

## Selected Mathematical Models in Hot Air Drying of Foods

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### Abstract

Food processing and preservation are major areas of interest for the food industry. Agricultural products having high amounts of water are highly perishable. Therefore, preservation methods are used to extend their shelf-lives. Drying is one of the oldest food preservation techniques. Among wide range of drying methods, hot air drying is one of the most frequently used drying methods for foods contain high amounts of water. Mathematical models for thin layer drying are useful in explaining heat and mass transfer mechanism and drying rate as well as predicting effective diffusion coefficient and activation energy of the drying process. The aim of the present study is to give fundamental information on both heat and mass transfer mechanisms in hot air drying of foods and selected mathematical models by deriving equations for predicting drying kinetics. It is expected that the present study provides basic background knowledge on hot air drying studies for the researchers.

*Keywords: Drying, Heat, Mass, Diffusivity, Moisture Content, Model*

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### 1. Introduction

Due to rapid growing world population, global warming and climate change, future projection of the limited food sources has been a great interest for the countries around the world. Many underdeveloped countries are in need of clean water and food supply whereas many others nearly face aridness and desertification. These facts bring researchers and governments to pay close attention and take proper actions especially on agricultural productions for future. High quality future foods are demanded and expected to be more nutritious, safe, natural, organic, functional, shelf stable as well as tasty. All these expectations could be matched to a certain degree with the benefits of food processing. Agricultural products are essential in human nutrition providing

bioactive components, water, carbohydrates, proteins, fat/oils, vitamins and minerals necessary for metabolic activities. Because of their highly perishable nature, they need to be preserved by using either thermal or non-thermal processing techniques such as drying, canning, freezing, cooling, smoking, salting, acidifying, microwaving, ohmic heating, dielectric heating, radio frequency processing etc.

Proper preservation technique is expected to lower water activity to a critical level where microbial, chemical and enzymatic control of food is possible meanwhile maintaining mechanical, textural, nutritional and physical properties of food (Arslan and Özcan, 2011). Among those techniques, drying is one of the oldest methods of food preservation (Orikasa et.al., 2008). There has been a growing interest in new and improved drying techniques over

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the past years. Although recent studies involve non-thermal drying methods as well as hybrid drying techniques, food industry still relies mainly on hot air drying. Hot air drying is a process where water removal from the food material is provided by the pre-heated air flow having constant velocity and relative humidity.

Drying process provides extended shelf life by lowering the water content and water activity of food being dried (Zhou et.al., 2019). Wide range of agricultural products are preserved by drying but dried products display altered organoleptic and nutritional properties as compared to their fresh counterparts. Moisture content of dried food is below its critical value where enzymatic, chemical and biochemical reactions are limited. Convective hot air drying is one of the most frequently used drying methods for food drying operations both in lab and industrial scale. Hot air drying process helps reduce product volume, facilitates handling and transportation, provides microbial, enzymatic and chemical stabilization of dried food, lowers storage expenses and offers a variety of processed foods to consumer (Zielinska and Markowski, 2010). Hot air drying also has some drawbacks such as longer drying time and undesired changes of food due to its heat sensitivity (Darvishi et.al., 2014). Studies on hot air drying of foodstuffs concentrate on the optimization of drying parameters, namely drying temperature, time, air velocity, air and food relative humidity, shrinkage, thickness, evaporation surface area and moisture content of food and type of drying equipment. All of these factors in return influence the rate of drying (Cruz et.al., 2015; Guine, 2018).

The aim of the present study is to give fundamental information on both heat and mass transfer mechanisms in hot air drying of foods and selected mathematical models by deriving equations for predicting drying kinetics. It is expected that the present study provides basic background knowledge on hot air drying studies for researchers.

## **2. Mechanisms of Heat and Mass Transfer**

The purpose of drying is the water removal from the food. Drying involves simultaneous heat and mass transfer for water removal. During hot air

drying, two simultaneous process occurs namely heat transfer from the heated drying air to the food surface and moisture (mass) transfer from the surface of the solid food to the hot drying air. Driving forces for mass transfer are capillary diffusion, concentration difference and pressure difference between food and hot drying air whereas driving forces of heat transfer are temperature difference and thermal conductivity of the drying food.

Drying behavior of food material is affected by internal (density, permeability, porosity, sorption characteristics, thermophysical properties of food) and external (temperature, velocity and relative humidity of heated drying air) factors (Kaya et.al., 2009). Knowledge on heat and mass transfer phenomena during hot air drying of foods greatly helps to reduce operational costs and preserve the quality of dried food via drying parameter optimisation studies.

Theoretical and experimental studies on heat and mass transfer phenomena during hot air drying of foods has been a major research area over the past decades. Diffusion theory, the capillary flow theory and evaporation-condensation theory are widely used to explain the physical phenomena of the hot air drying process in porous materials (Prommas, 2011).

## **3. Mathematical Models for hot air drying**

From the food engineering point of view, mathematical models are used as effective tools for describing drying mechanisms for process optimisation and analysis of food drying for wide range of foods. Fundamental understanding of drying characteristics is generally build on thin layer drying concept and models are theoretical, semi-theoretical or purely empirical nature (Mwithiga & Olwal, 2005). Thin layer drying is based on placing drying food onto drier trays as thin layered as possible to ease water removal from the surface of the food during drying. Most of the studies from literature use semi-theoretical models with a certain degree of success depending on the type of food and conditions of drying. Advantage of using of semi-theoretical models is in their less complicated solutions as compared to the theoretical models (Doungporn et.al., 2012). Most commonly used semi-theoretical

thin layer drying models from the selected literature are given in Table 1.

Table 1. Semi-theoretical thin layer drying model equations

Name of model	Model equation MR=	Reference
Lewis Newton	$\exp(-kt)$	Artnaseaw et.al., 2010; Mwithiga&Olwal, 2005
Page	$\exp(-kt^n)$	Artnaseaw et.al., 2010
Modified Page	$\exp(-kt^n)$ $\exp[-c(t/L^2)^n]$	Özdemir&Devres, 1999; Mwithiga &Olwal, 2005 Diamante&Munro, 1991
Henderson and Habis	$a \exp(-kt)$	Henderson&Habis, 1961
Modified Henderson and Habis	$a \exp(-kt) + b \exp(-gt) + c \exp(-ht)$	Karathanos, 1999
Logarithmic	$a \exp(-kt) + c$	Yaldız et.al., 2001
Two-term	$a \exp(-k_0t) + b \exp(-k_1t)$	Artnaseaw et.al., 2010
Two-term exponential	$a \exp(-kt) + (1-a) \exp(-kat)$	Sharaf-Eldeen et.al., 1980
Midilli and Kucuk	$a \exp(-kt^n) + bt$	Midilli et.al, 2002
Approximation of diffusion	$a \exp(-kt) + (1-a) \exp(-kbt)$	Demir et.al., 2007
Wang and Singh	$1 + at + bt^2$	Wang&Singh, 1978
Simplified Fick's diffusion	$a \exp[-c(t/L^2)]$	Diamante&Munro, 1991;
Thomson	$t=a \ln(MR) + b(\ln(MR))^2$	Paulsen &Thomson, 1973
Verma et.al.	$a \exp(-kt) + (1-a) \exp(-gt)$	Verma et.al., 1985

a,b,c,n and k are model constants.

Most of the studies on mathematical modelling of hot air drying focus on the semi-theoretical thin layer drying. Experimental data fits onto the selected model equations to find the best fit under constant drying conditions. Moisture ratio of samples during drying is calculated as (Guine et.al., 2011; Mota et.al., 2010):

$$MR = \frac{M_t - M_e}{M_0 - M_e} \quad 1$$

where M is the moisture content of the food (kg water/ kg DM), subscripts t, 0 and e denotes time t, initial and equilibrium respectively.  $M_e$  refers to the equilibrium of moisture content with surrounding medium namely drying air for a long period of drying time. For most drying operations  $M_e$  is relatively small as compared to  $M_t$  and  $M_0$  and therefore can be ignored for long period of drying time. Then, Equation 1 becomes:

$$MR = \frac{M_t}{M_0} \quad 2$$

Considering diffusion is, as in most case, the main mechanism for the mass transfer from the drying food surface, solution of Fick's second law of diffusion equation for a slab with no shrinkage can be given as (Singh and Pandey, 2012):

$$MR = \frac{M_t - M_e}{M_0 - M_e} = \sum_{n=1}^{\infty} \left( \frac{8}{(2n-1)\pi^2} \exp\left(\frac{-D_{eff}(2n-1)^2\pi^2}{4(L)^2} t\right) \right) \quad 3$$

where  $D_{eff}$ : effective moisture diffusivity ( $m^2/s$ ); L:half thickness of the slab (m), i: positive integer, number of terms that is taken into account and t: drying time (s). Using first term of series in Equation 3, moisture ratio is simplified to Equation 4:

$$MR = \frac{M_t - M_e}{M_0 - M_e} = \frac{8}{\pi^2} \exp\left(\frac{-\pi^2 D_{eff}}{4L^2} t\right) \quad 4$$

Equation 4 then can be rearranged for further simplification as in Henderson and Habis model and given as follows:

$$MR = \frac{M_t - M_e}{M_0 - M_e} = a \exp(-kt) \quad 5$$

Fick's law to explain moisture diffusion process also can be given for a cube geometry of food in series type of equation as (Zielinska and Markowski, 2010):

$$MR = \frac{512}{\pi^6} \left[ \sum_{n=1}^{\infty} \frac{1}{(2n-1)^2} \exp(-(2n-1)kt)^2 \right] \quad 6$$

where n: integer and k: model constant. Moisture

ratio can further be simplified using the first term of series in Equation 6 as follow:

$$MR = \frac{512}{\pi^6} \left[ \exp(-kt)^2 \right] \quad 7$$

Analytical solution of Fick's second law of diffusion in spherical geometry can be given as (Aghbashlo et.al., 2008):

$$MR = \frac{M_t - M_e}{M_0 - M_e} = \frac{6}{\pi^2} \exp \sum_{n=1}^{\infty} \frac{1}{n^2} \exp \left( \frac{-n^2 \pi^2 D_{eff}}{r_0^2} t \right) \quad 8$$

where  $r_0$  is the radius of the food material (m). When first term of the series Equation 8 is used:

$$MR = \frac{M_t - M_e}{M_0 - M_e} = \frac{6}{\pi^2} \exp \exp \left( \frac{-\pi^2 D_{eff}}{r_0^2} t \right) \quad 9$$

To simplify Equation 9 to a straight line equation:

$$\ln \ln (MR) = \ln \ln \left( \frac{6}{\pi^2} \right) - \left( \frac{\pi^2 D_{eff}}{r_0^2} \right) t = A + Bt \quad 10$$

where  $A = 6/\pi^2$ ;  $B = \pi^2 D_{eff}/r_0^2$ , slope of the straight line by which  $D_{eff}$  can be calculated.

Experimental data of MR and t is used to fit to model equations and goodness of the fit is determined by statistical analysis such as determination coefficient (R), correlation coefficient ( $R^2$ ), standart error of estimate, sum of squares, mean of squares, F test and P value (Guine et.al., 2011; Mota et.al, 2010). Statistical analysis on selection of best fit hot air drying equation is generally based on correlation coefficient ( $R^2$ ), reduced Chi-square ( $\chi^2$ ), root mean square error (RMSE) and mean bias error (MBE) as respectively follow (Evin, 2012):

$$\chi^2 = \frac{\sum_{i=1}^N (MR_{exp,i} - MR_{pre,i})^2}{N-n} \quad 11$$

$$RMSE = \left[ \frac{1}{N} \sum_{i=1}^N (MR_{pre,i} - MR_{exp,i})^2 \right]^{1/2} \quad 12$$

$$MBE = \frac{1}{N} \sum_{i=1}^N (MR_{pre,i} - MR_{exp,i})^2 \quad 13$$

where  $MR_{exp,i}$ : ith moisture content recorded experimentally;  $MR_{pre,i}$ : ith predicted moisture content by mathematical model in question; N: total number of recorded moisture content values, n: model

constant. Best fit model is decided by having the highest  $R^2$  and the lowest  $\chi^2$ , RMSE and MBE values.

Drying rate is also one of the important parameters in comparisons of drying operations. During hot air drying, moisture removal occurs at different rates namely constant rate and falling rate. For highly moist material as in most foods, both periods are present. Constant rate period is defined as the period of drying where the rate of moisture transfer from the center of the food to the evaporation surface is equal to the rate of moisture evaporation from the surface. Constant rate period continues as long as water supplied to the surface compensates the surface evaporation. Falling rate corresponds to the period where drying rate starts to decrease due to decreasing transfer of water to the evaporation surface. Drying rates of food can be calculated as:

$$DR = \frac{M_{t+\Delta t} - M_t}{\Delta t} \quad 14$$

where DR: drying rate (kg water/kg DM min);  $M_{t+\Delta t}$ : the moisture content at time  $t+\Delta t$  and  $M_t$ : moisture content at time t (min).

#### 4. Calculation of Effective Moisture Diffusivity and Activation Energy

Water diffusion is a complex phenomena during drying involving molecular diffusion, hydrodynamic, capillary and Knudsen flow and surface tension (Erbay & İcier, 2009). Lumped parameter model assumes only effective moisture diffusivity which technically corresponds to the conductive term of moisture transfer mechanism. Effective diffusivity is generally calculated by the use of experimental drying curve plots. From the experimental data, the plot of  $\ln(MR)$  versus drying time (t) gives a straight line and slope of this line is:

$$\ln \ln (MR) = \ln \ln (a) - \frac{\pi^2 D_{eff}}{4L^2} t \quad 15$$

where  $D_{eff}$ : effective moisture diffusivity ( $m^2/s$ ); k: drying rate constant, slope of the  $\ln(MR)$  versus t.

Effective diffusivity is affected both by internal conditions of food namely temperature, moisture content and microstructure and external conditions namely drying air velocity, air temperature and

relative humidity. Temperature dependency of  $D_{eff}$  is often constructed with Arrhenius type relation as follows (Fudholi et.al, 2016):

$$D_{eff} = D_0 \exp \left( -\frac{E_a}{RT} \right) \quad 16$$

Equation 16 can be linearized by taking natural logarithms of both sides:

$$\ln(D_{eff}) = \ln(D_0) - \left(\frac{E_a}{R}\right)\frac{1}{T} \quad 17$$

where  $D_0$ :effective diffusivity at infinitely high temperature ( $m^2/s$ ),  $E_a$ : activation energy ( $kJ/mol$ ),  $R$ : universal gas constant ( $8.314 \times 10^{-3}kJ/molK$ );  $T$ : absolute temperature ( $K$ ).  $E_a$  and  $D_0$  in Equation 17 can be calculated by the slope of the plot of  $\ln(D_{eff})$  versus  $1/T$ .

### Conclusion

Rapid increasing world population is in need of nutritious, safe, standardized and yet tasty foods with acceptable shelf-life. Food processing industry is constantly seeking new and improved methods for food processing and preservation. Drying has been and still is one of the most widely used method of food preservation and mainly relies on simultaneous transfer of heat and mass. Fundamentals of heat and mass transfer mechanisms help to improve present drying techniques as well as gives insight for innovations. Mathematical models are used to describe both water removal and heat penetration during hot air drying. Mathematical models for hot air drying of foods are used to develop new drying equipment, drying method and process parameters. Models are tools for process control. Considering rapid developments in artificial intelligence systems, such mathematical models have great potential for further integration with hands-on industrial drying operations for better process and product control. Present work is considered as useful summary for the students set their mind on getting engineering education.

### References

Arslan, D., & Özcan, M.M. (2011). Dehydration of red bell-pepper (*Capsicum annuum L.*): Change in drying behavior, colour and antioxidant content. *Food and Bioproduct Processing*, 89:504-511.

Artnaseaw, A., Theerakulpisut, S., & Benjapiyaporn C. (2010). Drying characteristics of Shiitake mushrooms and Jinda chili during vacuum heat pump drying. *Food and Bioproducts Processing*, 88:105-114.

Cruz, A.C.R., Guine, P.F. & Gonçalves, J.C. (2015). Drying kinetics and product quality for convective drying of apples (cvs. Golden Delicious and Granny Smith). *International Journal of Fruit Science*, 15(1):54-78.

Darvishi, H., et al. (2014). Study of the drying kinetics of pepper. *Journal of the Saudi Society of Agricultural Sciences*, 13:130-138.

Demir, V., Gunhan, T. & Yagcioglu, A.K. (2007). Mathematical modelling of convection drying of green table olives. *Biosystems Engineering*, 98:47-53.

Diamante, L.M. & Munro, P.A. (1991). Mathematical modelling of hot air drying of sweet potato slices. *International Journal of Food Science and Technology*, 26:99-103.

Doungporn, S., Poomsa-ad, N. & Wiset, L. (2012). Drying equations of Thai Hom Mali paddy by using hot air, carbon dioxide and nitrogen gases as drying media. *Food and Bioproducts Processing*, 90(2):187-198.

Erbay, Z. & İcier, F. (2009). A review of thin layer drying of foods: theory, modeling and experimental results. *Critical Reviews in Food Science and Nutrition*, 50:441-464.

Evin, D. (2012). Thin layer drying kinetics of *Gundelia tournefortii L.* *Food and Bioproducts Processing*, 90(2):323-332.

Fudholi, A., et al. (2016). Activation energy of thin layer drying kinetics of belimbing dayat fruit (*Baccaurea angulata*). *Research Journal of Applied Sciences, Engineering and Technology*, 13(4):295-300.

Guine, R.P.F. (2018). The drying of foods and its effect on the physicochemical, sensorial and nutritional properties. *International Journal of Food Engineering*, 4(2):93-100.

Guine, R.P.F., Pinho, S. & Barroca, M.J. (2011). Study of the convective drying of pumpkin

- (Cucurbita maxima). *Food and Bioproducts Processing*, 89:422-428.
- Henderson, S.M., & Habis, S. (1961). Grain drying theory. I. Temperature effect on drying coefficient. *Journal of Agricultural Research and Engineering*, 6:169-174.
- Karathanos, V.T. (1999). Determination of water content of dried fruits by drying kinetics. *Journal of Food Engineering*, 39:337-344.
- Kaya, A., Aydın, O. & Demirtaş, C. (2009). Experimental and theoretical analysis of drying carrots. *Desalination*, 237:285-295.
- Midilli, A., Kucuk, H. & Yapar, Z. (2002). A new model for single-layer drying. *Drying Technology*, 20(7):1503-1513.
- Mota, C.L., et al. (2010). Convective drying of onion: kinetics and nutritional evaluation. *Food and Bioproducts Processing*, 88:115-123.
- Mwithiga, G., & Olwal, J.O. (2005). The drying kinetics of kale (*Brassica oleracea*) in a convective hot air drier. *Journal of Food Engineering*, 71:373-378.
- Orikasa, T., et al. (2008). Drying characteristics of kiwi fruit during hot air drying. *Journal of Food Engineering*, 85(2):303-308.
- Özdemir, M., & Devres, Y.O. (1999). Thin layer drying characteristics of hazelnuts during roasting. *Journal of Food Engineering*, 42:225-233.
- Paulsen, M.R. & Thomson, T.L. (1973). Drying endysus of grain sorghum. *Transactions of the ASAE*, 16:537-540.
- Prommas, R. (2011). Theoretical and experimental study of heat and mass transfer mechanism during convective drying of multi-layered porous packed bed. *International Communications in Heat and Mass Transfer*, 38:900-905.
- Sharaf-Eldeen, Y.I., Blaisdell, J.L. & Hamdy, M.Y. (1980). A model for ear corn drying. *Transactions of the ASAE*, 5:1261-1265.
- Singh, N.J. & Pandey, R.K. (2012). Convective air drying characteristics of sweet potato cube (*Ipomoea batatas* L.). *Food and Bioproducts Processing*, 90(2):317-322.
- Verma, L.R., et al. (1985). Effects of drying air parameters on rice drying models. *Transactions of the ASAE*, 28:296-301.
- Wang, C.Y. & Singh, R.P. (1978). Use of variable equilibrium moisture content in modelling rice drying. *Transactions of American Society of Agricultural Engineers*, 11:668-672.
- Yaldız, O., Ertekin, C., & Uzun, H.I. (2001). Mathematical modelling of thin layer solar drying of sultana grapes. *Energy*, 26:457-465.
- Zhou, X., et al. (2019). Combined radio frequency-vacuum and hot air drying of kiwifruits: Effect on drying uniformity, energy efficiency and product quality. *Innovative Food Science and Emerging Technologies*, <https://doi.org/10.1016/j.ifset.2019.102182>.
- Zielinska, M. & Markowski, M. (2010). Air drying characteristics and moisture diffusivity of carrots. *Chemical Engineering and Processing: Process Intensification*, 49:212-218.

# Living or Nonliving? Reconsider Biology through the Concept of Viruses

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## Abstract

The concept of viruses has been a century-old debate among scientists due to their peculiar traits. Some viewed the virus as nonliving, initially seen as a poison and later as a simple protein molecule. Some challenged this nonliving nature of the virus due to its infectivity and filterability. The reason that scientists arrive to contrasted perspectives and theories in viruses derives from the fundamental perception of what constitutes life. While some scientists may overlook such a quest as a task in the philosophical scope, it is through philosophical lens that empirical scientific data have been processed, resulting in various theories. Upon examining the concept of the virus of André Lwoff, Patrick Forterre, and Luis Villarreal based upon their views of life, it is concluded that their respective understanding of viruses is not a direct reflection of the scientific data of the living traits (system, matter, chemical metabolism, complexity, reproduction, and evolution), but also reflects their employment of the philosophical lens and the perceptual principles. Thus, the approach to the study of biology requires philosophical process in perceptualizing life.

*Keywords: viruses, living, nonliving, life, biology, philosophy*

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## 1. Introduction

“A virus is an infectious particle consisting of little more than genes packaged in a protein coat,” as stated in the high school AP Biology textbook in the chapter on viruses (Reece et al., 2011). The definition is followed by a question: “Are viruses living or nonliving?” To answer this seemingly simple question, the authors describe briefly the changing definition of the virus over time and quickly conclude viruses are nonliving, except with an ambiguous tone: “Most biologists studying viruses today would probably agree that they are not alive” (Reece et al., 2011). The author’s indefinite word choices such as

“most biologists” and “probably” connote a controversial nature of the virus, and yet the authors’ conclusion as “nonliving” seems confusing, if not, oversimplified. The rest of the chapter primarily focuses on the structure and the replication of viruses without further mentioning any details about its fundamental nature. This ambiguity and dissatisfaction in explaining the nature of the virus prompted this research. Especially, due to COVID-19, viruses have been the most concerning topic presently, it is important to revisit its concept to better inform young biology students since, after all, the heart of biology lies in the matter of life. If we investigate a more comprehensive understanding of

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the living or nonliving nature of viruses, biology itself inevitably expands to philosophical conceptualization of life because the concept of life itself is comprehensive, beyond scientific facts and data. Therefore, the objective of this research is, through examining the debate of the virus as living or nonliving, to demonstrate the importance of a philosophical understanding of the biological concept in processing factual data. With only this broader approach, the complexities of life can be better understood and appreciated. In so doing, the uniqueness of viruses can be adequately perceived beyond the binary polarity between living and nonliving.

## **2. The History of the Concept of the Virus**

The virus has a long history of its enigmatic position. Its first recognition traces back to the ancient Greek period. The ancient Greeks had identified the virus as a “transmittable poison.” The famous philosopher Aristotle contributed to this notion based on the observation of the transmission of rabies from rabid dogs: “Dogs suffer from the madness. This causes them to become irritable and all animals they bite to become diseased” (Steele, 1991). This view of the virus was not challenged until the contribution Louis Pasteur made to the concept of the virus. Throughout his lifetime, Pasteur dedicated his life to finding vaccinations after inoculating cowpox to prevent smallpox. In the development of a smallpox vaccination, he discovered that disease was not caused by “poisons,” but rather by another entity. Pasteur proposed the germ theory to explain the role of this entity as the causal agent in all infectious diseases. According to the germ theory, diseases arise due to the activities of microorganisms. He defined microorganisms as any entity too small to be viewed by the unaided eye, as bacteria, protozoa, and some fungi and algae. He concluded that viruses were living microorganisms, to be more specific, a virulent bacterium (Berche, 2012). Pasteur had advanced the concept of the virus from a “poison” to a microorganism largely due to the fact that viruses exhibited the same traits as bacteria in terms of their infectivity and microscopic size. Although Pasteur mistakenly included viruses in the same category

with bacteria, he advanced the ancient metaphysical notion as poison to a more modern scientific notion based on empirical observation. Concurrently, with his theory, Pasteur had opened Pandora’s Box that has led to a 100-year-old debate on the nature of the virus: living or nonliving. Pasteur’s new point on viruses as microorganisms was based on the premise of their nature as living, like bacteria.

It was not until the end of the 19th century that the nature of the virus was rechallenge. Dmitri Ivanovski attempted to prevent the tobacco plants from a disease known as Tobacco Mosaic Virus (TMV). In the process Ivanovski discovered that TMV was able to pass through the porous membrane of unglazed ceramic. He reported his observation as follows: “[It] filtered the sap of diseased plants through a porcelain filter and stated the sap sterilized in this fashion, [but] retained its infectivity” (Lechevalier, 1972). Since bacteria were never able to pass through the membrane of unglazed ceramic due to their size, Ivanovski concluded TMV was a toxin produced by the bacteria. This brings the concept of the virus back to its original position: a poison. Although his claim demoted the concept of virus, his model of experiment was later repeated by another microbiologist to advance its concept further.

Martinus Beijerinck created a similar experiment and took a different perspective of the causal infectious agent and also concluded the infectious agent must be another being separate from a bacterium. Beijerinck observed that the infectious agent was more fluid than a cell, since he observed a drop of infected sap was able to diffuse slowly through an agar gel, an impossible task for a cell. In addition, he knew that the infectious agents from the TMV had the same characteristics, and toxins would not have the complexity to infect more plants with the disease. Upon discovering its unique nature, Beijerinck coined the term “virus,” a Latin derived term referring to venom or poison, to describe as he put “contagium vivum fluidum,” that is, living fluid contamination (Méthot, 2016). In his discovery, Beijerinck defined the virus as a living entity which had the capabilities of being soluble and still have the infectious abilities similar to a bacterium. Despite the shared infectious nature, Beijerinck noted that this new being must be differentiated from a bacterium

due to its significant size difference compared to bacteria. For this reason, he created a new term and was the first one to be credited to introduce the word “virus” to the world in a modern context (Machemer, 2020). This reintroduction of the concept of the virus became controversial from the beginning of the announcement. Having the toxic fluid in non-bacterial nature received heavy criticisms in the scientific circle because Beijerinck's new idea that pathogens can multiply inside the cell was “revolutionary and new” (Kammen, 1999). This idea was radical because the pathogen was a category used to define a living organism which causes disease, but Beijerinck presented an addition to the category of pathogen, which is non-organized, non-cellular but has a living nature (Bos, 1999).

Beijerinck's concept of virus as living invites the host of debates whether virus is living or nonliving. Wendell Meredith Stanley refuted Beijerinck's view of the virus as living with his discovery of the constituency of the virus. The crystallization of the TMV showed the inside of the virus: a combination of protein and nucleic acid, RNA. Based on this finding, he concluded that viruses are “inorganic, carbohydrate, hydrocarbon, lipid, protein, or organismal in nature” (Stanley, 1935). For Stanley, these inorganic chemicals are not complex enough to be considered life, such as lacking ribosomes, which is the necessary component to decode RNA for the replication process of all living organisms. Undoubtedly, his research contributed to a better understanding of the anatomy of the virus, and yet, his conclusion on the nature of the virus as an inanimate chemical added more controversy. How can this chemical-constituted agent without adequate qualities of life infect and replicate? Seeing the lack of essential anatomical parts, Stanley sided with the virus as the nonliving while his opponents argued that the presence of genetic material such as DNA or RNA and protein coat are the evidence that supports that viruses are the living (Hegde et al., 2009). It is noted that the same scientific materials were employed for Stanley to view as “the results demonstrating unequivocally that viruses are non-living” (Stanley, 1939), while others view they are the components to prove viruses are the living. In this sense, it is similar for one to ask, “Is the glass

half full or half empty?” Based on the same empirical scientific data, how scientists perceptualize them can be drastically different. Raising this question suggests that there is a gap between what the scientific reality is and how it can be perceptualized and articulated by humans, and it varies depending on the elusive definition of life one holds.

### **3. The Conceptual Principles of A. Lwoff, P. Forterre, and L. Villarreal in Defining the Virus**

At this point, it is important to further review in detail how other biologists after Beijerinck employed their conceptual principles in an effort to process the researched data on viruses. Three virologists' views will be considered: André Lwoff, Patrick Forterre, and Luis Villarreal. The table 1 shows their respective understanding of the virus based on living traits. It is interesting that each virologist projected different view, and I will analyze how each virologist arrived at different understanding.

André Lwoff (1957), in his famous article “The Concept of Viruses,” stated “viruses are viruses” (pg. 240). For this seemingly simple statement, he critically analyzed the behavior and properties of the bacteriophage at different stages of its life cycle: proviral, vegetative and infective phase. Placing infectivity as the distinctive trait of the virus, he viewed proviral and vegetative phase lack infectivity. Regardless of the absence, he stated that one cannot deny classifying proviral or vegetative phage as a virus because Lwoff emphasized the holistic or “the sum of the various phases of its life cycle” in defining viruses (Lwoff, 1957, pg 242). For him, the collection and integration of the properties from various phases of life cycle collectively contributes to a particular class identity. For this reason, Lwoff wanted to endow the virus with a separate class apart from other infectious agents and claimed that “viruses are viruses.” Then, he explained his conceptual principle in defining the virus as follows: “Our definition of viruses is valid only because. . . it includes a homogeneous class of entities, viruses, and excludes another homogeneous class of entities, micro-organisms” (Lwoff, 1957, pg 246). Recognizing the virus as its own kind, he compared

the virus to the micro-organism to further buttress his point that viruses have their own class contrasted to

the existence of different objects, categories, or concepts.

Table 1. Comparison of viruses based upon the six most common characteristics of life collected by Edward Trifonov (2011).

Living traits	Lwoff	Forterre	Villarreal
System (organized matter)	+	+ in virocell, - in virion	0 Only through the host cell (borrowed)
Chemical (metabolism)	+Through Lipmann system (i.e. a system of enzymes for the production of energy) during vegetative state	+ in the vegetative state of autonomous replication	0 only possible through the host cell
Complexity (information)	-Not acknowledge	+ in virocell, - in virion	-Lacks full critical complexity
reproduction	-Lack ability to binary fission	+	0 only possible through host cell (living or dead)
Evolution(change)	Not stated	+ viruses are evolved by virocells	+ viruses are fugitive host genes that have degenerated into parasites

+ found in virus, - not found in virus, 0 circumstantial

As shown in Table 2, Lwoff focused on individual traits in comparison to microorganisms. Upon comparing between microorganisms and viruses, Lwoff employed the similar conceptual principle that separated the virus from other infectious agents. This principle is sharply contrasted to Beijerinck’s or Stanley’s. Both Beijerinck and Stanley focused on particular traits in an effort to characterize the virus. For Beijerinck, filterability was the focal trait while Stanley focused on simple molecule constituency of the virus anatomy. For Lwoff, although he emphasized infectibility, the *integration* of various traits of the virus in defining it was more highlighted. In this train of thought, he viewed viruses lack dynamics in the process of integration of its various traits to become functionally independent. He claimed that life happens at this complex level of integration, and yet viruses lack this “transcendence” despite the evidence of shared organism qualities between viruses and microorganisms. This view is clearly evident when he stated:

“Worms and vertebrates possess a digestive tract, but this does not prove that worms are

vertebrates because insects also possess a digestive tract. Viruses and organisms have a few in common. These characters being also present in cellular organelles, they cannot be considered as supporting the conclusion that viruses are organisms” (Lwoff, 1957, pg. 247).

This view is contrasted to his contemporary virologist, Salvador Luria who defined living as one that presents individuality along with evolutionary independence rather than functional independence (Luria, 1959). Going back to the analogical question, “Is the glass half full or half empty?” can be redirected this way: Do biologists focus on the similarities or differences of the virus’ traits vis-à-vis other living beings? Or do they focus on individual, independent traits or the sum or integration of the dependent and interdependent traits? Depending on the emphasis placed by biologists, living and nonliving is defined, and so is the nature of the virus.

A more recent virologist, Patrick Forterre emphasized the evolving dynamics or process of life in defining a virus. He stated, “Life and living processes are simply names for complex evolving

forms of matter that are now present on our planet” (Forterre, 2017).

Table 2. Lwoff’s comparison between micro-organisms and viruses

<b>Micro-organisms</b>	<b>viruses</b>
Cellular size	Filterable size
Contain nucleic acids, DNA, RNA	Contain One type of nucleic acid
Reproduce	Replicate in the form of their genetic material
Have infectivity	Have infectivity
Able to grow	Unable to grow and to undergo binary fission
Replicate its nucleic acid	Multiply and reproduce (only in host cell)
presence of a “Lipmann system”	Devoid of a “Lipmann system”
Independent unit of integrated and interdependent structures and functions	Dependent on host-cell metabolism
Control its dependent and interdependent parts	Completely rely upon the cell
Forms a regular gradient of size	Forms a regular gradient of size

Forterre challenged the former perception of the virus often equated to a virion, which refers to the static structural aspect of the virus. Instead of virions, he suggested to focus on a biological process that includes a viral reproduction cycle to go beyond the static biological nature of the virus. In this sense, he clearly distinguished virions from virocells or “ribovirocell” as he coined the term to refer to the active state of the virus. Instead of virions, Forterre proposed to focus attention on the virocell, which is the intracellular phase in the virus reproduction cycle since virocells are cellular organisms that are living (Forterre, 2013). Forterre’s view somewhat resonates with F.C. Bawden’s proposal earlier. He argued classifying the virus as living or nonliving should depend on what medium one focuses on. Depending on the medium of the observation - the virus in a test tube or the virus in the infected plant or animal cell - it can be viewed as either living or nonliving. The virus in a test tube is a mere protein molecule while the virus in the infected plant or animal cell is clearly

living as it can multiply and mutate (Bawden, 1945). Similar to Bawden, Forterre treated the virocell as a living organism, but he remained uneasy defining the virus as a “living organism.” Just like a virion, which refers to one phase of the whole viral cycle, the virocell is simply another phase, not the whole process of the biological process of the virus. For Forterre, living means “a collection of integrated organs (molecular machines/structures) producing individuals evolving through natural selection” (Forterre, 2010, pg 158). Similar to Lwoff, he used integrative approaches by emphasizing the holistic aspect of the virus in its transition, except he furthered his view by emphasizing the virus as a major actor of variation and selection in the web of life (Forterre, 2012). In fact, this collective view of the virus by encompassing all phases of the virus life cycle has been embraced by many biologists recently (Nasir, Romero-Severson, & Claverie, 2020).

Another evolutionary virologist Luis Villarreal recognized a “spectrum” between living and nonliving in defining a virus’s position (Villarreal, 2004). He used a phrase, “a verge life” to refer to the nature of the virus because it can have “living” conditions such as metabolism, nucleic acid synthesis, protein synthesis, processing and transport, and all other biochemical activities viruses to multiply, but only through the host cell. For this perplexing nature of the virus, Villarreal suggested a “spectrum” of life. To better explain, he compared a virus to a seed, arguing that a seed itself may not be viewed as living but has a potential for life, which is also capable of being destroyed. Viruses having living qualities without autonomy resemble seeds in nature. Another comparison he proposed was the human brain as defining life as “an emergent property of a collection of certain nonliving things” (Villarreal, 2004, pg 103). He explained that a neuron by itself cannot be conscious but requires the whole brain complexity to be biologically alive and conscious. Although viruses lack this complexity, life itself as an emergent state is made from the same fundamental, physical building blocks that constitute a virus. He added that the discovery of Mimivirus in 1992, which is the largest and the most complex virus discovered, as an example to support the spectrum of life in the emergent nature in life since it carries genes that

cellular organisms possess. In this view, he categorized viruses as neither living nor nonliving. Especially, considering the capacity to grow and multiply in dead cells to revive the dead cells, a virus deserves its own space between living and nonliving. Villarreal concluded that it is in this middle position that viruses' innovative actions and constant invention of new genes enable them to contribute to evolutionary change. In short, Villarreal focused on the spectrum of emergent life to seek the role of viruses and attempted to seek a practical bearing from the debate on whether viruses are living or nonliving. He believed such a debate was often treated rhetorical among many scientists, but it has a practical bearing: "I think the issue is important, because how scientists regard this question influences their thinking about the mechanisms of evolution" (Villarreal, 2004, pg 104).

#### 4. Conclusion

A virus with its peculiar characteristics and traits has been inviting various theories over a century, and this quest always prerequisites the philosophical quest of the definition of life. Due to the nature of this quest, scientists have defined the virus not solely based on empirical, scientific facts and data, but through the perceptual lens to process those collected data. Therefore, in approaching the essence of the study of life, namely biology, one cannot deny the importance of the philosophical investigation of what life is, as being demonstrated in the century long debate on the nature of viruses. While some scientists ignore the quest of life as a rhetorical debate that has no practical bearing, the absence of it will significantly curtail the proliferation of scientific theories. In this sense, "disagreement" in the debate on the nature of viruses showcased that dissent should not be seen as negative, but a necessary factor to proliferate various perspectives in the research of biology. In the case of Villarreal's research, his "middle position" provided him a tangible way to enhance further his theory on viruses in the web of life and its contributions to the origin of species. Agreeing with Forterre, "the goal of biology should be to explore and understand exhaustively the mode of existence of living organisms" (Forterre, 2010, pg.

158). It is expected that the definitions of life must constantly evolve as biology progresses. Therefore, biology as the study of life inevitably requires conceptual and philosophical quests in order to invite broader new scientific views.

#### References

- Bawden, F. C. (1945). The nature of viruses. *The Scientific Monthly*, 60, 1, 48-50.
- Berche, P. (2012). Louis Pasteur, from crystals of life to vaccination. *Clinical Microbiology and Infection*, 18, 1-6. doi:10.1111/j.1469-0691.2012.03945.x
- Bos, L. (1999). Beijerinck's work on tobacco mosaic virus: Historical Context and Legacy. *Philosophical Transactions: Biological Sciences*, 354(1383), 675-685.
- Forterre, P. (2010, 03). Defining Life: The Virus Viewpoint. *Origins of Life and Evolution of Biospheres*, 40(2), 151-160. doi:10.1007/s11084-010-9194-1
- Forterre, P. (2012). Darwin's goldmine Is still open: Variation and selection run the world. *Frontiers in Cellular and Infection Microbiology*, 2. doi:10.3389/fcimb.2012.00106
- Forterre, P. (2012, 10). The virocell concept and environmental microbiology. *The ISME Journal*, 7(2), 233-236. doi:10.1038/ismej/2012.110
- Forterre, P. (2017). Viruses in the 21st Century: From the curiosity-driven discovery of giant viruses to new concepts and definition of life. *Clinical Infectious Diseases*, 65(Suppl\_1), doi:10.1093/cid/cix349
- Hegde, N. R., Maddur, M. S., Kaveri, S. V., & Bayry, J. (2009, 08). Reasons to include viruses in the tree of life. *Nature Reviews Microbiology*, 7(8), 615-615. doi:10.1038/nrmicro2108-c1
- Kammen, A. (1999). Beijerinck's contribution to the virus concept - An Introduction. *100 Years of Virology*, 1-8. doi:10.1007/978-3-7091-6425-9\_1
- Lechevalier, H. (1972). Dmitri Losifovich Ivanovski, (1864-1920). *Bacteriological Reviews*, 36(2),

135-145. doi:10.1128/membr.36.2.135-145.1972

Luria, S. E. (1959). Viruses as infective genetic materials. In V.Najjar (Ed.). *Immunity and Virus Infection*. (pp.188-195). New York, USA: Wiley.

Machemer, T. (2020). How a few sick tobacco plants led scientists to unravel the truth about viruses Retrieved January 31, 2021, from <https://www.smithsonianmag.com/science-nature/what-are-viruses-history-tobacco-mosaic-disease-180974480/>

Méthot, P. (2016). Writing the history of virology in the twentieth century: discovery, disciplines, and conceptual change Retrieved February 1, 2021, from <https://www.sciencedirect.com/science/article/pii/S1369848616300061>

Nasir, A., Romero-Severson, E., & Claverie, J. (2020). Investigating the concept and origin of viruses. *Trends in Microbiology*, 28(12), 959-967. doi:10.1016/j.tim.2020.08.003

Prud'Homme-Généreux, A. (2013, 01). What Is Life? An Activity to Convey the Complexities of This Simple Question. *The American Biology Teacher*, 75(1), 53-57. doi:10.1525/abt.2013.75.1.11

Reece, J. B., Urry, L. A., Wasserman, M. L., Minorsky, S. A., & Jackson, R. B. (2011). *Campbell biology, AP edition* (Ninth ed.). San Francisco, CA: Pearson Benjamin Cummings.

Stanley, W. M. (1935). Isolation Of a crystalline protein possessing the properties of Tobacco-Mosaic Virus. *Science*, 81(2113), 644-645. doi:10.1126/science.81.2113.644

Stanley, W. M. (1939). The architecture Of viruses. *Physiological Reviews*, 19(4), 524-556. doi:10.1152/physrev.1939.19.4.524

Steele, J.H., (1991). History of rabies and global aspects. In G.M. Baer (Ed.) *The natural history of rabies*. New York, USA: CRC Press.

Trifonov, E. N. (2011, 10). Vocabulary of Definitions of Life Suggests a Definition. *Journal of Biomolecular Structure and Dynamics*, 29(2), 259-266. doi:10.1080/073911011010524992

Villarreal, L. P. (2004, 12). Are Viruses Alive? *Scientific American*, 291(6), 100-105. doi:10.1038/scientificamerican1204-100

## Projected Impact of COVID-19 on the Reopening of Universities in Fall 2020

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### Abstract

In the summer of 2020, the United States faces a situation in which schools are forced to weigh the costs and benefits of reopening in fall 2020 while confronted with the COVID-19 pandemic, and to what extent they should do so. We chose to evaluate the risks of reopening by utilizing a simulation to model the effects of introducing one student infected with SARS-CoV-2 (COVID-19) to ten different university campuses in order to predict how the virus would spread amongst the student populations at each one. By developing case studies for each university, we were able to simulate the impacts COVID-19 could have at several different percentages of overall attendance. This representative modeling system helped us better judge the number of students that should be allowed on campus at different sizes of universities. Through our study, we determined that for US schools to proceed with in-class instruction, many safety measures, inspired by those successfully taken by other countries, will need to be put in place and enforced strictly. Our modeling demonstrated that larger universities should limit the number of students they allow back on campus, preferably to under 25% of regular attendance to reduce infections and deaths, and all but the smallest schools should not consider bringing more than half of their enrolled students back to campus in the fall. Through our research we were able to predict outcomes of 40 different potential upcoming situations and develop a rough guideline for universities to refer to.

*Keywords: COVID-19, SARS-CoV-2, novel coronavirus, coronavirus, university reopening fall 2020, college reopening, epidemiological modeling*

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### 1. Introduction

In the midst of the COVID-19 pandemic, universities throughout the United States of America were facing a dilemma of whether to reopen their campuses and pose a health risk to their students and faculty, or to go fully online and lose as much as half of their revenue and lower the quality of their students' education (Wood 2020). Despite attempts to contain the virus, COVID-19 spread throughout the

US in massive waves, with greater than 4.3 million diagnosed cases across the country and resulting in almost 150,000 deaths as of July 27, 2020 ("United States," 2020). This led to the widespread closing of schools and universities in March 2020 with most students being sent off-campus to complete the current term. Yet 5 months later, experts were still unsure of whether it was safe to return to school. Contrarily, in many other countries such as Denmark and Singapore, students returned to school and

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followed strict safety guidelines enforced by the government in order to stay healthy and limit the spread of the SARS-CoV-2 virus (henceforth referred to as COVID-19) (Melnick & Darling-Hammond, 2020). In France, primary schools reopened as early as May 11 with mild success. This reopening ultimately led to some social divide between the upper class that decided to return to school and the lower class that largely stayed at home for various reasons (Williamson, 2020). In Taiwan, universities never fully closed, but thorough guidelines to contain the virus were strictly enforced by various task force teams at universities, and with much success, resulting in only 7 confirmed cases in 6 Taiwanese universities as of June 18, 2020 (Cheng et al., 2020). However, these countries' successes in reopening schools and universities largely had to do with their containment of the virus early on in the year (Cheng et al., 2020; Domenico et al., 2020). The same policies would not be as effective in the US, where there were more than 4.3 million COVID-19 cases as of July 27, 2020, with more than 60,000 new cases per day as of July 29, 2020 ("United States," 2020). Therefore, it was important to examine the potential spreading scenarios if universities were to allow students to return to campus, in order to weigh the risks and benefits of reopening schools and universities in-person during the fall term. Looking at the methods other countries have used to contain COVID-19, and by analyzing data published by colleges, the purpose of our research was to simulate and model the behavior of COVID-19, if universities were to reopen at full, 75%, 50% or 25% capacity. Therefore, we put forth the question "by using data released by organizations and universities about COVID-19 cases and student population numbers through July 21, 2020, how was COVID-19 expected to impact American schools' reopening in Fall 2020?"

In order to learn as much as possible about the effects of COVID-19 and reopening, we first had to do background research on the virus, and then look to studies performed in other countries in order to determine how reopening could look in the US. To find the relevant literature available, we searched Google Scholar and other scholarly search tools using keywords such as "COVID-19", "school reopening",

"university plans", "Fall 2020", etc. We were able to come across valuable information that helped us understand better the impacts of COVID-19 on the public health of society as a whole, and learn more about the disease, how it spread, etc.

COVID-19 (coronavirus disease 2019) is a vascular illness caused by SARS-CoV-2 that most commonly affects the respiratory system of the body. It is spread through respiratory droplets, close person-to-person contact, and infected surfaces. Worldwide, there were over 15 million cases, with more than 600,000 deaths and more than 100,000 new cases per day as of July 24, 2020 (Centers for Disease Control and Prevention [CDC], 2020). According to the CDC (2020),

The coronavirus disease 2019 (COVID-19) pandemic may be stressful for people. Fear and anxiety about a new disease and what could happen can be overwhelming and cause strong emotions in adults and children. Public health actions, such as social distancing, can make people feel isolated and lonely and can increase stress and anxiety.

It is clear that COVID-19 has taken a toll on the mental health of Americans in addition to the adverse economic and physiological effects, and this may be part of the reason why many universities are pushing to reopen in fall 2020.

### 1.1 Education

Based on a review of the literature available at the time and based on other countries that have reopened schools, it seems clear that if universities are to be opened, strict safety guidelines need to be followed so as to spread COVID-19 as little as possible (Wood, 2020; Sheikh et al., 2020; Cheng et al., 2020). However, other countries have all handled the COVID-19 pandemic differently than the United States has, and this has led to differences in the way schools have been and should be reopened in each country.

#### France

A study performed in the area of Île-de-France looked at the different scenarios in which schools would reopen in the region, and performed statistical

tests to determine when and which methods should be used in the reopening of preschools to K-12 schools (Domenico et al., 2020). The researchers found that,

Reopening schools after lifting lockdown will likely lead to an increase in the number of COVID-19 cases in the following 2 months, even with lower transmissibility of children, yet protocols exist that would allow maintaining the epidemic under control without saturating the healthcare system (Dominica et al., 2020).

They also found that reopening preschools and primary schools alone would not overwhelm the healthcare system if opened on May 11. However, even with all necessary safety protocols, reopening middle and high schools would overload the healthcare system and rapidly increase the spread of COVID-19. The authors recommend against reopening middle and high schools at full capacity (Domenico et al., 2020). Many colleges in the US, with young adult/adolescent age students, were planning on reopening at full capacity, which is exactly what the study recommends against, even though it was written at a time when there were only about 56,000 active cases in all of France (around 139,000 total cases), specifically when the country was in lockdown and shortly after researchers had thought new cases had “peaked”. In addition, the US is a larger area with a larger population with many more cases of COVID-19 than Île-de-France, with comparatively less people inclined to wear masks and social distance. COVID-19 is spreading quicker than ever in the US currently, and the advice intended for a smaller region with a smaller population would not be fully applicable to the US; reopening colleges at full capacity would most likely have a larger impact on the spread of COVID-19 in the US than in France. However, healthcare systems and schools are both structured differently in the US than in France, so this also could have an impact on the spread of COVID-19.

### Taiwan

Another study examined how Taiwan, an island nation southeast of China that currently has fewer than 15 COVID-19 cases, handled the virus in the university setting (Cheng et al., 2020). Taiwan

maintained strict safety regulations from the very beginning of the epidemic, and universities never fully closed or went into lockdown, as they did in the US;

The guidelines delineated creation of a task force at each university; school-based risk screening based on travel history, occupation, contacts, and clusters; measures on self-management of health and quarantine; general hygiene measures (including wearing masks indoors); principles on ventilation and sanitization; regulations on school assemblies; a process for reporting suspected cases; and policies on school closing and make-up classes (Cheng et al., 2020).

In addition, if even one student on campus tested positive for COVID-19, class would be suspended, and if two or more students/faculty tested positive, the university would be closed for 14 days. These stringent safety guidelines are what kept the number of COVID-19 cases in Taiwan low, and helped the country make a quick economic recovery. However, the same advice on reopening universities could have different effects if implemented in the US, as cases in the country have been rising at a rate greater than ever before, greater than Taiwan had ever experienced. Nonetheless, it’s important to closely examine what Taiwan has done to keep the country safe.

