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AI Advances in Precision Medicine

Runsong Yu[1] *

[1]Beckman High School, Tustin, CA, USA
*Corresponding Author: russellyeet39@gmail.com

Advisor: Mary Zhao, maryz@astudentacademy.org

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Abstract

Medical care is a necessary aspect of human life. Even when someone is healthy, accidents happen. Additionally, as people grow older, there is an increasing likelihood of developing significant health problems. Some medical conditions require advanced medical care but the current standard of practice often limits the physician to generalizability, meaning that what works in the majority of patients can never be optimized for any single patient. This limitation has led to the development of precision medicine, which customizes diagnosis, prevention, and treatment based on an individual's genetics and hereditary risk, environmental exposures, and lifestyle choices. In general, precision medicine can be resource-intensive with the need for data mining, interpretation of various data classes for injury and illness prevention, and institutionalized infrastructure. This paper provides a narrative review of how public health computational tools and data-driven systems can help address these limitations. Using evidence from recent clinical studies and genomics initiatives, the paper considers how technology can support care for individualized patients or populations and reflects on ethical, regulatory, and accessibility considerations. The results suggest that careful consideration of the integration of computational techniques in precision medicine may further precision in the diagnosis, contribute to therapeutic drug safety, and facilitate better equity in healthcare. However, vigilance to location, context, and multi-disciplinary coordination should be kept to enable responsible practice in the future.

Keywords: Precision Medicine; Conventional Medicine; Artificial Intelligence in Healthcare; Genomics and Biomarkers; Ethics and Regulation of AI

1. Introduction

Healthcare has played a big role in people's lives. When someone feels fine, they might still run into sudden injuries—on top of that, getting older raises the chance of catching severe diseases. Over many years, doctors mostly stuck to standard methods: treatments shaped by studies done on broad crowds, aiming at an "ordinary person" type. That idea means averaging out how patients react instead of focusing on one unique body makeup. Sure, these strategies boosted community well-being quite a bit—yet they often ignore real differences in DNA, surroundings, or daily habits.

To close that gap, precision medicine has become a fresh take on healthcare. Rather than using one-size-fits-all treatments for people sharing a condition, it adjusts prevention, detection, and drugs based on individual traits. Usually, this involves spotting biological signals or gene differences that show how someone might react to a certain medication. One solid proof shows up in cancer care: people with HER2+ breast tumors do well on trastuzumab, whereas lung cancer patients carrying distinct EGFR changes tend to improve more with osimertinib instead of standard chemo. Precision medicine is moving into areas like heart care or even mental well-being, where DNA clues help pick treatments. Yet, even with potential, it's spotty in clinics—price tags, system needs, plus difficulty making sense of massive gene info slow things down.

This analysis stands out by linking medical, technical, and moral aspects of AI-driven precision care through a

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unified approach. Instead of viewing tech advances alongside policy issues separately, the review explores how they connect in actual healthcare environments. Drawing on results from cancer treatment and new uses beyond oncology, the paper shows opportunities as well as systemic barriers to deploying AI-powered tools ethically.

The main focus of this study is to determine the best way technology and number-crunching tools can enhance precise medical care without compromising trust, equal treatment, or patient harm. The goals break down into three parts:

1. To spot today's roadblocks in precise treatments—looking at diagnosis, cures, stopping illness before it starts, and also how information gets pieced together.
2. To examine the role of computer-driven and AI-powered methods in tackling those issues within real-world healthcare settings, while exploring their impact on day-to-day medical work.
3. To evaluate the moral issues and regulatory problems that arise when using these tools in everyday situations.

2. Methodology

This study uses a narrative style to collect results from research about AI applications in precision medicine, drug discovery, and diagnosis. Articles from 2015 to 2025 were searched in key platforms such as PubMed, Scopus, Nature Portfolio, along with Google Scholar. Trusted information from government resources such as the U.S. Food and Drug Administration (FDA) and the National Institutes of Health (NIH) was added to reflect up-to-date rules and health policies. References were also searched manually to capture additional relevant work.

The research selected articles containing terms such as "precision medicine," "artificial intelligence in healthcare," "machine learning diagnostics," "genomics and biomarkers," along with discussions on "AI ethics in clinical medicine." Only peer-reviewed English-language papers were included.