### 1.2 Distance Learning

A literature review on reopening schools after the COVID-19 lockdown examined the different methods that various countries have employed. Sheikh and his colleagues (2020) found that one of the best methods is one that has recently been used by Denmark- outdoor classrooms in which students wear masks and stay at least a 2 meters radius away from their peers. This method requires a lot of quiet outdoor space with minimal distractions and air pollution, which some schools may not have available to them in the US (especially in dense urban areas). Online learning was another one of the methods that was found to have worked the best (Sheikh et al., 2020). However, if universities in the US went all online, universities would lose a lot of money that’s crucial to paying their faculty/staff,

maintaining the campus, funding research and scholarships, etc. In addition, many students may prefer in-person classes to online classes for various reasons including peer motivation and escape from home environments that may be abusive or unsafe. Online classes are less effective at educating than in person classes have shown to be, and would likely result in a decrease in both overall learning and academic integrity (Protopsaltis & Baum, p. 1-3, 2019). On the other hand, if universities used Denmark’s strategy, they would need more space to do so, and both the universities in urban centers with limited land space and large universities with many students would find this a challenge.

Wood (2020) stated that going fully online for fall semester means universities would lose half their revenue, meaning they're likely to go bankrupt. Most schools are employing safety policies similar to Taiwan and South Korea on their campuses, but students are unlikely to strictly adhere to rules, meaning that universities could result in COVID-19 spreading at rates even faster than ever before.

### 1.3 Reopening in the US

Another author compiles the reopening plans of more than 1000 US universities and finds that about half of the universities are planning return to campus in the fall fully in-person, 35% are planning to use a hybrid model that combines virtual and in-person classes, 12% are planning for online, and 3.5% have not yet chosen a confirmed method of reopening (Figure 1). With half of universities inviting all students back to campus and with all in-person classes, they pose a major health concern to their students (Chronicle Staff, 2020). It is critical that the safety of the students is prioritized in all cases, and the universities must not only implement maximum safety and cleanliness requirements, but also understand the risks of following through with such plans.

#### England

A third analysis of the COVID-19 school reopening crisis analyzes various teachers’ responses to a survey on England’s school reopening strategy (See et al., 2020). See and colleagues found that the

majority of teachers in England had a high distrust of the government when it came to delegating the safety of returning to school. They had particularly negative responses in regards to their sense of safety upon a potential return to school June 1st, with most considering the situation to be much too dangerous. Most teachers felt unsafe and that the policies individual schools would put into place would not be nearly enough to create a safe environment for both students and teachers (See et al., 2020).

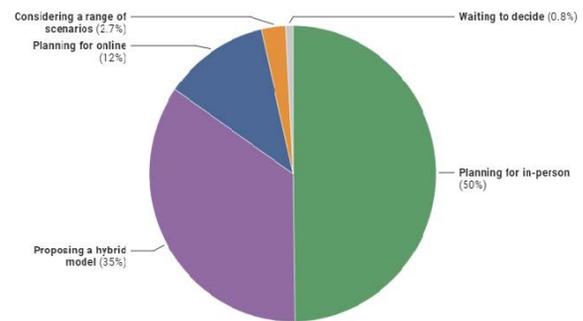


Figure 1. US University reopening plans (“The coronavirus”, 2020). Pie chart describing the range of universities planning to open “in-person”, “hybrid” (some in-person classes, some online classes), completely “online”, and those “waiting to decide”, or “in consideration”

## 2. Methods

As it became clear that guidelines needed to be established for universities to consider how they should reopen in the fall, we realized it was necessary for us to fill the void in research by answering the question of “by using data released by organizations and universities about COVID-19 cases and student population numbers, respectively, through July 21, 2020, along with data from other countries who have returned to school, how was the coronavirus expected to impact American schools’ reopening in fall 2020?” To do this, we gathered information from various sources which considered how other countries had managed a safe return to in-person educational practices. We understood that in order to make any predictions or to give universities valid claims to analyze and guide them, we would need to use a modeling system, where variables for each university

were calculated and set in order to give a realistic depiction of several case scenarios of what could happen in the fall. Given that the United States is much larger and suffered a much greater spread of COVID-19 than many countries who had returned to school thus far, it was widely understood that exactly the same practices would not be enough to contain the spread of the virus in universities. In order to test if this was true, and to show to what extent of danger universities faced, we chose to use a graphing simulator that would illustrate how many cases, deaths, and immunities would result from 40 different situations among 10 different sized universities. We hypothesized that as the number of students colleges allow on campus increases, the number of semester COVID-19 cases would increase exponentially.

In performing this study, we collected data from ten colleges across the United States (Harvard University, University of Southern California, Texas A&M University, University of Central Florida, Carnegie Mellon University, Brigham Young University, Johns Hopkins University, Tulane University, University of Alaska Southeast, and Purdue University) to perform an individual case study of each school. In making our model, we made sure to include an assortment of school sizes and locations so as to accurately represent universities in different settings. The entire student population of each school was calculated using current university data posted on their respective websites (as of July 21, 2020), other than Carnegie Mellon, who has not released current enrollment, hence we used 2019 enrollment numbers, and Purdue University, who has only released 2018 enrollment numbers. The number of students that would be permitted on campus at 25, 50, and 75 percent capacities were modeled using the original documented total population of students on campus (undergraduate and graduate), multiplied by the designated factor, and rounded down to the nearest person. Some of the data published on the websites of each college may not have been updated as of July 21, 2020, and the numbers we utilized in our modeling and analysis may have been enrollment records from 2019 or previous years if not noted online that they were current numbers. In addition, the use of modeling with both undergraduate students and graduate students harbors some error due to the

unlikelihood of graduate students spending similar amounts of time on college campuses as undergraduate students would.

The first variable that the simulator we used made use of was an initial population. We modeled situations in which 100%, 75%, 50%, or 25% of the enrolled undergraduate and graduate students were to be on campus with all classes being in-person in the fall (Table 1). We understand that many of these campuses, such as Harvard University, University of Southern California, and Texas A&M University to name a few, are offering all classes in an entirely online curriculum for students who wish not to risk exposure while taking classes on campus and classrooms. Six out of the ten universities we studied are adopting a hybrid model that combines online learning with in-person classes for fall 2020 as of July 28, 2020. Most universities have all virtual learning as an option for students that do not want to go on campus. The simulation we performed is solely based on specific set variables and is only modeling hypothetical situations that may occur at different schools if very specific guidelines are met. Despite this, through our study we would be able to produce viable estimates of how the disease could spread among different sizes of populations in an enclosed space with only one patient zero in each case. Using this, universities could begin to understand the effects of introducing not just one, but possibly more students back on campus who were infected with the novel coronavirus, and evaluate to what extent the risk is worthwhile.

### ***3. Instrumentation and Data Analysis***

In order to model our hypothetical situations, we used an online pandemic modeling simulator titled "Disease Epidemic Model" which utilized many different factors to create a model (Shodor, 2020). In our simulation, it is important to note that none of the included modeled universities took staff members into account (Figure 2). The simulations only model hypothetical situations for students. University staff is likely at the highest risk of contracting COVID-19, as members of older age groups and weakened immune systems have a much higher contraction, hospitalization, and mortality rate than the general

population of college-aged students.

Table 1. University Student Populations at Different Capacities; Initial populations of enrolled undergraduate and graduate students at 100%, 75%, 50%, and 25% attendance, and number of doctors assigned to each university (Association of American Medical Colleges [AAMC], 2020; Harvard, 2020; University of Southern California [USC], 2020; Texas A&M University, 2020; University of Central Florida [UCF], 2020; Brigham Young University [BYU], 2020; Johns Hopkins University, 2020; Carnegie Mellon University, 2020; University of Alaska Southeast, 2020; Purdue University, 2020; Tulane University, 2020)

University	100%	75%	50%	25%	Doctors
Harvard University	36,012	27,009	18,006	9,003	81
University of Southern California	48,500	36,375	24,250	12,125	67
Texas A&M University	69,465	52,098	35,732	17,366	78
University of Central Florida	69,525	52,143	34,762	17,381	92
Carnegie Mellon University	14,799	11,099	7,399	3,699	23
Brigham Young University	33,511	25,133	16,755	8,377	36
Johns Hopkins University	23,917	17,937	11,958	5,979	46
Tulane University	12,646	9,484	6,323	3,161	16
University of Alaska Southeast	2,561	1,920	1,280	640	3
Purdue University	43,411	32,558	21,705	10,852	50

Another variable we accounted for in the simulation was the number of doctors that treat COVID-19 at every university campus, respectively. To do this, we used data from the Association of American Medical Colleges (AAMC) as to how many clinical physicians corresponded to every 100,000 people in each state (AAMC, 2019). We then used that number to estimate how many doctors corresponded to the population of college students on the specific campus we studied. We divided that number in half, as we estimated only about 50% of doctors would be treating the novel coronavirus if they had no other choice. Physicians such as optometrists, dermatologists, surgeons, and many other specialties, would not be treating COVID-19 patients, but it impossible to know exactly how many physicians in the United States are capable and willing to treat those ill with COVID-19, so we made an estimate that we simply held constant in each

scenario for calculation purposes. These numbers aimed to provide a similar representative basis for each university, and may or may not be accurate or representative of each university. In addition, the model assumed that doctors cannot get sick. This is not the case; doctors fall ill from COVID-19 very frequently, due to exposure to the virus for long periods of time when treating patients. It is unlikely that all of the doctors would remain healthy in any scenario, but because the doctors were not considered to be part of the initial student population, if they had fallen ill, it would not have impacted our results in relation to each individual university. We thought it simply important to emphasize that this model does not perfectly adjust to realistic situations.

Additionally, the simulation we utilized had the ability to section off parts of our hypothetical campuses to limit travel to certain degrees. We chose not to include any barriers because we did not want

to create unknown variables. This is because students do not have the same probability of interacting with any other given person on campus at any given time (due to major and minor classes structure, living situation, friend groups, and many other variables), and it is impossible to know how many of these situations exist in one college campus. Hence, the simulation models the situation in which any one person has an equal chance of communicating or interacting with any other student on campus at a given time. This may change the risk of contraction by an unknown amount, because in this situation, the disease can spread to everyone on campus and doesn't take into account the different living situations and interactions of students at a given university in a completely closed campus.

Furthermore, within the model we accounted for a 3.7% infectiousness, as it was found that wearing masks reduces the risk of infectiousness from 17.4% to 3.7% (Dier, 2020). All universities that we studied and addressed it require all students, staff, and visitors to wear masks at all times upon return in the fall, unless the individual is alone in an office, or social distancing outside. It is not a guarantee that every student will follow these guidelines at all times, so it is likely that the infection rate will be slightly higher in reality. However, on a scale of 1-100%, we included an additional 15% of safety measures under the category of prevention and treatment, which held constant for each university. This was to account for the plans for the universities to clean high touch surfaces, some students and staff wearing additional PPE (Personal Protective Equipment), but also assuming that some students do not abide by the safety guidelines. Even though each university plans to implement different safety guidelines, it is hard to know how effective those will be at each school, so we chose to keep the prevention and treatment the same for all of them, in addition to including an infectiousness that assumes everyone wears a mask.

Additionally, we made sure not to account for a vaccine or successful medication into this model because both will likely not be readily available for COVID-19 by fall 2020. However, if such treatment is made available by this coming fall, it is likely that both cases and mortality rates would take a sharp decline.

In the "Days to Recover" variable, we implemented a 14 day average. In some situations it would take more or less than that time frame for a patient to recover, but, 14 days is the average length of recovery time for COVID-19. (Centers for Disease Control and Prevention [CDC], 2020)

Under the "fatality rate" setting, we used a rate of 0.121% (Berezow. 2020). This is the fatality rate for people in the age groups of 18-24 years old. Many graduate students fall out of that age range, and hence have an even higher mortality rate. Because ages of graduate students were unavailable for each university, we assumed the calculated death rate for the ages 18-24 would be accurate enough for our modeling purposes, but the potential death rate could be higher depending on the ages of the students at each university.

By implementing all of these variables for each university, we ran the simulation for 120 days to see how the hypothetical COVID-19 cases would spread. We found that within larger universities and with larger populations of students, the virus spread much more quickly. A university campus was simulated within the model, showing how many people were doctors in the situation (white figures), healthy (green figures), infected (red figures), or immune (blue figures). The fatalities were removed from the campus model.

For each day of the simulation, we recorded the ongoing cases during that day, the number of recovered and immune patients, and the number of ongoing deaths for each of the four capacity totals at each university. With all of that retrieved data, we created graphs and charts to illustrate the data in a different format, including 3 different graphs for each university (Appendix A). The first showed the ongoing cases, with four different lines representing cases at 100, 75, 50, and 25 percent capacity. The next showed ongoing deaths with the same four lines representing the different capacities. The last showed the ongoing immunities, also with the four representational lines.

Ten colleges were included in this case study (Table 1), including one college from each of the states with the most number of new cases per day as of July 23, 2020; Florida, Texas, and California.

It is important to recognize that this model does

not account for how quickly or how well the virus is spreading in the college's surrounding county or state. The infection rate is based solely on the global average, and not on regional averages for each university. This could result in actual numbers being different than those simulated. In addition, in many situations there is likely to be more than one student entering campus with the virus. This simulation is only intended to model the effects of if just one student with COVID-19 were to come onto campus upon reopening. The impacts of several initial infections have not been accounted for, but would almost certainly be much more serious.

In testing our research question, we used an online epidemiological simulator software to model the spread of COVID-19 throughout college campuses across the US. This simulator allowed us to enter the student population of each university (which we altered depending on the attendance rate we tested, 100%, 75%, 50%, and 25%), and the number of doctors relative to each university, which we calculated using AAMC data on the number of practicing physicians in the state each university was located in. The simulator also allowed us to input relevant constant variables that would make an impact on the spread of COVID-19, such as the limits on travel (we chose to use 0 limits on travel in our model), the overall sanitation of the university (which we kept at a constant 15/100), infectiousness (3.1%), average days to recover (14 days), and fatality rate for this age group (0.121%). After correctly setting up the simulator, we ran it 40 times (once for every one of the 10 universities tested for each of the attendance rates, see results below in the *Results* section and in Appendix A) and collected the data each time. Lastly, we created tables and graphs to analyze and visualize our data.

#### **4. Results**

We hypothesized that as the number of students colleges allow on campus increases, the number of semester COVID-19 cases will increase exponentially. To test our hypothesis, we used the "Disease Epidemic Model" by Shodor to predict the number and spread of COVID-19 cases at each university. ("Disease Epidemic Model," 2020). In

order to use the model, we had to plug in specific values that concerned the student population of each university and statistics that describes the virality, fatality, etc. of COVID-19. We ran simulations for each university, then downloaded the results from the simulator and created tables and graphs that represented the data using Google Data Studio. The first 5 days and last 5 days' predicted numbers of cases, deaths, and immunities are listed in Appendix B (Tables 3-32).

For the larger universities (University of Southern California, University of Central Florida, Texas A&M University, Purdue University, Brigham Young University, Harvard University and Johns Hopkins University to some extent), it looks as though our hypothesis was correct, as in all of our tables and graphs, an exponential curve can be seen in the number of COVID-19 cases as the percent attendance increases steadily/linearly. However, in the smaller universities (including Tulane University, University of Alaska Southeast, and Carnegie Mellon University), the exponential curve is much less accentuated, and is nonexistent in the smallest of those three, the University of Alaska Southeast. This is presumably because the model interprets these universities to be less dense in population, accounting for less interactions among students and less rise of COVID-19 cases.

Using the predicted data shown in the tables above from the simulator, the reopening of large universities at any attendance level (100%, 75%, 50%, or 25%) will likely lead to a surge in the number of COVID-19 cases that will overwhelm the healthcare system and inevitably lead to some student deaths. Looking at Harvard's predicted COVID-19 spread; if just one infected person were to come to the university, it becomes clear that at any level of attendance, there would inevitably be some deaths. In addition, our model is potentially a best case scenario, as it doesn't take into account the existing COVID-19 cases in the city, county, or state the university is located in, and it represents a situation in which only one student comes to campus infected. In reality, it is likely that more than one case 0 is to be expected on return to each campus, particularly on the campuses of the larger universities. As for smaller universities, such as the University of Alaska

Southeast, Tulane University, and Carnegie Mellon, the expected impact of reopening on COVID-19 cases is not so drastic. Rather, at each of these universities, there are no predicted COVID-19-related deaths for reopening at 75%, 50%, and 25% attendance.

This may not mean, however, that it is entirely safe for these universities to reopen, as our model does have some inaccuracies that impacts its results, and everything predicted by the model is subject to chance. These inaccuracies include the assumption that student population density uses the total student population number as a gauge for it. Campuses where students are more spread out (lower population density) may be less reliant on the actual population numbers of the campus to predict how the disease spreads. Our model also assumes that each university is a closed campus, and that no one can exit the campus and come back infected. Therefore, the model predictions could lead to results that are higher or lower than actual expected COVID-19 cases and deaths, so even though smaller campuses are at a much lower risk of having a high number of infections, other unaccounted for factors and variables, in addition to omnipresent chance, could lead to significantly different results in Fall 2020.

It is important for all colleges to evaluate all of the potential risks and benefits of returning to school, and at what allowed attendance of students. It is understood that moving to online education puts the universities in dangerous financial situations, puts the students in a far more suppressive learning environment, and creates many times more academic integrity risks; however, it does preserve the students' safety to the maximum amount (Wood, 2020). By using data visualizations that depict full data sets (Appendix A), parts of which are shown below in Appendix B (Tables 3-32), we saw an indication that opening at 25% attendance would be relatively the safest option, with the least number of cases projected of all the simulations. At 25% attendance, 475 cases was the highest number predicted (predicted for Texas A&M, Table 7) for any of the ten universities studied, more than quadruple the next largest predicted number of cases at this percent capacity, which was 93 cases.

Moving from 25% to 50% of the student

population on campus causes significant increases in cases and potential deaths, but not nearly as much as the increases between allowing 50% and 75% of the population back on campus. For instance, the predicted cases at Harvard University (at 25% attendance) by the end of the semester (120 days) increase by 42 times when increasing to 50% attendance. However, this is small when compared to the increase in cases from 25% to 75% attendance, which is a greater than 108 times the 25% projection (Table 1).

A similar, but less drastic increase difference is represented in Harvard's death rate (Table 4), as there are no projected deaths at 25% capacity, but the toll rises to 4 at 50%, and then to 13 at 75%. It sharply increases again if you were to introduce the entire population back to campus, with 25 projected deaths at Harvard by the end of the Fall term. Most of the other universities we studied emulate a similar pattern, some to an even greater degree, such as the University of Southern California and Texas A&M University.

At Johns Hopkins University (JHU), there are no projected deaths until 75% attendance (Table 20); insinuating that introducing a population of up to 50% could potentially be an acceptable number of students to have on campus. However, at the second largest campus studied, Texas A&M, even at 25% of total enrollment, 3 deaths were predicted by the simulation (Table 8). The University of Central Florida projects 2 and 21 deaths at 25% and 50% attendance respectively, which are dangerously high predictions for so little of the overall student population being allowed on campus. This has caused us to conclude that for larger universities especially, maximum safety requirements must be enforced at all times, with many doctors and hospitals available if universities so choose to have any fraction of students on campus, and they should not consider allowing any more than 25% of their total undergraduate and graduate enrolled students to come on campus if they value the health and safety of their student population.

A general pattern can be seen among all of the projection graphs other than Brigham Young University, Johns Hopkins University, the University of Central Florida, and the University of Alaska

Southeast (Appendix A), in which the difference in cases between 50% and 75% is incredibly dramatic, indicating that as a general case, maintaining a campus population of 50% of the total population enrolled is the maximum amount of students that should be allowed on campus to intermingle. This is not subjective, and as studied, each university and size will have to adjust to projections accordingly. However, bringing anywhere near to 100% of the full student population back to campus is an unsafe decision at most universities, with 7 of the 10 universities studied having over 10 projected deaths with most of their student body back on campus. Based on our model predictions (Appendix A), full attendance could be safe only at very small schools, such as those with 15,000 enrolled students and fewer (those studied include Tulane University, Carnegie Mellon University, and the University of Alaska Southeast; Tables 14, 23, and 26). This is because 1 or fewer deaths are projected at each while at 100% attendance. 1 is still a significant number, so if universities of these sizes decide it is safe to return at such high numbers, they still must follow maximum safety precautions, and maintain high observance and restriction to their student populations.

It is important to note that all graphs and charts of every university's case study, other than the University of Alaska Southeast, show an increase in cases, deaths, and immunities, as the percentage of students allowed on campus increases by the end of the semester. As the days draw closer to the end of the semester, there are no overlapping lines, (with the lines representing each of the four measured percent attendances; see Appendix A), and as the percent attendance increases, their corresponding graph lines reach higher. This is indicative of a highly positive correlation between the number of students who are allowed on campus and the number of cases of COVID-19 that would occur, and the number of deaths and immunities that would result because of the number of cases. Universities must be aware of the fact that the greater the student population they introduce to campus, no matter how seemingly insignificant, the greater the risk of contracting COVID-19 for each individual on campus.

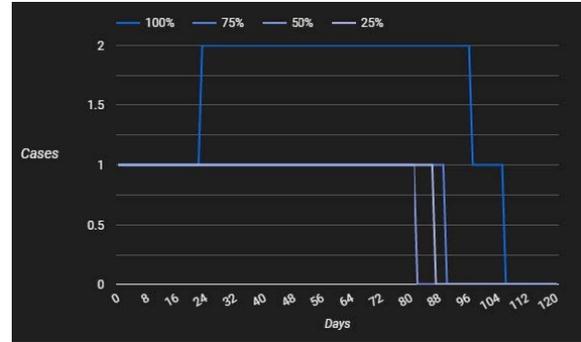


Figure 2. Projected COVID-19 cases at the University of Alaska Southeast: Graph depiction of predicted COVID-19 cases at the University of Alaska Southeast at each percent attendance (Appendix A contains more details)

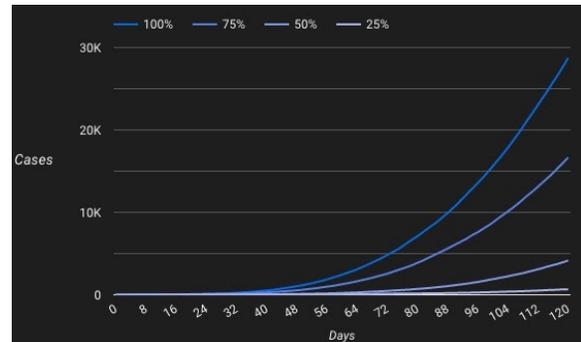


Figure 3. Projected COVID-19 cases at the University of Central Florida; Graph depiction of predicted COVID-19 cases at the University of Central Florida at each percent attendance (Appendix A contains more details)

The only graph and data depiction (Tables 25, 26, 27) that seemingly contradicts this positive correlation is the data for the University of Alaska Southeast (Cases graph depicted below in Figure 3). Although there are never any deaths, increasing the population on campus does have a positive correlation with the number of cases, as at 100% of their enrolled population returning, the projection reaches 2 cases at one time, as opposed to 1 at all other population amounts measured. This data is relatively insignificant however, because we worked with a projection that only estimates the spread of the disease, and 1 case is not enough to show a valid pattern for this university. This data does indicate that at very small schools, one case of the virus is often likely to get treatment fairly quickly and not infect

any or many other people. This leads us to conclude that at smaller universities (and in particular the University of Alaska Southeast where there are very few cases of coronavirus in general), there is a much lower risk of spreading COVID-19 even at 100% attendance, which may indicate that it is safer for smaller universities to return to school at relatively higher attendance percentages than larger universities (Figures 3 and 4; model comparison of small and large university projected cases).

## **5. Discussion**

In our research, we examined the projected impacts on COVID-19 cases, deaths, and resulting immunities in the event that various universities reopened at different capacities/attendance percentages (25%, 50%, 75%, and 100% attendance). Using a simulator by Shodor we modeled the spread and number of cases of COVID-19 in the university setting at these different attendance capacities and analyzed the results by creating graphs and tables to visualize the results of the simulations (“Disease Epidemic Model,” 2020) (See Appendix A). Before we started running simulations, we hypothesized that as the number of students colleges allow on campus increases, the number of semester COVID-19 cases will increase exponentially. Our hypothesis was correct in the context of the larger universities, as a clear exponential increase was observed when increasing the universities’ attendances by even as little as 25%. These results can also be seen in Appendixes A and B. However, for smaller universities that had fewer than 15,000 students, our hypothesis was less observable, but still proven correct. The only outlier was the University of Alaska Southeast, which had no predicted deaths at any of the attendance levels, and only 2 projected cases, even at 100% attendance. We concluded that no valuable and/or legitimate correlations could be drawn from the models for this university because there were so few cases and no pattern could be seen, and so we determined that in similarly small environments the virus would likely just filter out considerably quickly and affect a very small number of people.

By looking at the predicted COVID-19 cases

using our models generated by the simulator, we were able to conclude that it will likely be safer for smaller universities to return to campus in-person at a higher attendance (75%-100%) because there were far fewer cases and deaths resulting from a lower spread of the virus. In contrast, for larger universities, we concluded that it would be much more dangerous to return to campus in-person, especially at higher attendances. At such larger universities, a much more eminent exponential curve was observed when comparing higher attendance percentages to the number of COVID-19 cases. Even at 25% attendance, with the set conditions, these universities would inevitably have some deaths, which makes it particularly unsafe to return to campus with large amounts of students, and indicates that very strong measures and restrictions such as those modeled by Taiwan are a must for larger schools; everyone who returns is at a higher risk of contracting and spreading COVID-19, and those dangers must be met with more precautions. Given this data, it is imperative to recall the drawbacks and inaccuracies of our model, such as that it did not take into account the existing number of cases in the surrounding area of the university, the number of doctors may not have been completely accurate due to that we used state averages that will inevitably differ for each area of the state, and that our model used student population as a gauge for population density and interactions among said population, which is not always the case for different sized universities. In addition to this, our model was merely a prediction and will never represent the exact number of cases and spread of COVID-19 cases in a campus, as everything is subject to random chance in this situation.

As universities begin to reconsider their choices in reopening schools, our research becomes incredibly relevant in making important decisions that may impact the spread of COVID-19 not just throughout the university, but also the surrounding community that the university is a part of. Universities must weigh all the risks and benefits of reopening schools at different sized capacities in order to make informed decisions that will keep their students, faculty, and surrounding community safe from COVID-19. Our models and past precedent both indicate that even as few as 10 cases could result

in a much greater spread of COVID-19, not just to college-age students with healthy immune systems, but to their professors, their families, their friends, and the immunosuppressed whose bodies will not handle COVID-19 in the same way. The decision of whether to accept students' full tuition costs by allowing them to stay on campus this coming fall, despite the apparent risk of them contracting, spreading, and dying from COVID-19 examined in our models is entirely up to the universities, but we hope that our conclusive data may shed light on the potential dangers of reopening, in particular with full or near to full attendance from students. Looking at past data from the COVID-19 outbreak in Taiwan and other countries, it is clear that when even a few cases arise, safety precautions such as cancelling classes for weeks at a time must be taken in order to ensure safety of all students and faculty and to prevent the spread of the disease (Cheng, 2020). Universities' decisions of whether they are willing to lose part of their profits to ensure the health of their students and faculty will certainly help to determine the future spread of COVID-19 in the US, and so we hope that our research will allow them to make the most educated ones possible.

Given our hopes of helping universities make more informed decisions, we recognize our research only highlights a few major aspects when it comes to epidemiological modeling of the distribution and spread of communicable diseases like COVID-19. Our model had several limitations as formerly discussed, and there may exist a simulator or software that would more accurately depict the spread of COVID-19 and other similar diseases. Other than guaranteeing or disagreeing with our prediction models, future research should run simulations to determine what would happen if more people initially entered the university infected, in order to see the spread of COVID-19 in various instances in the individual university campuses. The simulator we used also did not allow us to account for the number of COVID-19 cases in the surrounding area of the university, the population demographics, or the density of the surrounding area, all of which would impact how the virus is likely to spread among the campuses. Looking into this variable of how COVID-19 may spread would help

to make more accurate predictions, as we only examined what would happen in a closed campus setting with few limits on student interaction with one another. Open campuses, especially those located within large cities, allow for more interaction with the surrounding people and city, and therefore would presumably spread COVID-19 faster.

A study with more case studies within it may create a more accurate prediction of the spread of COVID-19 in more situations, but due to time constraints we chose to study 10 universities of various sizes and locations so as to represent a wide array of learning environments that COVID-19 could affect differently if introduced to each campus. Most universities are also considering inviting students back to campus, but with many of their classes online. A future study should evaluate to what degree partially online school helps to stop the spread of the virus. An additional idea for future research would be to alter different variables on the simulator we used, such as the level of sanitation (which we kept at a constant 15/100 for all simulations) or the limits on travel (which we left unchecked and set to 0 for all simulations) to evaluate how each would impact the spread of COVID-19. In how we used the simulator we were unable to account for the staff on campus, who are at the highest risk of infection and death from the virus. It is critical that the dangers to staff and professors on campus are also evaluated before universities make decisions on how to implement learning in the fall. Accounting for the staff and examining how they would be affected in these instances would be valuable research to add to this quickly evolving field of study, and would help many universities come to a final and conclusive decision on their future plans, long anticipated by those enrolled and their families.

### 5.1 Review of Universities' Reopenings in Fall 2020

As universities were forced to adapt as a result of the COVID-19 crisis in the 2020-2021 school year, changes throughout every level of their educational structures occurred. Over 1,300 colleges and universities moved to hybrid or fully online formats, as the typical in-person classes and labs were cancelled in the Spring of 2020, and by the fall, only

27% of schools were planning to offer fully or mostly in-person classes (Smalley, 2021).

As described by a survey taken by the U.S. Census Bureau of college students in Fall of 2021,

- 15 million indicated their institution changed the content or format of classes. Among these:
- 9 million indicated this did not affect their plans for school in the fall
- 4 million indicated all plans to take classes had been canceled
- 2 million indicated classes would be different formats in fall
- 8 million indicated fewer classes would be taken
- 201,281 indicated more classes would be taken
- 709,132 indicated classes would be taken from a different institution
- 574,237 indicated classes would be taken from a different certificate or degree (Hanson, 2021)

Of note, the majority of universities saw declines in attendance rates, as students chose to drop out and defer as a result of COVID-19. Private for-profit colleges were 180 million cases worldwide with 3.91 million deaths attributed to COVID-19. The vast spread of the virus made it almost impossible for larger universities to continue to hold majority in-person classes throughout the 2020-2021 school year. The online and alternative formats to in-person classes created additional problems such as the major

drops in enrollment, particularly within black and low-income communities (St. Amour, 2020), as well as massive mental health issues worldwide, higher suicide rates, and dropping grades in all types of schools. The only grouping to see an increase in enrollment, undoubtedly as a result of their generally smaller population size and easier containment measures. In general, smaller colleges, unsurprisingly those with 15,000 students or less, were much better off than those with larger student populations (Figure 5). Note in said figure how every other grouping of colleges and universities suffered losses in enrollments during 2020.

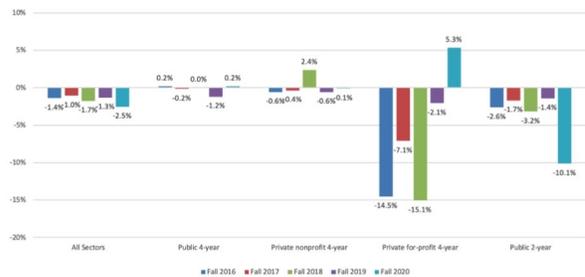


Figure 4. Penchant Change in Enrollment from Previous Year by Institutional Sector:2016 to 2020. Shown is the change in enrollment for each sector of college/university: Most notably is the comparison between the enrollment rates of private schools before and during 2020, and the notable surge in 2020 enrollment, as well as the decrease in enrollment overall (St. Amour, 2020).

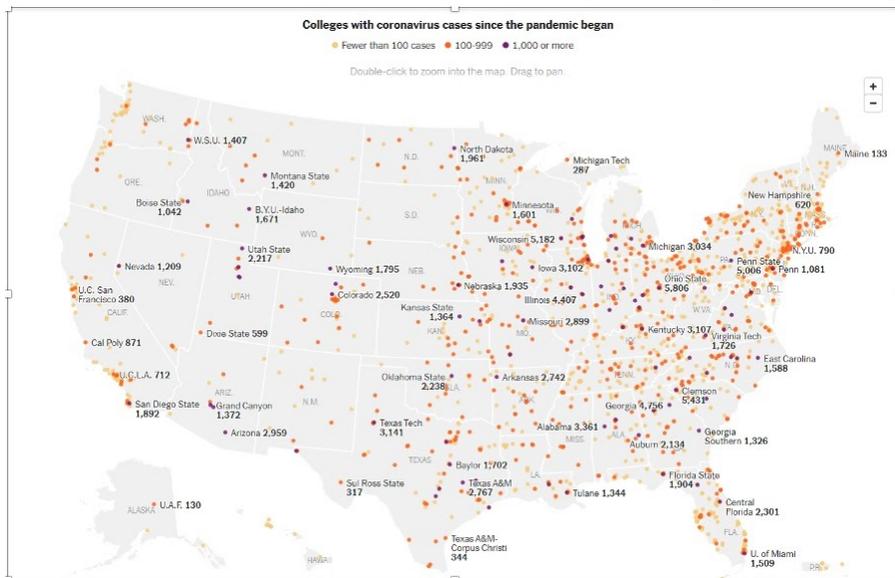


Figure 5. Colleges with Coronavirus Cases Since the Pandemic Began. A depiction of all of the known college cases across the US by school as of December 11, 2020. (New York Times, 2020)

By June 26, 2021, there had been 180 million COVID-19 cases worldwide with 3.91 million deaths. “More than 85 colleges have reported at least 1,000 cases over the course of the pandemic, and more than 680 colleges have reported at least 100 cases.” By December 11, 2020, there had been over 397,000 cases among college students in over 1,800 colleges (New York Times, 2020). In Figure 5 is shown the severity of colleges across the United States, including but certainly not limited to those in our case study. As depicted, thousands of colleges saw massive case numbers, as the map lights up in colorful dots across the nation. The Midwest and east coast saw the highest hotspots of cases within college-aged students, seen by the concentration of cases within the schools.

By Spring of 2021, the vast majority of surveyed universities were still not holding classes in a traditional classroom and college setting, and many of those who began the year entirely in person, had quickly been forced to send students home or online.

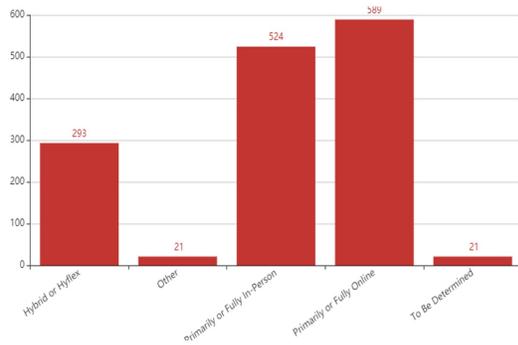


Figure 6. Spring Plans 2021. In a survey of 1,448 colleges and universities, this histogram depicts which learning format would be instantiated in the Spring semester of 2021. This is related to, but not indicative of the learning formats instantiated in the prior Fall semester (Davidson College, 2021).

As indicated by Figure 6, within the surveyed colleges and universities only ~36% were planning to return to a normal setting by the Spring semester. Of those returning fully in person, it was generally smaller universities who were able to do so, due to easier containment, contact tracing, sanitation measures, and enforcement of safety protocols. A prime example of a larger university who had to send

students back home was the University of North Carolina at Chapel Hill-within 2 weeks of admitting all students back to campus in the Fall, sent almost all back home to a virtual setting, after seeing an immediate surge in COVID cases. Almost every campus who had students on campus during the pandemic had to establish containment wards for exposed and infected students, where individuals had to isolate themselves and quarantine.

Few universities’ complete fall 2020 reopening plans are fully available to the public, and each university recorded their student cases differently for the semester (some provided combined faculty and student cases, and Harvard University did not have data for only Fall 2020). As a result, the chart below estimates the reopening capacity (based on the closest prediction of our model) of universities that did not provide exact data on their reopening capacities. These universities are denoted with an asterisk (\*) next to their reopening capacity. The rightmost column of the chart shows what our model predicted the number of cases to be, for the most similar capacity of students returning to the amount that actually returned (or the most similar number of cases for universities that did not provide data on their Fall 2020 reopening capacity). For five out of the ten universities studied, we found that our model prediction fell within a 25% range of the actual number of students that contracted COVID-19. Rather than looking at the size of a university to predict the number of COVID-19 cases, we believe that a more accurate predictor of its future cases were things that cannot be quantified in statistical models—such as the measures taken to slow the transmission of COVID-19, and how strictly they were enforced. Regardless, the recommendations we made to universities’ reopening were generally accurate to the universities’ Fall 2020 reopening plans, with the exception of larger universities such as Texas A&M University and Brigham Young University. As noted in Table 2 below, there was certainly a positive correlation between how many students were allowed back on campus, and the number of COVID-19 cases that occurred. In addition, the results of total reported cases generally reflect numbers similar to those predicted using our Shodor model under similar circumstances.

Table 2. Universities’ actual COVID-19 cases for Fall 2020 vs. our model’s prediction of cases

<i>University</i>	<b>Fall 2020 Reopening Capacity</b>	<b>Number of Cases</b>	<b>Our Model Prediction</b>
<i>Harvard University</i>	3.89%	388 (total undergraduate and graduate student cases as of June 20, 2021)	15 cases (25% capacity)
<i>University of Southern California</i>	9.25%	613 total undergraduate and graduate student cases in fall 2020	28 cases (25% capacity)
<i>Texas A&amp;M University</i>	75%*	4,890 cases in fall 2020 (w faculty included)	4695 cases
<i>University of Central Florida</i>	42.71%	2622 cases	2059 cases (50% capacity)
<i>Carnegie Mellon University</i>	75%*	29 cases	21 cases
<i>Brigham Young University</i>	100%	3,634 cases in fall 2020 (w faculty included)	2718 cases
<i>Johns Hopkins University</i>	50%	105 cases	107 cases
<i>Tulane University</i>	100%*	1381 cases	53 cases
<i>University of Alaska Southeast</i>	100%*	2 cases	2 cases
<i>Purdue University</i>	50%*	684 cases	302 cases

**6. Conclusion**

As COVID-19 cases continued to rise in the US, universities' fall 2020 reopening plans became increasingly complex and ambiguous- while some colleges planned to move to a hybrid or virtual format, the majority had opted for a completely in-person plan that disregards the value of the health of their own students, faculty, and cities, for personal gain and profit, and with the understanding that in-person is the best way to educate. Although this is true, more factors must be evaluated before such decisions can be made, and therefore in our study, we examined how altering the in-person attendance rate of ten universities of different sizes and locations would impact the spread and number of cases of COVID-19. To conduct our study and test our hypothesis, we used an epidemiological modeling software by Shodor to model our data for each of the universities in each of the different scenarios (100%, 75%, 50%, and 25% attendance) (“Disease Epidemic Model,” 2020). Keeping all other variables constant other than the population size, we found that as the in-person attendance grew linearly for each of the universities, we observed an exponential growth in the number of COVID-19 cases at each university, especially in the larger universities, leading to as many as 76 deaths (at Texas A&M University at

100% attendance, see Appendix B, Table 8). This pattern was visible in all universities other than the University of Alaska Southeast, where no pattern could be observed because of the low number of cases resulting from the small size of the university. Therefore, we can conclude that it is not safe for most universities to go back to in-person classes and residence life at full attendance, as this would likely cause a surge in the number of COVID-19 cases that would result in a positive feedback loop in which the disease spreads at an exponential rate. For larger universities such as the University of Central Florida and Texas A&M University, even going back at 25% capacity is anticipated to result in a few deaths (see Appendix B, Tables 8 and 11); contrarily, smaller universities like the University of Alaska Southeast and Carnegie Mellon University could supposedly go back at full attendance and experience minimal cases and COVID-19-related deaths. It is important to keep in mind that even though our models of these universities may predict no deaths, it does have inaccuracies and there will still be a small chance of death for any given individual that is on-campus and contracts the virus. In order to combat COVID-19, universities need very strict safety measures in order to pose the least risk to their students, faculty, and community, similar to those enforced in Taiwan (Cheng, 2020) and Singapore (Melnick &

Darling-Hammond, 2020). To conclude, unless universities move to a completely online format, there will inevitably be a risk of contracting and spreading COVID-19 as universities choose to allow students to return to campus at any capacity. Formerly mentioned measures can be taken to reduce this risk, including reducing attendance and employing strict safety measures on campus (mandatory daily temperature checks, face masks, contact tracing procedures, etc), but in several situations, there is only so much people will be able to do at the university level to contain the spread, as there will always be those who don't follow the guidelines. The most foolproof method of reducing the spread of COVID-19 is to limit as many interactions as possible, and larger universities in particular should do this by only allowing a percentage of their enrolled population of students to return to campus in the Fall.

## References

- Association of American Medical Colleges. (2019). 2019 State Profiles. <https://www.aamc.org/data-reports/workforce/data/2019-state-profiles>
- Berezow, A. (2020, June 25). Coronavirus: COVID Deaths in U.S. by Age, Race. American Council on Science and Health. <https://www.acsh.org/news/2020/06/23/coronavirus-covid-deaths-us-age-race-14863>
- Brigham Young University. (2020). Facts & Figures. <https://www.byu.edu/facts-figures>
- Carnegie Mellon University. (2019, September 16). University Enrollment by Degree Level. <https://www.cmu.edu/ira/Enrollment/pdf/fall-2019-pdfs/fall-2019-university-total-enrollment.pdf>
- Centers for Disease Control [CDC]. (2020). Quarantine If You Might Be Sick. <https://www.cdc.gov/coronavirus/2019-ncov/if-you-are-sick/quarantine.html>
- Centers for Disease Control [CDC]. (2020). Cases, Data, and Surveillance. <https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/index.html>
- Centers for Disease Control and Prevention [CDC]. (2020). Mental Health and Coping During COVID-19. Center of Disease Control and Prevention. <https://www.cdc.gov/coronavirus/2019-ncov/daily-life-coping/managing-stress-anxiety.html>
- Cheng, S., Center, H., Wang, C., Medicine, S., Shen, A., & Chang, S. (2020, July 12). How to Safely Reopen Colleges and Universities During COVID-19: Experiences From Taiwan. *Annals of Internal Medicine*. <https://www.acpjournals.org/doi/full/10.7326/M20-2927?journalCode=aim>
- Covid-19 Information. "Harvard University-Wide COVID-19 Testing Dashboard." [www.harvard.edu/coronavirus/testing-tracing/harvard-university-wide-covid-19-testing-dashboard/](http://www.harvard.edu/coronavirus/testing-tracing/harvard-university-wide-covid-19-testing-dashboard/)
- Davidson College. (2021). C2i Dashboard. <https://collegecrisis.shinyapps.io/dashboard/>
- Dier, A. (2020, June 03). Here's How Much a Mask Reduces Coronavirus Transmission. *Newser*. <https://www.newser.com/story/291760/heres-how-much-a-mask-reduces-coronavirus-transmission.html>
- Domenico, L., Pullano, G., Sabbatini, C., Boëlle, P., & Colizza, V. (2020, January 01). Expected impact of reopening schools after lockdown on COVID-19 epidemic in Île-de-France. <https://www.medrxiv.org/content/10.1101/2020.05.08.20095521v1>
- Harvard University. (2020). Harvard at a Glance. <https://www.harvard.edu/about-harvard/harvard-glance>
- Jahanian, F., & Garrett, Jim. (2020, May 14). Our Path Forward. <https://www.cmu.edu/leadership/president/campus-communications/2020/2020-05-14.html>
- Johns Hopkins University. (2020). Get The Facts: Undergraduate Admissions: Johns Hopkins University. <https://apply.jhu.edu/discover-jhu/get-the-facts/>
- Johns Hopkins University (2020, June 30). Johns Hopkins announces plans for fall undergraduate experience. Johns Hopkins University Hub. <https://hub.jhu.edu/2020/06/30/johns-hopkins-fall-2020-undergraduate-plans/>
- Johnson, E. (2020, June 23). BYU to hold in-person

classes fall 2020.

<https://www.abc4.com/news/byu-to-hold-in-person-cl asses-fall-2020/>

Melnick, H., Darling-Hammond, L., Leung, M., Yun, C., Schachner, A., Plasencia, S., & Ondrasek, N. (2020). Reopening schools in the context of COVID-19: Health and safety guidelines from other countries. Learning Policy Institute.

[http://www.nordcountryschool.org/uploads/5/2/3/3/5233925/1reopening\\_schools\\_covid-19\\_brief.pdf](http://www.nordcountryschool.org/uploads/5/2/3/3/5233925/1reopening_schools_covid-19_brief.pdf)

Pana-Cryan, R., Ray, T., Bushnell, T., & Quay, R. (2020). Economic Security during the COVID-19 Pandemic: A Healthy Work Design and Well-being Perspective. Centers for Disease Control and Protection [CDC].

<https://blogs.cdc.gov/niosh-science-blog/2020/06/22/economic-security-covid-19/>

Protopsaltis, S., & Baum, S. (2019). Does Online Education Live Up To Its Promise? A Look At The Evidence And Implications For Federal Policy. George Mason University.

<http://mason.gmu.edu/~sprotops/OnlineEd.pdf>

Purdue University. (2018). Student Enrollment, Fall 2018. Retrieved July 27, 2020, from <https://www.admissions.purdue.edu/academics/enrollment.php>

Purdue University (2020, July). Fall 2020 On-Campus Experience. <https://protect.purdue.edu/students/campus-2020/>

See, B., Wardle, L., & Collie, P. (2020, June 01). Teachers' responses to the school reopening strategy. Durham University. <http://dro.dur.ac.uk/31047/>

Sheikh, A., Sheikh, A., Sheikh, Z., & Dhami, S. (2020, June). Reopening schools after the COVID-19 lockdown. National Center for Biotechnology Information.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7321012/>

Shodor. (2020). Disease Epidemic Model (2020). <http://www.shodor.org/featured/ASLDiseaseModel/model>

Smalley, A. (2021, March 22). Higher Education Responses to Coronavirus (COVID-19). <https://www.ncsl.org/research/education/higher-education-responses-to-coronavirus-covid-19.aspx>

St. Amour, M. (2020, December 17). Final fall

enrollment numbers show pandemic's full impact.

<https://www.insidehighered.com/news/2020/12/17/final-fall-enrollment-numbers-show-pandemics-full-impact>

Staff, C. (2020, July 27). Here's a List of Colleges' Plans for Reopening in the Fall. The Chronicle of Higher Education.

<https://www.chronicle.com/article/heres-a-list-of-colleges-plans-for-reopening-in-the-fall/>

Texas A&M University. (2020). At a Glance - Texas A&M University, College Station, TX.

<https://www.tamu.edu/about/at-a-glance.html>

The New York Times. (2020, August 26). Tracking the Coronavirus at U.S. Colleges and Universities.

The New York Times.

<https://www.nytimes.com/interactive/2020/us/covid-college-cases-tracker.html>

Tulane University (2020, June 17). SPHTM FALL 2020 Reopening Academic Plan.

<https://sph.tulane.edu/sites/sph.tulane.edu/files/SPHTM%20Fall%202020%20Semester%20draft%20plan%20061220%20%281%29.pdf>

University of Alaska Southeast. (2020). University of Alaska COVID-19 Status.

<https://sites.google.com/alaska.edu/coronavirus/status?authuser=0>

University of Central Florida. (2020). UCF Facts 2019-2020. <https://www.ucf.edu/about-ucf/facts/>

University of Central Florida. (2020, June 1). UCF Return to Campus Plan Fall 2020.

<https://www.ucf.edu/coronavirus/document/return-to-campus-plan/>

University of Southern California. (2020). Facts and Figures. <https://about.usc.edu/facts/>

UNIVSTATS. (2020). Tulane University of Louisiana Student Population and Demographics.

<https://www.univstats.com/colleges/tulane-university-of-louisiana/student-population/>

Williamson, L. (2020, May 24). Coronavirus: Why reopening French schools is a social emergency.

British Broadcasting Corporation [BBC].

<https://www.bbc.com/news/world-europe-52769626>

Wood, G. (2020, April 28). There's No Simple Way to Reopen Universities. The Atlantic.

<https://www.theatlantic.com/ideas/archive/2020/04/co>

lleges-are-weighing-costs-reopening-fall/610759/

Worldometers. (2020, July 23). United States: Coronavirus. <https://www.worldometers.info/coronavirus/country/us/>

Young, M. K. A Thank You, Along With Plans For Summer And Fall. Texas A&M University, College Station, TX. <https://www.tamu.edu/coronavirus/messages/april-30-thank-you-and-plans-for-summer-fall.html>

Zukoski, C. F., & Wright, D. (2020, July 2). Letter on Student Housing and Course Schedules. USC Provost. <https://www.provost.usc.edu/letter-on-student-housing-and-course-schedules/>

**Appendix A**

[This links to a graphing tool where you can toggle between universities to see the projected number of COVID-19 cases and deaths & immunities associated with those cases](#)

**Appendix B**

**Harvard University**

Table 3. Predicted COVID-19 cases at Harvard University by day at each percent attendance				
Days	100%	75%	50%	25%
0	1	1	1	1
1	1	1	1	1
2	1	1	1	1
3	1	2	1	1
4	1	2	1	1
5	2	3	1	1
116	2417	1333	397	15
117	2490	1386	411	15
118	2542	1432	422	15
119	2610	1466	437	14
120	2705	1516	460	14

Table 4. Predicted COVID-19 deaths at Harvard University by day at each percent attendance				
Days	100%	75%	50%	25%
0	0	0	0	0
1	0	0	0	0
2	0	0	0	0
3	0	0	0	0
4	0	0	0	0
5	0	0	0	0

116	21	11	4	0
117	22	11	4	0
118	23	13	4	0
119	23	13	4	0
120	25	13	4	0

Table 5. Predicted COVID-19 immunities at Harvard University by day at each percent attendance

Days	100%	75%	50%	25%
0	0	0	0	0
1	0	0	0	0
2	0	0	0	0
3	0	0	0	0
4	0	0	0	0
5	0	0	0	0
116	39	15	10	3
117	41	15	11	3
118	46	16	12	3
119	49	18	12	4
120	52	20	12	4

**University of Southern California**

Table 6. Predicted COVID-19 cases at University of Southern California by day at each percent attendance

Days	100%	75%	50%	25%
0	1	1	1	1
1	1	1	1	1
2	1	1	1	1
3	2	1	1	1
4	2	1	1	1
5	2	1	1	1
116	4556	1974	150	25
117	4655	2040	159	26
118	4771	2112	170	26
119	4894	2177	178	28
120	5027	2247	181	28

Table 7. Predicted COVID-19 deaths at University of Southern California by day at each percent attendance

Days	100%	75%	50%	25%
0	0	0	0	0
1	0	0	0	0
2	0	0	0	0
3	0	0	0	0
4	0	0	0	0
5	0	0	0	0

<b>116</b>	49	24	1	0
<b>117</b>	51	24	1	0
<b>118</b>	52	24	1	0
<b>119</b>	53	24	2	0
<b>120</b>	54	24	2	0

Table 8. Predicted COVID-19 immunities at University of Southern California by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	71	11	1	1
<b>117</b>	77	11	1	1
<b>118</b>	84	12	1	1
<b>119</b>	91	13	1	1
<b>120</b>	98	16	1	1

**Texas A&M University**

Table 9. Predicted COVID-19 cases at Texas A&M University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	1	1	1	1
<b>1</b>	1	1	1	1
<b>2</b>	1	1	1	1
<b>3</b>	1	1	1	1
<b>4</b>	1	1	1	2
<b>5</b>	1	1	1	2
<b>116</b>	5866	4153	576	423
<b>117</b>	6026	4292	601	438
<b>118</b>	6187	4411	624	457
<b>119</b>	6349	4545	653	467
<b>120</b>	6506	4695	687	475

Table 10. Predicted COVID-19 deaths at Texas A&M University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0

<b>5</b>	0	0	0	0
<b>116</b>	52	39	5	3
<b>117</b>	53	41	5	3
<b>118</b>	54	42	5	3
<b>119</b>	58	43	5	3
<b>120</b>	61	45	6	3

Table 11. Predicted COVID-19 immunities at Texas A&M University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	45	65	2	9
<b>117</b>	56	69	2	10
<b>118</b>	62	78	2	10
<b>119</b>	73	82	2	10
<b>120</b>	86	85	2	10

**University of Central Florida**

Table 12. Predicted COVID-19 cases at University of Central Florida by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	1	1	1	1
<b>1</b>	1	1	1	1
<b>2</b>	1	1	1	1
<b>3</b>	1	1	1	1
<b>4</b>	1	1	1	1
<b>5</b>	1	1	1	1
<b>116</b>	6215	3959	1806	81
<b>117</b>	6370	4081	1848	83
<b>118</b>	6544	4204	1916	86
<b>119</b>	6729	4319	1979	91
<b>120</b>	6917	4417	2059	93

Table 13. Predicted COVID-19 deaths at University of Central Florida by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0

<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	68	44	21	2
<b>117</b>	69	44	21	2
<b>118</b>	72	48	21	2
<b>119</b>	73	50	21	2
<b>120</b>	76	50	21	2

Table 14. Predicted COVID-19 immunities at University of Central Florida by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	59	34	14	4
<b>117</b>	69	35	16	4
<b>118</b>	74	38	19	4
<b>119</b>	84	43	19	4
<b>120</b>	96	51	21	4

**Carnegie Mellon University**

Table 15. Predicted COVID-19 cases at Carnegie Mellon University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	1	1	1	1
<b>1</b>	1	1	1	1
<b>2</b>	0	2	1	1
<b>3</b>	1	2	1	1
<b>4</b>	1	2	1	1
<b>5</b>	1	2	1	1
<b>116</b>	58	18	4	0
<b>117</b>	61	20	4	0
<b>118</b>	63	20	4	0
<b>119</b>	69	21	4	0
<b>120</b>	75	23	4	0

Table 16. Predicted COVID-19 deaths at Carnegie Mellon University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
-------------	------	-----	-----	-----

<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	1	0	0	0
<b>117</b>	1	0	0	0
<b>118</b>	1	0	0	0
<b>119</b>	1	0	0	0
<b>120</b>	1	0	0	0

Table 17. Predicted COVID-19 immunities at Carnegie Mellon University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	1	3	1	1
<b>117</b>	1	3	1	1
<b>118</b>	1	3	1	1
<b>119</b>	1	3	1	1
<b>120</b>	1	3	1	1

**Brigham Young University**

Table 18. Predicted COVID-19 cases at Brigham Young University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	1	1	1	1
<b>1</b>	2	1	1	1
<b>2</b>	2	1	1	1
<b>3</b>	2	1	1	1
<b>4</b>	3	1	1	1
<b>5</b>	3	1	1	1
<b>116</b>	2438	725	330	21
<b>117</b>	2495	751	336	21
<b>118</b>	2574	780	347	22
<b>119</b>	2639	813	354	22
<b>120</b>	2718	844	367	22

Table 19. Predicted COVID-19 deaths at Brigham Young University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
-------------	------	-----	-----	-----

<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	20	9	1	0
<b>117</b>	21	10	1	0
<b>118</b>	21	11	2	0
<b>119</b>	21	11	2	0
<b>120</b>	21	11	2	0

Table 20. Predicted COVID-19 immunities at Brigham Young University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	30	7	5	6
<b>117</b>	36	7	6	6
<b>118</b>	40	8	6	6
<b>119</b>	46	9	6	6
<b>120</b>	53	10	6	7

**Johns Hopkins University**

Table 21. Predicted COVID-19 cases at Johns Hopkins University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	1	1	1	1
<b>1</b>	1	1	1	1
<b>2</b>	1	1	1	1
<b>3</b>	1	1	1	1
<b>4</b>	1	1	1	1
<b>5</b>	1	1	1	1
<b>116</b>	781	178	91	0
<b>117</b>	813	180	97	0
<b>118</b>	845	188	102	0
<b>119</b>	869	195	103	0
<b>120</b>	910	203	107	0

Table 22. Predicted COVID-19 deaths at Johns

Hopkins University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	11	1	0	0
<b>117</b>	11	1	0	0
<b>118</b>	11	1	0	0
<b>119</b>	11	1	0	0
<b>120</b>	11	1	0	0

Table 23. Predicted COVID-19 immunities at Johns Hopkins University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	7	4	5	1
<b>117</b>	10	4	5	1
<b>118</b>	10	4	6	1
<b>119</b>	11	4	7	1
<b>120</b>	11	4	7	1

**Tulane University**

Table 24. Predicted COVID-19 cases at Tulane University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	1	1	1	1
<b>1</b>	1	1	1	1
<b>2</b>	1	1	1	1
<b>3</b>	1	2	1	1
<b>4</b>	1	2	1	1
<b>5</b>	1	2	1	1
<b>116</b>	42	33	3	3
<b>117</b>	46	34	3	3
<b>118</b>	46	34	3	3
<b>119</b>	51	35	3	3

<b>120</b>	53	38	3	3
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Table 25. Predicted COVID-19 deaths at Tulane University by day at each percent attendance

Days	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	1	0	0	0
<b>117</b>	1	0	0	0
<b>118</b>	1	0	0	0
<b>119</b>	1	0	0	0
<b>120</b>	1	0	0	0

Table 26. Predicted COVID-19 immunities at Tulane University by day at each percent attendance

Days	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	3	3	2	1
<b>117</b>	3	3	2	1
<b>118</b>	3	3	2	1
<b>119</b>	3	4	2	1
<b>120</b>	3	4	2	1

**University of Alaska Southeast**

Table 27. Predicted COVID-19 cases at University of Alaska Southeast by day at each percent attendance

Days	100%	75%	50%	25%
<b>0</b>	1	1	1	1
<b>1</b>	1	1	1	1
<b>2</b>	1	1	1	1
<b>3</b>	1	1	1	1
<b>4</b>	1	1	1	1
<b>5</b>	1	1	1	1
<b>116</b>	0	0	0	0

<b>117</b>	0	0	0	0
<b>118</b>	0	0	0	0
<b>119</b>	0	0	0	0
<b>120</b>	0	0	0	0

Table 28. Predicted COVID-19 deaths at University of Alaska Southeast by day at each percent attendance

Days	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	0	0	0	0
<b>117</b>	0	0	0	0
<b>118</b>	0	0	0	0
<b>119</b>	0	0	0	0
<b>120</b>	0	0	0	0

Table 29. Predicted COVID-19 immunities at University of Alaska Southeast by day at each percent attendance

Days	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	2	1	1	1
<b>117</b>	2	1	1	1
<b>118</b>	2	1	1	1
<b>119</b>	2	1	1	1
<b>120</b>	2	1	1	1

**Purdue University**

Table 30. Predicted COVID-19 cases at Purdue University by day at each percent attendance

Days	100%	75%	50%	25%
<b>0</b>	1	1	1	1
<b>1</b>	1	1	1	1
<b>2</b>	1	2	1	1
<b>3</b>	2	3	1	1
<b>4</b>	2	3	1	1
<b>5</b>	2	4	1	1

<b>116</b>	3424	2397	250	29
<b>117</b>	3534	2467	262	33
<b>118</b>	3634	2530	274	35
<b>119</b>	3737	2604	288	35
<b>120</b>	3825	2677	302	35

Table 31. Predicted COVID-19 deaths at Purdue University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	37	21	5	0
<b>117</b>	41	22	5	0
<b>118</b>	42	23	5	0
<b>119</b>	44	23	6	0
<b>120</b>	46	24	7	0

Table 32. Predicted COVID-19 immunities at Purdue University by day at each percent attendance

<b>Days</b>	100%	75%	50%	25%
<b>0</b>	0	0	0	0
<b>1</b>	0	0	0	0
<b>2</b>	0	0	0	0
<b>3</b>	0	0	0	0
<b>4</b>	0	0	0	0
<b>5</b>	0	0	0	0
<b>116</b>	20	41	3	3
<b>117</b>	22	45	3	3
<b>118</b>	24	51	3	3
<b>119</b>	27	55	3	3
<b>120</b>	29	59	3	3

# Comparative Bioinformatics Analysis of SARS-CoV-2 and other Respiratory Viruses

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## Abstract

Viruses are sub-microscopic molecular parasites of cells that depend on and direct the host cell machinery to produce more copies of themselves. All viruses contain either DNA or RNA as their genetic material, which can potentially code for many proteins. The virosphere is very large and diverse, with almost 7000 unique species of viruses described to date. While the majority of these viruses are not disease causing and serve many important functions in the ecosystem, some viruses cause serious and debilitating diseases that have devastated human societies such as Ebola, Influenza, AIDS and SARS. Understanding the unique cell and molecular biology of these disease-causing viruses will aid in development of therapeutic strategies to target them. This study focuses on elucidating some unique features of the SARS-CoV-2 genome, which is the cause for the ongoing COVID-19 pandemic. Genomic and proteomic comparative analysis between SARS-CoV-2 and other known respiratory viruses such as SARS-CoV-1, MERS and Rhinoviruses and the intestine infecting human Rotavirus have been performed to characterize and extract selected novel features of the SARS-CoV-2 genome. These results can contribute to the existing and rapidly expanding knowledge of the biology of SARS-CoV-2.

*Keywords: SARS-CoV-2, COVID-19, Comparative Bioinformatics*

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## 1. Introduction

Viruses are rapidly evolving genetic entities that exist, reproduce, and evolve through principles of natural selection within the host cells of living organisms and are powerful instruments of molecular evolution that drive non-cyclical genetic exchange (Villarreal, 2008). While some viruses function as agents of mayhem and as agents of untold suffering, the vast majority of viruses are non-pathogenic and are integral to the health of organisms and are integral to supporting the ecosystem that we live in (Nuwer, 2020). As an evolutionary tool, viruses have

contributed to the formation of the placenta, a critical step in the history of mammalian evolution (Chuong, 2018). Within the human body, around 40% of the genome is derived from viral elements called transposons, and 8% has been derived from retroviruses (Arnold, 2020).

In order to reproduce and spread into new species, all viruses, regardless of classification or origin, must be able to subvert and transcend different molecular factors within their hosts. Viral binding and entry, recruitment of host factors necessary for viral replication, suppression of antiviral host factors, assembly and egress from the cell, and evasion of the

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host immune system are all dependent on various protein interactions with the host cell (Letko et al., 2020).

The slightest perturbations to these complex interactions, caused by changes in nucleotide or amino acid sequences, can make the difference between an increased or dead-end viral infection. Therefore, elucidating the different genomic and proteomic features of a virus can greatly enhance our understanding of the cell biology of viral infection of the host cell.

This paper focuses on genome-based characterization of COVID-19 virus (SARS-CoV-2) which is the cause for the current ongoing pandemic that is wreaking a deadly assault on the world as we know it. To highlight its unique features, we have compared the genome and proteomic characteristics of SARS-CoV-2 with other known respiratory viruses such as SARS-CoV-1, MERS and Rhinoviruses. To identify the common characteristics of respiratory viruses, the genomic sequences and the proteomic signature of the aforementioned respiratory viruses are compared with the human Rotavirus, which is a virus that infects the intestine. Brief descriptions of these viruses are given below.

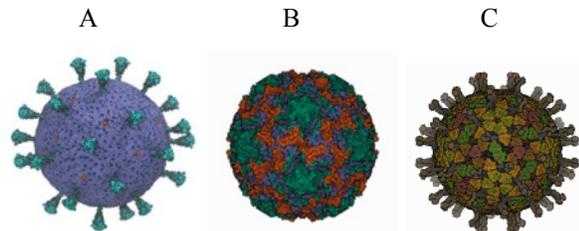


Figure 1. 3D model showing structural organization of A) Coronaviruses (Yu, 2020) B) Rhinoviruses (RSCB PDB 1R1A) and C) Rotaviruses (RSCB PDB 4V7Q) that are used in this study. These models can be found in the Protein Data Bank – a public repository for solved protein structures (www.rcsb.org).

Coronaviruses (CoVs) are members of the family Coronaviridae. CoVs are classified into four types based on phylogenetic (evolutionary) and genomic data: Alpha, Beta, Gamma, and Delta. SARS-CoV-1 and SARS-CoV-2 are both beta coronaviruses with large positive-sense single-stranded RNA genomes. Both SARS-CoV-1 and SARS-CoV-2 are

distinguished by crown-shaped (corona) spikes protruding from their surfaces (Pal, 2020). These spikes are glycoproteins that aid in binding to and infection of host cells. MERS is an abbreviation for Middle Eastern Respiratory Syndrome Coronavirus. It is a beta coronavirus with a positive-sense, single-stranded RNA virus genome, similar to SARS-CoV-1 and SARS-CoV-2. It is distinct, however, in that transmission occurs primarily between animals and people, while transmission between humans was uncommon and limited to spread among family members and healthcare settings (Pal, 2020).

Rhinoviruses (RVs) belong to the family of Picornaviridae. Of that, the specific Rhinovirus is the genus. They are common viral agents for humans and a leading cause of common colds, as well as upper respiratory tract infections. Like Coronaviruses, it contains a positive-sense, single-stranded RNA virus genome, however, it contains four different proteins that are projected as spikes on the viral surface, where three of them account for the virus antigenic diversity, and the last anchors the RNA core to the capsid (Palmenberg, 2015).

Rotaviruses belong to the Reoviridae family's Rotavirus class, which includes viruses with segmented, double-stranded RNA genomes. Rotavirus particles are massive and complex, with three concentric protein layers encasing an 11-segment double-stranded RNA genome (Kiefel and Itzstein, 2003).

We hypothesized that comparative bioinformatic analysis of SARS-CoV-2 relative to aforementioned viruses that cause respiratory diseases, will allow us to map the unique features of SARS-CoV-2 that can underlie its unique pathology. We also hypothesized that further comparative bioinformatic analysis of SARS-Cov-2 and the other respiratory viruses with the human rotavirus which is specialized to infect a different organ system, namely the gastrointestinal system, will allow us to attain a deeper understanding of the evolutionary adaptability of SARS-CoV-2 virus and the other respiratory viruses to the microenvironment of the lung. To that end, we have done a stepwise bioinformatics characterization using Python to analyze the previously mentioned viruses using sequences obtained from the National

Center for Biotechnology Information (NCBI) BLAST\* databases, and the Protein Data Bank (PDB). We present original data and conclusions regarding certain genomic and proteomic features of SARS-CoV-2.

## 2. Methods

The viruses were compared using bioinformatics in the following manner. The genomic sequences of viruses were obtained in the FASTA format from the NCBI's public database of nucleotide sequences at <https://www.ncbi.nlm.nih.gov/>. The files containing the entire genome's ORF (Open Reading Frame) sequences were created by merging the individual ORF sequences. Customized programs were developed in Python (3.6.13) to perform the following characterizations.

- a. Whole genome GC content
- b. Open reading frame GC content, where a count of the number of G's and C's were extracted and computed as the following fraction (number of G + number of C)/ total number of bases
- c. The influence of GC content on codon bias analysis was carried by measuring the number of G and the C that are present in the ORF of the various viral genomes.
- d. The genomic sequences were analyzed to find occurrences of nucleotide palindromes of different sizes.
- e. Proteomic analysis was carried out using BlastP on sequences obtained from the protein database of NCBI while protein structures are obtained from the public database of protein structures RCSB protein data bank

A detailed description of the steps and the source codes used for doing the analysis can be found in the following [GitHub](https://github.com/ananyabalaji/genomicseq) link: <https://github.com/ananyabalaji/genomicseq>

## 3. Results

3.1 Comparative analysis of GC content between the viruses causing respiratory illnesses reveal that SARS- CoV-2 has lower GC content and altered codon bias.

The GC contents vary amongst organisms and are regarded as genomic signatures which are specific to

a given organism. GC content plays a role in determining the amino acid selection, codon bias, genome, gene and promoter organization, the mutational bias of the genome, and gene silencing in different species (Elhaik and Tatarinova, 2012). Given the fact that the CoV-2 virus elicits differential physiological responses compared to other respiratory viruses, we performed a comparative analysis of the GC content of SARS-CoV-1, SARS-CoV-2, MERS, and Rhinovirus which are viruses that cause respiratory illness in humans. As a control, we also included the human Rotavirus, which infects the intestine to understand if there is a relation between the GC content and the environments that the viruses target within the human body. Figure 2 shows the viruses that were selected for analysis and the corresponding GC content distribution in their whole genomes, ORFs, and based on their position on codons.

In general, the whole genome GC content of various respiratory viruses was approximately 40%, while the whole genome GC content of the Rotavirus targeting the gut was approximately 33%. Human genomes have an average GC content of 35% to 60% across 100-Kb fragments, with a mean of 41% (International Human Genome Sequencing Consortium, 2001). Our whole genome GC content analysis revealed that there was approximately 2% less GC content in SARS-CoV-2 when compared to SARS-CoV-1 and MERS (37.97% CoV-2 vs 40.76% CoV-1 vs 41.24% MERS) (Figure 2A).

To determine whether this lowering of the GC content occurs in the coding regions of the genome, we examined the GC content only in the ORFs of the viruses, as shown in Figure 2. The GC percentages in the ORFs of the respiratory viruses followed a similar trend to that of the whole genome content, showing that SARS-CoV-2 has a lower GC content in its open reading frames (37.9% CoV-2 vs 40.90% CoV-1 vs 41.38% MERS). Interestingly the Rotavirus showed a larger decrease of GC content in the open reading frame (~40% for respiratory viruses vs 28.85% for the Rotavirus) further highlighting the link between the biodistribution and the genomic composition.

The lowering of GC content specific to the open reading frames can influence the amino acid composition, as reported in other retroviruses (Zhao,

2007). Particularly, it can influence the distribution of amino acids whose codons are GC rich such as Glycine, Alanine, Arginine, and Proline (GARP) amino acids. Whole-genome analysis of the GARP content in the open reading frame for the whole viral genomes, carried out in Figure 2C, revealed that the values were similar across the respiratory viruses. This suggests that the lower GC content of

SARS-CoV-2 does not translate to a differential codon usage. Interestingly, the GARP content of the respiratory viruses (~20%) was higher when compared with the Rotavirus (~16.79%), suggesting that the effect of the tissue microenvironment on the GC content has a dominant influence on the amino acid selection.

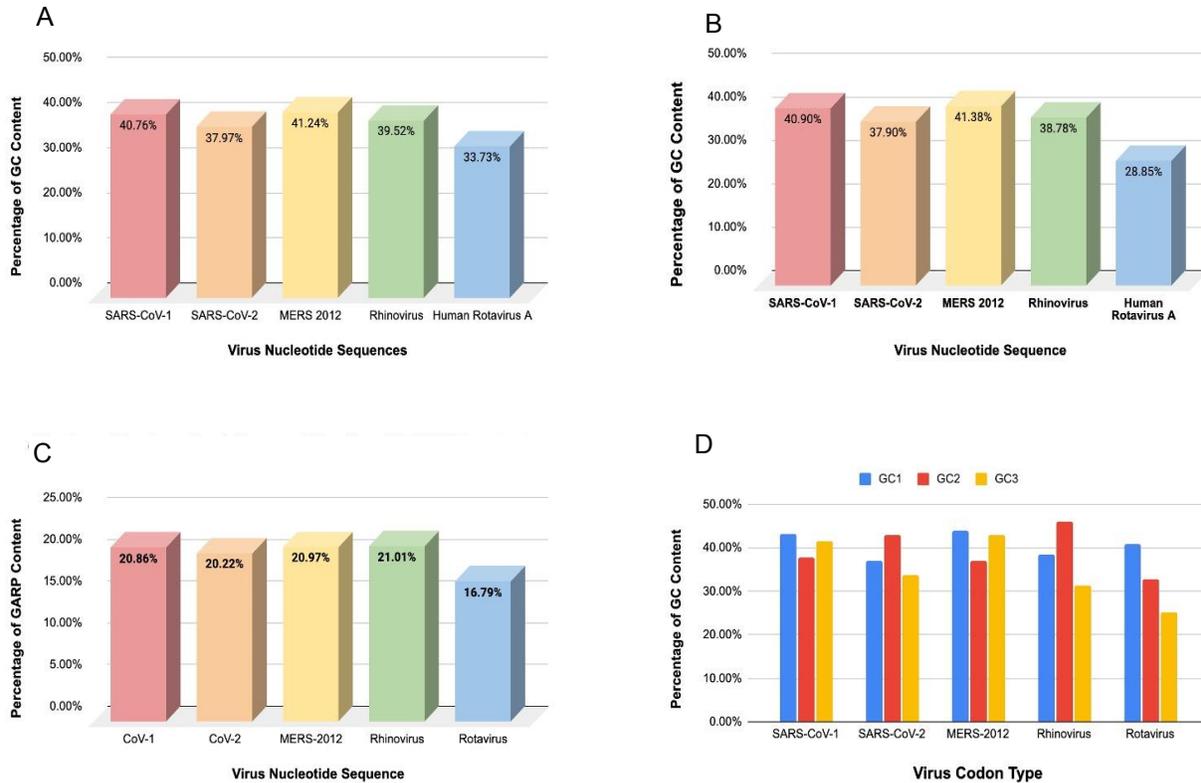


Figure 2. [A] GC content distribution for whole genome, [B] GC content in ORF for whole genome, [C] GARP content distribution for whole genome, and [D] Count of GC based on position in codon for whole genome.

### 3.2 Comparing count and distribution of palindromes of different sizes across viruses

In molecular biology, a palindromic sequence is defined as a sequence that, when read backwards, produces an exact complement of itself. Palindromic sequences in both DNA and RNA viruses have been implicated for viral packaging and defense mechanisms. While the biological significance of these sequences must be determined experimentally, we compared the palindromic features of different

respiratory virus genomes to filter and identify a few lead candidates that can have potential biological relevance in the pathophysiology of SARS-CoV-2 for future experimental investigations.

To analyze the palindromic features unique to SARS-CoV-2, we used our customized Python scripts to perform a comparative palindrome count analysis on the respiratory viral genomes. We determined that the largest palindrome in SARS-CoV-1 is a 22-mer palindrome, while the largest palindrome in SARS-CoV-2 is a 20-mer palindrome and the largest

palindrome in MERS is an 18-mer palindrome (Figure 3). The counts of the remaining palindromes ranging in length from 4 to 18 base pairs are shown in Figure 3 as a percentage coverage of the genome, while their positions in the genome are shown in Figure 4. For the majority of palindrome sizes, the percentage of the genome covered by palindromes was comparable between coronaviruses and significantly different from the rhinovirus. Amongst the coronaviruses, our analysis revealed that SARS-CoV-2 has a higher percentage (> 10%) of its genome covered by 4-mers, 6-mers, 8-mers, 12-mers, and 16-mers than SARS-CoV-1. While the number of 4-mers, 6-mers, and 8-mers in MERS was comparable to that of other coronaviruses, MERS had a higher percentage coverage of 10-mers and a lower percentage coverage of larger palindromes, as illustrated in Figure 3.

Published phylogenetic analyses by other groups revealed that MERS is a distinct coronavirus clade from SARS-CoV-1 and SARS-CoV-2. As a result, we limited our investigation to SARS-CoV-1 and SARS-CoV-2 for the frequency distribution studies between palindromes. We began by determining whether the distribution of palindromes across the genome was uniform or non-uniform. While 4-mers, 6-mers, and 8-mers were evenly distributed, 12-mers

and 14-mers palindromes were distributed in the extremities of both SARS-CoV-1 and SARS-CoV-2, rather than in the central 10,000 to 20,000 base pair regions, indicating a non-random distribution (Figure 4). Despite the fact that 4-mers and 6-mers are distributed uniformly throughout the genome, previous research established that 4-mers and 6-mers are statistically underrepresented in coronaviruses when compared to chance occurrence. To gain a better understanding of the biological consequences of this underrepresentation, we examined the frequency of different palindrome combinations in the SARS-CoV-1 and SARS-CoV-2 genomes. We discovered that the SARS-CoV-1 and SARS-CoV-2 contained all possible combinations of 4-mer palindromes, albeit at varying frequencies. We find that CoV-2 had a lower frequency (35%) of the 4mer palindromes 'TCGA', 'CATG', 'CCGG', 'CGCG', 'GCGC', while having a higher frequency of the AT-rich 4mer palindromes 'TTAA', 'TATA' (>20%). Figure 5 illustrates this. A similar analysis of the 6-mers revealed that, while the CoV-1 genome sampled 87.5 percent of all possible 6mer palindromes, the CoV-2 genome sampled 93.5 percent. Furthermore, 82% of the sampled 6mer palindromes were sequentially similar, with varying frequencies and positions in the genome.

Table 1. Palindrome distributions for SARS-CoV-1 and SARS-CoV-2

Palindrome Size	Selected Palindromic Sequence	Unique features of the selected palindromes
4	TTAA, TATA	These are present in <u>higher frequencies</u> in SARS-Cov-2 genome
4	TCGA, CATG, CCGG, CGCG, GCGC	These are present in <u>lower frequencies</u> in SARS-Cov-2 genome
6	GACGTC, CCGCGG, CGGCCG, GGGCCC	These 6-mers are <u>missing</u> from both SARS-Cov-1 and SARS-Cov-2. This could have possibly resulted from an antagonistic host interaction of an ancestral genome
8	TGTTAACA	This 8-mer occurs at the <u>highest frequencies</u> at both SARS-Cov-1 and SARS-Cov-2
10	TTGTTAACAA, TATAATTATA	These are conserved 10-mers that appear twice in SARS-Cov-1 and only once in SARS-Cov-2
12	TTATAATTATAA	This conserved 12-mer appears twice in SARS-Cov1 and only once in SARS-Cov-2
14	TAAAATTAATTTTA	This is the largest sequentially conserved palindrome in both SARS-Cov-1 and SARS-Cov-2
20	ACACTGGTAATTACCAGTGT	This is the <u>largest palindrome</u> found in SARS-Cov2 genome
22	TCTTTAACAAGCTTGTTAAAGA	This is the <u>largest palindrome</u> found in SARS-Cov1 genome

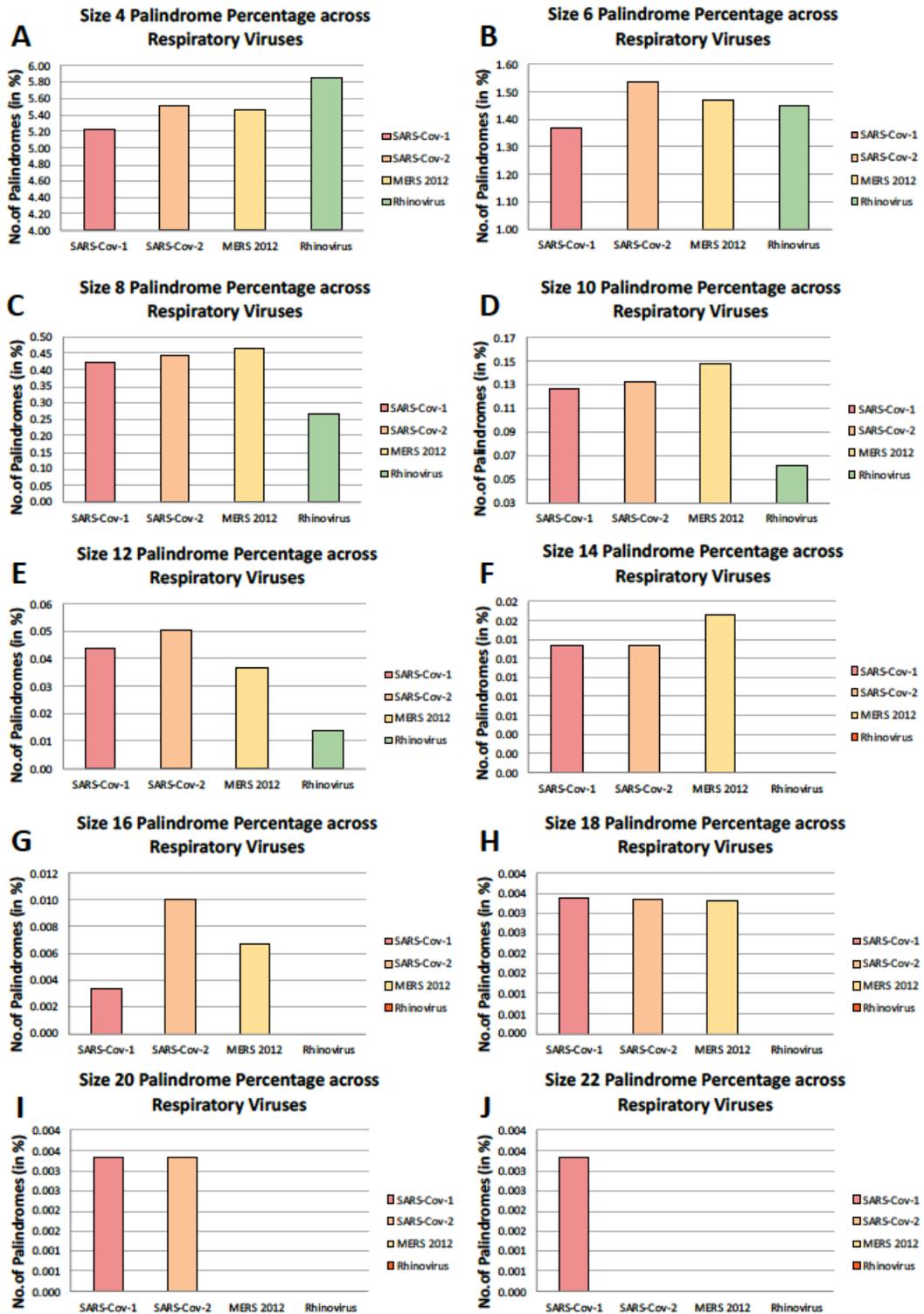


Figure 3. Palindromes of different lengths [A] 4-mer, [B] 6-mer, [C] 8-mer, [D] 10-mer, [E] 12-mer, [F] 14-mer, [G] 16-mer, [H] 18-mer, [I] 20-mer, [j] 22-mer are counted and expressed as percentage of genome coverage for the different respiratory viruses.

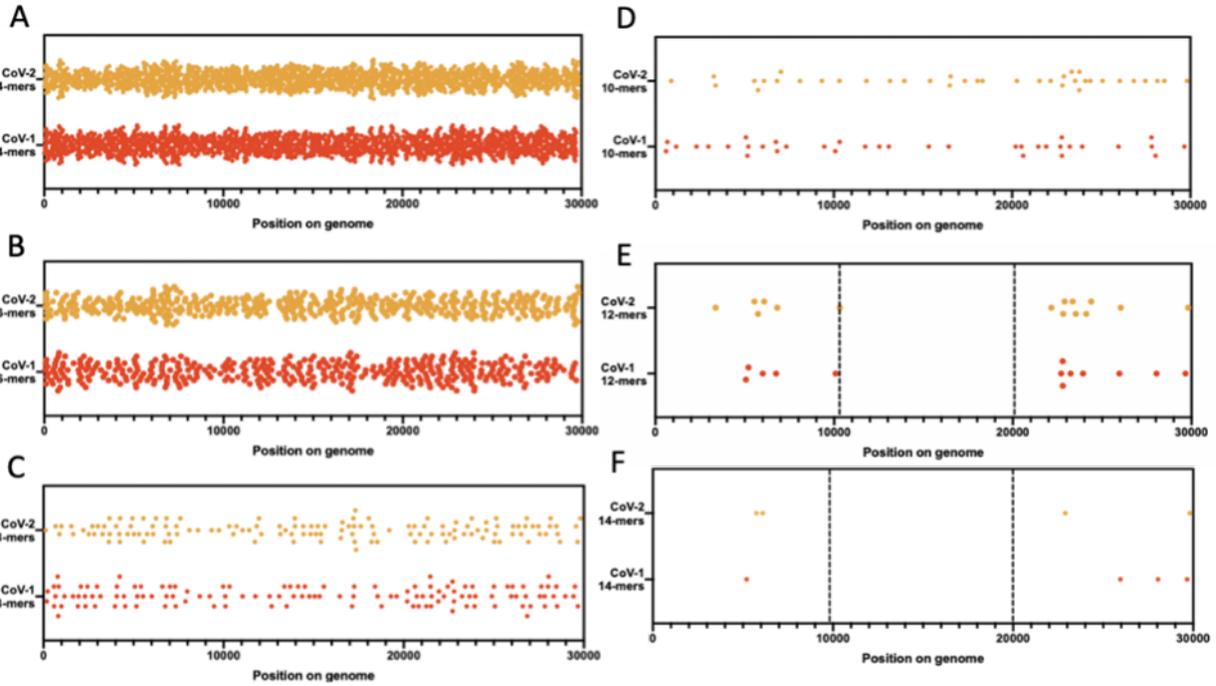


Figure 4. Distribution of [A] 4-mer [B] 6-mer [C] 8-mer, [D] 10-mer, [E] 12-mer and [F] 14-mer palindromes within whole genome of SARS-CoV-1 and SARS-CoV-2

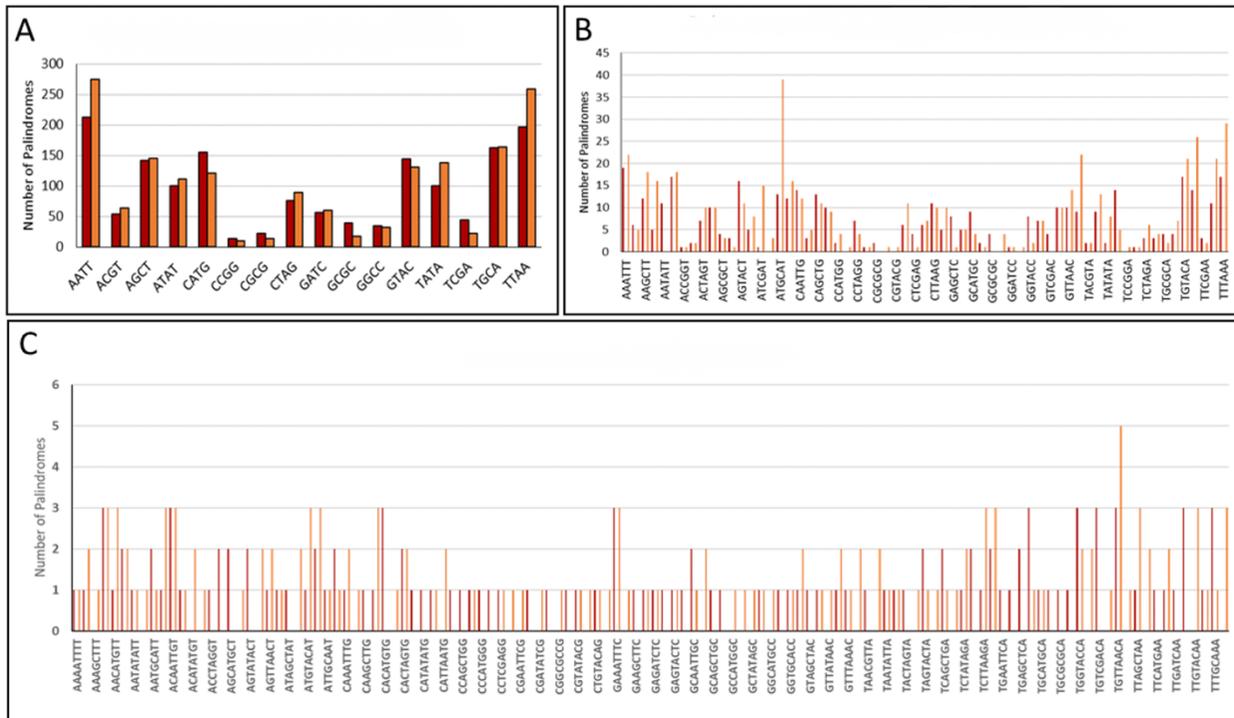


Figure 5. Frequency distributions of palindromes size [A] 4-mers, [B] 6-mers and [C] 8-mers versus SARS-CoV-1 and SARS-CoV-2. This reveals that the frequency of selected N-mers are altered in CoV-2 compared to CoV-1

While SARS-CoV-1 and SARS-CoV-2 sampled approximately 33% of all possible combinations of 8mer palindromes, 40% of the sampled 8mer palindromes were sequentially similar and appeared at different frequencies and locations in SARS-CoV-1 and SARS-CoV-2. SARS-CoV-1 and SARS-CoV-2 sampled between 3-4 percent of all possible 10mer palindromic sequences, and approximately eleven 10mer palindromes (18%) were sequentially similar, albeit at different frequencies and locations. Less than 0.5 percent of all possible combinations of 12 and 14-mers were sampled, and approximately four 12-mers and one 14-mer were conserved sequentially between SARS-CoV-1 and SARS-CoV-2. TTATAATTATAA' appeared twice in SARS-CoV-1 and once in SARS-CoV-2, amongst the conserved palindromic 12mers identified between SARS-CoV-1 and SARS-CoV-2. There were no sequentially conserved palindromes of size 16 or greater identified. Thus, the longest conserved palindrome between SARS-CoV-1 and SARS-CoV-2 is a 14-mer sequence identified as "TAAAATTAATTTTA". Based on these analyses, we have nominated lead candidate palindromes that can have potential biological relevance for future experimental investigations.

### 3.3 Comparing protein structures across viruses

Several unique features of viral genomes are imprinted in the structural proteins of viruses that serve to encapsulate the genome and protect it from degradation and reinfection. Similarities in structure of these proteins are the very basis of classification of viruses in terms of families, while minor alterations in structure are often the basis of differences in pathophysiological effects within members of the same family.

While earlier results focused on comparative analysis of genomic features between SARS-CoV-2, SARS-CoV-1, MERS, Rhinoviruses and Rotaviruses, this section focuses on comparative analysis of the proteomes of primarily the respiratory viruses. We carried out a whole proteomic signature comparison of the respiratory viruses by comparing the amino acid sequences of all proteins (proteome) in the viral genomes using NCBI Blast (BlastP) and comparing

protein sequences of different viruses. Results are shown in Table 2. The coverage percentage is a quantitative measure of the effective length of the sequences being compared following alignment, whereas the identity percentage is a quantitative measure of sequence similarity. Closely related species share a greater percentage of sequence identity than distantly related species. Our results indicated that the entire SARS-CoV-2's proteome alignment was 79.11 percent identical to SARS-CoV-1's, with an E-value of 0, indicating that this similarity is not coincidental. The similarity score between SARS-CoV-1 and SARS-CoV-2 was significantly higher than the similarity score (46.72 percent vs 37.56 percent respectively), implying that SARS-CoV-2 is more closely related to SARS-CoV-1 than MERS. This reinforces the previously published phylogenetic analysis that showed MERS belongs to a different clade than CoV-1 and CoV-2.

While structural interpretation is possible only if this proteomic analysis is extended to include comparisons of individual proteins within selected subcategories such as surface proteins and nucleocapsid proteins, this analysis is currently beyond the scope of this paper. However, the similarity and relatedness between the viruses revealed by the current analysis can be easily visualized by comparing the three-dimensional structures of the proteins that several laboratories are solving using cryo-electron microscopy and depositing in the protein database repository – PDB. This is demonstrated in Figure 6 by a comparison of surface spike proteins.

## 4. Discussion

The principle of biological amplification is often exemplified in virology, where a small modification of the genomic sequence changes the molecular structure and function of its proteins that results in a greater change in the pathophysiological presentation of a viral infection. In this study, we have attempted to elucidate key genomic signatures that are specific to SARS-CoV-2 by performing a comparative study with other known members of the Coronaviridae family such as SARS-CoV-1 and MERS. The comparison was extended to include Rhinoviruses

which belong to a different family of viruses but demonstrate similar physiological biodistribution of infecting the lung microenvironment. Finally, the comparisons were extended to include the Rotavirus

— which infects human intestines — to show a different tissue biodistribution and to understand the features in the context of its environment.

Table 2. Proteomic alignment scores for Coronaviridae viruses

Query Sequence	SARS-Cov-1			SARS-Cov-2			MERS		
	Coverage Percent	Identity Percent	E-value	Coverage Percent	Identity Percent	E-value	Coverage Percent	Identity Percent	E-value
SARS-Cov-1	100	100	0	79	78.37	0	89	46.72	0
SARS-Cov-2	79	78.37	0	100	100	0	70	37.56	0
MERS	89	46.72	0	70	37.56	0	100	100	0

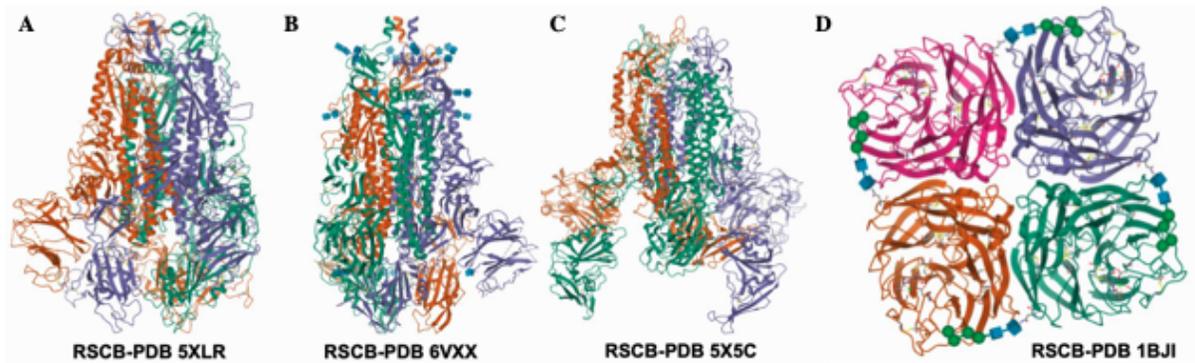


Figure 6. Surface protein structures for [A] SARS-CoV-1 spike protein, [B] SARS-CoV-2 spike protein, [C] MERS spike protein, [D] Rhinovirus Viral Coat Protein. These models can be found in the Protein Data Bank – a public repository for solved protein structures ([www.rcsb.org](http://www.rcsb.org)). The protein structure identifiers are within the figures. From the structures, we can see that the spike protein SARS-CoV-2 is more related to SARS-COV spike protein compared to MERS. Furthermore, the surface proteins of the coronaviruses are clearly distinct from the Rhinovirus, which belongs to a different family.

GC content plays a role in determining the genome, gene and promoter organization, amino acid selection, codon bias, the mutational bias of the genome, and gene silencing in different species. The variations of the whole genome GC content across viruses correlated with tissue preferentiality of the viruses, with the Rotavirus, demonstrating a distinctly lower GC content compared to the respiratory viruses. This suggests a selection of GC content in the viruses based on the microenvironment that they target. Thus, future studies can experimentally examine whether the GC contents of around 40% make the respiratory viruses more conducive for targeting the lung.

Amongst the respiratory viruses, SARS-CoV-2 had a lower GC content. From the molecular

perspective, lower-GC-content DNA is less stable than high-GC-content DNA and this stability difference is attributed to stacking interactions (Ninh, 2013). The biochemical cost of GC base synthesis is also quite high, and decreases in GC content across species has been hypothesized to be a consequence of energy efficiency (Chen et al., 2016). This indicates that lowering the GC content can make replication of the RNA genome a more thermodynamically viable process. Whether this contributes to the higher infectivity of SARS-CoV-2 needs to be experimentally determined by mutating the GC rich regions and observing the effect on infectivity in vitro and in vivo model systems.

Furthermore, the GC content analysis that we carried out across the total ORF of the viral genomes

revealed that this lowering of GC content occurs in the actively transcribed regions of the viral genome. Since lowering of GC content specific to the open reading frames can influence the amino acid composition, as well as codon bias, we investigated the distribution of GARP amino acids and discovered that the GARP contents were similar across the different viruses. Investigating the codon bias of SARS-CoV-2 revealed that compared to other respiratory viruses, SARS-CoV-2 uniquely preferred having G's and C's in the second position of the majority of its codons compared to the other viruses. While this is suggestive of a link between lower GC content and an altered codon composition, the causality as well as the biological underpinnings of the altered codon compositions have to be determined by controlled experimentation.

Palindromic sequences are intriguing features of viral genomes and are implicated in viral genome packaging and defense mechanisms. In addition, specific loss of function of palindromic sequences have revealed that some palindromic sequences regulate viral recombination (Gallaher, 2020) and viral replication capacity (Elmenofy and Jehle, 2015). Thus, palindromes represent novel modes of genomic regulation of viral behavior that are yet to be elucidated for SARS-CoV-2. An objective analysis of palindromes across different lengths (4-mers, 8-mers, 10-mers, 12-mers and 14-mers) revealed several unique features of the SARS-CoV-2 genome. While previous research has established that 4-mer and 6-mer palindromes are significantly under-sampled in coronaviruses in comparison to the frequencies predicted by random occurrence, the biological significance of this finding is unknown at the moment. Our findings add another layer of detail to this observation by demonstrating that the frequency distributions of the various possible 4-mers are not equal and that the frequency of certain 4-mer palindromes is significantly reduced in CoV-2 compared to CoV-1, while certain AT-rich palindromes are further enriched in CoV-2. The evolutionary selection pressure that resulted in this altered frequency distribution should be investigated because it may indicate that certain antagonistic host interactions have been overcome in CoV-2 compared to CoV-1.

A similar trend is observed in 6-mers, where the frequency distribution and positioning of the palindromes are altered for 82% of common 6-mer palindromes. Additionally, while there are 64 total combinations of palindromic six-mer sequences, four of these 6-mer sequences are not sampled in either the CoV-1 or CoV-2 genomes (GACGTC, CCGCGG, CGGCCG, and GGGCCC). Interestingly, these palindromes missing from CoV genomes are GC-rich, making it highly improbable that they were missed by chance and thus deserving of further investigation. While both CoV-1 and CoV-2 sampled 30% of the total number of 8-mers (256), they share approximately 40% of the palindromes with different frequency and position. A distinguishing feature of CoV-2 is that it contains a single 8mer palindrome that occurs five times throughout the genome, whereas every other palindrome occurs between one and three times, making it a candidate for experimental investigation. For 10-mer combinations out of ten thousand possible combinations, the CoV-1 and CoV-2 genomes sampled only 3-4 percent of all possible combinations, with only 18% of palindromes sequentially conserved. The number of palindromes decreased significantly for 12-mers, and it's worth noting that while 4, 6, 8, and 10-mers were distributed evenly and randomly throughout the genome, palindromes of 12bp were restricted to the extremities in both CoV-1 and CoV-2 genome thereby demonstrating a non-random distribution. Further comparison of conserved palindromic sequences revealed the presence of a specific palindromic 12-mer 'TTATAATTATAA', that appeared twice in SARS-CoV-1 and once in SARS-CoV-2. This could potentially be used for distinguishing SARS-CoV-1 and SARS-CoV-2. Indeed, previous studies have used palindromic sequence frequency patterns to cluster different viruses to the host they target (Lamprea-Burgunder, et al., 2011). The location and the conservation of this sequence suggests a potential biological role for this 12-mer that needs to be determined by experimentation. The largest palindrome that is conserved between CoV-1 and CoV-2 is a 14-mer, which makes it worthy of further experimental investigation. Thus, our study has identified a few lead candidates that are worthy of future

experimental investigation from thousands of palindromes in the CoV-2 genome.