3. Precision Medicine vs. Conventional Medicine

Conventional medicine has traditionally relied on treatments that were cut out for average patients. In this model, patients with the same diagnosis typically receive the same starting treatment, regardless of their underlying genetic or molecular diversity. While such an approach has facilitated the creation of broad public health guidelines and mass treatment schemes, it also tends to dilute therapeutic effectiveness (Hamburg & Collins, 2010). Those at lower probability of benefit are themselves threatened by the same toxicities, whereas those who might derive more benefit from alternative treatments may never receive them. Precision medicine shifts this therapeutic model by stratifying the patient into biologically defined subgroups. For example, patients with HER2-overexpressing early-stage breast cancer are treated with trastuzumab and chemotherapy, significantly increasing survival compared with HER2-negative patients, for whom the drug is worthless (Piccart-Gebhart et al., 2005; Romond et al., 2005).

Diagnostic methods show clear differences between both practices. While traditional care relies on physical checks, scans, and wide lab tests - sometimes adding tissue samples - it usually spots illness without uncovering the genetic causes behind progression or therapy outcomes. In contrast, precision tools bring in gene analysis, protein mapping, and blood-based biopsies capable of finding specific changes like EGFR or BRCA1/2 markers (Jameson & Longo, 2015). EGFR (epidermal growth factor receptor)changes cause unchecked cell division in some types of lung cancer, so drugs like osimertinib aim at these altered receptors. Instead of normal function, mutated BRCA1 or BRCA2 disrupts DNA repair processes, raising the chances of breast and ovarian tumors over time. Because detecting such variants shapes therapy choices, tests often check for them before starting treatment. Rather than using broad approaches, modern care uses this data to match patients with specific inhibitors - like PARP blockers - when appropriate. As a result, gene-based screening has become standard, shifting focus from general methods to individualized plans based on tumor genetics. One example is the FDA-cleared FoundationOne® Liquid CDx, allowing doctors to find treatable faults using just a blood draw if tissue isn't available (U.S. Food and Drug Administration, 2020. This test is notable because it can identify hundreds of clinically relevant genomic alterations using only a blood sample, making it especially valuable when tumor tissue is limited or inaccessible. It also represents one of several genomic profiling tools used in precision oncology, alongside alternatives such as Guardant360 and

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tissue-based next-generation sequencing panels. Conventional diagnostics offer limited snapshots; by contrast, molecular methods monitor how tumors change and resist treatment, so care plans can adapt quickly.

Precision medicine gains strength from how therapies are chosen. Instead of using standard chemo for everyone with the same type of tumor, which brings uneven results, targeted treatment looks at genetic changes in the cancer. For example, people with non-small cell lung cancer and an EGFR mutation now get osimertinib - this drug works better than older ones, improving both survival and brain-related outcomes (Ramalingam et al., 2019). While traditional methods apply one approach broadly, this method adjusts based on individual markers. In the same way, drugs like pembrolizumab used regardless of tumor type - when MSI-H or mismatch repair defects are present - show therapy can focus on molecular markers shared by different cancers (Marcus et al., 2019). Instead of just prescribing more treatments, precision care also means avoiding unnecessary ones when safe; take the 21-gene test in certain breast cancers - it helps identify individuals who skip chemo yet maintain outcomes (Sparano et al., 2018).

Risk grouping plus prevention differ greatly across both methods. Standard prevention uses wide-ranging risk tools along with age-driven checkups - good for groups, yet imprecise for people at high or low danger levels. On the flip side, tailored prevention adapts according to inherited tendencies and biological signals. As a result, women carrying faulty BRCA1/2 genes might begin tests much sooner than average folks or opt for preventive operations that sharply lower their chance of cancer. Folks with Lynch syndrome get colonoscopies more often than others at normal risk. Because prevention matches genetic risk, care is focused on those who gain most from it - skipping extra procedures for people less likely to need them.

There are also differences in how evidence is made in conventional versus precision medicine frameworks. Traditional RCTs are designed to test treatments in large and diverse populations, generating population-average estimates that seldom reflect the needs of small molecularly defined subgroups. As a result, these studies often lack adequate statistical power for rare biomarker-specific subgroups. Precision medicine has spurred the development of alternative designs—basket trials, umbrella trials, and adaptive platform trials—that enroll patients according to molecular alteration rather than tumor site (Woodcock & LaVange, 2017). The NCI-MATCH trial represents such a paradigm: it assigns patients to targeted therapies based solely on genetic mutation and independent of tumor type. Although clever, MATCH underscored the challenges facing precision trials: only about 17% of screened patients ultimately matched to a treatment arm, and numerous arms prematurely closed due to poor accrual (Flaherty et al., 2020). These designs nevertheless represent a meaningful step toward generating evidence that directly informs clinical decisions for narrowly defined molecular populations that conventional RCTs are not designed to address.