In addition to the comparison of genomic features, we compared the proteomic signatures of the respiratory viruses. At the whole proteome level, our comparison of SARS-CoV-1, MERS and SARS-CoV-2 amino acid alignments, and identities quantitatively measured that SARS-CoV-2 is more closely related to SARS-CoV-1 than MERS. While the analysis at whole proteomic level provides information regarding relatedness, understanding the similarities and differences in single protein structures paves the way forward to understand the biochemical, cellular and immune responses to SARS-CoV-1 and SARS-CoV-2 that contribute to the differences in pathophysiology.

## 5. Conclusion

This paper has characterized certain genomic and proteomic signatures of SARS-CoV-2 in relation to SARS-CoV-1, MERS, Rhinovirus and the Rotavirus. While SARS-CoV-2, SARS-CoV-1, MERS, and the Rhinovirus all infect the respiratory system, the Rotavirus infects the small intestine. We began by determining the GC content of the aforementioned viruses, as GC content is a species-specific genomic signature that contributes to the organization of the genome, genes, and promoters, as well as amino acid selection and codon bias in various species. Our findings indicate that respiratory viruses and rotaviruses had markedly different GC content values, implying that the GC content of viruses has evolved in response to the microenvironment they target. Amongst the respiratory viruses, SARS-CoV-2 has a lower whole genome GC content as well as lower GC content in the coding regions. To measure the effect of lower GC content in the coding regions, we investigated amino acid selection and codon usage bias in the different viruses. While this reduction in GC content in the coding regions had no effect on the amino acid selections as measured by GARP amino acid levels in respiratory viruses, our investigations into codon usage bias revealed that SARS-CoV-2 preferred G and C in the second position of the majority of its codons, which distinguished it from other coronaviruses.

Additionally, our findings indicate that this trend is comparable to that of rhinoviruses. These findings emphasize the evolutionary similarities and differences between respiratory viruses, while also emphasizing the relatively unique characteristics of the SARS-CoV-2 genome that may contribute to its unusual functional behavior.

Our subsequent investigations focused on studying palindromic distributions in the respiratory viruses. Palindromic sequences are intriguing viral genome features that are implicated in viral genome packaging and defense mechanisms. An initial palindromic count analysis revealed that while the coronaviruses SARS-CoV-1, SARS-CoV-2 and MERS showed similar distributions of palindromes of different sizes, the distributions were considerably different in Rhinovirus. The largest palindrome in SARS-CoV-1 is a 22-mer while the largest palindromes in SARS-CoV-2 and MERS are 20-mer and 18-mer respectively. We then focused on performing the palindromic frequency analysis with SARS-CoV-1 and SARS-CoV-2, which have been previously established to belong to the same clade. Our frequency analysis for the palindromes of different sizes indicated that A) the frequency distributions of the various possible 4-mers are not equal and that the frequency of certain 4mer palindromes is significantly reduced in CoV-2 compared to CoV-1, while certain AT-rich palindromes are further enriched in CoV-2. B) For the 6-mer, 8-mer and 10-mer palindromes, the frequency distribution and positions were altered in the sequentially conserved palindromes while several palindromes were unique. For the 12-mer palindromes, we found that there was a non-random distribution, while the largest sequentially conserved palindrome for CoV-1 and CoV-2 is a 14-mer. As a result of these studies, several unique characteristics of the CoV-2 genome have been identified, which may contribute to differential packaging and defense mechanisms against the host immune system. Additionally, we have proposed a set of lead candidate palindromes that we believe merit further experimental investigation. Future studies can mutate the specific palindromic residues highlighted in this study in order to gain a better understanding of their

biological significance.

Finally, by comparing the whole proteomes of the coronaviruses, we can quantify the degree of similarity between SARS-CoV-1, SARS-CoV-2, and MERS. Our findings corroborate previously published phylogenetic analyses by establishing that SARS-CoV-2 is more closely related to SARS-CoV-1 than to MERS. While our current analysis is limited to the entire proteome, additional comparative analysis of protein subgroups can provide additional insights.

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### References

Arnold C. (2020, January 9). The non-human living inside of you. Cold Spring Harbor Laboratory. <https://www.cshl.edu/the-non-human-living-inside-of-you/>

Chen, W. H., Lu, G., Bork, P., Hu, S., and Lercher, M. J. (2016). Energy efficiency trade-offs drive nucleotide usage in transcribed regions. *Nat. Commun.* 7:11334. doi: 10.1038/ncomms11334

Chew DS, Choi KP, Heidner H, Leung MY. Palindromes in SARS and Other Coronaviruses. *INFORMS J Comput.* 2004 Fall;16(4):331-340. doi: 10.1287/ijoc.1040.0087.

Chuong E. B. (2018). The placenta goes viral: Retroviruses control gene expression in pregnancy. *PLoS biology*, 16(10), e3000028. <https://doi.org/10.1371/journal.pbio.3000028>

COVID-19 virus uses heparan sulfate to get inside cells. (2020, September 15). EurekaAlert! [https://www.eurekaalert.org/pub\\_releases/2020-09/uoc--cvu091520.php](https://www.eurekaalert.org/pub_releases/2020-09/uoc--cvu091520.php)

Du M-Z, Zhang C, Wang H, Liu S, Wei W and Guo F-B (2018) The GC Content as a Main Factor Shaping the Amino Acid Usage During Bacterial Evolution Process. *Front. Microbiol.* 9:2948. doi: 10.3389/fmicb.2018.02948

Elmenofy, W. H., & Jehle, J. A. (2015). Possible

functional co-operation of palindromes hr3 and hr4 in the genome of *Cydia pomonella* granulovirus affects viral replication capacity. *The Journal of general virology*, 96(9), 2888–2897. <https://doi.org/10.1099/vir.0.000195>

Forster P, Forster L, Renfrew C, Forster M. Phylogenetic network analysis of SARS-CoV-2 genomes. *Proc Natl Acad Sci U S A.* 2020 Apr 28;117(17):9241-9243.

Gallaher, W.R. A palindromic RNA sequence as a common breakpoint contributor to copy-choice recombination in SARS-COV-2. *Arch Virol* 165, 2341–2348 (2020). <https://doi.org/10.1007/s00705-020-04750-z>

Gelderblom HR. Structure and Classification of Viruses. In: Baron S, editor. *Medical Microbiology*. 4th edition. Galveston (TX): University of Texas Medical Branch at Galveston; 1996. Chapter 41. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK8174/>

International Human Genome Sequencing Consortium (2001). "Initial sequencing and analysis of the human genome". *Nature*. 409 (6822): 860–921.

Jawaid Akhtar, M. (2020). COVID19 inhibitors: A prospective therapeutics. *Bioorganic Chemistry*, 101, 104027. <https://doi.org/10.1016/j.bioorg.2020.104027>

Kiefel MJ and Itzstein M-v (2003) Carbohydrates as Inhibitors of Rotaviral Infection. *Methods in Enzymology*, 363 (395-412)

Lamprea-Burgunder, E., Ludin, P., & Mäser, P. (2011). Species-specific typing of DNA based on palindrome frequency patterns. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 18(2), 117–124. <https://doi.org/10.1093/dnares/dsr004>

Letko M, Marzi A, Munster V. Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses. *Nat Microbiol.* 2020 Apr;5(4):562-569. doi: 10.1038/s41564-020-0688-y. Epub 2020 Feb 24. PMID: 32094589; PMCID: PMC7095430.

Liu, Z., Xu, W., Xia, S. et al. RBD-Fc-based COVID-19 vaccine candidate induces highly potent SARS-CoV-2 neutralizing antibody response. *Sig*

- Transduct Target Ther 5, 282 (2020).  
<https://doi.org/10.1038/s41392-020-00402-5>
- NCBI SARS-CoV-2 Resources. (n.d.). NCBI NIH National Library of Medicine. Retrieved May 5, 2021, from <https://www.ncbi.nlm.nih.gov/sars-cov-2/>
- Ninh, A.Q. (2013). Correlation Between GC-content and Palindromes in Randomly Generated Sequences and Viral Genomes. arXiv: Genomics.
- Nuwer, R. (2020, June 17). Why the world needs viruses to function. BBC Future.  
<https://www.bbc.com/future/article/20200617-what-if-all-viruses-disappeared>
- Pal M, Berhanu G, Desalegn C and Kandi V. Severe acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2): An Update (2020) *Cureus* 12(3): e7423 DOI 10.7759/cureus.7423
- Palmenberg AC and Gern JE (2015) Classification and evolution of human rhinoviruses. *Methods Mol Biol.* 2015; 1221: 1–10. doi: 10.1007/978-1-4939-1571-2\_1
- Payne S. (2017). Family Coronaviridae. *Viruses*, 149–158.  
<https://doi.org/10.1016/B978-0-12-803109-4.00017-9>
- Tatarinova, T., & Elhaik, E. (2012). GC3 Biology in Eukaryotes and Prokaryotes. In *DNA Methylation - From Genomics to Technology* (pp. 55-68)
- Villarreal L. P. (2008). Evolution of Viruses. *Encyclopedia of Virology*, 174–184.  
<https://doi.org/10.1016/B978-012374410-4.00706-8>
- Wesley A. Volk, Jay C. Brown. *Basic Microbiology* 8th Edition.
- Willwand, K., Moroianu, A., Hörlein, R., Stremmel, W., & Rommelaere, J. (2002). Specific interaction of the nonstructural protein NS1 of minute virus of mice (MVM) with [ACCA]<sub>2</sub> motifs in the centre of the right-end MVM DNA palindrome induces hairpin-primed viral DNA replication. *The Journal of general virology*, 83(Pt 7), 1659–1664.  
<https://doi.org/10.1099/0022-1317-83-7-1659>
- Yu A, Pak AJ, He P, et al., A multiscale coarse-grain model of the SARS-CoV-2 virion. *Biophysical Journal* 120, 1097-1104 (2020)
- Zhao X, McGirr KM and Buehring CG (2007). Potential evolutionary influences on overlapping reading frames in the bovine leukemia virus pXBL region. 89, 502-511
- Zhu, Z., Lian, X., Su, X. et al. From SARS and MERS to COVID-19: a brief summary and comparison of severe acute respiratory infections caused by three highly pathogenic human coronaviruses. *Respir Res* 21, 224 (2020).  
<https://doi.org/10.1186/s12931-020-01479-w>

# Convolutional Neural Network for Predicting Genetic Risks of Breast Cancer

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## Abstract

Breast cancer is a complex disease with a growing global prevalence whose genetic causes remain largely unexplored. The rise of next generation sequencing has significantly augmented genetic studies in identifying breast cancer-associated mutations, the most common of which are single nucleotide polymorphisms (SNPs). While SNPs offer insights into the genetic causes of breast cancer, they do not explain its biological underpinnings nor do they provide a context within which to judge sequence-based interactions between SNPs linked to the disease. Convolutional Neural Networks (CNNs) demonstrate higher performance in hierarchical and abstract feature learning for image classification compared to other deep learning methods. This study proposes a deep learning model, named SPRiNGS, to classify a sample's genetic breast cancer risk by analyzing the sequence contexts surrounding its SNP composition. Firstly, Monte Carlo simulations were implemented to generate a sample cohort and corresponding Polygenic Risk Scores (PRS). Secondly, each sample's sequence composition matrix was resized to highlight significant semantic patterns across sequences. Thirdly, a two-dimensional CNN was constructed for feature learning and classification. This research demonstrated the validity of its simulated cohort. Additionally, SPRiNGS elucidates the improved performance of sequence-based predictions compared to SNP-based methods. The robustness of SPRiNGS was proved by experimental variations of the number of loci considered and the sequence fragment length.

*Keywords: Breast Cancer, Risk Prediction, SNPs, Genomics*

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## 1. Introduction

Breast cancer is a complex disease with several subtypes and is influenced by myriad genetic and environmental factors. In 2020, the CDC categorized this disease among the “Top 10 Cancers” for its alarmingly increasing global prevalence and mortality rates (CDC, 2020). Current estimates suggest that approximately every 1 in 8 women could develop breast cancer in their lifetime (“U.S. Breast Cancer Statistics,” 2020). Advancements in next

generation sequencing technologies have greatly augmented nucleotide-based biomarker identification for various diseases, including breast cancer, primarily through genome-wide association studies (GWAS), which analyze the distribution of genomic mutations across cases and controls for a specified phenotype (Quezada, et al., 2017). These variants are mostly single nucleotide polymorphisms (SNPs), genetic mutations occurring at singular positions across a genome, and offer tremendous opportunity in precision medicine. While SNPs yield insights into

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the genetic causes of breast cancer, they alone do not explain its mechanisms nor do they provide a context to judge the underlying semantic interactions between SNPs. One strategy to overcome these issues is to incorporate the local DNA fragment surrounding each SNP into existing risk prediction models. By extracting DNA sequences around GWAS breast cancer mutations, this research hypothesizes that incorporating the local DNA sequence context around statistically significant mutations into disease prediction algorithms will outperform existing SNP-based methods in classifying genetic risks of breast cancer. This study proposes Sequence-based Polygenic Risk Network for GWAS SNPs (SPRiNGS), a novel computational method for classifying sequence-based breast cancer risks.

## 2. Materials and Methods

### 2.1 Data Collection and Preprocessing

This research utilized the SNPs available in the ‘Breast Carcinoma’ dataset from the online *GWAS Catalog* (Buniello, et al., 2019). To extract all SNPs with explicit corresponding genomic loci, the dataset was filtered to remove all entries missing both a risk allele and locus. Subsequently, for all entries without either an SNP or genomic coordinate, the missing information was manually extracted from *SNPedia* (Cariaso & Lennon, 2012) or *dbSNP* (Sherry, et al., 2001), thereby ensuring that each SNP had a corresponding locus. The remaining mutations were then filtered by statistical significance using the common GWAS  $p$ -value threshold  $\alpha = 5 \times 10^{-8}$  (Fadista, et al., 2016). Finally, the relative strength of each allele  $\beta$  was extrapolated to accurately characterize the individual effects of each locus on a sample’s breast cancer risk.

### 2.2 Sequence Extraction

The genomic location of each SNP was expanded into symmetric ranges about the risk allele. BEDTools, a powerful toolset for genomic arithmetic (Quinlan & Hall, 2010), then converted each of these ranges into DNA sequences using the *GRCh38* reference genome (Schneider, et al., 2017). A

reference genome is “a digital nucleic acid sequence database assembled by scientists as a representative example of the set of genes in one idealized individual organism of a species” (“Reference genome,” 2020). Extraction from a reference genome indicated that the emergent sequences were not associated with any disease (including breast cancer) because they lacked the risk-associated alleles (and were thus classified as “healthy”). To generate the breast cancer-associated sequences, risk alleles were substituted into the sequences surrounding their corresponding loci. This process generated one healthy and one risk-associated sequence for each statistically significant SNP location.

### 2.3 Monte Carlo Simulation

Previous genome-wide prediction studies primarily perform genomic sequencing on a sample cohort of cases and controls to extract their own specific SNP collection prior to risk analysis. This means that researchers would analyze the SNP composition of individuals who had a particular disease and those who did not. These data are then stored in databases for other researchers to use. However, these repositories often limit public access due to medical privacy and other ethical constraints. After searching popular databases including *cBioPortal* (Cerami, et al., 2012), *GWASkb* (Kuleshov, et al., 2019), and *GWAS Central* (Beck, et al., 2020) for SNP-based breast cancer case-control samples, it was found that the accessible data only described a sample’s mutated gene composition. However, since one gene can contain multiple SNPs, this type of data would not be suitable for this experiment. To circumvent this, Monte Carlo methods were implemented to emulate real-world conditions when generating a representative random sample of breast cancer risk scores. Monte Carlo methods rely on stochasticity to predict a deterministic result (Adekitan, 2014). For this study, each sample’s risk score was the deterministic result (see ‘Polygenic Risk Score Calculation’) and the sample’s sequence composition represented the stochastic component.

For this sample to be truly representative, all possible risk scores needed to be accounted for.

Across all samples, the Monte Carlo simulation randomly selected between healthy and risk sequences for each SNP location with varying probabilistic frequencies. This method ensured a random sample which accounted for all risk scores for the number of statistically significant SNPs.

The sequence data for all samples were stored in a 3D array whose height represents the total number of SNPs per sample  $s$ , width is the sequence length  $L$  (see ‘Sequence Encoding’), and depth represents the total number of samples  $N$  (Figure 1). The sample size was fixed at  $N = 20,000$  due to computational constraints. The other two variables were evaluated in a sensitivity analysis to measure how they impact the model’s performance. Specifically, the number of SNPs is strictly determined by statistical significance. Hence, variations in  $s$  were created by fluctuating the  $p$ -value threshold  $\alpha$ . The threshold was tightened ( $\alpha = 5 \times 10^{-9}$ ) and relaxed ( $\alpha = 5 \times 10^{-7}$ ) to obtain differing numbers of mutated loci while maintaining sufficient amounts of data required to train a machine learning algorithm.

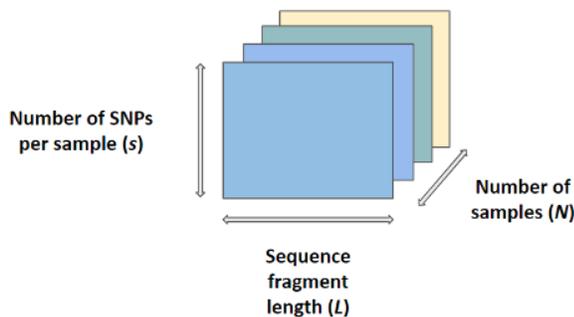


Figure 1. Three-dimensional data structure of Monte Carlo sample population. This simulation encodes each sample as an  $s \times L$  matrix which describes the sequence composition of a particular individual.

#### 2.4 Sequence Encoding

One-hot encoding is a popular technique to convert nucleotide sequences into binary sequences. For any given genomic sequence of length  $l$ , the length of the corresponding one-hot encoded sequence  $l_{ohc}$  is  $4l$  due to the four nucleotide possibilities (A, C, G, T) at each location along the nucleotide sequence. However,  $l_{ohc}$  explodes as  $l$

increases, making one-hot encoding impractical for large sequences. To avoid high-dimensional data, genomic sequences were converted to vectors of unique numbers between [1, 4], thereby preserving sequence length and explicitly differentiating alleles. This process encodes each sample as an  $s \times L$  matrix characterizing its sequence composition. Matrices were resized to dimensions  $28 \times 28$  to bring similar semantic patterns closer together and highlight important genomic features across samples. Moreover, making these matrices denser decreases the computational storage and time required for analysis.

#### 2.5 Polygenic Risk Score Calculation

Each sample’s breast cancer risk was calculated using a weighted Polygenic Risk Score (PRS) based on its genetic sequence composition, as seen in Equation (1), where  $i$  was an integer within [1,  $N$ ] representing the sample index,  $j$  represented the sequence number between [1,  $s$ ],  $s_{ij}$  was the sequence classification of ‘healthy’ or ‘breast cancer’ as 0 or 1 respectively, and  $\beta_{ij}$  represented the sequence’s relative strength based on its particular risk allele.

$$risk_i = \sum_{j=1}^s s_{ij} \times \beta_{ij} \quad (1)$$

While this risk calculation method assesses the cumulative impact of a sample’s sequence composition, it does not account for the occurrence-based or sequence-based interactions between SNPs. Therefore, machine learning is implemented to account for these complex underpinnings (see ‘Convolutional Neural Network’).

To categorize samples ‘healthy’ or ‘at risk of breast cancer,’ all risk scores were normalized between [0, 1]. Samples whose normalized risk scores were above the 50th percentile were classified as ‘at risk of breast cancer,’ and the remainder were classified as ‘healthy.’ This method yielded a population with 50% breast cancer prevalence, which ensures an equal number of cases and controls in the dataset to avoid a biased training procedure for the model.

## 2.6 Convolutional Neural Network

Convolutional Neural Network (CNN) is a subset of deep learning largely popularized for image classification because it adaptively learns and generalizes hierarchical spatial features (Indolia, et al., 2018). CNNs split their learning processes into “building blocks, such as convolution layers, pooling layers, and fully connected layers” to extract features from multidimensional data (Yamashita, et al., 2018). In convolution layers, the model iterates over samples using copious filters and stride windows of specified dimension to learn patterns among the input data. The pooling layers reduce the dimensionality of the model’s feature matrices as it continues to learn. Finally, the fully connected network makes predictions with the vector representations of the extracted features. These models specifically capture explicit and implicit patterns within data using fewer hyperparameters compared to other deep learning methods.

This research applied a two-dimensional CNN to classify breast cancer risks based on genomic sequence patterns around risk-associated loci. Binary cross entropy (Deng, 2012) was used as the loss function and the Adam algorithm (Kingma & Ba, 2015) was applied for optimization. Of the 20,000 samples in this study’s dataset, 70% were used to train the model and 30% were used to evaluate its performance. All hyperparameters were tuned using random grid search, a data analytics technique which trains copious models using randomly created hyperparameter combinations within user-specified ranges to extract the settings which yield the highest predictive accuracy. The model constructed in this study, named Sequence-based Polygenic Risk Network for GWAS SNPs (SPRiNGS), was implemented in Google Colab using the Keras platform in R because it allowed for free large-scale computation on a virtual machine.

## 2.7 Performance Evaluation

This experiment evaluated SPRiNGS with two metrics: Area Under the Receiver Operating Characteristics Curve (AUC) and normalized Matthews Correlation Coefficient (nMCC). In binary

classification problems, ROC Curves depict a model’s robustness by plotting the true positive classification rate against the false positive classification rate and calculating the area beneath the graph. Significant AUC values can range from [0.5, 1], where values tending toward 0.5 indicate poor classification ability while values closer to 1 indicate greater model performance.

Additionally, Matthews Correlation Coefficient (MCC) measures the model’s statistical accuracy in the context of its confusion matrix. This metric was used to assess the alignment between predicted risk classifications and actual risk classifications, ranging from [-1, 1]. nMCC is calculated by rescaling MCC values between [0, 1], where 0 indicates total misalignment, 0.5 indicates random alignment (as if the model was guessing), and 1 indicates total alignment amongst predicted and actual classes. Since AUC and nMCC depend on a model’s decision threshold, the threshold yielding the greatest accuracy was chosen prior to evaluation.

All code used for this study can be found here: <https://github.com/sivab468/SPRiNGS>.

## 3. Results

### 3.1 Simulation Validation

This research implemented Monte Carlo simulations to generate 20,000 samples whose breast cancer risks were dependent on their sequence composition. The validity of the simulation is examined based on whether this method extracts causal breast cancer variants, follows a normal PRS distribution, and associates higher PRS with greater chances of developing breast cancer. These criteria were found in “A Guide to Performing Polygenic Risk Score Analyses” (Choi, et al., 2020).

To assess whether causal breast cancer SNPs were extracted, all SNPs were graphed in a quantile-quantile (Q-Q) plot such that more significant SNPs would appear higher on the graph (Figure 2). Statistical significance was measured using  $-\log(p\text{-value})$  for ease of comparison. The black dots represent the observed data points and the blue line represents a normal distribution. While SNPs of lower significance somewhat align to the normal

distribution, the upward tail on the right indicates that the simulation used in this study extracted causal breast cancer variants amongst other mutations in the dataset.

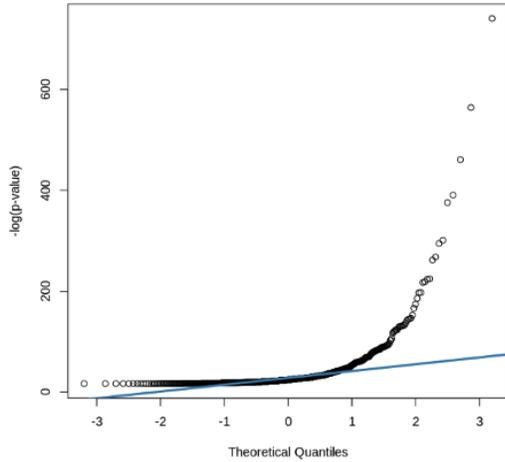


Figure 2. *Quantile-Quantile Plot of SNP Statistical Significance.* This graph depicts all SNPs in the dataset by their  $-\log(p\text{-value})$  such that more significant SNPs would appear higher on the graph. All points above the blue line represent causal breast cancer variants.

Next, this study analyzed the impact of PRS calculations on the breast cancer risk score distribution. Ideally, since risk scores are calculated as linear combinations of independent variables (SNPs), then standard PRS distributions should be normal (Choi, et al., 2020). To confirm the normality of the PRS distribution, a Q-Q plot of the breast cancer risk scores was created with the theoretical probability segments of a normal distribution on the x-axis and PRS on the y-axis (Figure 3). The black dots represent the observed risk scores and the red line represents a normal distribution. The more the data points align with the red line, the closer the distribution is to normal. This study quantifies the alignment between the PRS distribution and normal distribution using an R-squared value between [0, 1]. With R-squared = 0.99, this plot demonstrates this population's risk scores follow a near exact normal distribution.

The final measurement to validate this Monte Carlo simulation was to assess how breast cancer probabilities vary with PRS. Theoretically,

population strata with higher PRS are more likely to develop breast cancer since they have more SNPs (and therefore have a higher odds ratio for the disease). This research divided the population into 20 equal subgroups, calculated each sample's probability of developing breast cancer for each subgroup, and converted all probabilities into odds ratios of developing breast cancer. To better visualize the data, the  $\log(\text{Odds Ratios})$  were calculated (denoted as  $\Psi$ ) and plotted against PRS quantiles (Figure 4). Each point represents the mean  $\Psi$  for the population subgroup. The blue bars indicate the 95% confidence interval for each mean  $\Psi$ . The overall upward trend verifies that samples with higher PRS are more likely to develop breast cancer.

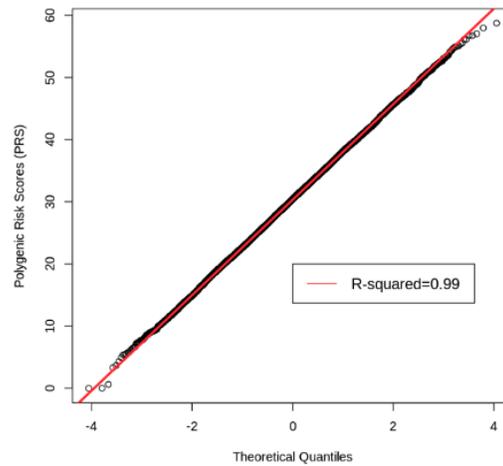


Figure 3. *Quantile-Quantile Plot of Breast Cancer Polygenic Risk Scores for Simulated Population.* This graph demonstrates the normality of the PRS distribution.

The three aforementioned figures confirm the validity of the Monte Carlo simulation presented in this experiment by extracting causal variants, observing a normal PRS distribution, and verifying the positive correlation between PRS and chances of developing breast cancer among the sample cohort.

### 3.2 Hyperparameters

This study consists of two hyperparameter categories: model-related and data-related. Model-related settings entail the various

hyperparameter combinations in SPRiNGS used during training and evaluation. Optimizing the model employed random grid search to sample 5% of all possible hyperparameter combinations and tune SPRiNGS with lower computational cost. The settings which minimized the loss value on the testing set were considered as the optimal hyperparameters. If more than one combination achieved the same minimum loss value, the combination which maximized the AUC value for the testing set was selected as optimal. All hyperparameters explored in SPRiNGS are summarized in Table 1 with the optimal settings bolded. All hyperparameters not explicitly mentioned remained at their default values.

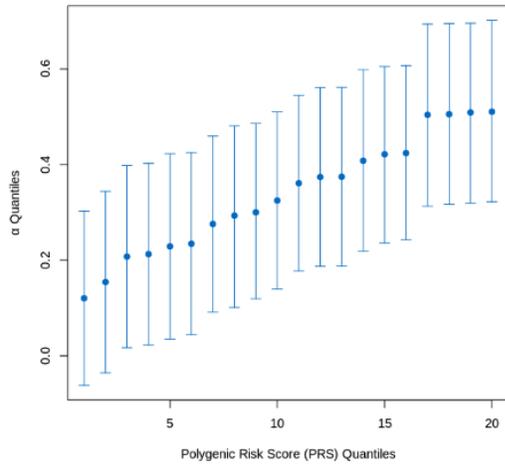


Figure 4. *Quantile-Quantile Plot of log(Odds Ratios) for Developing Breast Cancer across Stratified Polygenic Risk Scores.* This plot demonstrates the positive correlation between breast cancer PRS and the log(Odds Ratio) of developing breast cancer ( $\Psi$ ).

Previous SNP-based disease prediction studies demonstrate that including more polymorphisms in PRS calculations typically yield more robust results; however, this data characteristic has not been explored in sequence-based predictions. Moreover, the impact of the DNA context length on disease prediction remains unknown. Therefore, this research treated these values as data-related hyperparameters and discusses their impact below (see ‘Sensitivity Analysis’).

Table 1. *SPRiNGS Hyperparameter Combinations and Optimal Settings (bolded).* This table summarizes all settings considered when designing and tuning SPRiNGS. The settings which minimized the loss value on the testing set were selected as optimal (bolded).

Hyperparameter	Option
Convolution Filters 1	<b>32</b> , 64
Kernel 1 Length	3, 4, <b>5</b>
Kernel 1 Width	<b>3</b> , 4, 5
Convolution Filters 2	16, 32, <b>64</b>
Kernel 2 Length	<b>3</b> , 4
Kernel 2 Width	<b>3</b> , 4
Dense Nodes 1	<b>16</b> , 32
Dense Nodes 2	4, 8, <b>16</b>
Optimizer	<b>Adam</b> , RMSprop

### 3.3 SPRiNGS Performance Evaluation

To evaluate the impact of incorporating genomic sequence contexts into SNP-based predictions, this study developed two control models which only analyze the SNP composition across the sample cohort: a classical machine learning model (SVM\_RBF) and a deep learning model (1D CNN). SPRiNGS, on the other hand, analyzed the sequence composition of the simulated population. The ROC Curves for each model were plotted to compare the robustness of their predictions (Figure 5). SPRiNGS achieved the highest AUC at 0.91, while SVM\_RBF and 1D CNN followed at 0.88 and 0.84, respectively. This elucidates that the sequence-based model developed in this study extracted underlying semantic patterns and significant SNP-SNP interactions associated with breast cancer better than traditional SNP-based methods.

This study also measures the nMCC to discern the holistic statistical accuracy of each model in the context of its confusion matrix. nMCC values were calculated and plotted for their corresponding model (Figure 6). All models achieved significant nMCC scores, indicating that each applied its learned patterns to effective sample classification. However, SPRiNGS achieved the highest nMCC at 0.82, while SVM\_RBF and 1D CNN followed at 0.78 and 0.73, respectively. This demonstrates that incorporating the local DNA fragments into breast cancer predictions

improves their overall predictive accuracy compared to SNP-based methods.

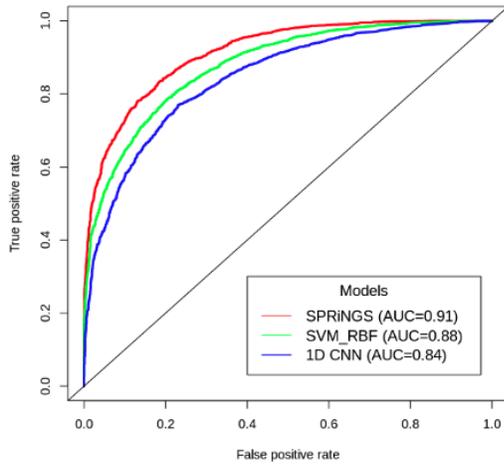


Figure 5. *ROC Curves for Breast Cancer Classification Models.* This graph demonstrates the robustness of breast cancer classifications achieved by SPRiNGS (red), SVM\_RBF (green), and 1D CNN (blue) using AUC.

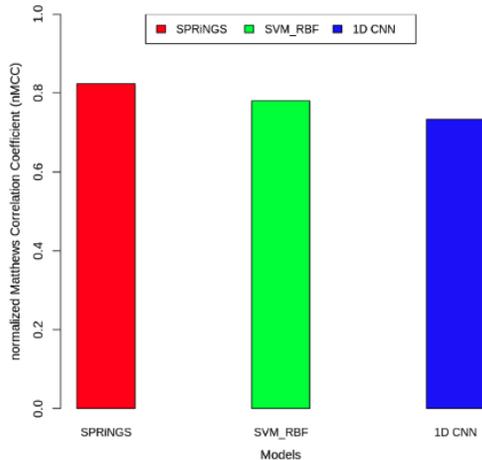


Figure 6. *nMCC Comparisons across Breast Cancer Classification Models.* This bar graph depicts the statistical accuracy of breast cancer classifications achieved by SPRiNGS (red), SVM\_RBF (green), and 1D CNN (blue) using nMCC.

### 3.4 Sensitivity Analysis

This research conducted a sensitivity analysis to explore the impact of data-related characteristics (the number of SNPs  $s$  and the sequence length  $L$ ) on

SPRiNGS' performance. Changing the number of loci considered allows the model to discern genomic patterns across more sequences. To vary  $s$ , the  $p$ -value threshold was relaxed, yielding 904 SNPs ( $\alpha = 5 \times 10^{-7}$ ). Additionally, the threshold was tightened, yielding 547 SNPs (to  $\alpha = 5 \times 10^{-9}$ ). AUC was measured for each variation and plotted (Figure 7). Considering fewer SNPs displayed a slightly lower AUC; however, including more SNPs caused a significant decrease in AUC, likely attributable to overfitting.

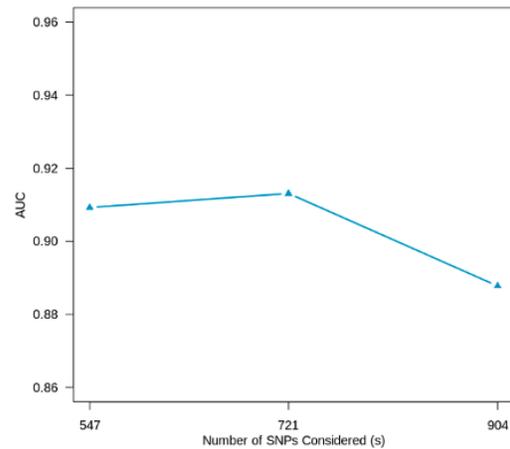


Figure 7. *Impact of number of SNPs ( $s$ ) on SPRiNGS performance.* This line graph displays the impact of the number of SNPs considered (which was varied by the  $p$ -value threshold  $\alpha$ ) on SPRiNGS AUC score.

Moreover, this study examined the effect of sequence length  $L$  on the model's performance using short DNA sequence fragments. Increasing  $L$  would allow the model to identify more encoding patterns within sequences to distinguish between case and control samples. This analysis varied  $L$  between 13, 37, and 61 nucleotides. Sequences shorter than 13 nucleotides were not explored to ensure minimal genomic encoding motifs were captured during model training. Sequence lengths larger than 61 nucleotides were not explored due to computational storage constraints. The AUC was plotted to understand the impact of each  $L$  variation on model performance (Figure 8). While showing fairly consistent performance overall, the fragment length  $L = 37$  displayed the highest AUC. The overall trend of the graph shows no significant correlation between model performance and sequence length.

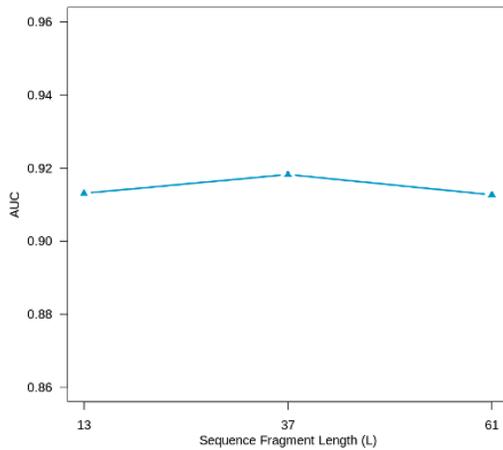


Figure 8. *Impact of sequence fragment length ( $L$ ) on SPRiNGS performance.* This line graph displays the impact of the DNA sequence fragment length on SPRiNGS AUC score and shows that no significant correlation was observed between the two.

#### 4. Discussion

This research proposes SPRiNGS, a two-dimensional convolutional neural network which analyzes genomic sequence patterns around statistically significant SNPs to classify breast cancer risks. After validating the Monte Carlo simulation used to generate a sample population, the results indicate that sequence-based breast cancer predictions outperformed SNP-based methods. Specifically, incorporating the sequence contexts of breast cancer-associated SNPs improved feature extraction and robustness (measured by AUC) and classification accuracy (measured by nMCC) compared to traditional SNP-based algorithms (such as SVM\_RBF and 1D CNN). SPRiNGS analyzed the occurrence patterns and genomic interactions among significant mutations while the control models only analyzed the former. Since SPRiNGS associated higher polygenic risk scores with greater chances of developing breast cancer (as seen in Figure 4), the model discerned how SNP occurrence patterns impact genetic breast cancer risks. Moreover, incorporating DNA sequence contexts around each SNP allowed SPRiNGS to understand various encoded semantic patterns across mutations, which improved robustness and accuracy compared to

SNP-based methods. These findings confirm the hypothesis that analyzing the local genomic fragments around statistically significant mutations will improve the quality of breast cancer predictions compared to SNP-based methods.

This study also explores the impact of data-related hyperparameters on SPRiNGS' performance. While previous genome-wide prediction studies have demonstrated that including more SNPs for PRS calculations improves predictive accuracy (Antoniou, et al., 2018; Hajiloo, et al., 2013; Lee, et al., 2019; Cecile, et al., 2019), this research observed the inverse. Decreasing the number of SNPs elicited a slight decrease in AUC; however, increasing the number of SNPs noticeably lowered the model's performance. Since tightening the  $p$ -value threshold yielded fewer SNPs, SPRiNGS learned more influential semantic patterns across more statistically significant mutations. Inversely, since relaxing the threshold yielded more SNPs, less significant mutations likely contributed to noise around otherwise important semantic features during matrix resizing. Adding more mutations to consider caused the model to overfit, thereby achieving a lower AUC.

The other data-related characteristic explored was the sequence length  $L$ . As previously mentioned, SPRiNGS (which performed sequence-based classifications) outperformed SVM\_RBF and 1D CNN (which performed SNP-based classifications), indicating that analyzing sequence contexts improves classification robustness and accuracy. The sensitivity analysis isolated the sequence length to measure its impact on model performance. SPRiNGS performed relatively consistently across all tested fragment lengths, but observed the highest AUC when  $L = 37$  nucleotides. This sequence length likely captured significant sequence motifs which elicited better predictions. While decreasing  $L$  did not capture these semantic features, increasing  $L$  incorporated more information as noise when the matrices were resized, thereby leading to slightly lower performance. Although no significant correlation was observed between  $L$  and model performance, this study demonstrates the importance of analyzing the local DNA sequence contexts around statistically significant SNPs in genome-wide breast cancer prediction studies.

#### 4.1 Limitations

This experiment contained plenty of limitations to consider. First, the Keras platform used to implement SPRiNGS prevents users from seeing the algorithm's inner workings, meaning that more research is required to understand which particular genomic features helped SPRiNGS outperform the SNP-based control models. Second, breast cancer has several molecular subtypes which this model did not account for; SPRiNGS simply determined whether a sample was healthy or at risk of breast cancer, but not which type of breast cancer. One method to overcome this limitation is by using a larger sample size with subgroups for each molecular subtype. Third, there are other genetic mutations associated with breast cancer besides SNPs. Including other mutation types (insertion, deletion, and genetic amplification) would provide a more holistic mutation-based prediction. Fourth, while the simulation in this study met the previous validation criteria, it does not account for genetic variations among global populations. This means sequence-based SNP interactions could fluctuate depending on geographic regions, causing changes in SNP statistical significance and allele frequencies. Exploring other simulations to understand how SPRiNGS' performance varies based on population-specific parameters would offer greater insights into the global variations of genetic breast cancer risks caused by dynamic sequence-based SNP interactions.

#### 4.2 Future Work

The results of this study inspire further inquiry into the biological application of genomic sequence interactions in disease prediction. The model developed here, SPRiNGS, can be generalized to predict other common complex diseases, including cardiovascular, immune, and respiratory traits alongside other cancer types. Also, as mentioned earlier, SPRiNGS can be used to subtype various diseases based on their genomic and biological features. After analyzing the semantic patterns associated with copious genetic diseases, future research could explore the biological implications of these sequence-based interactions in protein binding,

transcription factor motif identification, and gene regulation. In clinical settings, medical professionals can use SPRiNGS to recommend therapeutic action depending on a patient's risk classification for a certain disease. This study has identified a link between sequence contexts and breast cancer predictions; future research should explore how these semantic interactions impact an individual's biological susceptibility to this disease and others.

#### 5. Conclusion

Ultimately, this research confirms the hypothesis that analyzing the local DNA sequence around statistically significant mutations will improve the quality of breast cancer risk classifications compared to SNP-based methods. SPRiNGS outperformed the SNP-based control models in both robustness and statistical accuracy. Moreover, an exploration of data-related characteristics revealed that including more SNPs decreased predictive accuracy (contrary to previous literature) and that the sequence fragment length has no significant correlation with model performance. While more research is required to understand the genomic features responsible for SPRiNGS' improved performance, this model holds exciting potential for precision medicine. Hopefully, as our knowledge of high-throughput sequencing and disease prediction mechanisms grow, so too will our ability to promote human health and longevity.

#### References

- Adekitan, A. I. (2014). *Monte Carlo Simulation*. University of Idaban.
- Antoniou, A. C., et al. (2019). Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, 104(1), 21-34. doi:10.1016/j.ajhg.2018.11.002
- Beck, T., et al. (2020). GWAS Central: a comprehensive resource for the discovery and comparison of genotype and phenotype data from genome-wide association studies. *Nucleic Acids Research*, 48(D1), D40-D933. Retrieved from <https://doi.org/10.1093/nar/gkz895>

- Buniello, A., et al. (2019). The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. *Nucleic Acids Research*, Vol. 47 (Database issue): D1005-D1012. <https://doi.org/10.1186/1471-2105-14-S13-S3>
- Cariaso, M., & Lennon, G. (2012). SNPedia: a wiki supporting personal genome annotation, interpretation and analysis. *Nucleic Acids Research*, 40 (Database issue), D1308–D1312. <https://doi.org/10.1093/nar/gkr798>
- CDC. (2020). *Breast Cancer Statistics*. <https://www.cdc.gov/cancer/breast/statistics/index.htm>
- Cecile, A., et al. (2019). Polygenic risk scores that predict common diseases using millions of single nucleotide polymorphisms: Is More, better? *Clinical Chemistry*, 65(5), 609-611. doi:10.1373/clinchem.2018.296103
- Cerami, E., et al. (2012). The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. *Cancer Discovery*, 2(5), 401-404. doi:10.1158/2159-8290.CD-12-0095
- Choi, S. W., et al. (2020). Tutorial: A guide to performing polygenic risk score analyses. *Nature Protocols*, 15(9), 2759-2772. doi:10.1038/s41596-020-0353-1
- Deng, L. (2012). The Cross-Entropy Method: A Unified Approach to Combinatorial Optimization, Monte-Carlo Simulation, and Machine Learning. *Technometrics*, 48(1), 147-148. <https://doi.org/10.1198/tech.2006.s353>
- Fadista, J., et al. (2016). The (in)famous GWAS P-value threshold revisited and updated for low-frequency variants. *Eur J Hum Genet*, 24, 1202–1205. <https://doi.org/10.1038/ejhg.2015.269>
- Hajiloo, M., et al. (2013). Breast cancer prediction using genome wide single nucleotide polymorphism data. *BMC Bioinformatics*, 14, S3. <https://doi.org/10.1038/ejhg.2015.269>
- Indolia, S., et al. (2018). Conceptual Understanding of Convolutional Neural Network- A Deep Learning Approach. *Procedia Computer Science*, 132, 679-688. <https://doi.org/10.1016/j.procs.2018.05.069>
- Kingma, D. P., & Ba, J. L. (Eds.). (2015). *Adam: A Method for Stochastic Optimization*. ICLR. <https://arxiv.org/pdf/1412.6980.pdf>
- Kuleshov, V., et al. (2019). A machine-compiled database of genome-wide association studies. *Nat Commun*, 10, 3341. <https://doi.org/10.1038/s41467-019-11026-x>
- Lee, A., et al. (2019). BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. *Genet Med*, 21, 1708–1718. <https://doi.org/10.1038/s41436-018-0406-9>
- Quezada, H., et al. (2017). Omics-based biomarkers: Current status and potential use in the clinic. *Boletín Médico Del Hospital Infantil De México (English Edition)*, 74(3), 219-226. doi:10.1016/j.bmhime.2017.11.030
- Quinlan, A. R., & Hall, I. M. (2010). BEDTools: a flexible suite of utilities for comparing genomic features. *Bioinformatics (Oxford, England)*, 26(6), 841-842. <https://doi.org/10.1093/bioinformatics/btq033>
- Reference genome*. (2020, Dec 25). Wikipedia. Retrieved January 27, 2021, from [https://en.wikipedia.org/wiki/Reference\\_genome](https://en.wikipedia.org/wiki/Reference_genome)
- Schneider, V. A., et al. (2017). Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. *Genome Research*, 2017(27), 849-864. doi:10.1101/gr.213611.116
- Sherry, S. T., et al. (2001). dbSNP: the NCBI database of genetic variation. *Nucleic Acids Research*, 29(1), 308-311. <https://doi.org/10.1093/nar/29.1.308>

Wen, J., et al. (2019). A classification model for lncRNA and mRNA based on k-mers and a convolutional neural network. *BMC Bioinformatics*, 20, 469. <https://doi.org/10.1186/s12859-019-3039-3>

Wu, T., et al. (2021). DeepDist: real-value inter-residue distance prediction with deep residual convolutional network. *BMC Bioinformatics*, 22, 30. <https://doi.org/10.1186/s12859-021-03960-9>

*U.S. Breast Cancer Statistics*. (2021, February 4). BREASTCANCER.ORG. Retrieved April 14, 2021, from [https://www.breastcancer.org/symptoms/understand\\_bc/statistics#:~:text=About%20in%208%20U.S.,\(in%20situ\)%20breast%20cancer](https://www.breastcancer.org/symptoms/understand_bc/statistics#:~:text=About%20in%208%20U.S.,(in%20situ)%20breast%20cancer)

Yamashita, R., et al. (2018). Convolutional neural networks: an overview and application in radiology. *Insights Imaging*, 9, 611–629. <https://doi.org/10.1007/s13244-018-0639-9>

## Fibonacci Numbers in the Number of Seeds and Carpels of Rosaceae and Rutaceae Fruits

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### Abstract

The Fibonacci Sequence is a sequence of numbers that has been observed greatly in nature. One aspect of the Fibonacci Sequence and nature that has been studied minimally is with fruits. Thus, the research question that guided this study is: what trends can be seen in the relationship between the numbers of the Fibonacci Sequence without any manipulation and numerical values including the number of seeds and the number of carpels present in Rutaceae and Rosaceae fruits? The goal of this study was to examine how much of a relationship there is between the Fibonacci numbers and fruits. The method of descriptive research was used to describe the naturally occurring phenomenon. The number of seeds and the number of carpels from 140 fruits were recorded; there were 7 types of fruits from each of the two fruit families and 10 pieces of each fruit. The data was then analyzed to find the percentage of numbers that were Fibonacci numbers. The major conclusion is that Fibonacci numbers tend to be more present in the number of seeds and carpels of Rosaceae fruits when compared to Rutaceae fruits.

*Keywords: Fibonacci Sequence, Fruit, Carpels, Seeds, Rutaceae, Rosaceae*

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### 1. Introduction

Leonardo Bigollo Pisano, also known as Fibonacci, was a mathematician during the late 12th and early 13th centuries. His most famous work includes his book, *Liber Abaci*, which translates to the Book of Calculation. In this book, Fibonacci discusses the answer to a theoretical math question that he created (Gies, 2021). The theoretical situation reads, “[a] certain man had one pair of rabbits together in a certain enclosed place, and one wishes to know how many are created from the pair in one year when it is the nature of them in a single month to bear another pair, and in the second month those born to bear also” (Sigler, 2003). His solution to this

question was the sequence of numbers now known as the Fibonacci Sequence. This sequence is recursive, and a term of the sequence is found by adding the two previous terms. It follows the pattern 0,1,1,2,3,5,8,13,21 and continues infinitely.

The applications of the Fibonacci Sequence have been discovered in a wide variety of fields with the most prominent being in nature. One example of the sequence in nature is that the number of petals on a flower tends to be a number of the Fibonacci Sequence. Sudipta Sinha (2017), from the Department of Mathematics at Burdwan Raj College, finds that lilies and irises have 3 petals while delphiniums have 8 petals. Both of these numbers are Fibonacci numbers. The sequence is also found in the

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number of spirals in pinecones and even in the lengths of the bones in the human finger.

One application of the Fibonacci Sequence that has not been studied to the extent that it has in other fields is in fruits. There has been some evidence of the Fibonacci numbers in fruits, but the research is very limited and broad. Some of the surface level evidence includes the fact that apples have five sections which is a Fibonacci number and bananas have three sections which is also a Fibonacci number (Allen, 2018). Aside from this basic evidence of the Fibonacci Sequence in fruits there are a few scholarly studies that expand upon these ideas. Dr. Grzegorz Skorny and Jakub Śledziowski (2015) from the University of Technology and Economics in Szczecin conducted research on the presence of Fibonacci numbers in the symmetry of selected fruits. They used “[t]he method of visual and theoretical analysis” to complete their research and came to the conclusion that “Fibonacci numbers in botany are interpreted in fruit cross-sections of various fruits” and that in some fruits the multiples of Fibonacci numbers can be observed. They ultimately did find some evidence of the Fibonacci numbers in fruits however their research is very broad since they do not explain any connections or trends. They also focus on random fruits and the multiples of Fibonacci numbers as opposed to the original numbers of the sequence. This does not make their research any less accurate or reliable since they did find evidence of the numbers in a broader sense. Other researchers have looked more in depth into this topic by focusing on one specific fruit. For instance, both Judithlyne Carson and Paul C. Erken examined the phyllotaxy of the pineapple fruit and plant. Ekern (1968), in his article for the *Botanical Gazette* published by the University of Chicago press, discovered that the “ratio between the number of turns about the plant axis and the number of leaves between two leaves superimposed in the vertical” in pineapple plants were values of the Fibonacci Sequence. Specifically, he found that Cayenne Pineapples have a phyllotaxy of 13/34; both of these numbers are Fibonacci numbers. His research proves that different varieties of pineapples have phyllotaxies that consist of Fibonacci numbers. Carson (1978) conducted similar research and found that the number of hexagons on the outside of

different types of pineapples are also Fibonacci numbers. She goes further, however, and gives some potential reasons for why these numbers could be present in pineapples and the outside factors that could have contributed to the variation she discovered. She explains that “[t]he *Ananas* genus grows in an area of wide geographic distribution on the South American continent, in altitudes ranging from sea level to 6000 feet, and from conditions of semi-aridity to hot, humid forests” (Carson, 1978). This wide variety of factors is a potential reason why different pineapples have different phyllotaxies, but it does not change the fact that the majority had numbers of the Fibonacci Sequence.

Beata Zagórska-Marek from Wroclaw University, Institute of Botany conducted similar research on the phyllotaxy of magnolia fruits. Zagórska-Marek (1994) found that certain types of magnolia fruits have phyllotaxis values such as 5:8 and 8:13 that contain Fibonacci numbers. Instead of simply identifying these values like Carson and Ekern did, Zagórska-Marek goes even further and examines the frequency at which the Fibonacci number appear in the phyllotaxy of the different magnolia fruits. She concluded that “most magnolia fruits show the Fibonacci pattern in their carpel arrangements about 75% of the time” (Figlar, 2002; Zagórska-Marek, 1994).

From these examples, it is clear that there is some relationship between Fibonacci numbers and different types of fruits. However, the research conducted has focused mainly on the phyllotaxy of the plants that the fruits come from as opposed to the fruits themselves. The research has also either examined a random selection of fruits or focused on one specific fruit; no research has been conducted examining different categories of fruits or comparing them. This is one of the major gaps in this topic of study because there has been very little research conducted related to the trends that can be seen in the relationship between the numbers of the Fibonacci Sequence and numerical values present in the fruits themselves.

In order to examine trends, specific groups of fruits must be selected so that connections and comparisons can be made. There are a variety of different ways in which fruits are categorized including “kingdom, division, class, subclass, order,

family, genus, species, variety, cultivar, and strain” (International Agency et. al., 2003). Two specific families of fruit that are extremely popular in the United States are Rosaceae and Rutaceae. Rosaceae is the rose family and some of the common fruits that fall under this category are apples, apricots, and pears; Rutaceae, on the other hand, is the rue family and consists of fruits like lemons, limes, and oranges (International Agency et. al., 2003). Within a fruit, there are many different numerical values that can be calculated, including the number of seeds and carpels. Seeds can be defined as “the structures containing the embryo plant for the next generation” (Rost, 2006). Their structure and appearance vary drastically based on what plant they are coming from. The number of seeds in a fruit depends on the number of carpels; a carpel is “the structure which includes both the ovary and its associated ovule(s) in a flower” (Seed & Fruit Development, n.d). These carpels fuse when fruit grow and therefore can be seen in fruit as well. They hold seeds which is why the number of seeds depends on the number of carpels (Rost, 2006). Both of these values can be easily identified and measured without any equipment necessary.

The question that comes up when discussing this topic is: what trends can be seen in the relationship between the numbers of the Fibonacci Sequence without any manipulation and numerical values including the number of seeds and the number of carpels present in Rutaceae and Rosaceae fruits? This question guided the research conducted in this study. As explained, there is very broad evidence of the Fibonacci numbers in fruits and there have not been any connections made between the different types of fruits and their relationship to the sequence. The reason Rosaceae and Rutaceae fruits were chose specifically was because they were the most accessible fruits and most popular fruits in the United States. None of the existing research has studied the number of seeds and very minimal research has examined the number of carpels in relation to the Fibonacci Sequence. Most of the research has instead focused on phyllotaxy. The purpose of the research that was conducted in this study was to identify any trends in the relationship and understand the extent to which the Fibonacci Sequence and the number of

seeds and carpels are connected. The results of the experiment will help to identify what trends are present and determine whether or not there is a connection between these fruits and the Fibonacci Sequence. The original hypothesis is that there will be a greater relationship between the number of carpels and Fibonacci numbers when compared to the number of seeds. This is speculated because carpels are a more structured component of fruits with less variation than seeds.

## **2. Materials and Methods**

Researchers who conducted similar research on the applications of Fibonacci numbers used a wide variety of methods, however the method used for the purpose of this study was descriptive research. Descriptive research “is defined as a research method that describes the characteristics of the population or phenomenon studied” (Descriptive Research, 2021). The research conducted in this study focused on describing the naturally occurring relationship between the Fibonacci Sequence and fruits which is why this method was the best option. This research was also quantitative which provided the numerical evidence that was lacking in the previous studies in the field. The analysis of the data was accomplished using descriptive statistics. Descriptive statistics ensures that the data is not altered so much that it is no longer relevant while also ensuring that the data can be described properly. Since the purpose of the study was to describe this natural phenomenon, using descriptive research to analyze the data allowed for the data to be presented without too much alteration. Using this method of descriptive research and descriptive statistics will answer the research question by providing the trends and relationships between the two variables. Mirroring how Zagórska-Marek analyzed her data in her study, the research conducted in this study will provide what percentage of the times the trends occurred. The limitation of this method, however, is that it will not explain why such trends occur but instead simply identify them. For the time frame and purpose of this study, explaining the reason why these trends occurred was simply not feasible and would require much more time and higher knowledge of the subject.

This is something that can be researched in the future, though, to provide an explanation as to why the trends discovered in this study exist.

### 2.1 Sample

A wide variety of fruits were used in this study because having a large sample allows for more connections to be made and for the results to be more accurate. The two fruit families that were used in the research were Rosaceae and Rutaceae. These specific families were chosen because they are the most popular in the United States and the fruits that come from these families are easily accessible. Seven fruits were then selected from each family so that there would be enough data to analyze and find connections. The seven Rosaceae fruits that were selected included peaches, Fuji apples, Granny Smith apples, Honey Crisp apples, Gala apples, pears, and cherries. The seven Rutaceae fruits that were selected included lemons, limes, Navel oranges, Cara Cara oranges, grapefruits, tangelos, and mandarin oranges. These specific fourteen fruits were chosen based on local availability and accessibility. Some fruits such as kumquats and loquats are not easily accessible and therefore were not included in the research. This, however, is a potential limitation of the study as certain fruits were excluded. Future research could be conducted including those fruits which were not included in this study. Furthermore, ten pieces of each of these fourteen fruits were examined leading to a total of 140 fruits. The reason why ten pieces of each fruit were used in the research is so that the data is as accurate as possible; by having multiple pieces of the same fruit, it allows for any potential variances or outliers in the data to be accounted for. It also provides enough data for the percentages to be calculated. Most existing research in the field did not include this repetitive data collection component making their results more general. In order for the results of this study to be detailed and applicable, multiple pieces of each fruit were used.

### 2.2 Data Collection

The data that was collected using these 140 pieces of fruit was the number of the seeds and the number

of carpels. First, the number of carpels was collected by cutting the fruit so that the cross section shows all the carpels. For instance, in Figure 1, a Gala apple is cut so that its cross section shows the five carpels that are present. If the number of carpels was unclear because they were not fully formed or if they were merged with other sections, then the number of carpels that were clear was recorded.

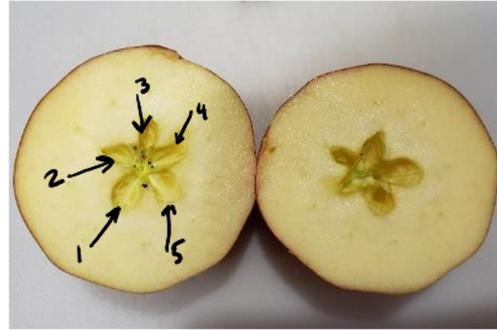


Figure 1. Cross-section of Gala Apple.



Figure 2. Navel Orange with Unclear Carpels.

As seen in Figure 2, the carpel that is outlined in blue was not included in the total count because it was not a distinct carpel. Since it does not reach all the way to the peel of the orange, it was excluded from the data. Therefore, that Navel Orange had 10 carpels. Next, the number of seeds per fruit was collected by simply removing the seeds from each piece of fruit and counting them. This data was also recorded so that it could be analyzed later. Seeds that were not fully developed were not counted in the data. This included seeds that were flat or those that were significantly smaller than other seeds in the same piece of fruit. If these seeds had been included in the data, the results could have been exaggerated. These seeds are not fully developed and therefore do

not qualify as a seed that should be counted for the purpose of this study. These steps were then repeated for each of the 140 pieces of fruit.

### 2.3 Data Analysis

Once all the data was collected, it was analyzed. The first step was to calculate the percentage of fruit whose number of seeds were Fibonacci numbers. This was done by dividing the number of data points that were a Fibonacci number by the total number of data points which was ten. Since ten pieces of each fruit were used, there were ten total data points for the number of seeds. This was then repeated for each of the 14 types of fruits. Next, the percentage of fruit whose number of carpels were Fibonacci numbers was calculated and repeated for each of the 14 different fruits using the same method as previously but instead with the data points for the carpels (see Appendix A for all data points). Although 0 is technically a Fibonacci number, for the purposes of this study 0 was not considered a Fibonacci number because this would skew the results. Since 0 was a commonly occurring number in the data, if it were considered a Fibonacci number then it would seem like there was a greater relationship when in reality there was not. The next calculation that was made was finding the percentage of fruits within each family whose number of seeds were Fibonacci numbers. Then, the percentage of fruits within each family whose number of carpels were Fibonacci numbers was calculated. These percentages were calculated using the same method as earlier but this time with all the fruits in each family as opposed to the individual fruits. These percentages provided the trends between Fibonacci numbers and fruits and thus answered the research question. A trend was considered significant if it had a percentage that was greater than 40%. This specific percentage was chosen because there was a 40% chance that a number from the data set was a Fibonacci number. This number was calculated by finding the probability that a number in the data set was a Fibonacci number. The highest and lowest numbers in the data were identified and then the probability that one of those numbers was a Fibonacci number was calculated.

### 3. Results

There were many trends that were identified upon completion of this study; some of which supported the original hypothesis and others which did not. First, the results of the Rosaceae fruits will be discussed. 100% of Rosaceae fruit used in this study had carpels that added up to Fibonacci numbers which means in each of 70 Rosaceae fruits examined, the number of carpels was a Fibonacci number. Furthermore, in 65.71% of the Rosaceae fruits, the number of seeds was a Fibonacci number. Some fruits, however, had much higher percentages while others had much lower ones; 100% of the peaches and cherries, for instance, had a number of seeds that added up to a Fibonacci number while only 20% of Fuji apples had the same; this can be seen in Figure 3 along with the percentages from the rest of the Rosaceae fruits. This percentage (65.71%) is an average of all the Rosaceae fruits and is considered significant because it is higher than 40%. As explained in the previous section, any percentage greater than 40% is considered significant. While the Rosaceae fruits had significant correlation with the Fibonacci numbers (100% & 65.71%), the Rutaceae fruits had a much less drastic relationship.

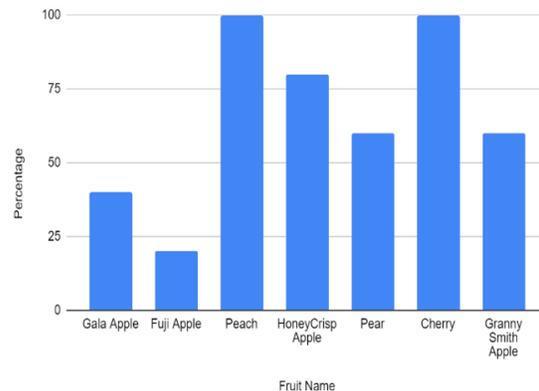


Figure 3. The Percentage of Rosaceae Fruits Whose Number of Seeds Added Up to a Fibonacci Number.

In only 21.43% of Rutaceae fruits, the number of seeds was a Fibonacci number; similarly, in only 18.57% of Rutaceae fruits, the number of carpels was a Fibonacci number. This shows a clear trend when comparing the two fruit families: Fibonacci numbers tend to be more present in the number of seeds and

carpels of Rosaceae fruits in comparison to Rutaceae fruits. Figures 3 and 4 clearly show this distinction in the number of seeds; the blue represents Rosaceae fruits while the orange represents Rutaceae fruits. It is clear that the Rosaceae fruits have much higher percentages than the Rutaceae fruits do showing that Fibonacci numbers are more present in the number of seeds of Rosaceae fruits.

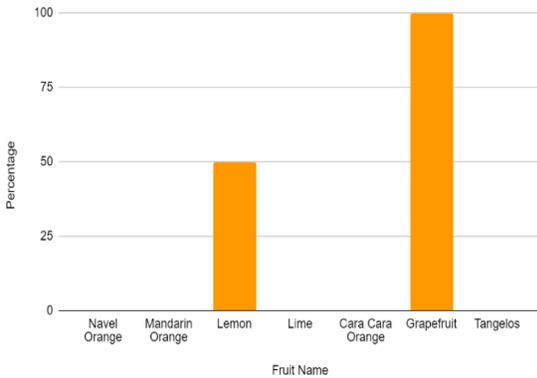


Figure 4. The Percentage of Rutaceae Fruits Whose Number of Seeds Added Up to a Fibonacci Number

Figures 5 and 6 show the drastic difference between Rosaceae and Rutaceae fruits in regard to the number of carpels. It is clear that the Fibonacci numbers are more present in the number of carpels of Rosaceae fruits than they are in the Rutaceae fruits. Thus, the major trend that can be seen when comparing the two families is that Fibonacci numbers tend to be more present in the number of seeds and carpels of Rosaceae fruits in comparison to Rutaceae fruits.

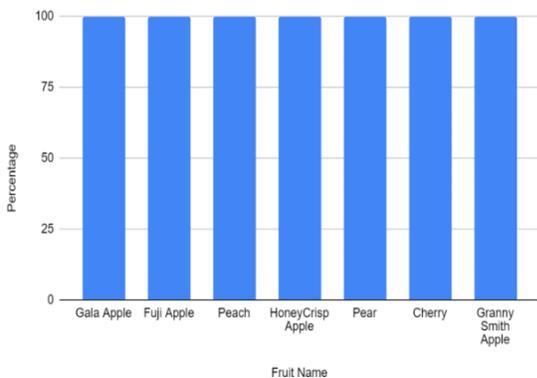


Figure 5. The Rosaceae Fruits Whose Number of Carpels Added Up to a Fibonacci Numbers

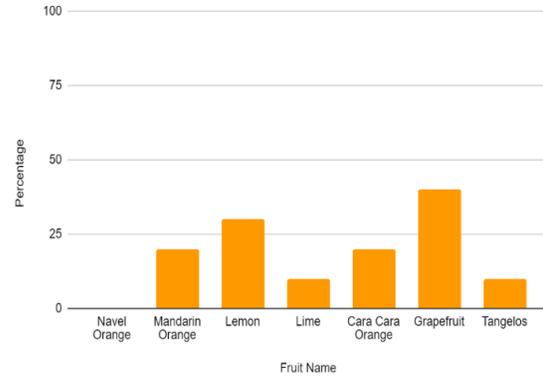


Figure 6. The Percentage of Rutaceae Fruits Whose Number of Carpels Added Up to a Fibonacci Number

#### 4. Discussion

While there were trends when comparing the two different fruit families, there were also some trends and conclusions that could be made when comparing fruits within a family. Within the Rosaceae family, for instance, there was much more variation with the percentages when looking at the number of seeds as opposed to when looking at the number of carpels. One of the most significant trends in the Rosaceae family is that in 100% of Rosaceae fruits, the number of carpels was a Fibonacci number. There were not any significant trends like this in the Rutaceae family, however there were some outlying percentages. In most of the Rutaceae fruits, the number of seeds was not a Fibonacci number. Most of the percentages were 0%, however 100% of the grapefruits had seeds that added up to a Fibonacci number and 50% of the lemons had seeds that also added up to a Fibonacci number (as seen in Figure 4). This is drastically different than the rest of the Rutaceae fruits. Besides these conclusions, most of the data was extremely varied and no additional trends could be identified.

The key finding of this study is that Fibonacci numbers tend to be more present in the number of seeds and carpels of Rosaceae fruits in comparison to Rutaceae fruits. The purpose of this study was to examine what trends occur in the relationship between Fibonacci numbers and these selected fruits. The results of this study prove that while there are some patterns that can be seen, there are also lots of variances in the data. The major trend that was discovered supports the idea that the presence of

Fibonacci numbers in fruits and more generally in nature is purposeful. However, the drastic variances that were seen in the data also support the opposite: that the presence of Fibonacci numbers in fruits and nature is a coincidence and there is no pattern.

#### 4.1 Limitations & Future Research

There are some limitations, however, with the research that was conducted. Only 14 fruits were examined which is just a fraction of the possible fruits to be studied. Also, only 10 pieces of each fruit were used; this is a potential idea for future research. Future research could be conducted to see whether the trend discovered in this study applies to other categories of fruit and other fruit families. Future research could also include a larger sample size to ensure that the trends are valid and are consistently present. This would help to better understand the presence of the Fibonacci numbers in nature as well as to identify whether the relationship is simply coincidental or if it is reoccurring. Researchers could use more than 10 pieces of each fruit to make sure the trends they find are more accurate. They could also use more than 14 types of fruits. Another limitation of this study is that it does not explain why these trends occur; this is a limitation of the method because it only identifies the trends. For the purpose of this study, explaining why the trends occurred was not feasible or necessary. Future research, however, could attempt to explain why the conclusions of this study exist and what factors impact the presence of Fibonacci numbers in fruits. This is important to study because it would help explain why the Fibonacci Sequence is present and nature as well as because it would open up a whole new field of study that could have real-life implications.

#### 5. Conclusion

Despite these limitations, there are many implications of this study. For instance, the results of the study reflect the overall complexity of the topic. While the conclusion supports the idea that Fibonacci numbers are present in nature, the variances in the data support the idea that this

relationship is coincidental. There has been no definitive conclusion made yet on why these numbers appear in nature. One of the major theories is that of optimization. Cristina Olimpia (2008) from the University of Agricultural Sciences and Veterinary Medicine in Romania explains that “the reason for this arrangement forms seems to be an optimal packing to obtain an maximum efficiency.” This theory that nature follows the pattern of the Fibonacci Sequence to achieve optimal sunlight and optimal growth could potentially explain the results found in this study. The Fibonacci numbers could have been present in the Rosaceae fruits in order to optimize the number of seeds for further growth. However, as Dan Reich from Temple University explains “almost any reasonable arrangement of leaves has the same sunlight-gathering capability” which disproves Olimpia’s claim. Despite this, the results of this study could be used in the future to help create a new idea for why Fibonacci numbers are present in nature. Moving away from why the Fibonacci Sequence is present in nature since that has not yet been thoroughly identified, there are other reasons why the trends discovered in this study are important. Since nature is full of patterns, by understanding these patterns it helps to understand how nature develops. Having a better understanding of how fruits develop as well as what patterns are present can lead to a greater understanding of nature itself. These conclusions address a topic that has been studied minimally, but also supports similar existing conclusions. Skorny and Śledziowski, Carson, Ekern, and Zagórska-Marek all concluded, in some manner, that Fibonacci numbers are present in certain fruits, but not all fruits. The research conducted in this study supports this claim. However, many new questions are presented from these conclusions with the biggest one being why the Rosaceae fruits had a larger correlation to the Fibonacci Sequence than the Rutaceae fruits did. Since the gap in the field of study was addressed, the present research contributes to a growing body of knowledge surrounding the presence of the Fibonacci Sequence in nature.

**References**

Allen, S. (2019). *Master Fibonacci: The Man Who Changed Math*. Fibonacci Inc. Carson, J. (1978). Fibonacci Numbers and Pineapple Phyllotaxy. *The Two-Year College Mathematics Journal*, 9(3), 132-136. doi:10.2307/3026682

*Descriptive Research: Definition, Characteristics, Methods, Examples and Advantages*. QuestionPro. (2021, April 20). <https://www.questionpro.com/blog/descriptive-research/>

Ekern, P. (1968). Phyllotaxy of Pineapple Plant and Fruit. *Botanical Gazette*, 129(1), 92-94.

Figlar, R. B. (2002). Phyllotaxis in Magnolia Fruits. *The Journal of the Magnolia Society International*, 37(72), 26– 28.

Gies, F. Carney (2021, January 22). Fibonacci. Encyclopedia Britannica. <https://www.britannica.com/biography/Fibonacci>

International Agency for Research on Cancer, IARC Working Group on the Evaluation of Cancer-Preventive Strategies, World Health Organization, Vainio, H., & Bianchini, F. (2003). Definitions and classifications for fruit and vegetables. In *Fruit and Vegetables* (Vol. 8, pp. 1–21). Amsterdam, Netherlands: Amsterdam University Press.

Meisner, G. (2016, August 31). *Is the Nautilus shell spiral a golden spiral?* The Golden Ratio: Phi, 1.618. <https://www.goldennumber.net/nautilus-spiral-golden-ratio/>.

Olimpia, C. (2008). Fibonacci Numbers in Horticulture. *Bulletin of the University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca Horticulture*, 65(2), 603-607.

Reich, D. (n.d.). The Fibonacci Sequence, Spirals and the Golden Mean. <https://math.temple.edu/~reich/Fib/fibo.html>.

Rost, T. L. (2006). *Plant biology*. Thomson.

Salingaros, N. A. (2018). Applications of the Golden Mean to Architecture. *Symmetry: Culture and Science*, 29(3), 329–351.

[https://doi.org/10.26830/symmetry\\_2018\\_3\\_329](https://doi.org/10.26830/symmetry_2018_3_329)

*Seed & Fruit Development*. Seed & Fruit Development - Fruit & Nut Research & Information Center. (n.d.). [http://fruitandnuteducation.ucdavis.edu/generaltopics/AnatomyPollination/SeedFruit\\_Development/#%3A~%3Atext%3D](http://fruitandnuteducation.ucdavis.edu/generaltopics/AnatomyPollination/SeedFruit_Development/#%3A~%3Atext%3D)

Sigler, L. E. (2003). *Fibonacci's Liber Abaci: a Translation into Modern English of Leonardo Pisano's Book of Calculation*. Springer.

Sinha, S. (2017). The Fibonacci Numbers and Its Amazing Applications. *International Journal of Engineering Science Invention*, 6(9), 7–14.

Skorny, G., & Śledziowski, J. (2015). Interpretation of Fibonacci Numbers in Botany on the Example of Selected Fruits. *Problems of Applied Sciences*, 3, 209-216.

Spinak, M. (2011). *The Golden Section Hypothesis: A Critical Look*. Naturography. <https://patterns.architexturez.net/doc/az-cf-172990>

Zagórska-Marek, B. (1994). Phyllotaxic diversity in Magnolia flowers. *Acta Societatis Botanicorum Poloniae*, 63(2), 117–137. <https://doi.org/10.5586/asbp.1994.017>

**Appendix**

Table A1: Number of Seeds and Carpels in Rosaceae FruitsNote.

Fruit Name (Number)	Number of Seeds	Number of Carpels
Gala Apple (1)	6	5
Gala Apple (2)	4	5
Gala Apple (3)	6	5
Gala Apple (4)	9	5
Gala Apple (5)	6	5
Gala Apple (6)	3	5
Gala Apple (7)	3	5
Gala Apple (8)	8	5
Gala Apple (9)	7	5
Gala Apple (10)	5	5

Fuji Apple (1)	8	5
Fuji Apple (2)	9	5
Fuji Apple (3)	6	5
Fuji Apple (4)	11	5
Fuji Apple (5)	8	5
Fuji Apple (6)	10	5
Fuji Apple (7)	9	5
Fuji Apple (8)	9	5
Fuji Apple (9)	9	5
Fuji Apple (10)	10	5
Peach (1)	1	1
Peach (2)	1	1
Peach (3)	1	1
Peach (4)	1	1
Peach (5)	1	1
Peach (6)	1	1
Peach (7)	1	1
Peach (8)	1	1
Peach (9)	1	1
Peach (10)	1	1
Honeycrisp Apple (1)	3	5
Honeycrisp Apple (2)	1	5
Honeycrisp Apple (3)	8	5
Honeycrisp Apple (4)	4	5
Honeycrisp Apple (5)	1	5
Honeycrisp Apple (6)	3	5
Honeycrisp Apple (7)	2	5
Honeycrisp Apple (8)	3	5
Honeycrisp Apple (9)	5	5
Honeycrisp Apple (10)	7	5
Pear (1)	1	5
Pear (2)	3	5
Pear (3)	1	5
Pear (4)	2	5
Pear (5)	0	5

Pear (6)	1	5
Pear (7)	0	5
Pear (8)	0	5
Pear (9)	8	5
Pear (10)	0	5
Cherry (1)	1	1
Cherry (2)	1	1
Cherry (3)	1	1
Cherry (4)	1	1
Cherry (5)	1	1
Cherry (6)	1	1
Cherry (7)	1	1
Cherry (8)	1	1
Cherry (9)	1	1
Cherry (10)	1	1
Granny Smith Apple (1)	7	5
Granny Smith Apple (2)	11	5
Granny Smith Apple (3)	3	5
Granny Smith Apple (4)	5	5
Granny Smith Apple (5)	11	5
Granny Smith Apple (6)	1	5
Granny Smith Apple (7)	7	5
Granny Smith Apple (8)	13	5
Granny Smith Apple (9)	5	5
Granny Smith Apple (10)	8	5

Note. The numbers in blue font are Fibonacci numbers.

Table A2: Number of Seeds and Carpels in Rutaceae Fruits

Fruit Name (Number)	Number of Seeds	Number of Carpels
Navel Orange (1)	0	11
Navel Orange (2)	0	10
Navel Orange (3)	0	10
Navel Orange (4)	0	9
Navel Orange (5)	0	10

Navel Orange (6)	0	12
Navel Orange (7)	0	10
Navel Orange (8)	0	11
Navel Orange (9)	0	10
Navel Orange (10)	0	12
Mandarin Orange (1)	0	8
Mandarin Orange (2)	0	9
Mandarin Orange (3)	0	8
Mandarin Orange (4)	0	9
Mandarin Orange (5)	0	9
Mandarin Orange (6)	0	9
Mandarin Orange (7)	0	10
Mandarin Orange (8)	0	11
Mandarin Orange (9)	0	9
Mandarin Orange (10)	0	9
Lemon (1)	0	8
Lemon (2)	13	7
Lemon (3)	1	9
Lemon (4)	13	10
Lemon (5)	9	8
Lemon (6)	8	10
Lemon (7)	12	10
Lemon (8)	11	11
Lemon (9)	1	8
Lemon (10)	14	11
Lime (1)	0	11
Lime (2)	0	11
Lime (3)	0	11
Lime (4)	0	9
Lime (5)	0	10
Lime (6)	0	11
Lime (7)	0	9
Lime (8)	0	11
Lime (9)	0	8
Lime (10)	0	10

Cara Cara Orange (1)	0	11
Cara Cara Orange (2)	0	9
Cara Cara Orange (3)	0	10
Cara Cara Orange (4)	0	9
Cara Cara Orange (5)	0	10
Cara Cara Orange (6)	0	8
Cara Cara Orange (7)	0	8
Cara Cara Orange (8)	0	9
Cara Cara Orange (9)	0	9
Cara Cara Orange (10)	0	10
Grapefruit (1)	3	14
Grapefruit (2)	3	11
Grapefruit (3)	2	13
Grapefruit (4)	1	12
Grapefruit (5)	1	11
Grapefruit (6)	1	14
Grapefruit (7)	2	12
Grapefruit (8)	3	13
Grapefruit (9)	1	13
Grapefruit (10)	2	13
Tangelos (1)	0	14
Tangelos (2)	0	11
Tangelos (3)	0	13
Tangelos (4)	0	10
Tangelos (5)	0	11
Tangelos (6)	0	11
Tangelos (7)	0	10
Tangelos (8)	0	10
Tangelos (9)	0	10
Tangelos (10)	0	10

Note. The numbers in orange font are Fibonacci numbers.

# The South Asian Second Generation in the USA: Representation on Identity

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## Abstract

Cultural representation and preventing stereotyping are major areas of importance for modern American society. Immigration from the South Asian ethnic community has contributed to a higher regard for the accuracies in media and social representation of South Asian culture and people in the ethnic minority. While the definition of misrepresentation is subjective, common examples include the model minority, sexualization, Islamophobia, and cultural appropriation. A lack of proper representation has the potential to harm second generation adolescents who may participate both ethnic and popular culture. A qualitative survey gathered detailed information through open-ended responses, and multiple choice questions were qualitatively analyzed to find patterns within the sample and characterize them using the South Asian Identity Development Model (Ibrahim et al., 1997). The purpose of the results is to garner for improved representation and action against cultural stereotyping. The goal of the current study is to further research on ensuring adequate cultural representation to protect the psychological development of second generation South Asian American adolescents and other ethnic groups.

*Keywords: Cultural Representation, South Asian, Model Minority, Stereotyping, Psychology, Identity*

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## 1. Introduction

Within the United States having a diverse population, the extent and importance of cultural representation of minorities and immigrants have been contested. Regarding South Asian migration, the US experienced a rise in immigrants following President Lyndon Johnson's signing of the INS Act of 1965, replacing per-country quotas on immigrants with prioritizing skilled and educated immigrants (Jha, 2001); such immigration led to the creation of the Asian American identity. Generations of Asians have grown up surrounded by American popular culture and their ethnic culture, and as mixed cultural interactions occur, the way cultures are represented comes to importance to prevent generalizations.

While misrepresentation is harmful to minorities in general and poses a challenge to the formation of ethnic identity, second generation immigrants may react in different ways.

Second generation South Asian Americans refers to children of immigrant(s) from South Asia; second generation immigrants have not internationally migrated themselves. The model minority is a representative stereotype where an intellectual minority within a racial group is idealized. Cultural assimilation is the process of completely absorbing the dominant culture and leaving traditional practices of one's ethnic culture. Panethnicity is a term used to group various ethnic groups together based on related characteristics; for the purpose of this study, the term groups the diverse Asian cultures together based on

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geography under the “Asian American” label.

To understand the position of South Asians in American society, the tendency of South Asians to be marginalized within American society and also Asian American society is relevant. For instance:

[They] have the dubious distinction of being Caucasian, and yet not white...in a country where race has crucially assigned the immigrant's place in the nation...Perceived as being outside the histories of racial struggle in the United States, South Asian Americans have remained largely invisible in mobilizations of the Asian American community (Menon, 2006, p. 349).

Therefore, as the South Asian American identity is heavily marginalized and encompassed with external influences, misrepresentation, possibly presenting itself with the model minority (Ng et al., 2007), sexualization (Lee & Vaught, 2003), and Islamophobia (Singh, 2017), further harms the hierarchical standing of second generation immigrants. In modern society, the issue of misrepresentation increased following September 11, 2001 as “there have been incidents of discrimination against Pakistanis, and occasionally Indians have been attacked in mistake for Pakistanis” (Jha, 2001, p. 321-322). Essentially, the South Asian American community is subject to generalizing, which has the potential to spread and result in hate crimes; perspectives, harmful and positive, can easily be spread in current society, demonstrating the reach of representation.

My research addresses the responses of second generation adolescents to misrepresentation. Adolescence is remarked as a time of identity construction; analyzing misrepresentation and its correlation, if any, with ethnic identity is critical in conserving ethnic identities in American multicultural society and validating marginalized ethnic minorities.

The expected outcome is that harmful representation of South Asian culture in American society can negatively impact an individual's confidence in their ethnicity, possibly shown in participants exhibiting a desire to assimilate. In a larger context, the results can show how proper representation of ethnic cultures is vital in

maintaining a multicultural society. These results may support in advocating for diverse and accurate representation of minority cultures, specifically South Asian.

For the purpose of this study, the assumption was made that participants have an influence from their ethnic culture. If individuals' ethnic culture is not relevant to their daily life, representation in society may not be as much of a concern compared to an individual that is more connected to their homeland. Therefore, this study assumes that participants experience their ethnic culture at home and popular culture in American society.

Ergo, the research question follows: In the United States, to what extent does stereotypical misrepresentation of South Asian culture in society impact second generation South Asian American adolescents' self-assessment of their ethnicity? The scope of this study is national but seeks to extrapolate a connection within second generation South Asian Americans between the ages 13-20.

## **2. Literature Review**

Previous literature serves to address the inquiry regarding the extent to which stereotypical misrepresentation of South Asian culture in American society impacts second generation South Asian American adolescents' self-assessment of their ethnicity. Intense sociocultural and scientific analysis is required to delve into an anthropological study of South Asian Americans, cultural representation, and associated psychological effects.

### **2.1 Social Attitudes on Asian Americans**

Despite the progress that society has made, stereotypes still lead to the misrepresentation of Asian Americans in the United States. Dr. Jennifer Ng and colleagues report that “Contemporary characterizations of Asian Americans reveal the persistence of the foreigner and model minority stereotypes in mainstream culture” (Ng et al., 2007, p.197). Similarly, society commonly embodies a sexualized perception of Asian American women. Anthropologist Stacey Lee and her colleague concur with Ng et al. on the presence of misrepresentation as they display that Asian Americans become fetishized

and labeled as “exotic” (Lee & Vaught, 2003); this elucidates that misrepresentation in American society that allows for the existence of the model minority and sexualization of Asian women inhibits multiculturalism as individuals are perceived as foreign or exotic.

Furthermore, Professor of Philosophy Erich Matthes presents that the prevalence of cultural appropriation in society is harmful as the dominant culture benefits from aspects of an ethnic culture that causes minorities to be marginalized (Matthes, 2019). Members of minority groups, such as Asian Americans, are witness to the misrepresentation, exploitation, and manipulation of their own culture; it is hypocritical for society to alienate minorities and simultaneously selectively choose which aspects of ethnic cultures are acceptable. Thus, Ng et al., Lee and Vaught, and Matthes establish the presence of negative stereotypes from the dominant culture in American society towards Asian Americans.

#### Religious Misrepresentation

However, in addition to facing general Asian stereotypes, South Asians are susceptible to Islamophobia. Jasleen Singh elaborates that while post-9/11 society can misrepresent Islamic culture and depict Muslim Americans as terrorists, society generalizes all South Asian Americans to where even Sikhs and Hindus may be subject to stereotypical religious misrepresentation (Singh, 2017). Ultimately, Singh contributes to the discussion regarding Asian misrepresentation by highlighting an additional negative factor South Asian Americans have to overcome in society, bringing attention to the possibility of negative implications faced by this community.

#### 2.2 Second Generation Immigrant Responses

Analyzing negative implications of misrepresentation should consider the responses of second generation immigrants to cultural misrepresentation as second generation immigrants simultaneously deal with ethnic pressures to maintain cultural loyalty and pressures of the dominant society to participate in popular culture. Sociologists Portes and Hao quantitatively demonstrated in a study with

5,000 second generation immigrants that second generation immigrants enter a process of losing ethnic culture, proven by an increase in English monolingualism in the second generation (Portes & Hao, 1998). While Portes and Hao analyzed the overall trend of decreasing bilingualism and the likelihood of passing culture through generations, their perspective fails to consider the detriments of cultural bereavement on personal identity formation.

#### Personal Responses to Misrepresentation

Assimilation is an evident response among second generation immigrants that poses a threat to respective ethnic cultures. Psychologist Derek Iwamoto and colleagues qualitatively researched 12 Asian Indian Americans and discovered that “Many participants relayed their realization of being physically or culturally different from Whites. Most reported hiding their cultural self because of a desire to fit in...” (Iwamoto et al., 2013, p. 230). On the other hand, South Asian Americans may also respond to assimilation pressures and stereotypical cultural misrepresentation with increased ethnic nationalism. Sociologist Prema Kurien counters Iwamoto et al., stating that “Multiculturalism leads to the institutionalization of ethnicity and to ethnic formation among immigrant groups as individuals face pressure... to organize into groups,” and post 9/11 racism has led to Muslim Americans and South Asian Americans as a whole congregating to oppose racist public perceptions (Kurien, 2007, p. 763). This perspective is evident with the formation of cultural societies and religious groups, which is made feasible if an individual contains a strong intrinsic motivation to preserve their culture or lives in an ethnic enclave where their culture is predominant. Thus, as Iwamoto et al. and Kurien display two differing results of individual responses of second generation South Asian Americans, the possible reactions of individuals require deeper insight.

#### Panethnicity

However, within the two extremes, an individual can also integrate into society under a panethnic label that allows for embracing one’s ethnicity and social inclusion. According to Erika Lee, the problem with panethnicity is that “despite their diverse origins,

Asian Americans have been consistently lumped together and treated as one monolithic group” (Lee, 2015, p. 136). The adoption of a label that does not entirely represent one’s core ethnicity has potential for creating a conflict between one’s private and public cultural identity as members of the same Asian American racial minority can have different beliefs. Lee, Iwamoto et al., and Kurien would acknowledge the personal challenges that come with the responses they analyzed; a person can develop a conflict if they feel underrepresented with panethnicity, pressures to assimilate, or discrimination for embracing their culture respectively.

### 2.3 Psychological Review

Therefore, members of an ethnic minority in the United States can develop conflicts in one’s concept of identity. As such, Sociologist Krycia Mossakowski elaborates that ethnic identity can fluctuate with external influences, commonly creating a weakened sense of identity in minority groups that can catalyze mental health issues (Mossakowski, 2003). However, it is critical to understand how external factors can impact adolescents in their process of identity formation. Therefore, Psychologist Lisa Kiang and colleagues report that adolescent development is heavily influenced by intercultural interactions (Kiang et al., 2019). While members of minority groups can suffer from self-concept issues as a result of social pressures, adolescents in specific are at risk due to their presence in initial stages of development. Consequently, second generation South Asian adolescents may react differently to misrepresentation compared to their adult counterparts evaluated in previous literature.

### 2.4 Research Implementation

Ultimately, preserving the identity and ethnic self-concept of South Asian Americans should be a priority for society as second generation immigrants contain the potential to contribute to society. While holistic studies on Asian American identity exist that connect misrepresentation to various individual responses of ethnic-identification, it is necessary to contribute a study in specific of second generation adolescents in the South Asian ethnic community to

analyze whether the implications of their responses follow the same pattern, if not more dramatic, due to the prevalence of the additional Islamophobic misrepresentation, disparities between social and ethnic pressures, and fragility of self-concept faced by this cohort.

### 3. Method

This section proposes a mixed study that will compare the impacts of stereotypical misrepresentation of South Asian culture in American society on the ethnic self-assessment of second generation South Asian American adolescents. In this section, the format and the composition of the survey are described, along with the procedure for the study.

The dependent variable is the impact misrepresentation has on an individual’s identity. Therefore, this approach is non-experimental, seeking to characterize the responses of second generation South Asian American adolescents to misrepresentation and the resulting impacts on their ethnic self-concept. Participants are presented with a survey with open and closed ended questions to allow for participants to express complete thoughts and reflect on how society has impacted their understanding of their ethnicity. Flexibility in open ended responses allows for evaluation of how cultural misrepresentation can impact individuals in specific as participants can share their personal experiences. Qualitative analysis of personal experiences and in-depth responses is required to evaluate the extent to which second generation South Asian American adolescents are impacted by misrepresentation. However, quantitative analysis of results is also vital to report the general patterns among the responses of participants; data can depict the proportion of the study population that feels negatively impacted by stereotypical misrepresentation, embodies a negative perception of their ethnicity, exhibits conflict in their own ethnic label, etc.

Participants involved in this study are second generation South Asian American adolescents, meaning participants are American-born citizens with parent(s) who have immigrated from a South Asian country. Common characteristics in this cohort

include education level (secondary education or undergraduate studies) and religious affiliation (examples include Hinduism, Islam, Buddhism or Sikhism).

All ages between 13-20 were represented in the study, with 16 year-olds (21.9%) and 15 year-olds (18.8%) making up most of the 32 respondents. The gender demographics are as reported: 50% female, 46.9% male, and 3.1% genderfluid. 75% of participants were in secondary education and 25% in undergraduate programs. Represented states include Texas, California, and Georgia, with Texans being the large majority. Participants were predominantly Hindu (78.1%), but individuals were also Muslim, Jain, Sikh, or not religious. Additionally, respondents were mostly of Indian origin, with Pakistani and Bangladeshi origin having one participant each. 68.8% of participants had an *Indian American* ethnic label, with the next common label being *Asian American* (9.4%).

The survey mostly takes the form of multiple choice questions to allow for empirical conversion. Initial questions seek characterizing information about the participant: age, education, gender, parents' country of origin, religious affiliation, and ethnic label. The participants are also encouraged to respond to short answer questions asking about possible instances of stereotypical misrepresentation, other personal experiences, the confidence level one has in their identity, and how one assesses their ethnicity. The remainder of the multiple choice questions reflect the South Asian Identity Development Model (Ibrahim et al., 1997); each involves a statement regarding American portrayal of South Asian culture, second generation cultural pressures, ethnic cultural expectations, the possible presence of an ethnic identity conflict, or the extent one embraces their ethnic culture. Participants must indicate whether they *strongly agree*, *agree*, *disagree*, *strongly disagree*, or remain *neutral*.

All data was stored electronically in a private file accessible only to the researchers to protect participants' confidentiality.

### 3.1 Procedure

Institutional Review Board approval is obtained

prior to data collection. To achieve variance in the sample population, the survey is distributed on nationally accessible digital platforms. Following the completion of receiving parental and informed consent from participants, the survey is administered. A phenomenological approach is taken where significant responses from individuals are identified, and participants' multiple choice responses are numericized in relation to the participant's information: age, ethnic label, etc. Patterns will be visible from the way the majority of participants respond to questions regarding their relationship with their ethnic culture. Correlations can be determined between misrepresentation and adolescent responses if the majority of the participants align themselves towards *agree* or *disagree*. Responses will be determined as significant if they elaborate on misrepresentation and ethnic identity; the significance of a response is not determined by the opinion of the researcher.

The South Asian Development Model by Ibrahim et. al (1997) involves the Acceptance Stage (individuals have ethnic pride and believe that hard work will overcome sociocultural differences), Dissonance Stage (individuals realize that sociocultural differences with American society cannot be overcome), Resistance and Immersion Stage (individuals reject mainstream cultural values and stereotypes), and the Synergistic Articulation and Awareness Stage (individuals reject popular and ethnic culture values for individuality) (pg. 42-43). The stages will be used to measure the level of ethnic security that participants have and possibly the change in ethnic security, if any, with misrepresentation.

## 4. Results

A holistic perspective to the multiple choice questions are as follows in Appendix 1.

Additionally, all participants, when rating their satisfaction with their ethnic label scaled with 10 being completely satisfied, answered between 6 and 10; the mean is 8.97, median is 9, and mode is 9.

However, open-ended questions showed diversity in responses. Regarding examples of positive South Asian representation, opinions of participants include

portrayals in "Quantico" and "Never Have I Ever," representations of Hijabi women, Hasan Minhaj, Vice President Kamala Harris, Google and Microsoft CEOs, and cultural appreciation. Participant A recorded that "some media portrayals normalize Indians being average, which is sometimes a good thing, because of this overwhelming stereotype that [Indians] are all smarter than the average person." On the other hand, people believed that negative examples of South Asian representation include cultural appropriation, "mocking" religious symbols, and depictions of South Asians as "the typical nerdy kid." Participant A remarked that "[o]utward racism or xenophobic rhetoric is a pretty big red flag in all cases... For all means and purposes, Raj from Big Bang Theory... fit a stereotype as an immensely nerdy, not very attractive, and awkward guy who had a terrible fashion sense and couldn't talk to girls sober."

Most individuals exhibit pride in embracing their ethnicity in public as "there's nothing embarrassing about being prideful," (Participant G) and "[p]eople are usually welcoming of diversity and seem more interested in learning..." (Participant H). Others expressed ethnic confidence over time; Participants A and B's responses, respectively, include "I used to not be, but as a college student, I've grown more comfortable with it...because I've been given the space and support to feel proud," and "I used to not be because American society is largely ignorant and intolerant. With age, I have come to embrace and stand up for it." However, while no participants stated a complete lack of ethnic confidence, responses did include a sense of discomfort in public: "I don't like speaking anything other than English outside," (Participant C) and "if I know that there will be other people expressing their ethnic identity I feel comfortable but otherwise I feel uncomfortable," (Participant D).

Moreover, Participant B chose a pan-ethnic label since "government documentation only has an option for Asian American." As participant E explained, "[m]any of my friends are Asian, but not Indian, and share many of the same sociocultural experiences as I do..."

When comparing ethnic and popular American culture, while one response stated that no difference

exists, others referenced differing lifestyles, religions, languages, and cultural values. Participant F explained that "American society is far more individualistic and focuses on the value of a person [while] Indian identity is rooted in collectivism."

Lastly, when asked about the impact of misrepresentation on their view of their ethnicity, participants expressed: "I subconsciously ignore the stereotypes and perspectives and continue to have pride in my culture," (Participant F) and "[t]here is no single portrayal or what an Asian person is like," (Participant A). There were outliers that explained that the way South Asians are represented in society is "degrading" and have caused "shame in [youth]."

## 5. Discussion

Ultimately, representation of South Asian culture in American society needs to improve to prevent stereotyping and offensive connotations. As participants documented instances of negative and inaccurate representation, even though there was no particular mention of sexualization or Islamophobia, the model minority was mentioned by Participant A (see page 7). While representation of South Asians as overly intelligent is not inherently offensive, the connotation upholds the stereotype that South Asians are antisocial, smart students; the model minority originates as ethnic parents teach their children that working harder in comparison the majority is required to have equal opportunities (Ng et al., 2007, pg. 117). Therefore, the model minority essentially represents the efforts marginalized groups have to achieve in a competing society and should not be idealized and misrepresented. Portrayals that contribute to the belief that all or most people of South Asian descent are highly intellectual take away from the marginalization of the South Asian community and create pressure for young individuals to aspire to social expectations or contest misrepresentation. Ergo, positive representation in media and popular culture would prevent the proliferation of the 'nerdy' stereotype. Correspondingly, Matthes (2019) claims that ethnic minorities are subject to a vulnerability clause where social oppression causes cultural groups to be vulnerable to further exploitation (pg. 1006). The

vulnerability clause can be seen as participants referenced cultural appropriation and the “mocking” of ethnic culture (see page 7); the proliferation of cultural appropriation and misrepresentation of South Asian culture will only further marginalize the ethnic minority. Inhibiting stereotyping and employing accurate cultural representations can serve to protect marginalized groups that are already socially threatened. Regardless of the various extent of impacts misrepresentation may have on individuals, as the United States is a multicultural society, the country has an ethical obligation to improve social representation to hinder stereotypical misrepresentation.

Such action is required as self-concept issues can arise as a result of cultural misrepresentation. The observation that the majority of participants reported cultural representation having minimal impact on their view of identity was contrasted as a few individuals felt degraded by misrepresentation and most participants expressed some degree of care over South Asian representation (Appendix 1). Such juxtaposition can be reasoned as Kiang et al. (2019) state that “ethnic identity itself has a strong association with fewer depressive symptoms,” (pg. 325); as poor representation harms the relationship an individual can have with their ethnicity or make them feel excluded, a threat to ethnic identity is formulated, which can bring poor health consequences depending on the individual. However, since there were people who had experienced ethnic conflicts before and settled on a South Asian ethnic label or people that grew confident with their identity over time, second generation South Asian adolescents adapted to their environment (Appendix 1). Individuals have mostly grown accustomed to the influences in American popular culture, but some people may carry a degree of vulnerability to misrepresentation. Essentially, cultural misrepresentation can be harmful to individuals who are young and learning their way in a multicultural society. Especially since “perceived discrimination and stereotyping experiences outside of the home can come together and subsequently predict adolescents’ identity and outcomes,” maintaining proper representation in society is vital in allowing individuals to increase their comfort with their

ethnicity (Mossakowki, 2003, pg. 533). The impacts of cultural misrepresentation vary from each person, but with the potential to hinder even a minority of second generation South Asian adolescents, stereotypical misrepresentation contributes to the ethnic groups’ marginal status or possible self-esteem issues and therefore must be reformed with accurate and culturally appropriate portrayals.

On the other hand, the majority of second generation South Asian adolescents exhibit confidence in their ethnicity. Since most participants responded as having ethnic pride, associating within ethnic groups, and being raised with cultural values, they express an influential presence by their ethnic culture (Appendix 1); the average ethnic confidence level among participants was also very high (see page 7). Conversely, an examination of immigrant families by Portes and Hao (1998) that showed a common loss of culture is supported through current research as 62.6% of participants stated that they were more connected American culture than their parents, and only 12.5% of participants felt that they were closer to their ethnic culture as compared to their parents (Appendix 1). Essentially, second generation South Asian Americans find themselves with ethnic ties, but unable to be as connected to ethnic culture as their parents. These sentiments manifest themselves through assimilation tendencies as 40.6% of participants expressed a desire to assimilate, and a minority stated a history with determining their ethnic identity (Appendix 1). Having results that show second generation immigrants as having ethnic pride but also assimilation tendencies is reported as a common phenomenon as Iwamoto et al. (2013) and Kurien (2007), respectively, state that people can either assimilate or embrace their identity when marginalized in society. Assimilating into American society or embracing a full sense of ethnic nationalism both exist more as a spectrum of responses where individuals can tend towards one side over the other. Ultimately, cultural misrepresentation and stereotyping creates a sense of ethnic frustration among second generation South Asian American adolescents and possible assimilation desires but not to the extent where people give up their culture; personal connections to ethnic culture ultimately result in ethnic pride.