Outcome metrics further distinguish the two paradigms. Traditional medicine usually judges effectiveness through general goals like total survival rates - or time without relapse - across big patient samples. Although helpful when looking at populations, such indicators tend to hide major differences in personal risk levels. Precision medicine instead incorporates individualized endpoints informed by genetic and molecular features. The DYNAMIC trial in stage II colon cancer shows this change: researchers measured ctDNA levels to decide if patients needed chemo after surgery. Those with no detectable ctDNA avoided treatment safely - with only 7% relapsing compared to 13% under standard care - while people with positive tests got tailored therapy cutting their risk of return (Tie et al., 2022). Applying ctDNA like this cut excess treatments, reduced adverse reactions, improved use of medical resources, and highlighted how precision methods move away from broad solutions toward plans matching a person's unique condition.

4. Limitations of Precision Medicine

Precision medicine changed how care works - by matching treatments, checks, or prevention to a person's genes and body makeup. Even though it's helped in cases like targeting HER2 in breast cancer or EGFR in some lung cancers, real-world use still hits roadblocks tied to biology and logistics. Take trastuzumab: it boosts survival without relapse in HER2+ breast cancer, cutting return odds almost by half when stacked against chemo only (Piccart-Gebhart et al., 2005; Romond et al., 2005). But using it means ongoing heart scans due to possible damage like weak pumping function, plus plenty of people stop responding over time - which leads doctors to switch gears mid-course (Zhang et al., 2023). Just like that, osimertinib - today's top choice for early treatment in EGFR-driven NSCLC - boosts average

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time without worsening to 18.9 months, way past the 10.2 months seen with earlier TKIs (Ramalingam et al., 2019). Even so, stubborn changes like EGFR C797S tend to pop up, showing how tough cancer biology still is for targeted therapy (Song et al., 2023).

These limits aren't just about therapy. Tools that spot issues, like blood tests - take the FDA-backed FoundationOne® Liquid CDx - are able to catch treatable gene changes from just a vial of blood. Still, how well they work relies on how much cancer DNA gets released into the bloodstream. When tumors release little DNA, these checks might miss them entirely, whereas uncommon genetic blends can lead to unclear or shaky outcomes (U.S. Food and Drug Administration, 2020; Heitzer et al., 2023). While regular tissue checks come with drawbacks, blood-based tests bring extra doubt - especially when cancer signals are barely there.

Preventive genomics hits roadblocks just like other fields. Testing often spots DNA changes scientists don't fully understand, making it tough to know if they're dangerous or harmless. Because of that uncertainty, doctors hesitate - and people might stress out or get tests they don't need (Richards et al., 2015; Vears et al., 2022). When it comes to treatments, even targeted studies such as NCI-MATCH struggle to pair patients with suitable drugs. Usually, under one in five folks tested actually qualify - leading to tiny groups in trials and weaker results (Flaherty et al., 2020).

Big genome efforts - like the UK's 100,000 Genomes Project - show how useful DNA info can be when built into public healthcare, boosting diagnosis rates for uncommon conditions while guiding tailored treatments. Still, such programs face ongoing issues: aligning different data formats, enrolling enough patients, uneven gene testing accuracy between labs, alongside lasting worries over keeping genetic details private (Turnbull et al., 2018; Parliamentary Science & Technology Committee, 2018). In reality, the main bottleneck isn't lack of breakthroughs - it's people struggling to handle, connect, and make sense of the massive amounts of information precision medicine produces today.

5. Artificial Intelligence Techniques Supporting Precision Medicine

These challenges highlight one key problem - precision medicine produces vast quantities of intricate data, but existing healthcare systems often fail to handle or make sense of it efficiently. While AI has stepped forward as a potential answer, providing tools able to detect trends, predict results, or combine insights far surpassing what people can do alone.

In therapy tracking, deep learning methods - like CNNs or gradient-boosted setups - help spot early toxicity signals while also forecasting treatment resistance (Yagi et al., 2024). Take trastuzumab-linked heart issues: prediction is now possible long before clinical signs emerge. Models using vast collections of echo images, ECG patterns, along with biomarker values identify minor heart shifts better than standard visual reads (Zhang et al., 2023). On another front, RNN systems examining repeated tumor DNA data foresee resistance changes like EGFR C797S, giving doctors time to shift approaches ahead of progression (Sun et al., 2023; Li et al., 2023). Data shows these tools might shorten lag times in recognition by multiple months - an edge when tumors change fast (Attia et al., 2020).