Therefore, wanting to assimilate due to the desirability of American culture or misrepresentation of ethnic culture and expressing confidence in an ethnic identity can occur simultaneously.

Also, the adoption of a pan-ethnic label does not have a personal significance to second generation South Asian American adolescents. With the aspect of transnationalism, identities extending borders and connections being forged with homeland affairs, many differences exist between Asian cultures, and embodying a general ethnic label fosters distance from unique aspects of one's ethnic culture (Lee, 2015). Choosing a pan-ethnic label over a more specific ethnic label may render itself as an individual not fully embracing their identity; however, participants did not mention any shame of guilt regarding a specific ethnic label, elucidating an extent of personal pride or acceptance of ethnicity despite external pressures (see page 7). While South Asian Americans may have frustrations regarding their ethnicity and cultural representation in society, ethnic pride protects against internalizing misrepresentation into possible identity conflicts.

Ergo, according to the South Asian Identity Development Model by Ibrahim et. al (1997), with most participants exhibiting ethnic pride and self-exclusion from misrepresentation, participants fall into the Resistance and Immersion stage; second generation South Asian American on average hinder desires to assimilate and embrace their ethnic culture. While some participants expressed passing through a Dissonance Stage of ethnic frustration regarding a desire to assimilate, with maturity, ethnic pride was embraced. However, attention should be brought to the potential of misrepresentation to hold individuals in ethnic dissonance. Even though, participants expressed ethnic security over time regardless of stereotypical misrepresentation, second generation immigrants were held to a degree of personal responsibility to eventually restrict the personal impacts of misrepresentation.

## **6. Conclusion**

This study has served to expand the knowledge regarding the nature of second generation South Asian Americans responding to cultural

representation and constructing a suitable ethnic identity. The correlation between stereotypical misrepresentation of South Asian culture and the ethnic identity of second generation South Asian American adolescents varies with each individual. While stereotypical misrepresentation of South Asian culture has the potential to instigate identity conflicts in second generation adolescents, many individuals have successfully separated society's view of their culture from their own view. Representation in society can have the ability to instill assimilation tendencies into modern youth while also creating an opportunity for others to empower themselves and their ethnicity. However, with possibilities that affected persons can suffer with ethnic identity conflicts and younger individuals can be more susceptible to social pressures, American society has the responsibility to maintain accurate cultural representation and prevent stereotyping.

This responsibility, however, is not inherently straightforward. The definition of accurate cultural representation can certainly differ from person to person depending on many factors. A person from the South Asian ethnic group who does not hold their culture to a high level of importance may not regard misrepresentation as much or be less likely to isolate stereotyping compared to someone who is attentive surrounding their culture. As American society becomes increasingly diverse and people get exposed or accustomed to other cultures, people may become increasingly aware as to what is considered "harmful" to ethnic minorities. Ergo, as the definition of misrepresentation and stereotyping can broaden in the future with the expected increasing social awareness, the consensus remains fluid. As of the moment, the instances of misrepresentation within the media that seem agreeable among Ng et al., Lee & Vaught, Matthes, and the study participants include the model minority, sexualization, and cultural appropriation. Nevertheless, maintaining accurate cultural representation via media involves inhibiting listed common forms of misrepresentation and an accommodating awareness to future grievances regarding cultural portrayals at the least.

### **6.1 Limitations**

This study was conducted with mostly Indian Americans who identified themselves as Hindu. Generalizing this study to extend across multiple religious affiliations may not be accurate as Sikhism and Buddhism were not represented in this study.

Additionally, despite gaining participants from the west and east coasts as well, the survey had respondents from mostly Texas; outreach through social media platforms proved unsuccessful. As most surveys, this study may have involved a sense of sampling bias. Systematically, second generation South Asian American adolescents in Texas were more likely to participate in the survey.

Even though participants were encouraged to convey reflections on their identity and express complete opinions regarding cultural representation, such responses were minimal. Open ended questions were not made required in the survey to allow for minimal risk to participants (if a certain question was deemed harmfully intrusive due to past cultural trauma or other reasons, participants could choose to skip that question). However, since questions were optional, not all questions were answered by each participant or participants indicated "N/A". For those who chose to respond, there was no essential motive for detailed responses other than contributing to the body of cultural knowledge.

Furthermore, the researcher is of the South Asian American community, and possibly biased towards the area of research. No personal biases have obscured the results of the study; data from the multiple choice questions were objectively quantified and statements from respondents were quoted. The collected data responses were not modified.

## 6.2 Implications

Despite such relevance to the Muslim community within the United States, the lack of reference of Islamophobia by participants may be attributed to the insufficient number of Muslim American respondents. Likewise, participants being mostly of Indian origin cannot entirely represent South Asia as a whole as individuals with origins of Bhutan, The Maldives, and Sri Lanka went unobserved.

Since participants were from urban areas, rural second generation South Asian Americans were left

as a gap. Urban areas have a higher density of people and can possibly contribute to more interaction between various cultures. As assimilation is connected to the stigma against minorities and a sense of cultural inferiority, living in areas without diversity may foster greater experiences of racial stigma and vulnerability to cultural misrepresentation. However, outreach to nonurban communities may not occur as easily as advertising a study to an urban or suburban population.

## 6.3 Future Directions

The possibility exists that responses to misrepresentation may vary with different countries of origin or religious background. As ethnic enclaves and religious groups contribute to the rise in nationalism amongst immigrants, the demographic of the United States is a significant factor. Ethnic enclaves can form as immigrants interact with others with a similar cultural or religious background; different affiliations within South Asian Americans may be unable to achieve a rise in ethnic acceptance if affiliates are an extremely small minority within the country. As the study primarily showed the impact of second generation Indian Americans, future research can be done to compare how responses of individuals with different backgrounds differ from second generation Hindu Indian Americans.

Moreover, children who have immigrated into the United States themselves but at a very young age, also experience a similar environment to second generation immigrants. Examining the responses between such first generation South Asian Americans to stereotypical misrepresentation and possibly drawing similarities with second generation immigrants become relevant. As this study showed the different varying responses to cultural misrepresentation, the spectrum of responding with assimilation tendencies or embracing ethnic pride may be attributable to first generation immigrants who lack recollection of their home country.

Age also was a major contributing factor in the study, and since this study showed the pattern appeared to be individuals adapting to misrepresentation over time and accepting their

identity, examining younger adolescents and older adolescents separately may highlight changes in responses to stereotyping through adolescence. The differences in maturity and vulnerability to external influences between young teenagers and young adults might be a significant variable in measuring psychological impacts to identity construct. Younger individuals may be vulnerable to misrepresentation or encompass feelings to integrate into society; aging and gaining additional exposure to other cultures and one's own culture can possibly result in increased ethnic nationalism.

Lastly, as cultural representation had a negative impact on some participants, this study can be used to support the need for inhibiting misrepresentation. The influences of proper representation on the ethnic identity of second generation South Asian adolescents, if researched, can serve to contrast the negative experiences of individuals lacking positive cultural influence. Adolescents who grow in a positive environment depicting their culture in an accurate late may present their relationship with their identity to be more secure. To further research on cultural representation, a larger study should be conducted with more diversity and emphasis on detailed responses.

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### References

- Ibrahim, F. A., Ohinishi, H., & Sandhu, D. (1997). Asian American identity development: A culture-specific model for South Asian Americans. *Journal of Multicultural Counseling and Development*, 25, 34-50. <https://doi.org/10.1002/j.2161-1912.1997.tb00314.x>
- Iwamoto, D. K., Negi, N. J., Partiali, R. N., & Creswell, J. W. (2013). The racial and ethnic identity formation process of second-generation Asian Indian Americans: A phenomenological study. *Journal of*

*Multicultural Counseling & Development*, 41(4), 224-239. <https://doi.org/10.1002/j.2161-1912.2013.00038.x>

Jha, N. (2001). Indian Americans: The growing force. *India Quarterly*, 57(3), 55-78. <http://www.jstor.org/stable/45073246>

Kiang, L., Supple, A. J., & Stein, G. L. (2019). Latent profiles of discrimination and socialization predicting ethnic identity and well-being among Asian American adolescents. *Journal of Research on Adolescence (Wiley-Blackwell)*, 29(2), 523-538. <https://doi.org/10.1111/jora.12403>

Kurien, P. (2007). Who speaks for Indian Americans? Religion, ethnicity, and political formation. *American Quarterly*, 59(3), 759-783. <http://www.jstor.org/stable/40068449>

Lee, E. (2015). A part and apart: Asian American and immigration history. *Journal of American Ethnic History*, 34(4), 28-42. <https://doi.org/10.5406/jamerethnhist.34.4.0028>

Lee, S., & Vaught, S. (2003). "You can never be too rich or too thin": Popular and consumer culture and the Americanization of Asian American girls and young women. *The Journal of Negro Education*, 72(4), 457-466. [www.jstor.org/stable/3211196](http://www.jstor.org/stable/3211196)

Matthes, E. H. (2019). Cultural appropriation and oppression. *Philosophical Studies*, 176(4), 1003-1013. <https://doi.org/10.1007/s11098-018-1224-2>

Menon, S. (2006). Disrupting Asian America: South Asian American histories as strategic sites of narration. *Alternatives: Global, Local, Political*, 31(3), 345-366. <http://www.jstor.org/stable/40645189>

Mossakowski, K. (2003). Coping with perceived discrimination: Does ethnic identity protect mental health? *Journal of Health and Social Behavior*, 44(3), 318-331. Retrieved August 24, 2020, from <http://www.jstor.org/stable/1519782>

Ng, J., Lee, S., & Pak, Y. (2007). Contesting the model minority and perpetual foreigner stereotypes: A critical review of literature on Asian Americans in education. *Review of Research in Education*, 31, 95-130. <http://www.jstor.org/stable/20185103>

Portes, A., & Hao, L. (1998). E pluribus unum: Bilingualism and loss of language in the second generation. *Sociology of Education*, 71(4), 269-294. [www.jstor.org/stable/2673171](http://www.jstor.org/stable/2673171)

Singh, J. (2017). Desire, patriotism, and Sikh subjectivity. *Sikh Formations: Religion, Culture, Theory*, 13(4), 254– 267. <https://doi.org/10.1080/17448727.2017.1382632>

Appendix 1. Multiple Choice Question Response

American society (media, pop culture, public perceptions) correctly represents my ethnic label.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
6.3%	12.5%	31.3%	50%	0%
I am satisfied with South Asian representation in American society.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
6.3%	15.6%	31.3%	43.8%	3.1%
The way my ethnic culture is socioculturally represented in American society matters to me.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
21.9%	50%	25%	3.1%	0%
I am socioculturally closer to my South Asian ethnic culture than to American culture.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
12.5%	18.8%	34.4%	28.1%	6.3%
I strongly identify with many elements of my South Asian ethnic culture (language, religion, traditions, etc).				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
21.9%	53.1%	18.8%	3.1%	3.1%
I associate with others in my ethnic group.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
31.3%	59.4%	9.4%	0%	0%
I believe that I fit into American society.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
21.9%	59.4%	18.8%	0%	0%

I have a desire to assimilate into American society.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
3.1%	37.5%	43.8%	15.6%	0%
I believe that I fit into my ethnic society.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
3.1%	62.5%	18.8%	15.6%	0%
I have strong ethnic pride.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
9.4%	59.4%	21.9%	9.4%	0%
I am more connected with American culture and society compared with my South Asian immigrant parent(s).				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
31.3%	31.3%	18.8%	15.6%	3.1%
I am more connected with ethnic culture and society compared with my South Asian immigrant parent(s).				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
0%	12.5%	18.8%	43.8%	25%
My South Asian ethnicity is not relevant to my daily life in the United States.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
9.4%	12.5%	37.5%	34.4%	6.3%
American society accepts my cultural differences.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
3.1%	46.9%	28.1%	18.8%	3.1%
I have never experienced an internal conflict regarding which ethnic group I am a part of.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
15.6%	46.9%	6.3%	28.1%	3.1%
I have experienced an internal conflict regarding which ethnic group I am a part of, but I have chosen a South Asian ethnic label.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
6.3%	28.1%	21.9%	34.4%	9.4%

I am currently experiencing an internal conflict regarding which ethnic group I am a part of.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
0%	3.1%	9.4%	50%	37.5%
I acknowledge the positive aspects of my ethnic culture				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
40.6%	59.4%	0%	0%	0%
I have knowledge regarding the cultural values, expectations, and history associated with my ethnic label.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
21.9%	62.5%	15.6%	0%	0%
I have grown up in an ethnic household that emphasizes the following: reputation, respect for age, and respect for community.				
Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
53.1%	40.6%	3.1%	3.1%	0%

# New Jersey High School Students' Perceptions of Full-time Online Learning

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## Abstract

The usage of online learning has dramatically increased since the start of Covid-19. Though the novel form of learning has seen sizeable economic growth and futuristic potential, it has received heavy critique from students worldwide. For these reasons, research on the viability of online learning is increasingly relevant. I analyzed New Jersey High School students' perceptions of online learning in comparison to in-person learning. I utilized an online survey to obtain results. Ultimately, I discovered that students have adapted to online learning, and, consequently, student perceptions of online learning have been generally positive. I also researched the factors that impact student perceptions of online learning and student perceptions of the potential of online learning. Some positive attributes of online learning are its convenience and comfort, while negative features include its lack of interaction, worsened learning quality, technological issues, and lack of engagement. Despite these flaws, Students have generally shown that they believed in the future of online learning. Future research in this field should further analyze the factors that impact student perceptions of online learning so that educators, school boards, and programmers can foster a positive learning environment for online students.

*Keywords: Online Learning, High School, Student Perceptions, New Jersey*

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## 1. Introduction

In 1728, Caleb Phillips advertised a “private correspondence [course]” (Georgie, 2021), one of the first recorded instances of distanced learning, in the Boston Gazette. In this course, Phillips taught through the mail rather than in person. As technology advanced over time, distance learning improved as well. Distance learning involved the radio, records, and television by the mid-twentieth century. In 1976, the first virtual college, Coastline Community College, was formed (Thompson, 2021). Today, distance learning is rapidly developing both technologically and logistically. Now primarily online, distance learning has spurred economic

growth within multiple industries. Educators commonly utilize applications such as “Zoom” and “Google Meet” as the means of communication.

Since the onset of Covid-19, the utilization of online learning has drastically increased. In Wuhan, China, Covid-19 “resulted in the largest “online movement” in the history of education with approximately 730,000, or 81% of K-12 students, attending classes via the Tencent K-12 Online School in Wuhan” (Li, 2020). As the virus spread to the United States, so did online learning. Going into the 2020-2021 school year, many United States schools have remained entirely online, while others have switched to hybrid schedules. For example, on July 6, 2020, Harvard University decided to hold all classes

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online for the 2020-2021 school year but still charge full tuition (Algar, 2020). This “injustice” led a Harvard Law student to sue the school “over tuition prices as classes remain online.” The student felt “overall disrespected and unheard by the administration” (Lantry, 2020). Harvard University is one of many universities currently facing lawsuits, as “students at more than 25 U.S. universities who have been sent home to learn online during the coronavirus pandemic are filing lawsuits against their schools.” These lawsuits generally claim that the quality of online education is not of the same quality that the school promised the students, and thus, refunds are required (Betz, 2020). Parents have extensively complained about online learning as well. In September 2020, parents who believed their children received inadequate education online sued the Los Angeles Unified School District (Esquivel, 2020). The students within this district believed they had the right to quality education, and they believed online learning did not meet this quality. Reactions have been similar around the United States in all levels of education. Going forward, School boards should determine student perceptions of online learning to help foster a positive online learning experience. Understanding student perceptions can help teachers better understand student needs and adjust accordingly in this novel online learning environment.

Online learning has seen significant economic growth within the last year. According to the World Economic Forum, “even before Covid-19, there was already high growth and adoption in education technology ... the overall market for online education projected to reach \$350 Billion by 2025” (Li, 2020). Many investors and application programmers hold an interest in online learning, as it has immense economic potential. Therefore, understanding student perceptions of the potential of online learning and the changes that students believe would positively impact the online learning experience would be highly beneficial. For application programmers, understanding student perceptions of online learning would increase the understanding of student needs and thus allow developers to program the best possible online learning service. This understanding of student perceptions of online learning would bring

essential data about the economic potential of online learning, which is of utmost interest to many investors. Covid-19 has catalyzed considerable growth in online learning usage. Given futuristic improvements, the growth will continue.

Understanding student perceptions of online learning and what students believe would improve online learning are increasingly relevant for these social and economic reasons. This study will overview the current information in terms of student perceptions of online learning and conduct additional research to bolster the body of knowledge within the field.

## **2. Literature Review**

While news outlets have extensively shown that students negatively perceive online learning, researchers must also consider formal research. Since online learning has existed since the infancy of the internet, there are many studies on student perceptions of online learning. In a study that researched university student perceptions of online learning in Indonesia, researchers found that, of those surveyed, 77.5% of students were very satisfied with online learning, 18.75% of students were satisfied with online learning, and only 2.5% of students were dissatisfied with online learning (Maskun, 2020). Maskun performed this study before the Covid-19 outbreak became a pandemic, and the students all voluntarily took online classes. In another study that researched United States university students' opinions on online learning, 13.1% of students felt completely satisfied with online courses, 39.9% felt mostly satisfied, 24.4% felt somewhat satisfied, while 11.9% felt somewhat dissatisfied, 8.9% felt mostly dissatisfied, and 1.8% felt completely dissatisfied (Rodriguez, 2008). Rodriguez conducted this research in 2008 on roughly seven hundred university students who took part-time online classes. In general, research in this area strongly supports the notion that University students positively evaluate online learning, which contradicts what many news articles have implied through their reporting of student complaints towards online learning.

In a study conducted in May 2020, during the onset of Covid-19, researchers researched 407 Indian

online students on their perceptions of online learning. "The results of the survey showed that 87.1% of the students reported that they preferred classroom teaching method more than online teaching mode. 12.9% preferred online classes" (Nambiar, 2020). Overall, this study showed the exact opposite of previous studies, as students in this survey showed negative perceptions of online learning. Other studies conducted during or after the onset of Covid-19 show similar negative student opinions of online learning. In a study that surveyed 261 Indonesian university students, only 3.8% of students stated that they preferred online learning, while 96.8% of students answered that they preferred in-person learning (Widodo, 2020). While there will be differences between student perceptions of online learning depending on the country and class, this incongruency between perceptions of online learning is much too large to ignore. Some external factors may be the cause of this inconsistency.

I hypothesize that Covid-19 has skewed student perceptions of online learning from positive to negative. The logical explanation for this skew is that the students surveyed are very different before Covid-19 than after. Before Covid-19, if one took an online course, they likely did so voluntarily, meaning that they specifically chose to attend an online course alternative rather than an in-person course. Therefore, those surveyed would likely already have a positive perception of online learning. After Covid-19, online learning was enforced internationally due to safety concerns. Because many of the students likely had little to no experience with online learning, those surveyed would likely negatively perceive online learning. Research in student perceptions of online learning generally corroborates with this hypothesis, as shown in the four studies provided above.

I also hypothesize that because students now have experience in online learning (many students who took online courses due to Covid-19 have been online for over a year), students may more positively evaluate online learning. In the Los Angeles School District, which, as mentioned prior, had received lawsuits from the parents about its "flawed" online learning system, the majority of students have chosen remote learning over the in-person school. Although all schools within the school district have fully

opened, only "7% of high schoolers, 12% middle schoolers and 30% of elementary children are back in the classroom" (City News Service, 2021). I believe that student perceptions of online learning over time and experience have shifted from negative to positive. Since all previous research likely does not accurately represent current student perceptions of online learning due to environmental changes, researchers must conduct new studies.

Previous research has shown that convenience and comfort are advantages of online learning. Various studies "indicate that convenience, time flexibility, lack of a commute to campus and the need to "sit through" a class" (Reisetter, 2004) are integral reasons for student participation in online courses. In general, students feel that not having to commute to class at a designated time is a significant advantage of online learning. Conversely, previous research suggests that lack of interaction and technological issues negatively impact the online learning experience. According to a study on student perceptions of online learning, "the most dominant theme in student explanations for preferring face-to-face classes (92%) was related to interaction" (Tichavsky, 2015). Many students believed that seeing a "real" teacher and interacting with "real" classmates significantly improved their learning experience. In another study about online learning, students "talked about their frustration with technology glitches and how these glitches affected the quality of their interactions." (McBrien, 2009) Other students suggested that the overwhelming nature of flipping through videos, PowerPoints, speaking, listening hindered their learning ability. This field needs new research regarding the factors that impact student perceptions of online learning for the same reasons mentioned above. Environmental factors, like Covid-19, have dramatically changed the sample of online learners, and, therefore, this field requires new research on this changing sample.

The main goal of this study is to determine student perceptions of online learning. Additional goals are to identify factors that impact student perceptions, determine student perceptions of the potential of online learning, and identify specific changes that would positively impact the online learning experience. Although online learning has

shown remarkable futuristic growth, very little research has targeted the potential of online learning; therefore, new research about online learning potential would be beneficial. I also want to understand what changes would positively impact the online learning experience because understanding this will help improve online learning. I hypothesize that students in this study will positively rate online learning compared to in-person learning, contradicting what much research after Covid-19 has shown. I also hypothesize that students believe in the futuristic potential of online learning.

### **3. Methods**

To understand student perceptions of online learning, one must question students themselves on their evaluation of online learning, which eliminates the possibility of using an experimental procedure or a meta-analysis. The only methods that would rationally make sense for this research are focus groups, interviews, and surveys. I ultimately conducted a survey. The most utilized method in measuring student perceptions is a survey. I believed that following similar methods to previous expert research would prove beneficial. Surveys also do not involve face-to-face contact, an essential trait during the Covid-19 pandemic. Furthermore, surveys generally require less time commitment from the subjects in comparison to interviews and focus groups. I believe that subjects are more likely to participate in a study that requires less time. Therefore, to ensure that the study's sample size is large, this study utilized an online study.

For the survey, I researched New Jersey, full-time, online, high school students. I chose to research New Jersey since it was one of the states with the longest enforcement of online learning. Consequently, these students would have a more nuanced understanding of online learning. I used similar logic when choosing to research full-time students. These students spent the longest time in online classes, and their perspectives on online learning would likely be more constructive. I researched high school students since it would be easiest to research personally, allowing me to obtain a larger sample.

The survey consists of eleven questions that pertain to the online learning experience. These questions range from semi-structured (open response) to a 5-point Likert scale (strongly agree, agree, neutral, disagree, strongly disagree). There was also a section where the subject could list their demographic information. This information was solely utilized to understand if the sample size was skewed. For example, if substantially more females respond to the survey than males, the sample may not accurately represent student perceptions of online learning. The Likert scale questions in the survey are as follows:

1. Overall, I would rather attend full-time online learning rather than in-person learning.
2. My overall level of comfort was greater in online school than in in-person school
3. I learn better in online school than in in-person school
4. I believe online learning is more convenient than in-person learning
5. I believe online learning is lacking in terms of interaction
6. Technological difficulties have, to some degree, hindered my online learning experience
7. I believe online learning has the potential to permanently replace in-person learning in the future
8. I will take an online course in the future

As opposed to free-response questions, Likert scale questions provide more concrete answers. The student responses are separated into five categories, making organizing student responses and interpreting general student evaluations of online learning more straightforward. Although many questions are quite general, such as number one, which asks if students would rather attend full-time online learning over traditional learning, they are integral for analyzing how students generally view online learning in relation to in-person learning. Other questions are more specific, such as questions four through six, which revolve around specific factors that have been commonly associated with student perceptions of online learning. These questions are essential in understanding the factors that impact student perceptions of online learning. Finally, questions seven and eight hope to gauge student perceptions of

the potential of online learning. All of these questions were specifically designed to reach one of my four research goals. The semi-structured questions in the survey are as follows:

1. If any, what change in online learning would most improve your opinion of online learning?
2. If any, name the most prominent factor that positively impacted your perception of online learning?
3. If any, name the most prominent factor that negatively impacted your perception of online learning?

Semi-structured questions give the respondents opportunities to express their views with more nuance. They contain fewer barriers that constrict the respondent from thinking critically. These questions hoped to catalyze critical thinking amongst the respondents. I hoped that respondents answered question one with detail, as it was an integral part of understanding how online learning can be improved in the future. Question two and three deal with potential positive and negative factors that impact student perceptions of online learning. In contrast to questions four through six in the Likert scale questions, the respondents can answer the question freely and possibly identify new factors that have not been commonly considered throughout past research.

The survey was distributed to high school students across New Jersey via social media and messaging. I also distributed the survey through various teachers across New Jersey high schools. To ensure balanced demographics, I contacted teachers within schools of varying locations and economic classes. Students filled out an informed consent form; after completed, they were given a link to the online survey. I utilized the Google Forms program for the survey, as it was the most familiar to the respondents. It also was the most advanced in the user interface, allowing a detailed analysis of the respondent's answers to the various questions. This survey must have a relatively large sample size to be accurate. Therefore, I marketed for the survey accordingly to ensure a sufficient sample size.

There were various limitations associated with conducting the survey. It naturally was challenging to make sure the sample size was representative of the student population of New Jersey. At times, males

and Asians were much over-represented in my survey, which would lead to inaccurate results. I mitigated this limitation by periodically checking if my respondents' demographics matched up with the New Jersey averages. Therefore, when I spotted significant skews in my sample, I adjusted accordingly by targeting specific groups. Another challenge in the surveying process was obtaining a sufficient sample size. I marketed my survey extensively on social media and sent my survey to numerous teachers within various schools to prevent this limitation.

## 4. Results

### 4.1 Quantitative Data

The survey received one hundred and four results from students across over ten high schools in New Jersey. Most responses came from schools in Camden County, which is located in southern New Jersey. Student populations within these schools ranged from 8%-55% economically disadvantaged (gross income for household size of four less than \$52,000). Most schools within this area had relatively diverse student populations. Other responses came from schools in northern New Jersey, which generally had wealthier students. Every high school student surveyed partook in full-time online learning for over a semester. The economic, gender, and racial demographics can be found in Figures 1, 2, and 3.

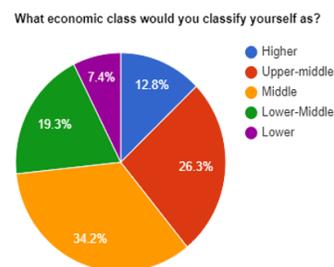


Figure 1. Pie-chart showing the economic-class distribution of the surveyees.

The Likert-scale question results are presented in the quantitative data section, while the open-response question results are presented in the qualitative data section. The responses to the Likert-scale questions can be found in Figures 4 through 11. (Note: 1=Strongly Agree, 2=agree, 3=neutral, 4=disagree, 5=strongly disagree).

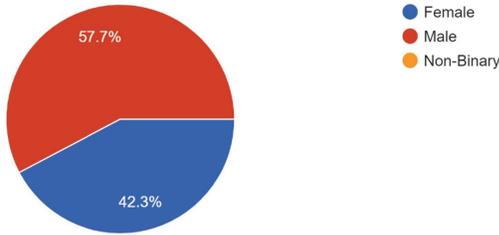


Figure 2. Pie-chart depicting the gender distribution of the respondents.

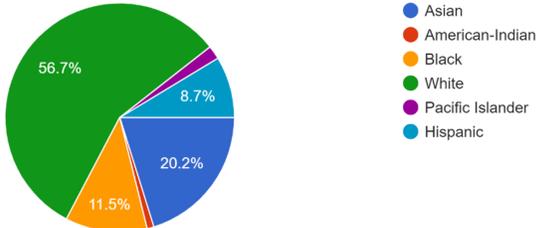


Figure 3. Pie-chart portraying the racial demographics of the respondents.

The demographic information shown in Figures 1, 2, and 3 shows the respondents' economic, gender, and race distribution. Figure 1 shows that respondents classified themselves as primarily middle to upper-middle class, with slightly fewer lower-class individuals than higher-class. These results were self-classified based on the student's perception of their wealth, meaning I did not give set guidelines for which income bracket meant which class. I thought this was preferable because there is no "official" definition of how each income bracket matches up with each class, so I did not want my question to be subjective to my personal classifications. Figure 2 illustrates that there were slightly more respondents identifying as male than female. Figure 3 shows that most respondents were White, followed by Asian and Black. While the distributions of the demographic results are not perfect, I believe they are close enough to represent New Jersey student perceptions of online learning accurately.

#### 4.2 Likert-Scale Questions

In Figure 4, I asked students if they would rather attend online learning than in-person learning. 31.7% of students strongly agreed with that statement, 20.2% agreed, 15.4% were neutral, 11.5% disagreed, and 21.2% strongly disagreed. Students generally agreed that they would rather attend online learning

than in-person learning; though, a substantial portion of students still prefer in-person instruction.

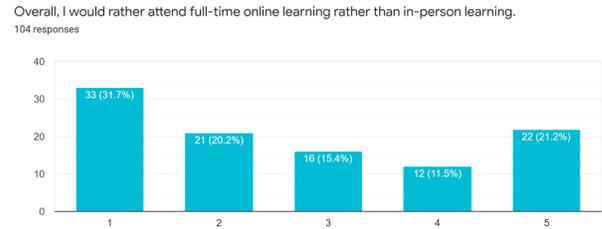


Figure 4. Bar graph depicting whether respondents agree that they would rather attend full-time online learning than in-person learning

In Figure 5, I questioned students if they believed that they had a greater level of overall comfort in online learning. 38.5% strongly agreed with that assertion, 21.2% agreed, 15.4% were neutral, 9.6% disagreed, 15.4% strongly disagreed. Comfort is a positive attribute of online learning, according to students. Interestingly, a portion of students agreed that while online learning is more comfortable than in-person instruction, they would still rather attend in-person learning.

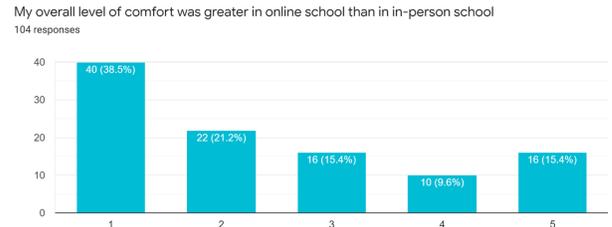


Figure 5. Bar graph showing if students agreed that their comfort was greater in online school than in in-person school

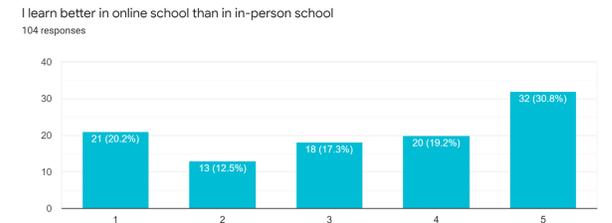


Figure 6. Bar graph showing whether students believe they learn better in online school than in in-person school.

In Figure 6, I asked students if they thought they learned better online than in an in-person environment. 20.2% strongly agreed with that statement, 12.5% agreed, 17.3% were neutral, 19.2% disagreed, 30.8% strongly disagreed. Figure 6 is the

only figure that received more responses with disagreements than agreements. Students' responses show that students believe they learn better in an in-person setting. One might think that because students negatively perceive their ability to learn in an online setting, they would dislike online learning; however, this is not the case for this sample of students as they generally positively rated online instruction.

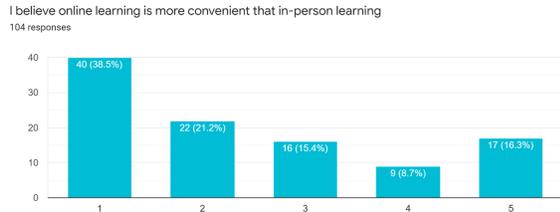


Figure 7. Bar graph depicting whether students believed online learning was of greater convenience than in-person learning.

In Figure 7, I questioned students if they believed online learning is more convenient than in-person learning. 38.5% strongly agreed with that assertion, 21.2% agreed, 15.4% were neutral, 8.7% disagreed, 16.3% strongly disagreed. Similar to comfort, students believe that convenience is a positive attribute of online learning. Figure 7 and Figure 5 nearly have identical distributions, likely because convenience and comfort are similar attributes.

In Figure 8, I asked students if they thought online learning was lacking in interaction. 35.6% strongly agreed with that assertion, 23.1% agreed, 16.3% were neutral, 9.6% disagreed, 15.4% strongly disagreed. Lack of interaction seems to be a substantial negative factor in students' perceptions of online learning; although, it seems that other positive attributes, like comfort and convenience, outweighed the lack of interaction in impacting students' overall opinion of online learning.

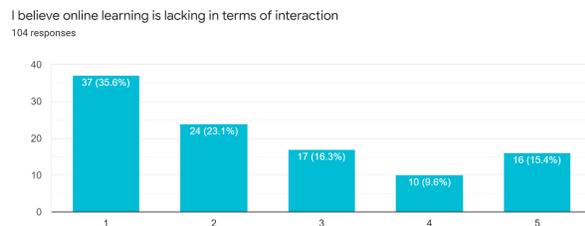


Figure 8. Bar graph portraying if students believe online learning is lacking in terms of interaction.

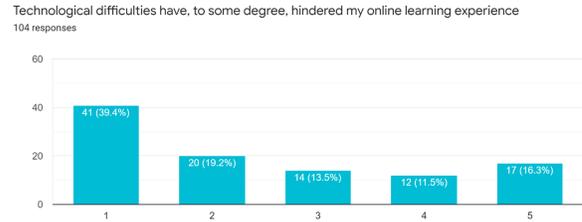


Figure 9. Bar graph depicting whether students believe technological difficulties have hindered their learning experience.

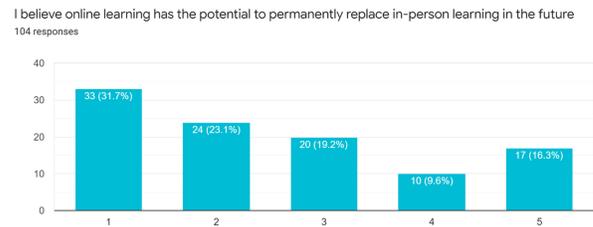


Figure 10. Bar graph showing if students believe online learning has the potential to replace in-person learning in the future.

In Figure 9, I asked students if technological issues have, to some degree, hindered their online learning experience. 39.4% strongly agreed with that statement, 19.2% agreed, 13.5% were neutral, 11.5% disagreed, 16.3% strongly disagreed. Students most strongly agreed with the statement in this figure. This result logically makes sense as online learning has only become widespread recently, thus the technology is far from perfect.

In Figure 10, I inquired students if they believed that online learning could permanently replace in-person learning in the future. 31.7% strongly agreed with that assertion, 23.1% agreed, 19.2% were neutral, 9.6% disagreed, 16.3% strongly disagreed. Despite various negative attributes of online learning, students still believe in the potential viability of online learning. This figure had the highest percentage of "neutral" responses, which is likely caused by the theoretical nature of the question. Many students may not surely understand what the future entails for online learning.

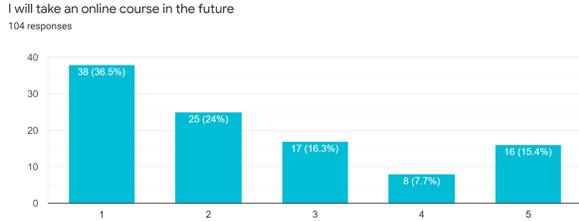


Figure 11. Bar graph depicting if students would be willing to take an online course in the future.

In Figure 11, I questioned students if they would take an online course in the future. 36.5% strongly agreed with that assertion, 24% agreed, 16.3% were neutral, 7.7% disagreed, 15.4% strongly disagreed. Even though this question did not receive the most “strongly agree” responses, it received the most “agree” responses, which is likely because students are still uncertain about online learning, and, consequently, they would not “strongly agree” about their future participation in online learning. Overall, it makes sense that students would be willing to take an online class in the future as students generally positively evaluated online learning.

#### 4.3 Qualitative Data

The open-response questions yielded mostly short responses (2-3 words); I sorted the responses for each question into different categories. For instance, if, in Figure 14, a respondent believed that their inability to foster connections with peers most negatively impacted their perception of online learning, I would manually sort this answer into the “social related” section. If another respondent believed that the continual technological issues encountered in online learning most negatively impacted their opinion of online learning, I would put this response as “technology related.” If I found that the response could not be sorted into any group, or if the question was not adequately answered, I labeled this response as “other.” The pi-chart of the types of responses can be found in Figures 12, 13, and 14.

In Figure 12, I questioned the respondents on what would most improve their perception of online learning. 35% of respondents agreed that an increased sense of community and collaboration with peers would improve their perception of online learning. One student believed that online school should foster

“more time spent on collaborative projects rather than independent work.” Other respondents believed improved technology and more engaging teaching styles (both 10%) would improve their online learning experience.

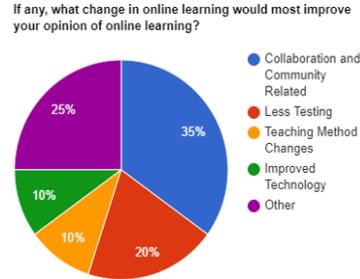


Figure 12. Pie chart showing how students generally responded when asked what change would most improve their opinion of online learning.

In Figure 13, I asked respondents which factor most positively impacted their online learning experience. The most common trend by far, yielding approximately 50% of responses, pertained to convenience. Many students mentioned that “later school start times” and “more lenient schedules” positively impacted their online learning experience. 20% of students also believed that the comfort of learning online greatly improved their perception of online learning, with one student stating that “being able to learn from the bed made online learning all the better.” Another trend within the responses, about 10%, was that the less time-consuming nature of online learning allowed students to “better pursue non-school related hobbies.”

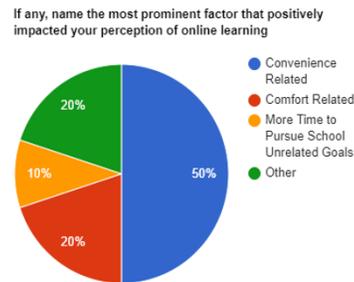


Figure 13. Pie chart showing how students generally responded when asked what factor most positively impacted their perception of online learning.

In Figure 14, I asked respondents which factor most negatively influenced their perception of online learning. 40% of responses were social related, with many respondents believing that online learning had

a “lack of social interaction.” 20% of respondents believed that lack of engagement most negatively impacted their perception of online learning, which I did not consider beforehand. Multiple students declared that online learning was “repetitive.” One student believed that “online learning is a lot more boring than in-person school.” 15% of students believed that online learning had a lesser quality of learning than in-person learning. To many, “online learning did not mimic the traditional school atmosphere,” and distractions hindered their learning ability.

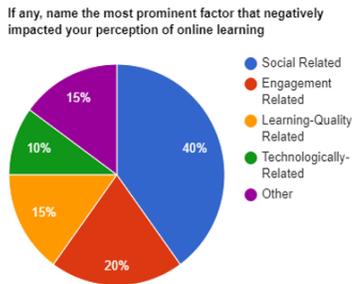


Figure 14. Pie chart portraying how students generally responded when asked what factor most negatively impacted their perception of online learning.

### 5. Discussion

Through Figure 4, I found that most full-time high school students would rather attend online than in-person school. 51.9% of students strongly agreed or agreed that they would rather than online school than an in-person school (compared to the 32.7% who disagreed or strongly disagreed). These results are congruent with the research done before Covid-19, where online learners voluntarily chose online learning over in-person learning; However, this contradicts the research done during the infancy of Covid-19. During this time, many studies showed that students abhorred online learning and would much rather return to in-person school. I deduce that student perceptions of online learning have improved due to students’ adaptability to their environment. At the time of surveying, all surveyees have attended over a semester of fully online school. This experience has allowed many students to adjust their learning techniques and thus perceive online learning positively.

Figure 10 and Figure 11 portray those students who believe in the futuristic potential of online learning. In figure 10, 54.8% of students strongly agreed or agreed that online learning could potentially replace traditional learning, while only 25.9% disagreed or strongly disagreed. These results surprised me, and it shows how the students’ experiences with online learning have improved their perceptions. In Figure 11, 60.5% of students strongly agreed or agreed that they would take an online class in the future, while 23.1% disagreed. The results show that students believe that online learning can overtake in-person learning with some technological improvements. Figure 10, which shows that 58.6% of students faced technical difficulties that hindered their online learning experience, suggests that student perceptions of online learning will also improve with improved technology.

Through the research, I have identified various areas of improvement that can positively impact student perceptions of online learning. Figures 9, 12, and 14 suggest that technological difficulties hinder student perceptions of online learning. Therefore, technological improvements that foster faster internet, higher-quality cameras, and more fluid conversations will naturally result in improved perceptions of online learning. Figure 14 shows that the most prominent factor that negatively impacts perceptions of online learning is the lack of social interaction. Futuristically, improved technology can encourage increased online social interaction amongst peers. Many students believe that online learning does not mimic traditional learning well, which technological improvements can change. Students will naturally socialize in an online learning setting that more accurately mimics traditional learning, thus improving their perceptions of online learning. Research also portrayed that a teaching style that fosters group interaction and less individual work would improve student perceptions of online learning. Figure 8 shows that students believe increased collaboration and a sense of community would improve their perceptions of online learning. Consequently, a teaching style that allows students to team-build and creates a sense of community would drastically improve online students’ experience. Figure 14 illustrated that students believed online

school lacked engagement. With a more personalized and engaging teachings style, student perceptions of online learning will naturally improve.

I have identified six factors that I believe most prominently impact student perceptions of online learning. The first factor is convenience, which of course, is a positive factor. In Figure 13, 50% of students believed that convenience most positively impacted their online learning experience. The ability to attend class anywhere in the world certainly benefits the case for switching to online learning. The next factor is comfort: the second most prominent factor in Figure 13 that positively impacted student perceptions of online learning. Figure 5 showed that 59.7% of students strongly agreed or agreed that their level of comfort in online learning was greater than in-person learning (25% strongly disagreed or disagreed). Comfort plays a significant role in the online learning experience. The following four factors are all negative, and the most prominent of these factors is a lack of social interaction (Figure 8, 12, 14). Other negative factors found in the results are as follows: general learning quality (Figure 6, 14), technological issues (Figure 9, 12, 14), and lack of engagement (Figure 14). While there are more prominent negative factors than positive ones, the two positive factors, convenience, and comfort outweigh the negative ones. Interestingly, students seem to prioritize their time over their learning quality.

## **6. Conclusion**

The utilization of online learning has drastically increased due to Covid-19, and, likely, this newly popularized form of learning is here to stay. Previous research has shown conflicting results about student perceptions of online learning. This research definitively shows full-time online high-school students' evaluations of online learning, as well as the specific factors that impact these evaluations. Teachers and school boards must consider the factors that impact student perceptions of online learning when adapting their teaching styles and curriculum respectively; software engineers should also consider student perceptions when constructing new online learning platforms. The research shows that lack of

engagement and lack of community hinder students' online learning experience. Therefore, teachers and school boards must adjust accordingly to foster engagement and community in an online setting within their schools. The research shows that despite various flaws, students strongly believe in the futuristic potential of online learning. While to some, it is far-fetched, others believe that online learning can replace in-person learning in the future. For investors, understanding student perceptions of the potential of online learning is vital for their investments in the growing online learning market. Many of the pitfalls of online learning today can be solved through improved technology and software updates. With the knowledge of what specifically hinders students' online learning experience, software engineers can better construct a system that fosters the requests of its students. For example, the research shows that a lack of social interaction strongly hinders students' perceptions of online learning. With this knowledge, software engineers are encouraged to create a system that makes socialization amongst peers more appealing a fluid. Wholistically, this research provides valuable information for various groups that, through time, can drastically improve the online learning experience for students.

In the process of my research, I have found various limitations that must be addressed. While the results may be accurate for the time being, they likely will become outdated very quickly. Student perceptions of online learning are drastically changing as technology and society change. Future generations will likely evaluate online learning more positively because they have acclimated to advanced technology. The same applies to the factors that impact student perceptions of online learning. In the coming years, societal changes may influence the different factors that students believe positively and negatively impact online learning. Becoming outdated is inevitable for studies on this topic, and future researchers should be aware of this fact. Another limitation is a relatively small sample size of one hundred and four responses. While distributing surveys to students through their respective schools seemed logical, the survey did not receive as many responses as I initially hoped. I would recommend future research to conduct a more widespread

distribution to ensure a holistic representation of students. The final limitation pertains to the surveyees themselves. Although all have attended full-time online school for over a semester, and some for about a year, very few would consider themselves “full-time online students.” Most view online learning as a temporary replacement for in-person learning during Covid-19. This lack of experience and commitment towards online learning may slightly skew my results. For future researchers, it would be ideal for surveying those with ample experience in full-time online learning. These individuals may provide a more nuanced perspective on online learning and provide a more accurate evaluation of online learning as a whole.

Future research on perceptions of online learning can be conducted on different samples. While it is important to understand student perceptions of online learning, it is also crucial to understand parental perceptions of online learning. Therefore, future research could potentially target the parental perspective of online learning. In terms of student perceptions of online learning, researchers could perform statistical analyses on the factors that impact student perceptions. I performed a more qualitative approach in my analysis of these factors, so additional research that quantifies these factors could further the body of knowledge. Finally, the research portrayed that students believe online learning could benefit from increased engagement. Future research should construct an in-depth analysis of this relationship so that teachers can further understand how their online teaching style impacts their students.

## References

Algar, S. (2020, July 6). *Harvard will hold all classes online next year — but still charge full tuition*. New York Post.

<https://nypost.com/2020/07/06/harvard-will-hold-all-classes-online-next-year-charge-full-tuition/>

Betz, B. (2020, May 4). *College students file lawsuits seeking refund from schools moved online during coronavirus lockdowns*. Fox News.

<https://www.foxnews.com/us/university-students-law-suit-refunds-schools-online-coronavirus-lockdowns>

City News Service. (2021, May 10). *Majority Of*

*LAUSD Students Choose Not To Return To School*. NBC Los Angeles.

<https://www.nbclosangeles.com/news/local/majority-of-laUSD-students-choose-not-to-return-to-school/2592123/>

Esquivel, P. (2020, September 25). *Parents sue LAUSD for online learning “educational crisis.”* Los Angeles Times.

<https://www.latimes.com/california/story/2020-09-24/parents-sue-laUSD-blasting-its-online-learning-for-creating-an-educational-crisis>

Georgie, M. G. (2021, June 18). *The History of Distance Learning | An Online Education Timeline*. World Wide Learn.

<https://www.worldwidelearn.com/articles/history-of-distance-learning/>

Lantry, L. (2020, June 23). *ABC News Exclusive: Harvard Law student sues university over tuition prices as classes remain online*. ABC News.

<https://abcnews.go.com/US/abc-news-exclusive-harvard-law-student-sues-university/story?id=71345292>  
[abcnews.go.com/US/abc-news-exclusive-harvard-law-student-sues-university/story?id=71345292](https://abcnews.go.com/US/abc-news-exclusive-harvard-law-student-sues-university/story?id=71345292).

Li, C. L. (2020, April 29). *The rise of online learning during the COVID-19 pandemic*. World Economic Forum.

<https://www.weforum.org/agenda/2020/04/coronavirus-education-global-covid19-online-digital-learning>

Maskun, M., Rusman, T., Suroto, S., & Rahmawati, F. (2020). Student Perceptions of Online Learning. *International Journal of Multicultural and Multireligious Understanding*, 7(2), 67-73.

McBrien, J. L., Cheng, R., & Jones, P. (2009). Virtual spaces: Employing a synchronous online classroom to facilitate student engagement in online learning. *International review of research in open and distributed learning*, 10(3).

Nambiar, D. (2020). The impact of online learning during COVID-19: students’ and teachers’ perspective. *The International Journal of Indian Psychology*, 8(2), 783-793.

Reisetter, M., & Boris, G. (2004). What works: Student perceptions of effective elements in online learning. *Quarterly Review of Distance Education*, 5(4), 277.

Rodriguez, M. C., Ooms, A., & Montañez, M. (2008). Students' perceptions of online-learning quality given comfort, motivation, satisfaction, and experience. *Journal of interactive online learning*, 7(2), 105-125.

Thompson, E. T. (2021, May 27). *History of Online Education*. TheBestSchools.Org. <https://thebestschools.org/magazine/online-education-history/>

Tichavsky, L. P., Hunt, A. N., Driscoll, A., & Jicha, K. (2015). " It's Just Nice Having a Real Teacher": Student Perceptions of Online versus Face-to-Face Instruction. *International Journal for the Scholarship of Teaching and Learning*, 9(2), n2.

Widodo, A., Ermiana, I., & Erfan, M. (2020). Emergency online learning: How are students' perceptions. In *4th Sriwijaya University Learning and Education International Conference (SULE-IC 2020)* (Vol. 513, pp. 263-268).

# Diurnal Variations of Carcinogenic Soil Radon Emissions and Various External Factors

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## Abstract

In this study, we made many radon measurements in an area where we know that carcinogenic soil radon is intense to investigate the daily radon emission changes and the external factors affecting these changes. In this study, we realized the measurements in three different points that are very close to each other (such as 13 m, 7 m). Lemon trees with shallow roots affected the radon emission values more than Oleander trees with relatively deep roots, while the third point, a tree-free point, measurements were intermediate of both. We believe that the roots of trees absorb and collect natural radon gases, and upon planting around the buildings, the trees may prevent radon leakages towards the basements.

*Keywords: Medical Geology, Radon, Emission, Daily variation, Carcinogen, Prevention, Tree roots*

## 1. Introduction

The radioactive decay series of <sup>238</sup>U produces radon, a natural (<sup>222</sup>Rn, half-life 3.84 days) radioactive, inert, colorless, and odorless noble gas (Bonotto & Santos, 2007). The radioactive decay series of <sup>238</sup>U is complex and produces alpha, beta, and gamma radiation. We present them with their half-lives in Figure 1.

Radioactive decay is a natural, spontaneous process in which an atom of one element decays or breaks down to form another element by losing atomic particles (protons, neutrons, or electrons) (Otton, 1992). Although uranium and thorium are naturally present in all types of rocks, their concentration is maximal in silica-rich rocks like granites, syenites, pegmatites, aplite, rhyolites, dacites, or their metamorphic counterparts such as gneiss, schists, and migmatites (Aydar & Diker,

2021).

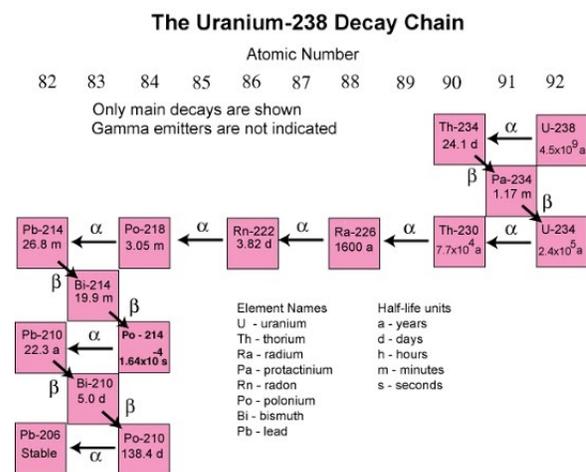


Figure 1. Radioactive decay of <sup>238</sup>U and its products (figure from USGS Glossary: <https://pubs.usgs.gov/of/2004/1050/uranium.htm>)

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USEPA (2021), (Environmental Protection Agency-USA) states that radon gas, which can cause serious health problems such as cancer, is constantly produced in nature through the  $\alpha$ -decay of  $^{226}\text{Ra}$ . Outdoor radon dissipates rapidly due to atmospheric conditions and is generally not a health concern. However, indoor radon exposure, where daily exposure can take long hours in living, work, and school areas, negatively affects health. Higher indoor accumulation capacity of radon than outdoor makes indoor exposure critical (Petrovic, 2017). There is an increased risk of lung cancer with indoor radon exposure higher than 100 Bq/m<sup>3</sup>. (Fucici, 2012)

Radon gas enters buildings through cracks in the foundations and other weak spots and condenses inside. Various methods and devices exist in radon measurement for short and long term periods, such as Alpha-TrackDetector, Activated Charcoal, Electret Ion Chamber, Electronic Integrated Device, Continuous Radon Monitor (El-Taher, 2018). Some of these can be expensive systems. However, indoor radon can be controlled and managed with proven, cost-effective techniques (USEPA, 2021), like commercialized portable devices.

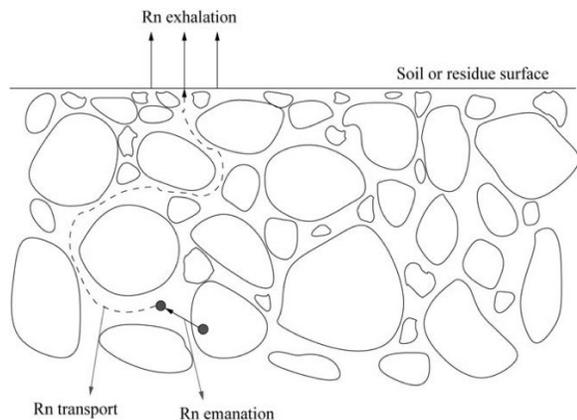


Figure 2. Mechanism of the radon release to atmosphere (from IAEA, Technical Report, Ishimori et al., 2013)

Ishimori, et al. (2013) explain the mechanism of the radon released to the atmosphere from the ground in a technical report of the International Atomic Energy Agency (IAEA) (Figure 2) that radon atoms are not released into the atmosphere due to their very low diffusion coefficient. However, if they are located in the intermediate space between the grains,

they can spread to the surface (Ishimori et al., 2013). Therefore, the diffusion of radon from its location to the atmosphere is mainly due to (a) Emanation — radon atoms escape from the grains to the spaces between them (b) Transport — diffusion and advective flow cause the radiated radon atoms to move to the ground surface (c) Emission — radon atoms carried to the earth's surface are then released into the atmosphere (Moed et al., 1998).

Diffusion, convection, and general flow of air or water are the principal mechanisms for the transport of Radon (IARC, 1988). High soil porosity increases the diffusion rate. Also, modest amounts of moisture enhance radon release, whereas high moisture levels decrease it because of slowed diffusion (UNSCEAR-United Nations Scientific Committee on the Effects of Atomic Radiation, 1982; Aydar and Diker, 2021).

It is explained by UNSCEAR, (1982) that after radon enters the water or air environment in the soil, it is transported by mechanisms such as diffusion, percolation, and mechanical and convective flows. Radon alone can be transported over minimal distances by diffusion; for example, radon can be carried by diffusion up to 5 m in the air, 5 cm in water, or up to 2 m in soil (UNSCEAR, 1982). In addition, earthquakes or artificial quakes can help radon transport within the ground (Aydar and Diker, 2021).

Radon was classified as a human carcinogen (in the same carcinogen group as tobacco smoke, asbestos, and benzene) in 1988 by the International Commission on Radiation Protection (IARC) (Baskaran, 2016). WHO (World Health Organization), (2009) recommends that countries adopt reference levels of the gas of 100 Bq/m<sup>3</sup>, equivalent to 2.7 pCi/L. Besides, each country has its action level threshold values for indoor radon changing between 148 to 400 Bq/m<sup>3</sup>. Upon inhalation of radon, high-energy ionizing alpha particles are produced from the decay of  $^{222}\text{Rn}$ , and each of the alpha particles can interact with biological tissue in the lungs leading to significant damage to the DNA of a cell (Moore et al., 2014; WHO, 2009). Such DNA damage can, in principle, occur at any level of  $^{222}\text{Rn}$  exposure (Moore et al., 2014).

It is generally accepted that there should be at least one mutation and proliferation of intermediate cells that have sustained some degree of DNA damage, significantly increasing the pool of cells available for cancer development (WHO, 2009).

WHO, (2009) also stated that radon could be related to some other diseases other than lung cancer for example, when an individual spends time in an atmosphere that contains radon and its decay products, the part of the body that receives the highest dose of ionizing radiation is the bronchial epithelium. However, the extrathoracic airways and the skin may also receive appreciable doses (Aydar and Diker, 2021). In addition, Kendall and Smith, (2002) propose the low dose receipt of radon by the kidney and the bone marrow. Moreover, some DNA damages in peripheral lymphocytes increase with high indoor radon concentrations have been proposed by Hellman et al., (1999). Similarly, Walczak et al., (2020) offer statistically significant differences in levels of DNA damage in peripheral lymphocytes (Aydar & Diker, 2021). A considerable increase in female breast cancer incidence in Iceland has been reported in geothermal areas where the geothermal fluids have a high concentration of Radon (Kristbjornsdottir and Rafnsson, 2012).

Radon levels are never constant even in the same measuring point and change hourly, daily, and seasonally (Chambers et al., 2011; Siino et al., 2019; Aydar and Diker, 2021). Usually, the radon concentrations were lower during daylight than during the night. However, during the hours just before dawn, the air frequently becomes still, and the radon and radon daughter concentrations rise to a maximum (UNSCEAR, 1982).

In this study, we investigate the daily soil radon gas concentration changes and possibly external factors affecting it by measuring soil radon gas at the same sector but at different very close points for periods ranging from 24 hours to 48 hours.

## 2. Materials and Methods

We reported a radon survey during July-August 2021 using the Radon Eye+ device of Radon FTLab company. To examine the effect of external factors, we selected three different, very close to each other

measuring points on the same geological ground, where physical parameters change such as near/far from the building, presence of trees, etc. Therefore, the maximum distance between the three selected points was measured as 13 meters. (Figure 3). The first point was under the lemon tree, 50 cm from the building. The second point was selected as the bottom of the oleander tree, 13 meters from the first point. The third point was determined 7 meters ahead of the first point, again close to the building. The third point lacks the trees.



Figure 3. Location of outdoor measurement points

Aydar and Diker, (2021) previously realized the radon measurements on this region and stated that the region contains very high carcinogenic soil radon gas. We used the same method described in Aydar and Diker,(2021), in which we put our device in a sealed, isolated PVC bucket with soil during outdoor measurements. The measurement started after the first 10 minutes, which was necessary for air stabilization within the chamber (Figure.4). We used in this work Radon eye+, a pulsed ion chamber type device with a high sensitivity of 0.5cpm/pCi/l, about 20–30 times more than a conventional radon detector (Aydar and Diker, 2021). It can measure till to 9700 Bq/m<sup>3</sup> of radon, with gas temperature and humidity (Aydar and Diker, 2021). Regardless of the measurement time (day, week etc.), Radon Eye+ also gives the average of the measurements (without any statistical error margin).Its first reliable data out time is below 60 min from measurement start with an accuracy of <10% at 10pCi/l according to the producer of the detector. The accuracy and precision

spec were tested by the KTL (Korea Testing Laboratory administrated by the Korean government) (Aydar and Diker, 2021).



Figure 4. Radon measurement within an isolated PVC bucket, together with atmospheric humidity and soil humidity measurement

In addition to the outdoor measurements, indoor measurements were also carried out in a flat room on the garden floor with the same device. The possible airflow that may affect the measurement values is prevented by closing the window and door of the room, so we did not use a bucket during indoor measurement. While making the radon measurements, air humidity, temperature, air pressure, soil humidity values were also measured (Figure.4). Radon Eye+ device instantaneously measures the soil gas humidity and temperature together with radon concentration. In addition, we measured meteorological conditions with the ADC-Silva device, illustrated in Fig.4. The ADC-Silva measures altitude, barometric pressure, temperature, wind, and air humidity. Moreover, we carried out soil moisture measurements at the points where radon was measured with Rapitest Digital Moisture Meter. The approximately 15 cm long probe was inserted into the soil, and the soil moisture value was read digitally.

### 3. Results

#### 3.1. Meteorological and Soil conditions

The air humidity ranged between 54-72%, while the air temperature was about 35°C max. At night, this value drops to 24°C. The air pressure varied between 1002-1014 mbar.

Our moisture meter, inserted 15 cm into the soil, did not read any humidity value at the measurement points, meaning that the soil where the Radon Eye+ was installed is very dry.

We also observed the insolation hours of the measurement points, as the direct exposure of the sun's rays to the soil may be important for radon emission. The sunlight time interval of the first spot is around 3-5 in the afternoon, while it remains in the shade during the other hours. Sunlight hits the second spot at 7:40 a.m., while the detector is in the shadow of the tree around 2 p.m. At the third point, the sun's rays hit 8:30 a.m. It arrives until 2:30 p.m.

#### 3.2. First Point

We present the measurement device in Figure 4. This measuring point, which is very close to the building wall, is also protected from direct sunlight as it is located under the lemon tree. Radon measurements after 50 hours are given in Figure 5. In these measurements, the radon emissions fluctuate throughout the day. While a maximum soil radon value of 2667 Bq/m<sup>3</sup> is measured, this value decreases to 1064 Bq/m<sup>3</sup>. The average soil radon value was around 2113 Bq/m<sup>3</sup> at 50 hours of measurement. The lowest values were around 4-5 p.m., while the highest was reached between 05-09 a.m. In Figure 5, we present the gas humidity and temperature relationship measured by the device. The humidity and temperature relationship graph is very similar to the Radon Emission graph measured as a function of time, and the curve represent a smooth periodic oscillation along the measurement interval. While the gas humidity recorded by Radon Eye+ varies between 75-99%, the highest gas temperature values are kept in the measurements with the lowest humidity (37-39°C). Gas humidity is directly proportional to the Radon concentration, and the radon content increases with moisture. However, the temperature is inversely proportional.

#### 3.3. Second Point

We selected to install our device under an Oleander tree, 13 meters far from the building (Figure 3). At this point, the detector received direct sunlight at 7:40 a.m. At the end of the 24 hours of

uninterrupted measurement, we wanted to quickly move the sensor to the first measurement point close to the building and to see the radon emission difference. We obtained a maximum of 1589 Bq/m<sup>3</sup> and a minimum of 887 Bq/m<sup>3</sup> radon emission values (Figure 6). The daily average radon value is around 1276 Bq/m<sup>3</sup>. While the highest values were measured between 05-08 a.m., the lowest soil radon yield was measured between 10 a.m.-4 p.m. It should be mentioned that these time intervals are the hours that the soil is exposed to direct sunlight. Simultaneously with the radon measurement, we also measured the humidity and temperature values and give in Figure 6. The relationship between humidity and temperature show that the humidity is inversely proportional to the increase in temperature, and the humidity values decrease with the temperature rise.

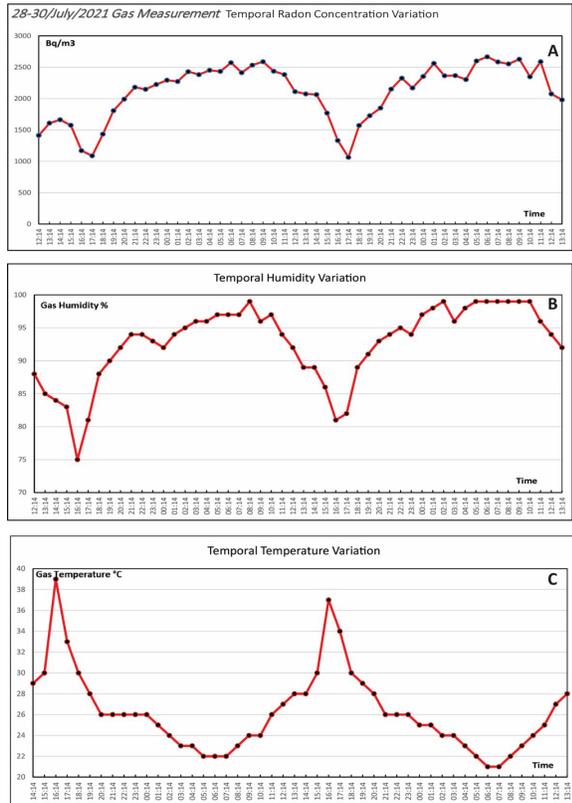


Figure 5. Time dependant Soil Gas measurement. A. Hourly Radon Emission during two days, B. Simultaneous radon gas humidity, C. Simultaneous radon gas temperature measurements in First Point (very close to building).

At the same time, we observe that radon values

decrease at low humidity and high-temperature values. For example, humidity is between 63-72%, and temperature values vary between 24-29°C, whereas the radon values are between 1322-1589 Bq/m<sup>3</sup>. In addition, between the hours when the humidity was between 52-57%, the gas temperature was between 31-37°C, and the radon values were between 911-1290 Bq/m<sup>3</sup>.

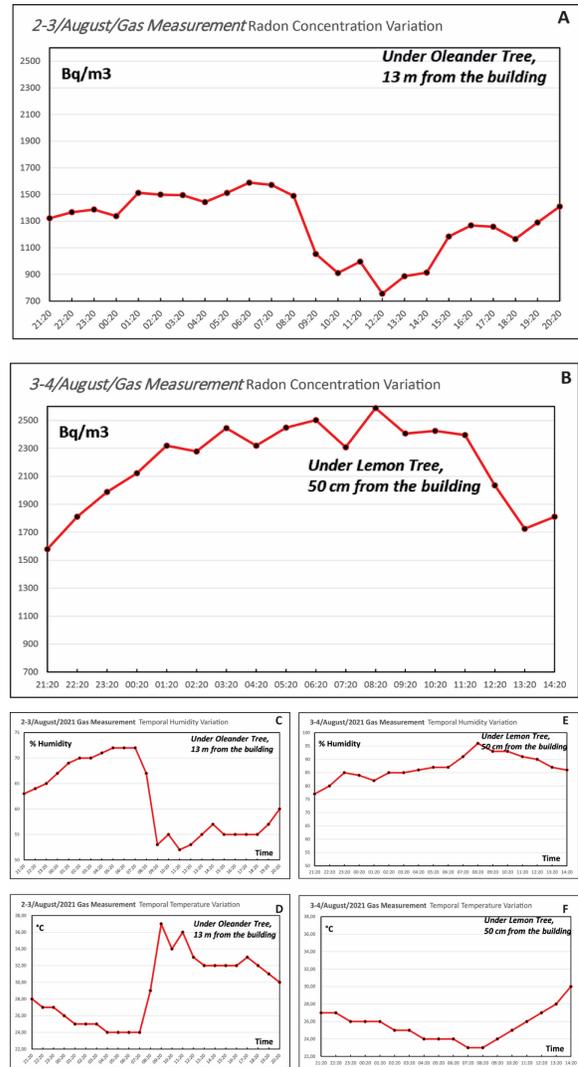


Figure 6. Continuous radon measurement in two different points. A. The measurements in the first 24 hours have been realized under the oleander tree, B. the second 24 hours below the lemon tree. C. Radon gas humidity variation during the measurement under Oleander tree, D. Temperature variation of Radon gas under Oleander tree, E. Radon gas humidity variation during the measurement under Lemon tree, F. Temperature variation of radon gas under Lemon tree

### 3.4. Third Point

The graphical representation of this point, which is close to the building but has no trees around it (Figure 3), is given in Figure.7. The graphic profile of the third point is very similar to that of the second point.

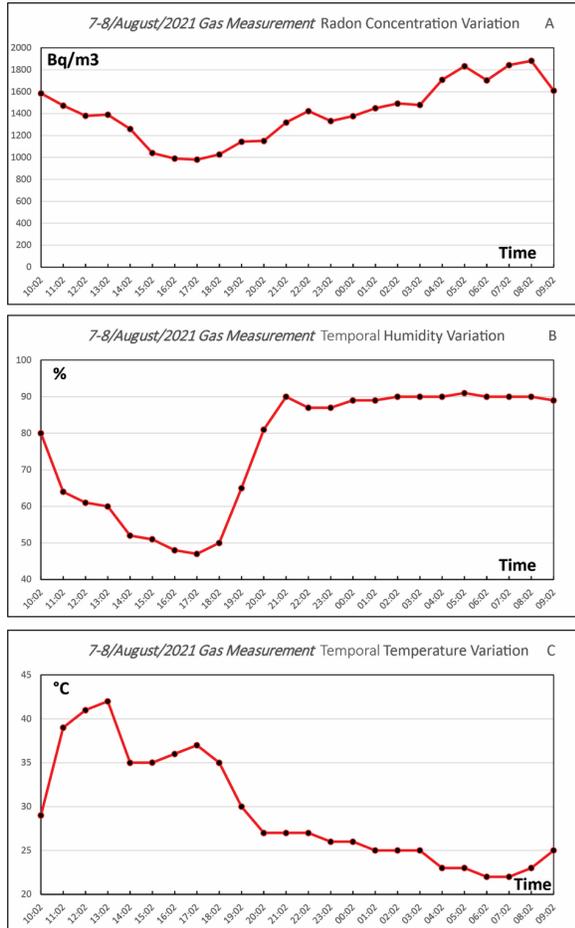


Figure 7. Time dependent A. Daily radon emission, B. Simultaneous humidity variation, C. Simultaneous temperature variations at Point 3.

The radon values fluctuate between 970-1881 Bq/m<sup>3</sup>. The daily average radon concentration is 1406 Bq/m<sup>3</sup>. While we get the highest values in our measurements between 04-09 a.m., and the lowest was calculated between 3-6 p.m. The relationship between humidity and temperature is the same, with low humidity (47-80%), high temperature (29-42°C), and relatively low radon concentration (970-1547 Bq/m<sup>3</sup>).

### 3.5. Indoor Measurement

We also made a 24-hour measurement in the garden floor flat of the building. In Figure 8, we present the daily variation of indoor radon concentration. Indoor radon values ranged between 25-61 Bq/m<sup>3</sup>, while the daily average indoor radon value was 41 Bq/m<sup>3</sup> as calculated by the device. While the radon values rise at dawn towards the morning, they do not show a particular order and fluctuate according to the hours.

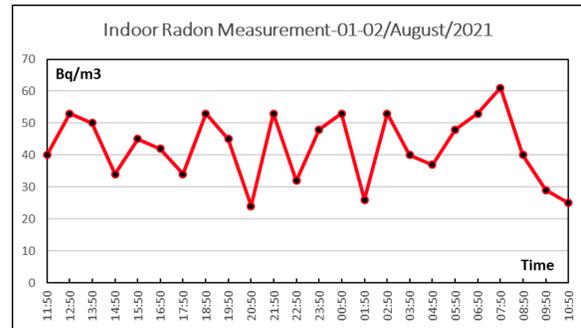


Figure 8. Indoor radon variation for 24 hours

## 4. Discussion

Radon has carcinogenic properties and causes mainly lung cancer. Many studies also indicate it as a possible cause of leukemia, breast, skin, and gastrointestinal cancers (Aydar and Diker, 2021). We know that the geological characteristics of the bedrock strongly influence radon emission. Aydar and Diker,(2021) mention that the ground's physical properties, such as permeability, porosity, humidity, water level, rock cracks, etc., control radon migration adequately. Radon gas emission helps explore some radioactive mineral resources, geothermal fluids, or buried faults in geology (Khattak et al., 2011). Radon flux increases before the seismic activities in fault zones (Soldati et al., 2020).

Radon is a heavy gas 7.5 times heavier than air and is the only naturally radioactive gas (Heiserman, 1992), so it cannot be easily carried and needs a transporting agent. However, geothermal fluids (Whitehead, 1984), seismic waves, negative pressures around fractures (Baskaran, 2016), even ground vibrations due to the influence of anthropogenic induced seismic waves (Schmid and Wiegand, 1999) help moving radon toward the

surface (Aydar and Diker, 2021).

The USEPA (United States- Environmental Protection Agency) set 148 Bq/m<sup>3</sup> value as an action level for indoor radon ([https://www.radon.com/radon\\_levels/](https://www.radon.com/radon_levels/)). Besides, most European countries accept 400 Bq/m<sup>3</sup> for indoor and 1000 Bq/m<sup>3</sup> for outdoor radon as standard threshold. It is estimated that a reduction of radon levels to below 74 Bq/m<sup>3</sup> would likely reduce the yearly lung cancer deaths attributed to radon by 50% ([https://www.radon.com/radon\\_levels/](https://www.radon.com/radon_levels/)). We conducted this research in the Davutlar region, western Turkey, which has high levels of carcinogenic soil radon (Aydar and Diker, 2021). The average radon gas concentration values we obtained vary between 1406 and 2113 Bq/m<sup>3</sup>, although they vary according to the measurement point. In other words, our values are above 1000 Bq/m<sup>3</sup> in our study area, which corresponds to the accepted action level threshold for outdoor radon. Our measurement points are very close to point 1 of Aydar and Diker (2021) (on the other side of the building). For their point 1, Aydar and Diker (2021) gave an average radon value of 902 Bq/m<sup>3</sup>. This difference may be because we took approximately two days of continuous measurements for each station, not hourly. We know that there has been a definite increase in seismic activities (a 6.9 magnitude earthquake called the Samos earthquake/İzmir earthquake occurred in the region on October 30, 2020, and continuous aftershocks have occurred in the region since that date). We can also think that seasonal drought has advanced, reducing soil moisture, evaporating pore water, and allowing radon to reach the surface more. In our outdoor measurements, we found that radon gas concentrations fluctuate throughout the day. While these fluctuations generally present a certain pattern, they offer the most regular oscillation, especially at the first point. The highest values are reached in the early morning hours, while the lowest are observed around 4-5 p.m. Porstendörfer et al., (1994) propose similar results.

In addition to the high outdoor radon values, indoor radon measurements are quite low (daily average Radon: 31Bq/m<sup>3</sup>), below the action level. Indoor measurements are made by paying attention to the absence of airflow, so there is no dilution of radon

values in the air. The distance between the measurement room and the first measurement point is around 3-4 meters. Besides, indoor measurement does not show a clear increasing or decreasing trend even though we have the highest value in the early morning. In general, we observe that it oscillates with short intervals. In the building built in the 1970s, there is no basement, the room where we measure is on the ground floor. Therefore, it is possible to attribute low radon values to the fact that the foundation insulation of the building is good and that there are no cracks. However, we can also say that cracks formed inside the buildings in this seismic region, albeit small and insignificant, after the Samos/İzmir earthquake. It should be noted that this old building was built without being designed for radon isolation.

In particular, radon emission is positively related to the moisture content of the air and temperature (Kulalı et al., 2017). Faheem and Matiullah (2008) examined the relationship between moisture content and radon emission and stated that radon concentration increased with increasing humidity. Our measurements found that the graphs of radon concentration versus time and the graphs of gas humidity and temperature measured by the radon detector simultaneously showed the same behavior, and the curves were similar. Thus, we can read from the graphs that humidity and radon concentration is directly proportional. However, we would like to point out that gas temperature is inversely proportional to humidity and radon concentration.

While the direct effect of radon in the soil on human health is very low, cancer risks arise as a result of radon leaking from the foundations of the houses, via cracks in the walls of the homes, pipe joints, etc., especially into the basements, reaching high concentrations and long-term interaction with people (exposure). In order to avoid being affected by radon exposure, it is recommended to ventilate homes all over the world constantly. Thus, the radon gas accumulating inside the building will be diluted, and the exposure effect will be reduced (USEPA, 2021).

Furthermore, we have results that can draw attention to another critical point in our study. Namely, our first measurement point was at the

bottom of a lemon tree, which has shallow but widespread roots, very close to the building. The lemon roots stay mainly in the top 24 inches of soil because a system of woody roots develops laterally from the trunk in all directions, traveling horizontally well beyond the tree's drip line (Spengler, 2021). The values we obtained at this point are very high, reaching 2667 Bq/m<sup>3</sup>. Even the smallest value we get is much higher than the outdoor action level value. This is because the amount of radon gas in the pores of the soil increases its concentration 4 times up to 80 cm from the surface (Magonigal et al., 2019). Magonigal et al., (2019) propose that the trees absorb the soil radon gas and release them to the atmosphere. Thus, trees act as radon pumps, bringing the gas to the surface (<https://www.sciencedaily.com/releases/2012/03/120321105525.htm>).

On the other hand, we measured under the oleander tree at our measuring point number two. At this point, our radon values reach a high value of 1589 Bq/m<sup>3</sup>. However, this value is not as high as the value taken under the lemon tree, 13 meters away. Considering that geological control cannot be at such a short distance, this can be explained by the fact that the roots of the tree are deeper. The oleander tree reaches 4 meters in height, that its roots may go to 2 meters. Therefore, radon alone can only advance a few tens of centimeters at most. In this case, the radon absorbed by the oleander roots does not reach the surface thoroughly. Our measurement point number three also has a radon value and graphical profile similar to number two, confirming this hypothesis. Since there are no trees and no roots at our measurement point number three, the values were relatively low at this measurement point, which is approximately equidistant from the first point to the building.

## 5. Conclusion

In this study, we investigated the daily variation of outdoor radon emission and possibly external factors affecting it in an area where carcinogen soil radon is previously known to be high. Radon emission rises at dawn in the morning and decreases to a minimum value in the afternoon. Graphically,

outdoor radon concentrations oscillate throughout the day, while indoor concentration changes hourly within a small concentration range. In our outdoor measurements, radon concentrations are maximum in the early morning hours, while they decrease to a minimum around 4-5 pm.

The measurements taken under the lemon tree with a shallow root system reached the highest values, while the measures under the oleander tree with deeper roots were lower. In addition, the measurements taken from the point close to the building wall, where there is no tree, gave lower values than the values measured under the lemon tree and higher than the oleander. In the meantime, we would like to point out that indoor radon values are pretty low in a place with a soil radon value of >2600 Bq/m<sup>3</sup>. This high radon level may indicate that the foundation of the building is highly impermeable, or it may indicate that the radon entering the building from the foundation of the building is absorbed by the tree roots. In response to radon exposure, ventilation of houses and some special foundation designs are classically recommended.

As demonstrated in our study, in radon-threatened areas, planting trees with shallow root systems, such as lemons, close to buildings, where there is no basement, may absorb soil radon preventing leakage inside the buildings in some percentages. Perhaps deeper rooted trees could be considered for facilities with basements, but this hypothesis needs to be tested.

As a result, we can suggest that trees should be planted close to the buildings and that the roots of these trees absorb radon gas in order to partially or significantly prevent radon leaks into structures.

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## References

Aydar, E. & Diker, C. (2021). Carcinogen Soil Radon Enrichment in a Geothermal Area: Case of

- Güzelçamlı-Davutlar District of Aydın City, Western Turkey. *Ecotoxicology and Environmental Safety*, 208, 111466, 1-8.
- Baskaran, M. (2016). *Radon: A Tracer for Geological, Geophysical and Geochemical Studies*. In: Springer Geochemistry, p. 260
- Bonotto, D.M. & Santos, T.O. (2007). Health risk related to radon in a thermal spa utilizing waters from Guarani aquifer, in: *Brebbia, C.A. (Ed), Environmental Health Risks IV. WITPress, Southampton, UK, 269p.* doi:10.2495/EHR070281
- Chambers, S., et al. (2011). Separating remote fetch and local mixing influences on vertical radon measurements in the lower atmosphere. *Tellus*, 63B, 843–859.
- El-Taher, A. 2018. An Overview of Instrumentation for Measuring Radon in Environmental Studies. *Journal of Radiation and Nuclear Applications*. 3/3, 135-141.
- Faheem, M., Matiullah, 2008. Radon exhalation and its dependence on moisture content from samples of soil and building materials. *Radiation Measurements*. 43, 1458 – 1462.
- Fucici, A., 2012. The main health hazards from building materials. In: Pacheco-Torgal, F., Jalali, S., Fucic, A. (Eds.), *Toxicity of Building Materials*. Woodhead Publishing, Cambridge.
- Heiserman, D.L. (1992). *Exploring Chemical Elements and their Compounds*. TAB Books, Blue Ridge Summit, PA, p. 376.
- Hellman, B., et al. (1999). Alkaline single cell gel electrophoresis and human biomonitoring for genotoxicity: a study on subjects with residential exposure to radon. *Mutat. Res.* 442 (2), 121–132.
- IARC (International Agency for Research on Cancer-WHO), 1988. IARC Monographs on the Evaluation of Carcinogenic Risks to Humans: Man-made Mineral Fibres and Radon, Vol: 43, ISBN 92 832 12436.
- Ishimori, Y. Et al., (2013). Measurement and Calculation of Radon Releases from NORM Residues. *IAEA (International Atomic Energy Agency), Technical Reports Series No. 474*.
- Kendall, GM. & Smith, TJ (2002). Doses to organs and tissues from radon and its decay products. *J Radiol Prot.* 22, 389–406.
- Khattak, N.U., Khan, A.M., Ali, N., Muntazir Abbas, S., 2011. Radon Monitoring for geological exploration: A review. *Journal of Himalayan Earth Sciences*, 44/2, 91-102
- Kristbjornsdottir, A. & Rafnsson, V. (2012). Incidence of cancer among residents of high temperature geothermal areas in Iceland: a census based study 1981 to 2010. *Environ. Health* 11 (73). <https://doi.org/10.1186/1476-069X-11-73>
- Kulali, I. Akkurt, I., Özgür, N., 2017. The Effect of Meteorological Parameters on Radon Concentration in Soil Gas. *Acta Physica Polonica A*. 132/3-II, 999-1001.
- Megonigal, J.P., Brewer, P.E., Knee, K.L., 2019. Radon as a natural tracer of gas transport through trees. *New Phytologist*, doi: 10.1111/nph.16292
- Moed, B.A. et al., (1988). Soil as a source of indoor Radon: Generation, migration and entry. Radon and its Decay Products in Indoor Air in *Nazaroff, W.W., Nero Jr., A.V., Eds*), John Wiley and Sons, New York, 57–112.
- Moore, S., Stanley, F. K. and Goodarzi, A. A., 2014. The repair of environmentally relevant DNA double strand breaks caused by high linear energy transfer irradiation—no simple task. *DNA Repair (Amst)* 17, 64–73.
- Otton, J.K. (1992). *The Geology of Radon*. USGS, Open-File Report. <https://pubs.usgs.gov/gip/7000018/report.pdf>
- Petrovic, E.K., 2017. An overview of health hazards from materials: application of principles. In Petrovic, E., Vale, B., Zari, M. (Eds), 203-236. (Elsevier) Woodhead Publishing, 416p, e-ISBN: 9780081007068
- Porstendörfer, J., Buttenveck, G., Reineking, A., 1994. Daily variation of the radon concentration indoors and outdoors and the influence of meteorological parameters. *Health Physics*. 67/3, 283-287.
- Schmid, S., and Wiegand, J. (1999). Seismic waves in the urban environment triggering radon release

from the soil. *Il Nuovo Cimento*, 22C, (3-4), 475-481.  
<http://eprints.bice.rm.cnr.it/13444/>

Siino, M et al., (2019). Multiple seasonality in soil radon time series. *Scientific Reports*, 9:8610.  
<https://doi.org/10.1038/s41598-019-44875-z>.

Soldati, G., Valentina Cannelli, V., Piersanti, A.,  
2020. Monitoring soil radon during the 2016–2017  
central Italy sequence in light of seismicity. *Scientific  
Reports*, volume 10, Article number: 13137 (2020)

Spengler, T. (2021) *The Root System of a Lemon  
Tree*.  
<https://www.hunker.com/13428599/the-root-system-of-a-lemon-tree>

Trees may play role in electrifying the atmosphere,  
study suggests. (March, 12, 2012). Science Daily  
retrieved August, 10, 2021 from  
<https://www.sciencedaily.com/releases/2012/03/120321105525.htm>

UNSCEAR, 1982. Ionizing radiation: sources and  
biological effects, *Report to the General Assembly,  
United Nations Scientific Committee on the Effects of  
Atomic Radiation*, 210p.  
[https://www.unscear.org/docs/publications/1982/UNSCEAR\\_1982\\_Annex-D.Pdf](https://www.unscear.org/docs/publications/1982/UNSCEAR_1982_Annex-D.Pdf)

USEPA, 2021 (Environmental Protection  
Agency-USA) report. Radiation protection. *What is  
radon gas? Is it dangerous?* (web site: last updated at  
July, 12, 2021  
<https://www.epa.gov/radiation/what-radon-gas-it-dangerous>)

USGS Glossary, Uranium.  
<https://pubs.usgs.gov/of/2004/1050/uranium.htm>

Walczak, K. et al., (2020). Residential exposure to  
radon and levels of histone gH2AX and DNA  
damage in peripheral blood lymphocytes of residents  
of Kowary city regions (Poland). *Chemosphere* 247.  
<https://doi.org/10.1016/j.chemosphere.2019.125748>

*What is a safe and acceptable level of radon gas?*  
(2021), Retrieved 08,10,2021 from  
[https://www.radon.com/radon\\_levels/](https://www.radon.com/radon_levels/)

Whitehead, N.H. (1984). Geothermal prospecting by  
ground radon measurements. *J. Volcanol. Geotherm.  
Res.* 20 (3–4), 213–229.

WHO, (2009). Handbook on Indoor Radon: A public  
Health Perspective. *World Health Organization  
Report 110p*.  
[https://apps.who.int/iris/bitstream/handle/10665/44149/9789241547673\\_eng.pdf](https://apps.who.int/iris/bitstream/handle/10665/44149/9789241547673_eng.pdf)

# Synthetic and Natural Phytohormones: A Review and Analysis of their Development, Functions, and Impacts

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## Abstract

Plant hormones are compounds synthesized naturally by plants, which regulate growth and development. In this paper, we survey recent developments in understanding the complex roles of eight small molecule plant hormone classes—abscisic acid (ABA), auxins, brassinosteroids, cytokinins, gibberellins, jasmonates, salicylic acid, and strigolactones—of which we primarily focus on cytokinins and auxins regarding their natural and synthetic versions. We then analyze the environmental and societal impacts of commercial usage of these hormones<sup>7</sup> on an industrial scale. While plant hormones have potential in stimulating antioxidant production in certain plants and stem cell growth, excessive plant hormone usage in the agricultural sphere can have negative consequences which must be considered prior to application.

*Keywords: Plant hormones, Phytohormones, Auxins, Cytokinins*

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## 1. Introduction

Phytohormones are shown to regulate various functions of plants, including cell differentiation and division, organ formation, seed dormancy and germination, and senescence, while monitoring external activity and its effect on plant stress (Dobrev, 2005). These compounds are vital in maintaining essential systems within the plant, such as opening and closing the stomata and boosting immunity against stressors and pathogens. Plant hormones have been studied as potential avenues for research in promoting the biosynthesis of therapeutically-

relevant compounds, as well as promoting antioxidant properties of specific plants to fight a variety of illnesses.

Additionally, synthetic plant hormones mimic their natural counterparts' structure and function and are frequently used in the agricultural industry to improve plant growth dynamics and crop yield, both of which are beneficial to combating global population growth. Due to these abilities, plant hormones, and the potential social and environmental consequences of their application, have become a significant area of interest for scientists and

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agriculturalists alike. Learning to utilize synthetic hormones efficiently to our advantage is crucial in such industries as specific amounts of hormones, when applied to plants, can effectively enhance reproduction rates. This paper explores both natural and synthetic hormones and their wide-spread use in commercial agriculture and beyond.

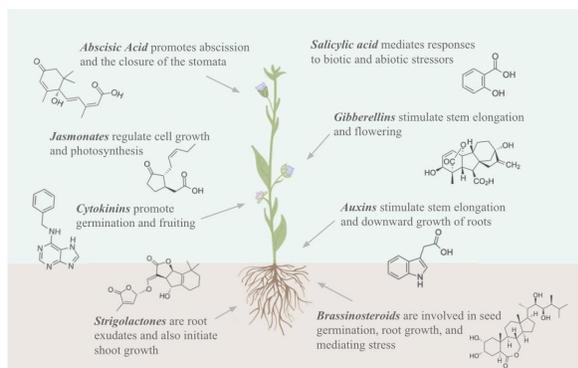
**2. Overview**

Each class of plant hormones is produced uniquely within specific plant regions and helps maintain all aspects of growth and development, ranging from pathogen defense to stress tolerance and reproductive

development. For example, indole-3-acetic acid (IAA), a natural auxin synthesized from tryptophan primarily in the plants' leaf primordia and developing seeds, is later transported to the vascular cambium and procambial stand, where it produces a growth response (Davies, 2010). On the other hand, cytokinins are biosynthesized in root tips and prevalent in plant tissue. From there, the hormones are concentrated in areas of heightened cell division, such as the subapical root zone, where it can stimulate cell division, differentiation of axillary buds, and regulate shoot growth.

Table 1. The physiological effects and biological targets of each specific plant hormone group: abscisic acid, auxins, brassinosteroids, cytokinins, gibberellins, jasmonates, salicylic acid, and strigolactones.

	<b>Physiological Effects</b>	<b>Biological Targets</b>
<b>Abscisic Acid (ABA)</b>	Promote senescence and stress responses in abscising organs, seed desiccation tolerance (Finkelstein, 2002; Finkelstein, 2013; Sah, 2016)	1. CH1H/ABAR: seed development and stomatal movement 2. GTG1/GTG2: stomatal opening and closing (Guo, 2011)
<b>Auxins</b>	Apical dominance, phototropism, gravitropism, vascular tissue differentiation, delays ripening (Palmiye, 1970; Abel, 2020)	1. AFB2, AFB4, AFB5: seedling development 2. TIR1 and AFB2: encourage auxin signaling (Prigge, 2016)
<b>Brassinosteroids</b>	Germination, senescence, responses to biotic and abiotic stressors (Yang, 2015)	1. BRL1: cell development, extreme temperature tolerance (Caño-Delgado, 2004) 2. BRL2: targeted protein degradation, vesicle trafficking, signal transduction (Ceserani, 2009) 3. BRL3: drought tolerance (Fàbregas, 2018)
<b>Cytokinins</b>	Release of apical dominance, delay senescence, chloroplast development (Amasino, 2005; Palmiye, 1970)	1. CRE1/AHK4, ZmHK1: promote signals transmission (Lomin, 2012)
<b>Gibberellins</b>	Flowering, enzyme production, implementation of maleness in dioecious plants (Gomi, 2003)	1. GID1: crucial in regulating transcription within the GA-signaling network (Gomi, 2003)
<b>Jasmonates</b>	Respond to various abiotic and biotic factors, regulates the plants' immunity (defense) and development (Wasternack, 2002; Katsir, 2008)	1. MYC2/3/4 receptor: promote expression of catabolic enzyme genes (Zhu, 2015) 2. COI1 receptor: mediates signaling and degradation of JAZ repressor proteins (Katsir, 2008; Sheard, 2010)
<b>Salicylic Acid</b>	Thermogenesis, disease resistance (Klessig, 1994)	1. NPR1 receptor: direct Ref to gene activation 2. NPR3/NPR4 receptors: negative regulators of immunity (Kuai, 2015)
<b>Strigolactones</b>	Induce germination of parasitic weeds, inhibit shoot branching (Zwanenburg, 2015)	1. DWARF14 receptor: strigolactone detection and degradation (Yao, 2016; Seto, 2019)



**Figure 1:** The locations at which the main classes of plant hormones are most commonly found in plants are illustrated above. In addition to others, these hormones occur in varying amounts depending on plant species and surrounding conditions, among many others.

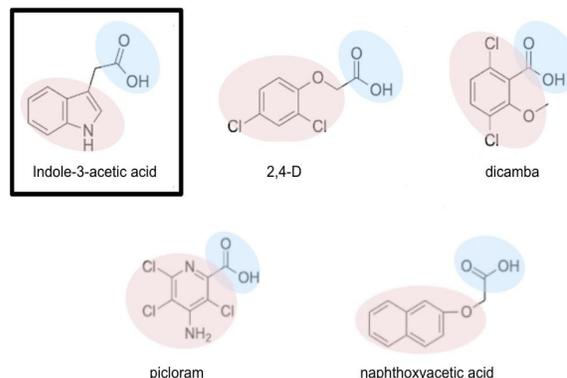
### 3. Natural versus Synthetic

The foremost differences between natural cytokinins and synthetic cytokinins are exemplified in biological studies concerning their effects on plants' growth and development. Previous studies tested the variation between benzylaminopurine (BAP) and natural cytokinins found in *Moringa oleifera* extract (MLE), although both natural and synthetic hormones significantly helped produce more vegetative and flowering branches, natural cytokinins had more antioxidant activities, correlating with increased defense against stressors and nutrient quantity within plants (Anantharaj, 1970). The studies' findings indicate that while both synthetic and natural cytokinins help increase plant production, most natural phytohormones possess other functions that synthetic plant hormones are unable to mimic completely.

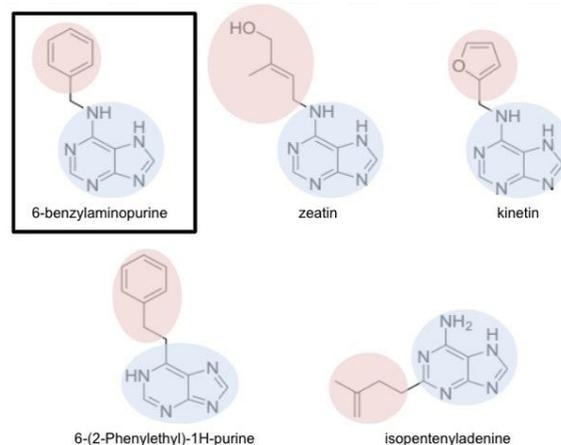
#### 3.1 Structural and functional mimicry

Structural variations between natural and synthetic hormones result in differing interactions within plants. Due to their difference in structure, many synthetic and natural plant hormones will also differ in size, their polarity in the head group, the number of hydrophobic and hydrophilic chains the molecule has, as well as their saturation degrees. These subtle differences will result in different properties as well as in their fulfillment in biological

activity (Flasiński, 2014). For instance, the auxin IAA can influence and interact with lipid monolayers more profoundly than that of 1-naphthaleneacetic acid (NAA), a synthetic auxin, due to the difference regarding aromatic ring size between the two hormones (Calderon-Villalobos, 2010). Similarly, all cytokinins have adenine and function in plant growth and development. Figures 2a and 2b highlight the structural similarities and differences between natural and synthetic auxins and cytokinins respectively.



**Figure 2a:** Naturally occurring auxin, IAA, structurally compared to various synthetic auxins. Structural similarities are highlighted in blue, and structural differences are highlighted in red.



**Figure 2b:** Synthetic cytokinin, 6-benzylaminopurine, structurally compared to various naturally occurring cytokinins. Structural similarities are highlighted in blue, and structural differences are highlighted in red.

### 4. Structural Relationships

Most auxins contain similar features that help facilitate interactions with auxin receptors and are

critical for auxin activities: an aromatic ring and a carboxylic acid group. In general, the binding affinity of auxins depends on the size of the aromatic ring and its hydrogen-bonding partner. For instance, one auxin receptor called ubiquitin protein ligase SCF(TIR1), or just the TIR1, is commonly bound to auxins by having the auxin's carboxyl interact with a negative charge on the bottom of the TIR1. However, due to the various ring sizes/structure of different auxins, the binding affinities differ. IAA, which contains a hydrogen-bonding group in the aromatic ring (NH group), can form a hydrogen bond with TIR1 carboxyl group, thus having a stronger binding affinity compared to those without a hydrogen-bonding group (Calderon-Villalobos, 2010). Unlike most hormones, auxins bind with the protein without needing to alter the shape of the receptor. This is due to the fact that the binding site of TIR1 is indifferent to the different aromatic sizes of the various auxins, thus easily taking in different analogs (Ma, 2018).

Another major binding interaction can be found in the IAA receptors: Aux/IAA and auxin response factor (ARF), both of which regulate auxin-induced gene expression. (Figure 3a) The two work closely together to regulate gene expression efficiently. Typical ARF proteins would have a C-terminal domain similar to the domains III and IV of the Aux/IAA, allowing the two to interact with each other (Reed, 2001).

An example of a protein binding with cytokinin can be found between the 17-kD protein acceptor, generally found in mungbeans (*Vigna Radiata*) and zeatin. (Figure 3b) In the past, most cytosolic proteins involved with protein modifications, mRNA degradation, metabolic processes, and cell death, were found to bind with cytokinins with low binding affinity. However, the discovery of the cytokinin-binding 17-kD protein *Vigna Radiata* Cytokinin-specific binding protein (Vr CSBP) with a high binding affinity, signal sequences, and transmembrane domain presented an exception. The group, including Vr CSBP, has evolved to bind with small-molecule ligands such as plant hormones like zeatin.

The structure of Vr CSBP has // Their binding pockets are much larger than these small molecules,

allowing other molecules to enter the binding cavity along with solvent, sealing off the site. For example, the zeatin binding site is located deep inside the large cavities between the beta-sheet and C-terminal helix alpha 3, where Vr CSBP and other proteins bind to and later seal off with two compact water molecules (Pasternak, 2006).

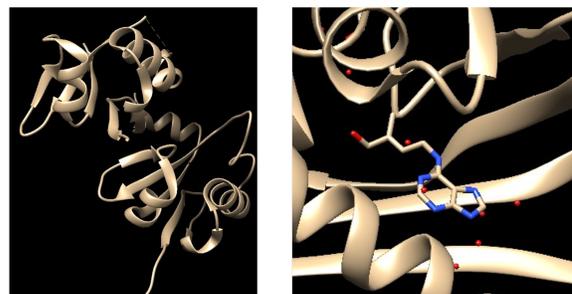


Figure 3a: 6L5K (ARF5) Figure 3b: 2FLH (Crystal Structure of cytokinin-specific binding protein from mung bean in complex with cytokinin)

Obtaining the crystal structures of the auxin and cytokinin complex's from the Protein Data Bank (PDB), and utilizing UCSF Chimera to view the structures, Figures 3a and 3b show the crystal structure of the auxin or cytokinin specific binding proteins respectively.

## 5. Impacts

### 5.1 Environmental Impacts

Plant hormones are primarily studied and utilized to improve agricultural yield on a large, commercial scale. By using synthetic phytohormones, crops can withstand disease more effectively and grow healthier efficiently, which is critical in sustaining the increasing agricultural demand due to the growing human population. From a controlled administration of plant hormones to plants' prolonged flowering, the hormones help result in overall growth as well as in a greater seasonal crop yield on a global scale (Raza, 2019). They can also be utilized to repair ecosystems after a drought (Basu, 2016). Plant hormones such as cytokines, which promote cell growth, can help alleviate water stress on plants (Othman, 2016).

Additionally, since each plant species is naturally

accustomed to varying quantities and types of phytohormones, one species may be more receptive to large quantities of phytohormones while others may have inhibited function, such as stomatal closure, bud and seed dormancy, and stunted stem growth (Plant Hormones). This can foster deleterious mutations and could potentially harm both the plant and the ecosystem (Adamse, 1988; Batt, 2005).

Aside from environmental effects, other pressing problems regarding food chain impacts remain with phytohormones being utilized on a mass scale, such as their negative side effects on humans and other organisms. One study highlights how the regenerative properties of auxins might not have been favored through evolution due to a potential risk of cancer as a result of increased cell proliferation (Cernaro). These negative side effects on humans and the environment deter the use of phytohormones as growth stimulators in the agricultural industry.

## 5.2. Health Impacts

Despite potential environmental concerns, plant hormones have the potential to greatly benefit society, both pharmaceutically and commercially. For instance, cytokinin ribosides have recently been studied for potential usage as anti-cancer agents. They are known to inhibit growth and cause apoptosis in numerous cell lines, exhibiting activity that counteracts cancer, such as anti-angiogenic activity and the ability to stimulate immune responses (C. Amiable, 1970; Voller, 2010). Many other such applications of plant hormones exist in the pharmaceutical industry. By studying the role of various plant hormones within plants in regulating cell development, scientists have been able to translate many such ideas into the field of medicinal chemistry, which continues to be a growing area of interest in phytohormone research.

## 5.3. Social Impacts

Commercially, auxins can be utilized in plant nurseries to increase crop production through the formation of adventitious roots and synchronized initiation of senescence among flowers and fruits in crops. On the other hand, cytokinins may be utilized

to deter pests and pathogens due to their disease-fighting abilities (Albrecht, 2017). This not only results in a higher crop yield but also improves the quality of crops produced in terms of food security. Pests are known not only to stunt crop growth but are also oftentimes harmful to humans when consumed. By reducing pests and the need to use toxic pesticides, both cytokinins and auxins provide a safer alternative to improve food security when harnessed correctly (Agrawal, 1998). Continuing studies with such phytohormones provide scientists and agriculturalists with new ideas surrounding developments in commercial agriculture and tackling these issues in particularly low-income regions. In these communities, food insecurity causes many people to struggle with chronic illnesses as a result of horrific management of nutritional needs, pest control, and toxicity measurements in foods (Seligman, 2010). It is especially crucial in these areas to have a better understanding of plant hormones and their properties to put an end to the cycle of lives being claimed by diseases associated with poor nutrition.

Phytohormones also promote microalgae production, which is beneficial in biotechnological applications. Found to enhance production, metabolite contents, and lipid aggregation, certain hormones partake in metabolic mechanisms and cell cycle regulation, further promoting metabolite and biomass production. They foster more resilient microalgae able to withstand abiotic stress in their local environments (Stirk, 2020).

## 6. Conclusion

Plant hormones have been found to have significant effects on several aspects of plant development, including stem and leaf growth, increased germination rates, and cell differentiation. Major plant hormones – auxins and cytokinins – have especially been studied using numerous biological assays, computational analyses, and pharmaceutical testing. Despite their seemingly beneficial nature, these phytohormones also have detrimental effects on the environment and beyond when synthesized for commercial use. These damaging effects can be examined by understanding the functions and primary

usage of synthetically produced hormones versus their naturally occurring counterparts. As plant hormones continue to be utilized in agriculture and medicine, scientists and agriculturalists alike should be mindful of these environmental drawbacks and utilize these hormones both effectively and ethically.

Although their excessive use for industrial production poses many threats, the future of plant hormones is one with much potential. Due to their abilities to promote cell growth, plant hormones have been considered as possible avenues for research in promoting the biosynthesis of therapeutically-relevant compounds (Giannakoula, 2012; Bhullar, 2013). Other applications in the medical field include harnessing plant hormones for modifying stem cell production and enhancing the potential antioxidant properties of certain plants to fight various illnesses.

As the field of plant hormones becomes an increasingly prevalent topic in agricultural and scientific endeavors, it is important to consider both the benefits and possible detrimental effects of plant hormone usage. Despite these seemingly large challenges, the future of phytohormones is one with many applications, from agriculture to medicine.

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### References

Adamse, Paulien, et al. (1988). *Photophysiology and Phytochrome Content of Long-Hypocotyl Mutant and Wild-Type Cucumber Seedlings*. Plant Physiology. American Society of Plant Biologists. <http://www.plantphysiol.org/content/87/1/264>

Agrawal, AA., et al. (1998). *Tackling the Threat to Food Security Caused by Crop Pests in the New Millennium*. Food Security. Springer Netherlands. <https://link.springer.com/article/10.1007%2Fs12571-010-0061-8>

Albrecht, Tessa, et al. (2017). *Should I Fight or Should I Grow Now? The Role of Cytokinins in Plant Growth and Immunity and in the Growth-Defence Trade-Off*. Annals of Botany. Oxford University Press. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5379597/>

*Algal Bloom*. Science Daily Science Daily. [https://www.sciencedaily.com/terms/algal\\_bloom.htm](https://www.sciencedaily.com/terms/algal_bloom.htm).

Amasino, Richard. (2005). *1955: Kinetin Arrives: the 50th Anniversary of a New Plant Hormone*. Plant physiology. American Society of Plant Biologists. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1176392/#bib21>

Amiable, C. et al. (1970). *Anti-Cancer Activities of Cytokinin Ribosides*. Phytochemistry Reviews. Springer Netherlands. <https://link.springer.com/article/10.1007/s11101-019-09620-4>

Bashir, Ishrat, et al. (2020). *Concerns and Threats of Contamination on Aquatic Ecosystems*. Bioremediation and Biotechnology: Sustainable Approaches to Pollution Degradation. U.S. National Library of Medicine. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7121614/>

Basu, Supratim, et al. (2016). *Plant Adaptation to Drought Stress*. F1000Research. F1000Research. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4937719/>

Batt, Angela L., et al. (2005). *Evaluating the Vulnerability of Surface Waters to Antibiotic Contamination from Varying Wastewater Treatment Plant Discharges*. Environmental Pollution. Elsevier. <https://www.sciencedirect.com/science/article/abs/pii/S0269749105005129>

Bhullar, Khushwant S., et al. (2013). *Polyphenols: Multipotent Therapeutic Agents in Neurodegenerative Diseases*. Oxidative Medicine and Cellular Longevity. Hindawi. <https://www.hindawi.com/journals/omcl/2013/891748/>

Calderon-Villalobos, et al. (2010). *Auxin Perception--Structural Insights*. Cold Spring Harbor perspectives in biology. Cold Spring Harbor

Laboratory Press.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2890193/>

Caño-Delgado, Ana, et al. (2004). *BRL1 And BRL3 Are Novel Brassinosteroid Receptors That Function in Vascular Differentiation in Arabidopsis*.

Development. The Company of Biologists Ltd.  
<https://dev.biologists.org/content/131/21/5341>.

Cernaro, Valeria, et al. *Auxin Induces Cell Proliferation in an Experimental Model of Mammalian Renal Tubular Epithelial Cells*. Taylor & Francis.

<https://www.tandfonline.com/doi/full/10.3109/0886022X.2015.1015683>

Ceserani, Teresa, et al. (2009). *VH1/BRL2 Receptor-like Kinase Interacts with Vascular-Specific Adaptor Proteins VIT and VIK to Influence Leaf Venation*. The Plant journal : for cell and molecular biology. U.S. National Library of Medicine.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2793540/>.

*Cytokinin*. US EPA - Pesticides - Fact Sheet for Cytokinin.

EPA.[https://www3.epa.gov/pesticides/chem\\_search/eg\\_actions/reregistration/fs\\_G-29\\_29-Feb-96.pdf](https://www3.epa.gov/pesticides/chem_search/eg_actions/reregistration/fs_G-29_29-Feb-96.pdf).

Davies, Peter J. (2010). *The Plant Hormones: Their Nature, Occurrence, and Functions*. Davies P.J. (eds) Plant Hormones. Springer, Dordrecht.

[https://doi.org/10.1007/978-1-4020-2686-7\\_1](https://doi.org/10.1007/978-1-4020-2686-7_1).

Dobrev, P.I., et al. (2005). *Purification and Determination of Plant Hormones Auxin and Abscisic Acid Using Solid Phase Extraction and Two-Dimensional High Performance Liquid Chromatography*. Journal of Chromatography A.

Elsevier.<https://www.sciencedirect.com/science/article/abs/pii/S0021967305007612>

Fàbregas, Norma, et al. (2018). *Overexpression of the Vascular Brassinosteroid Receptor BRL3 Confers Drought Resistance without Penalizing Plant Growth*. Nature News. Nature Publishing Group.

<https://www.nature.com/articles/s41467-018-06861-3>

Finkelstein, Ruth. (2013). *Abscisic Acid Synthesis and Response*. The arabidopsis book. American Society of Plant Biologists.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3833200/>

Finkelstein, Ruth R., et al. (2002). *Abscisic Acid Signaling in Seeds and Seedlings*. Plant Cell. American Society of PlantBiologists.

[http://www.plantcell.org/content/14/suppl\\_1/s15.full](http://www.plantcell.org/content/14/suppl_1/s15.full)

Flasiński, Michał, et al. (2014). *Natural vs Synthetic Auxin: Studies on the Interactions between Plant Hormones and Biological Membrane Lipids*.

Environmental Research. Academic Press.<https://www.sciencedirect.com/science/article/abs/pii/S001393511400173X>

Giannakoula, Anastasia E., et al. (2012). *The Effects of Plant Growth Regulators on Growth, Yield, and Phenolic Profile of Lentil Plants*. Journal of Food Composition and Analysis. Academic

Press.<https://www.sciencedirect.com/science/article/abs/pii/S088915751200110X>

Gomi, Kenji, et al. (2003). *Gibberellin Signaling Pathway*. Elsevier.

[http://www.cetice.universite-paris-saclay.fr/2007/ogm/doc/5\\_en\\_savoir\\_plus/construction\\_de\\_la\\_plante/hormones\\_vegetales/gibber.pdf](http://www.cetice.universite-paris-saclay.fr/2007/ogm/doc/5_en_savoir_plus/construction_de_la_plante/hormones_vegetales/gibber.pdf)

Guo, Jianjun, et al. (2011). *Abscisic Acid Receptors: Past, Present and Future*. Wiley Online Library.

John Wiley & Sons.  
<https://onlinelibrary.wiley.com/doi/full/10.1111/j.1744-7909.2011.01044.x>

Jochem, Greta. (2017). *Algae Toxins In Drinking Water Sickened People In 2 Outbreaks*. NPR.

NPR.<https://www.npr.org/sections/health-shots/2017/11/09/563073022/algae-contaminates-drinking-water>

Katsir, Leron, et al. (2008). *COII Is a Critical Component of a Receptor for Jasmonate and the Bacterial Virulence Factor Coronatine*. PNAS.

National Academy of Sciences.  
<https://www.pnas.org/content/105/19/7100.short>

Klessig, Daniel F., et al. (1994). *The Salicylic Acid Signal in Plants*. Plant Molecular Biology. Kluwer Academic Publishers.

[http://www.esalq.usp.br/lepse/imgs/conteudo\\_thumb/The-salicylic-acid-signal-in-plants.pdf](http://www.esalq.usp.br/lepse/imgs/conteudo_thumb/The-salicylic-acid-signal-in-plants.pdf)

Kuai, Xiahezi, et al. (2015). *Integrating Data on the Arabidopsis NPR1/NPR3/NPR4 Salicylic Acid Receptors; a Differentiating Argument*. Frontiers.

- Frontiers.  
<https://www.frontiersin.org/articles/10.3389/fpls.2015.00235/full>
- Lomin, S N, et al. (2012). *Receptor Properties and Features of Cytokinin Signaling*. Acta naturae. A.I. Gordeyev.  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3491891/pdf/AN20758251-04-031.pdf?tool=EBI>
- M. Anantharaj, et al. (1970). *Morphological and Physiological Response of Tomato (Solanum Lycopersicum L.) to Natural and Synthetic Cytokinin Sources: a Comparative Study*. Acta Physiologiae Plantarum. Springer Berlin Heidelberg.  
<https://link.springer.com/article/10.1007/s11738-014-1662-1>
- Ma, Qian. (2018). *Auxin Signaling: a Big Question to Be Addressed by Small Molecules*. Journal of experimental botany. Oxford University Press.  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5853230/>
- Michalak, Anna M., et al. (2013). *Record-Setting Algal Bloom in Lake Erie Caused by Agricultural and Meteorological Trends Consistent with Expected Future Conditions*. PNAS. National Academy of Sciences. <https://www.pnas.org/content/110/16/6448>
- Othman, Eman M, et al. (2016). *The Plant Hormone Cytokinin Confers Protection against Oxidative Stress in Mammalian Cells*. PloS one. Public Library of Science.  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5179003/>
- Palmiye. (1970). *What is growth hormone in plants?*  
<http://provacyl-tm.blogspot.com/2015/11/what-is-growth-hormone-in-plants.html>
- Pasternak, Oliwia, et al. (2006). *Crystal Structure of Vigna Radiata Cytokinin-Specific Binding Protein in Complex with Zeatin*. The Plant cell. American Society of Plant Biologists.  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1626604/>
- Plant Hormones*. Plant Hormones - an overview. ScienceDirect  
Topics.  
<https://www.sciencedirect.com/topics/neuroscience/plant-hormones>
- Prigge, Michael J, et al. (2016). *The Arabidopsis Auxin Receptor F-Box Proteins AFB4 and AFB5 Are Required for Response to the Synthetic Auxin Picloram*. Genetics Society of America.  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4856089/>
- Raza, Ali, et al. (2019). *Impact of Climate Change on Crops Adaptation and Strategies to Tackle Its Outcome: A Review*. Plants (Basel, Switzerland). MDPI.  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6409995/>
- Reed, Jason W. (2001). *Roles and Activities of Aux/IAA Proteins in Arabidopsis*. Trends in Plant Science. Elsevier CurrentTrends.  
<https://www.sciencedirect.com/science/article/abs/pii/S1360138501020428>
- S. Ahmad, et al. (1970). *The Role of Phytohormones in Enhancing Metal Remediation Capacity of Algae*. Bulletin of Environmental Contamination and Toxicology. Springer US.  
<https://link.springer.com/article/10.1007/s00128-020-02880-3>
- Sah, Saroj K, et al. (2016). *Abscissic Acid and Abiotic Stress Tolerance in Crop Plants*. Frontiers in plant science. Frontiers Media S.A.  
doi:10.3389/fpls.2016.00571
- Seligman, Hilary K, et al. (2010). *Food Insecurity Is Associated with Chronic Disease among Low-Income NHANES Participants*. The Journal of nutrition. American Society for Nutrition.  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2806885/>
- Seto, Yoshiya, et al. (2019). *Strigolactone Perception and Deactivation by a Hydrolase Receptor DWARF14*. NatureNews. Nature Publishing Group.  
<https://www.nature.com/articles/s41467-018-08124-7>
- Sheard, Laura B, et al. (2010). *Jasmonate Perception by Inositol-Phosphate-Potentiated COII-JAZ Co-Receptor*. Nature. U.S. National Library of Medicine. doi:10.1038/nature09430
- Steffen, A., & Theologis, A. (1996). *Early Genes and Auxin Action*. Plant Physiol.  
<http://www.plantphysiol.org/content/plantphysiol/111/1/9.full.pdf>

Stirk, Wendy A., et al. *Potential of Phytohormones as a Strategy to Improve Microalgae Productivity for Biotechnological Applications*. Biotechnology Advances. Elsevier.  
<https://doi.org/10.1016/j.biotechadv.2020.107612>

Trevino-Garrison, et al. (2015). *Human Illnesses and Animal Deaths Associated with Freshwater Harmful Algal Blooms-Kansas*. MDPI. Multidisciplinary Digital Publishing Institute.  
<https://www.mdpi.com/2072-6651/7/2/353>

Voller, Jiří, et al. (2010). *Anticancer Activity of Natural Cytokinins: A Structure–Activity Relationship Study*, Phytochemistry. Pergamon.  
<https://www.sciencedirect.com/science/article/abs/pii/S0031942210001421>

Wasternack, Claus. *Jasmonates and Octadecanoids: Signals in Plant Stress Responses and Development*. Institute of PlantBiochemistry.  
DOI: 10.1016/S0079-6603(02)72070-9

Yang, Cang-Jin, et al. (2015). *The Mechanisms of Brassinosteroids' Action: From Signal Transduction to Plant Development*. Molecular Plant. Cell Press.  
<https://www.sciencedirect.com/science/article/pii/S1674205214606845>.

Yao, Ruifeng, et al. *DWARF-14 Is a Non-Canonical Hormone Receptor for Strigolactone*. Nature. Letter.doi:10.1038/nature19073.

Zhu, Xiaoyu, et al. (2015). *Jasmonic Acid Promotes Degreening via MYC2/3/4- and ANAC019/055/072-Mediated Regulation of Major Chlorophyll Catabolic Genes*. Wiley Online Library. John Wiley & Sons.  
<https://onlinelibrary.wiley.com/doi/full/10.1111/tpj.13030>.

Zwanenburg, Binne, et al. (2015). *Structure and Activity of Strigolactones: New Plant Hormones with a Rich Future*. Molecular Plant. Cell Press.  
<https://doi.org/10.1093/mp/sss141>

# Studies of collective behavior in bounded and exterior domains with repulsion

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## Abstract

In this note, we perform numerical studies of the Cucker-Smale system for a group of agents confined to a bounded domain or to its exterior. The purpose of this study is to test several hypotheses related to the long-time behavior of the system. Our most definitive observation suggests that in a convex bounded domain, the agents either settle away from the influence of the wall or congregate to a point circulating periodically near the boundary. In the exterior case, we observe a critical ratio between the radius of the flock and the radius of the obstacle that serves as a threshold between two distinctly different limiting behaviors - bouncing back from the obstacle or passing around it.

*Keywords: Alignment, Flocking Behavior, Cucker-Smale system.*

## 1. Introduction

Collective behavior of agents can be used to model many swarming phenomena in biology, such as flocking of birds or milling formations of schools of fish. One collective phenomenon that is abundant in nature is called alignment – convergence of all velocities in the flock to a common vector  $v_i \rightarrow v_\infty$ , as  $t \rightarrow \infty$ . The actual interpretation of the term “alignment” may change depending on the circumstances. For instance in biological systems this may literally mean convergence of a flock to a single direction of motion. In the context of opinion dynamics it may mean reaching a consensus. We refer to Tadmor (2021) and Shvydkoy (2021) for recent overviews and surveys on the subject.

Mathematical models can be used to predict the alignment as well as the rate at which it occurs using the techniques of ordinary or partial differential equations. A particular swarming model that has recently received considerable attention in the

mathematical literature is called the Cucker-Smale system as introduced by F. Cucker and S. Smale (2007). The system involves a positive communication function  $\phi(r) > 0$  which depends only on the Euclidean distance  $r$ , monotonely decreasing at infinity, which regulates the strength of connection between each pair of agents  $x_i \in R^n$ , and is stated as follows

$$x_i' = v_i; \quad v_i' = \frac{1}{N} \sum_{j=1}^N \phi(|x_i - x_j|) (v_j - v_i) \quad (1)$$

Here,  $v_i$  is the velocity of the  $i$ th agent. The main result states that if the communication function does not decay too fast at long range, i.e., there is sufficient connection remaining between even remotely distant agents, the alignment will occur exponentially fast. Here is the precise statement.

**Theorem 1.1** (Cucker and Smale, 2007). *If  $\phi(r) = \frac{H}{1+r^\beta}$ , where  $\beta \leq 1$ , then for any initial condition the solution to the system (1) satisfies*

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$$\max_i |v_i - v_\infty| \leq C e^{-\delta t}$$

where  $C, \delta > 0$  depend only on the kernel and the initial condition.

Much analysis of this original system or systems with various interaction forces was focused on the case when the flock environment is an open space or periodic torus  $T^n$ . In other words, an environment without boundaries. The main objective of this note is to address the situation when the environment does have boundaries. In particular, we focus on two complementary scenarios: the flock is confined into a bounded region (interior problem) or is located in an open space with obstacles (exterior problem). The motivation for such study comes from an attempt to place the system (1) in a more realistic setting where various obstacles or boundaries are unavoidable. In this situation the swarm is confronted not only with the alignment forces but also the forces that keep agents from colliding with the walls. The basic question we ask is does the flock still reach a collective outcome in presence of boundaries? And what that collective outcome might look like?

Previous research on this problem is scarce. The work of Shu and Tadmor (2020) addresses a somewhat similar situation when the flock is being confined to a bounded region with strong attractive forces, but with no boundaries involved. Here the collective outcome is described by a limiting condition in which the flock aggregates around a pair of phase variables  $(x, v)$  satisfying the harmonic oscillator equation

$$x' = v; \quad v' = -x.$$

The work of Bae et. al. (2019) studies the case of a cylindrical domain with specular boundary conditions (perfect reflection). In this situation the flock aggregates near the boundary and with an additional push force along the cylinder does align parallel to the cylinder. The agents of the flock are allowed to collide with the walls in this model.

We will study the situation when the agents are perceptive enough to avoid collisions. To achieve this effect wall interactions will be modeled through a strong repulsive force. We will be interested in testing computationally several conjectures related to the possible collective behavior in these physically reasonable settings. Our findings show that generally

in the case of a bounded domain the limiting behavior of a flock depends on whether the domain is convex or not. In the convex case the flock either stalls in the interior away from the boundaries or aggregates to a common position and velocity and behave like a single particle circling around the boundary, somewhat similar to the open space confinement situation of Shu and Tadmor (2020). In a non-convex domain, the system exhibits a much more complicated behavior and may settle on chaotic billiard-like dynamics. Lastly, in the case of the exterior problem, we find that the flock can either bounce back from the boundary, stall near the boundary, or circumvent the boundary and pass the obstacle. These scenarios depend on the ratio between the initial radius of the flock and radius of the obstacle (ball in our case) under a fixed initial velocity. We will find that ratio to be approximately 7.5.

These and other observations will be detailed in the forthcoming sections. We finish the introduction by introducing precisely the model we are studying.

Let us describe the repulsive force first. It will have a common structure regardless of the situation we consider. The repulsion force starts at zero within one unit length from the boundary, then intensifies and approaches infinity as the agent position closes into the boundary. Otherwise, the force remains smooth and differentiable away from the boundary. This force is the gradient of a potential defined below, where  $r$  is the distance from the boundary,

$$U(r) = \frac{(r-1)^2}{r}, \text{ if } 0 < r < 1$$

$$U(r) = 0, \quad \text{if } r \geq 1.$$

So, for each agent  $x$  the actual force acting on it is defined as follows

$$F(x) = -\nabla_x V, \quad V(x) = U(\text{dist}\{x, \partial\Omega\}).$$

The agents will also have an alignment force as in the classical Cucker-Smale system, that gets weaker as the agents are farther away from each other:

$$\phi = \frac{1}{1+r}.$$

Note that this is the weakest kernel in the range of applicability of Theorem 1.1. Thus, the system we study reads as follows:

$$x'_i = v_i; \quad v'_i = \frac{1}{N} \sum_{j=1}^N \phi(|x_i - x_j|)(v_j - v_i) + F(x_i)$$

## 2. Bounded Domains

In this section, we are testing the conjecture that with any initial conditions, the agents inside a circular bounded domain will achieve limiting behavior in one of two ways.

*Conjecture 2.1.* As time goes to infinity one of the following two behaviors occur:

(1) Velocities will align  $v_i \rightarrow v_\infty$  and particles will aggregate  $x_i \rightarrow x_\infty$  to a couple  $(x_\infty, v_\infty)$  satisfying the following Hamiltonian system:

$$x'_\infty = v_\infty; \quad v'_\infty = -\nabla V(x_\infty)$$

(2) The particles come to rest at some point inside the domain and out of range of the repulsive forces of the boundary.

At first, we explored the behavior of three particles starting with random initial conditions in the circular bounded domain. After completing 30 trials we determined that the system would eventually converge to the same end behavior as described in parts (1) and (2) of the conjecture. A sample experiment showing the first possibility is depicted in Figure 1. After a transient period of oscillatory motion the particles aggregated and settled on a looping pattern near the boundary marked by the green curve. Given the circular symmetry of the domain the particles in their limiting state satisfy the harmonic oscillator

$$x'_\infty = v_\infty; \quad v'_\infty = -c x_\infty,$$

where the constant “c” is determined by the distance of the limiting circle from the boundary, which is always positive.

The simplest scenario where the agents didn’t end up looping around the edge of the boundary was achieved when they started off with symmetric initial conditions. This scenario would still lead to aggregation, but the particles, after a transient oscillatory period, eventually ran out of energy and came to a complete stop in the interior of the disc away from the influence of the wall, as shown in Figure 2.

On a relevant note, we mention that a conjecture similar to our 2.1 was in fact confirmed analytically by Shu and Tadmor (2020) in the case of open space with quadratic confinement potential  $U$ . The result relies in an essential way on convexity of the

potential, which is suggestive of the fact that our conjecture in the convex domain, and hence under convex potential force, may have a similar analytic validation.

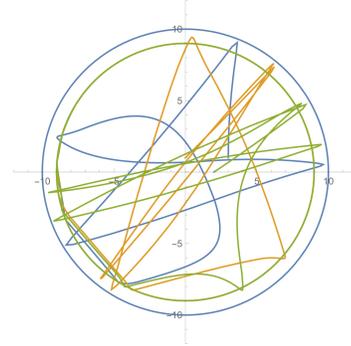


Figure 1: The blue circle is the boundary of the circle, with the boundary repulsive force beginning to take effect one unit inside it. The green circle just inside the boundary of the domain represents the end behavior of the particles. In this simulation, the particles bounced around in random fashion before merging together and settling in a consistent path, which is shown by the green circle just inside the blue boundary circle. The starting conditions were as follows:  $x_1 = (3, 1)$ ,  $v_1 = (0, 3)$ ,  $x_2 = (3, 1)$ ,  $v_2 = (3, 3)$ ,  $x_3 = (3, 1)$ ,  $v_3 = (3, 2)$

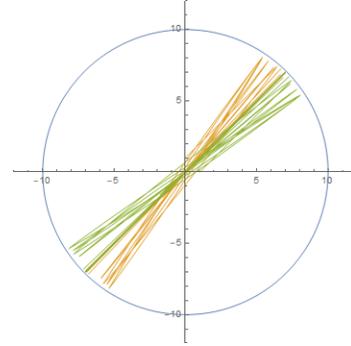


Figure 2: In this case, the blue boundary represents the boundary of the domain, while the end behavior of the particles is represented by the darker green line that makes a  $45^\circ$  angle with both axes. The starting conditions were as follows:  $x_1 = (1, 1)$ ,  $v_1 = (3, 3)$ ,  $x_2 = (0, 1)$ ,  $v_2 = (0, 1)$ ,  $x_3 = (1, 0)$ ,  $v_3 = (3, 3)$

We attribute the difference in collective outcomes to the presence of residual total energy. Let us recall that the energy of the system is given by

$$E = \frac{1}{N} \sum_{i=1}^N V(x_i) + \frac{1}{2N} \sum_{i=1}^N |v_i|^2$$

The energy law can be computed directly from

system (1), see (Shvydkoy, 2021):

$$(EL) \quad E' = -\frac{1}{N} \sum_{i,j=1}^N |v_i - v_j|^2$$

As we can see, the longer the agents remain misaligned, the more energy will be burned by the alignment forces. On the other hand, if the system settles into an aligned configuration before the energy is fully depleted, that residual conserved energy drives the system into a perpetual motion.

We also tested the same system of three particles in an irregular, convex bounded domain as shown in Figure 3. In this irregular domain, the three particles would still aggregate. However, the limiting path is no longer showing any regular pattern. The aggregated system follows a chaotic and unpredictable trajectory, which exhibits transient periods of traversing the boundary of the domain, especially near the convex parts of it, and other times bouncing off of the boundaries in a billiard-like fashion. The system loses energy if velocities remain misaligned  $v_i \neq v_j$  according to (EL). If the misalignment persists for a long time the system comes to a complete stop. If the system aggregates and aligns with residual energy left, the agents settle into a perpetual billiard-like motion.

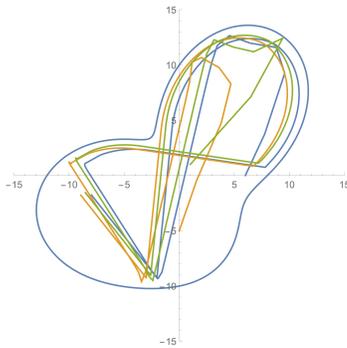


Figure 4: The blue line represents the boundary of the domain. Starting conditions:  $x_1 = (6, 0)$ ,  $v_1 = (4, -2)$ ,  $x_2 = (0, -5)$ ,  $v_2 = (0, 3)$ ,  $x_3 = (1, 1)$ ,  $v_3 = (5, 5)$ . The particles align and settle into a perpetual billiard-like dynamics. Domain is given by  $r = 10 + 4\sin(2\theta) - 2\cos(3\theta)$

### 3. Conclusion of the Bounded Domains case

The results of our computations indicated rather convincingly that the limiting behavior of the Cucker-Smale system in a bounded convex domain

follows one of the two outcomes described under Conjecture 2.1. The system settles either into an oscillatory motion near the boundary, or to an equilibrium in the interior of the domain. In the former case the energy of the system remains positive and the agents move perpetually. In the latter case the energy burns down to zero and the agents come to a complete stop.

In the case of a non-convex domain we found that the limiting behavior does not fall under the general conclusions of Conjecture 2.1. The system undergoes a period of chaotic motion before settling into an equilibrium state inside the domain if misalignment persists for a long time. Otherwise, the system settles into a perpetual chaotic motion. We believe that in non-convex domains the complete description of collective outcomes depends on the particular shape of the domain and is no longer universal as in the convex case. We anticipate that any attempt to classify the behavior in this setting would rely on the theory of dynamical systems, which we plan to investigate in future studies.

### 4. Exterior Domains

With exterior domains, we would have a group of particles with initial velocities  $v_0 = (1, 0)$  and starting positions at  $x = -40$ , and a number of exterior domains in the path of the particles to test out how the particles would react. We conjectured that there would be one of the three outcomes from these experiments.

*Conjecture 3.1.* The simulation, as time goes to infinity, will follow one of the following three behaviors:

- (1) The particles successfully pass the exterior domains and continue with a positive velocity in the x direction.
- (2) The particles rebound from the obstacles and aggregate to a negative velocity in the x direction.
- (3) The particles are almost completely stopped by the obstacles, and continue with a near-zero velocity in the x-direction.

#### 3.1 One Obstacle

First, we tested this conjecture on a case with the

exterior of a ball. We had to flip the boundary force equation so that it acted outside the boundary instead of inside. We increased the number of particles to ten, and spread them out evenly on the range  $[-10, 10]$ . We made the radius of the ball a variable that could be easily changed to test which different radii result in the particles rebounding backwards or going around. Figures 5,6, and 7 show examples of various scenarios.

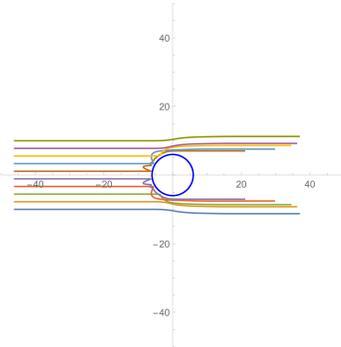


Figure 5: Particles successfully managed to pass around the obstacle, with the radius of the tree being 6.

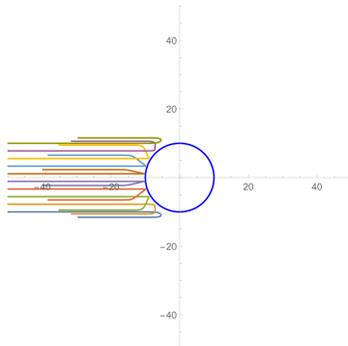


Figure 6: Particles did not pass around the obstacle and instead got turned around, with the radius of the obstacle being 10.

After testing the simulation 40 times and making the corresponding adjustments, we figured out the exact radius of the obstacle such that the particles wouldn't pass by or get rebounded, instead come to an almost complete stop. This threshold value of the radius just about 7.5, with the particles ending with slight forward velocities with magnitudes around  $10^{-6}$  when the radius is exactly 7.5. Figure 7 shows how the particles stalled and slowed down drastically.

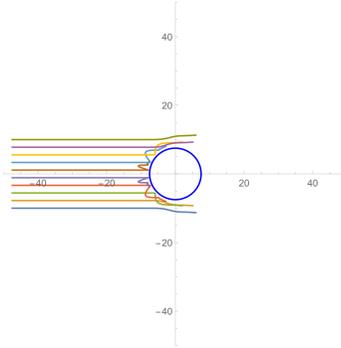


Figure 7: Particles stalled and came to an almost complete stop, with the radius of the obstacle being 7.5.

### 3.2 Multiple Obstacles

Another model we tested out using exterior boundaries was a configuration of many smaller obstacles in a random distribution, reminiscent of a forest. The forest would consist of 30 trees (boundary circles with radius one) on random integer coordinates in a 45 by 60 rectangle. To make sure that the trees wouldn't overlap, we would produce a random integer on the range -10 to 10, then would be multiplied by 3 in order to produce the desired random y coordinate, with a similar procedure used to produce the x coordinate. The three particles we used would be placed far left, at  $x = -40$ , and have random y values. All the particles would have initial velocity  $v = (1, 0)$ . Because we had 30 random boundaries, each with their own repulsive force, we had to have a sum of all the forces in the differential equations of each particle,

$$F = - \sum_{i=1}^{30} \nabla V_i.$$

We ran the simulation many times, and the particles would sometimes manage to get through the trees, and other times not, as seen in Figures 8 and 9.

We found that whether the particles pass through the "forest" or not was highly dependent on the random starting positions. With the density of obstacles and starting values as described in the beginning, the particles did not pass through the forest most of the time. However, there were still multiple cases where they managed to successfully do so as seen in Figure 9.

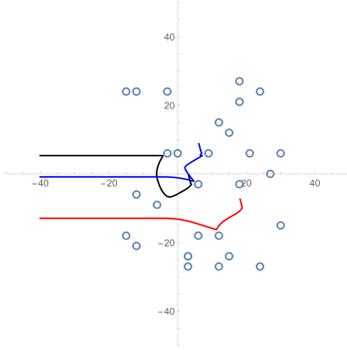


Figure 8: Particles did not manage to get through the trees.

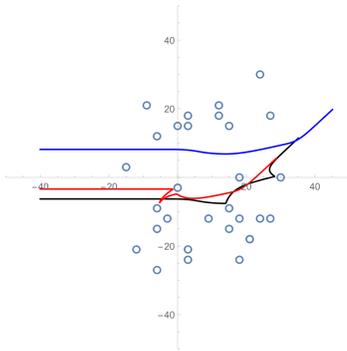


Figure 9: Particles successfully pass through the trees.

### 5. Conclusion of the Exterior Domains case

Through the testing of the behavior of the agents in presence of one exterior domain and multiple exterior domains, we can conclude that our hypothesis as stated in Conjecture 3.1 is correct. In both scenarios we tested (one obstacle vs. many), the particles always followed one of the three behaviors as outlines in Conjecture 3.1: the particles get around/through and end with a positive x-velocity, the particles get stopped and continue with a near-zero velocity, or the particles are rebounded and continue with a negative x-velocity.

For the case of one circular exterior domain, after testing the simulation 40 times and adjusting the radius of the obstacle, we found that the critical ratio between the range on which the particles are distributed and the diameter of the obstacle to be 7.5. This threshold value was found to be robust. It is independent of the actual characteristic dimensions of the system as long as the ratio remains unchanged. However, it still varies with the initial energy of the system. This observation calls for a more rigorous

analysis of universality of the passing threshold value, which we plan to undertake in near future.

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### References

Cucker, F and Smale, S. (2007). Emergent behavior in flocks. *IEEE Trans. Automat. Control*, 52(5), 852–862

Cucker, F. and Smale, S. (2007). On the mathematics of emergence. *Jpn. J. Math.*, 2(1), 197–227

Shu, R. and Tadmor, E. (2020). Flocking hydrodynamics with external potentials. *Arch. Ration. Mech. Anal.*, 238(1), 347–381

Bae, H., et al. (2019). Flocking Behaviors of a Cucker--Smale Ensemble in a Cylindrical Domain. *SIAM Journal on Mathematical Analysis*, 51, 2390–2424

Shvydkoy, R. (2021). Dynamics and analysis of alignment models of collective behavior. *Necas Center Series*. Birkhäuser/Springer, Cham, ©2021

Tadmor, E. (2021). On the mathematics of swarming: emergent behavior in alignment dynamics. *Notices Amer. Math. Soc.*, 68(4), 493--503

## Breaking the Spheres: The Effect of World War I on Traditional Gender Roles

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### Abstract

World War I was the first occasion where the most powerful countries of the world turned against each other, leaving 20 million people dead. Millions of men were drafted into their countries' armies and eventually sent to fight and kill all around the world. Stuck at home with empty positions left by men, millions of women began filling in those jobs, aiding the cause of war in any way that they could. That said, their roles drastically changed over the four years of the war, paving the path for changes that would slowly emerge following the end of the war. Men's gender roles were reinforced during the war, as they fought vigorously and continued where they had left off before they were drafted. Women, however, temporarily fulfilled men's vacant jobs only to return to their domestic work. Nevertheless, the end of the war was the beginning of landmark social changes that slowly opened the gates for women to become full participants in society.

*Keywords: World War I, Women's Roles, Traditional Gender Roles, Women's Rights*

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### 1. Introduction

After the two Balkan Wars, Serbians looked toward "liberating" the South Slavs of Austria-Hungary, which they believed would be accomplished by the death of Franz Ferdinand, the Austrian Archduke (Royde-Smith and Showalter, 2021). The Archduke's assassination was plotted after learning about his visit to Bosnia. On that fateful June day, at 11:15 AM, in Sarajevo, Bosnia, Franz Ferdinand, and his wife, Sophie, were shot dead by Gavrilo Princip, a member of Young Bosnia, a movement promoting Yugoslavist aims of pan-South Slav unification of territories into Yugoslavia (Banac, 1988; Barkan et al., 2004), as well as Serbian nationalist aims of pan-Serb

unification into Serbia. Ferdinand's assassination led to a chain of events that would spark Austria-Hungary to declare war on Serbia, igniting one of the world's most horrific and bloodiest wars (History.com Editors, 2009). The world's greatest powers turned their industrial weapons and soldiers on each other for the first time in history, resulting in four years of blood, sweat, and tears. The Allied Powers, consisting of the British Empire, France, the Russian Empire, the United States, and many more countries, lined up against Austria-Hungary, Germany, the Ottoman Empire, and all parts of the Central powers, and fought to prevail democracy and peace throughout the world (History.com Editors, 2009).

Before the war, "[w]omen were considered

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nurturers and supporters, objectified as something to be protected and as prizes to be won by the brave” (Showalter, 2002). Occupying the private and domestic spheres, women served as mothers, wives, and daughters who tended to housework and childbirth. Middle- and upper-class women enjoyed more flexibility in their daily schedules, and some single women were allowed to work “outside the home to supplement family income” under very few exceptions. Women were actively discouraged from venturing outside “their spheres,” as some aspired to be entrepreneurs or politicians (Showalter, 2002). Even if they crossed into the male-dominated public, political, or economic spheres, they did so “without absolute security.” Women earned considerably less in the workplace than men, even when working on similar jobs. The societal boundaries between men and women’s work barred women from engaging in any skilled trade that required apprenticeship or lengthy training. Even as teachers, women were blocked from teaching at many universities because of their gender (Braybon, 1998). Society told women that male-dependency was necessary to succeed and survive. In Russia’s strongly patriarchal society, women were under the control of their husbands or fathers, and suffered abuse and domestic violence, both of which were common and acceptable (Braybon, 1998). In many countries, society restricted women from aspiring to achieve high roles that require education (or training of some sort) and instead placed them at home as loyal companions and child-bearers, not breadwinners (Boehnke, & Gay, 2020).

Men, the established breadwinners of the family, occupied the public, political, and economic spheres before the war. Many of the “masculine duties included that of provider, and protector, both for their families and their nations” (Showalter, 2002). They exercised authority over family members under their protection. In rural areas, men dominated the workforce in farms and factories. Many men were dragged into the war myth, and for boys, war was a rite of passage to manhood. Requiring virtues of courage, decisiveness, and vigor, men had to maintain these war-like qualities to avoid slipping back into a “boyish condition.” Thus, war was a rite of passage to manhood and a guarantor of that

passage (Showalter, 2002). One soldier wrote in a letter, “The story-books were coming true, and by an extraordinary piece of luck, I was privileged to be a participator” (Wiesner-Hanks et al., 2014).

The war forced both men and women to take on roles that they had never dealt with before, and abruptly altered the lives of millions. During World War I, women challenged gender stereotypes by entering traditional spheres designated for men, while men reinforced their manhood through war. Although after the war, these gender roles shifted back as women were forced out of their newly gained jobs, their social attitudes drastically changed forever. While the gender role shift due to the change of the social and international relationship occurred during World War I, it has been difficult for the author to compare gender roles pre-, during, and post-World War I. This study, therefore, investigated the reinforcement of traditional gender roles during World War I, and how they shifted during the post-war period.

## **2. Gender Role Movement during the War**

World War I provided women with new opportunities as they took on jobs that were previously dominated by men. With so many men drafted, there was a phenomenal rise in demand for women to fill the now-vacant white-collar jobs (Anderson et al., 2000). Driven by patriotism and money, often double of what they previously earned, many rushed to work in factories, supporting their troops globally. In munition factories, for example, thousands of women worked tirelessly, making shells, explosives, aircrafts, and other war supplies. In other countries, such as France, women found different ways to contribute toward the war effort, such as constructing wooden huts. With so many women rushing to get jobs, by 1917, countries like Russia saw an industrial workforce in which nearly half were women. Other countries and their industries also witnessed rising numbers of women’s participation (Braybon, 1998). Within a few years, it was now common to see women road sweepers, lamplighters, delivery van drivers, or shop assistants, something that would have been thought of as absurd a few years ago. Along with an initial lack of white-collar

workers, the war also created a demand for educated women who took on jobs in banks, the government, and public services.

Apart from factories and labor, women began participating near the frontline as medical specialists, tending to the wounded. Some women, like Marie Curie, drove ambulances, while others, like Elise Inglis, organized hospitals. As shown in Figure 1, women were convinced to join the Red Cross, an organization that gave medical services to armies and brought relief to many civilians across Europe. In the US, the Army and Navy enlisted over 20,000 nurses, all of whom were women, to serve close to home and overseas (Women During World War I, 2019). However, even nursing was arduous and dangerous for women who served near the front lines, close to the bloodshed of the battlefield. Women also enlisted in these wartime organizations in great numbers to aid the war effort as they felt a deep sense of obligation. In some cases, women were able to participate in active services, fighting, and aiding soldiers. Most notably, in Russia, privileged women organized combat battalions after the February Revolution of 1917. As shown in Figure 2, women were even given distinctions and decorations, and were instructed to inspire new recruits. This war would also be the first time that women, who were not nurses, were allowed to enlist in the US Armed Forces. By the end of the war, the US accepted 13,000 women into active duty in the Navy and Marines, while accepting a smaller number into the Coast Guard. Moreover, some women risked their lives to act as spies; an example is Marthe Ricard, who the French Secret Service enlisted and eventually awarded the Legion of Honor. Other women risked their lives to help military communication, such as the Hello Girls and telephone operators stationed inside the trenches in countries such as France (Taylor, 2014).

The focus on turning boys into men through war upheld the traditional societal standards for men. Many young men and boys, lured by the war myth, were encouraged by posters expressing that their country needed them to risk their life for the world, honor of the regiment, and the safety of their fellow comrades. Men were expected to uphold their virtues of courage and bravery in combat. In those grueling

years, men suffered immense trauma and pain, and were constantly exposed to death, bullets, and explosions at every moment (Wiesner-Hanks et al., 2014). However, even war seemed to be too strong of a burden for men. Many men fell into a trance-like state, and were traumatized by the experiences of the war. Rather than the strong, immovable forces men were expected to be, thousands returned from the war as the “living dead” (Meyer, 2007).



Figure 1. WWI Women Marines. Photograph. WWI: Thirty Thousand Women Were There. <http://userpages.aug.com/captbarb/femvets4.html>.



Figure 2. Library of Congress. Young Russian women, having won distinction at the front with decorations, are part of the staff of instructors to inspire new recruits. February 1918. Photograph. The Atlantic. April 27, 2014. <https://www.theatlantic.com/photo/2014/04/world-war-i-in-photos-global-conflict/507335/#img25>.

### 3. Gender Role Movement after the War

The world witnessed a shift in gender roles after World War I. While most men left their careers for the military, women were left to return to their previous jobs and manage their homes. Such changes led to sustainability and improved cultural performance, specifically in terms of how women performed their duties. During this period, several societal changes affected the status quo by shifting the performance of women’s roles in society. This section reflects on these changes in gender roles after

World War I.

The US experienced several gender role changes after World War I. First, women were allowed to join the military and assist the wounded soldiers (Irwin, 2016). For instance, most of them became nurses, implementing specific programs to help injured men undergo medical procedures, which caused a shift in the cultural phenomenon where women were expected to perform domestic functions. Entry into service of the country instituted better services and revolutionized the significance of women in the contemporary world (Lopez, 2016). These changes were the beginnings of professionalism and a shift in the working methods of women in the country. It facilitated changes that revolutionized ineffective cultural supremacy, which had previously demoralized women due to male dominance (Grant, 2014). After the war, the changes enabled improvements that later developed and enhanced sustainability to advance human rights.

Women were allowed to vote by the Constitution. These efforts were initiated by pioneers such as Margret Mead, who stood firm to organize and fight for women's rights. During this period, the constitution underwent changes that allowed women to have democratic rights and votes (Scott, 2018). These new rights were a developmental milestone because women were considered domestic workers for many years and were denied constitutional practice and democratic rights. Therefore, the changes improved sustainability in the country and recognized women as having contributions to the US national leadership that were significant enough for them to represent their issues.

Professionalism equalized performance in the country. It influenced the displacement where women were involved in economic revolutions due to the improvement of the working culture in the country (Johnson, 2018). Women resumed office functions to ensure that the government ran effectively to enhance development. Before the war, society recognized women as a minority (Belarmino and Roberts, 2019). They were considered unable to contribute to the economy because of the cultural context of the country. In addition, the country saw new revolutions due to the feminist movement that enabled effective government policies, including those for women in

the corporate industry. Therefore, the changes in gender roles facilitated changes in the economy, and women acted as the frontiers of building the economy.

In addition, women experienced dramatic changes in their dressing styles. Modernity began entering the fashion industry, and most women began wearing short clothes and shaping their hair using various techniques (Wingate, 2017). Changes in the fashion industry made women undertake roles in the clothing industry to make clothes for men in the military and sell them in the market. Such subsequent changes have transformed, enhanced growth, and helped women become pioneers in the fashion industry.

In summary, women's roles changed after the war as men entered military service for the country. Most women assumed the roles of men by participating in elections, nursing the injured soldiers, entering offices, and improving the fashion industry. Such changes facilitated cultural shifts and changes, and have improved the social and economic spheres. The onset of modernity has shaped the foundation and future of the American economy, including women in the labor industry.

#### 4. Conclusion

Women experienced dramatic changes in their daily lives during the war, especially when the society expected men to reinforce their traditional roles and virtues. Although, eventually, women had to return to their original professions, they gained suffrage and social freedom in the process. Today's society continues to challenge gender roles in all aspects of life; even the definition of gender has changed. However, discrimination still exists, as certain opportunities are still presented only to certain genders. This indicates that progress is not linear, as society continues to experience constant improvements and setbacks in social change for many different groups.

#### References

Anderson, B. S., et al. (2000). *A History of Their Own: Women in Europe from Prehistory to the Present*. Oxford University Press.

- Banac, I. (1988). *The National Question in Yugoslavia: Origins, History, Politics*. United Kingdom: Cornell University Press.
- Barkan, E. R., et al. (2004). *The Former Yugoslavia's Diverse Peoples: A Reference Sourcebook*. United Kingdom: ABC-CLIO.
- Belarmino, M., & Roberts, M. R. (2019). Japanese Gender Role Expectations and Attitudes: A Qualitative Analysis of Gender Inequality. *Journal of International Women's Studies*, 20(7), 272-288.
- Boehnke, J., & Gay, V. (2020). The Missing Men World War I and Female Labor Force Participation. *Journal of Human Resources*, 0419-10151R1.
- Braybon, G. (1998). *Women, War, and Work in World War I: A History*, (H. Strachan, Ed.). Oxford University Press, 149-62.
- Grant, S. (2014). Nurses Across Borders: Displaced Russian and Soviet Nurses After World War I and World War II. *Nursing History Review*, 22(1), 13-36.
- Hankey, D. W. A. (2009). *The making of a man*, in *A Student in Arms*. Cornell University Library.
- History.com Editors. (2009, October 29). World War I. HISTORY.  
<https://www.history.com/topics/world-war-i/world-war-i-history>
- Irwin, J. F. (2016). Beyond Versailles: Recovering the Voices of Nurses in Post-World War I US-European Relations. *Nursing History Review*, 24, 12.
- Johnson, A. (2018). The War to End All Wars on Ideal Female Figures: An Analysis of WWI and its Effects on US Women's Fashion from 1917-1927. *Ursidae: The Undergraduate Research Journal at the University of Northern Colorado*, 7(3), 4.
- Lopez, P. J. (2016). American Red Cross posters and the cultural politics of motherhood in World War I. *Gender, Place & Culture*, 23(6), 769-785.
- Meyer, G. J. (2007). *A World Undone: The Story of the Great War, 1914-1918*. Bantam Dell.
- Royde-Smith, J. G. & Showalter, D. E. (2021, July 21). World War I. *Encyclopedia Britannica*.  
<https://www.britannica.com/event/World-War-I>
- Scott, J. (2018). Patterns of Change in Gender-Role Attitudes 1. In *Rewriting the Sexual Contract* (pp. 126-140). Routledge.
- Showalter, D. E. (2002). *Gender Roles: Were Women Excluded from the Great War?* In *History in Dispute*, 8, 124-31. St. James Press.
- Taylor, A. (2014, April 27). *World War I in Photos: Soldiers and Civilians*. The Atlantic.  
<https://www.theatlantic.com/photo/2014/04/world-war-i-in-photos-soldiers-and-civilians/507329/>
- Wiesner-Hanks, M. E., Evans, A. D., Wheeler, W. B., & Ruff, J. (2014). *Discovering the Western Past, Volume II: Since 1500*. Cengage Learning.
- Wingate, J. (2017). *Sculpting Doughboys: Memory, Gender, and Taste in America's World War I Memorials*. Taylor & Francis.
- Women During World War I*. Delaware Historical and Cultural Affairs.  
<https://history.delaware.gov/world-war-i/women-roles-wwi/>