Diagnostics now gain a lot from AI. Though liquid biopsies often overlook tumors releasing little ctDNA, causing missed results, newer methods spot hidden signs through pattern analysis. Traditional liquid biopsies often miss mutations due to low ctDNA, leading to false negatives. In contrast, they may flag normal variations as cancer signals, resulting in false positives. However, AI-driven fragmentomics identifies tiny shifts in fragment length, alongside irregular methylation or skewed allele ratios - patterns standard tests overlook. By focusing on these markers, machine learning cuts down both types of mistakes. Instead of relying on volume, systems use traits like fragment size or chemical tags on DNA. By applying machine learning types - such as random forests or support vector machines - detection becomes sharper even when signal is weak. This helps catch elusive cancers earlier while reducing mistakes in identifying rare changes like NTRK fusions. As a result, fewer patients get treatments they don't actually need. Food and Drug Administration, 2020. Better interpretation improves test advice while lowering errors.

AI has also transformed therapeutic decision-making. Knowledge-graph–based platforms, including decision-support systems such as IBM Watson for Oncology, integrate patient genomic information, prior treatment responses, and global clinical trial data to suggest optimized therapeutic regimens (Santra et al., 2024). At the molecular level, reinforcement learning models simulate tumor evolution, rewarding strategies that delay resistance, while deep

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learning–based docking algorithms predict three-dimensional drug–protein interactions (Sun et al., 2023). These models prioritize effective drug options in minutes—replacing weeks of manual review—and accelerate the development of next-generation inhibitors targeting resistance mutations (Li et al., 2023).

AI has played a critical role in prevention and genetic risk assessment as well. Tools such as REVEL, CADD, DeepVariant, and protein-structure models like AlphaFold2 improve interpretation of variants of uncertain significance by analyzing evolutionary conservation, structural stability, and predicted protein function (Vears et al., 2022). By leveraging extensive variant databases, these algorithms reduce inconclusive results, enabling clinicians to offer more definitive guidance to individuals with BRCA1/2 or Lynch syndrome mutations and decreasing unnecessary prophylactic procedures (Richards et al., 2015).

Clinical trial design and enrollment have also evolved. Precision medicine trials such as NCI-MATCH face persistent challenges including limited match rates and small sample sizes. Natural language processing systems and platforms such as Deep Lens VIPER analyze pathology reports, genomic data, and health records to identify eligible participants. By extracting details such as “EGFR exon 19 deletion” from unstructured notes and aligning them with trial criteria, AI significantly reduces recruitment time. Pilot programs report enrollment increases exceeding 30%, improving efficiency and diversity in clinical research (Flaherty et al., 2020).

Data integration plus ongoing oversight offer a key shift in practice. Though genomic, radiologic, pathologic, or clinical datasets are usually isolated - this limits effective precision care. With federated learning setups, organizations can build joint models without sharing unprocessed health records, thus boosting confidentiality; at the same time, natural language tools structure insights from written reports (Habli et al., 2020). Systems using multimodal deep learning merge genetic results, scans, alongside medical histories to deliver practical risk predictions. For instance, the UK’s 100,000 Genomes Project demonstrates how AI-backed merging increases diagnosis success for uncommon conditions while cutting down analysis delays (Turnbull et al., 2018).

Lastly, AI improves forecasting results through better tracking of recurrences. Traditional approaches depend mostly on tumor stage - yet often miss minor signs of return. By combining ongoing ctDNA data with scans and patient records, machine learning offers tailored forecasts (Tie et al., 2022). These systems use sequential neural setups alongside enhanced Cox models to catch early warnings - even if markers appear normal. For colorectal cases, such tools spot at-risk individuals nearly half a year sooner than usual practices, allowing closer follow-up plus timely treatment.

Taken together, these tools show how vital AI is throughout precision medicine. Using smart algorithms designed for particular medical issues, AI goes beyond human limits in reading data - while adding forecasting and combining functions never seen before. As a result, this blend marks real progress toward broader, lasting personal treatment in today’s health systems.

6. Dangers

Although AI can assist in improving precision medicine, it simultaneously introduces notable risks that need careful oversight. Since this healthcare method relies heavily on genetic evaluation, laboratory assessments, and customized therapies, errors or biased outputs from artificial intelligence might affect clinical decisions, prevention methods, or research designs. One key issue centers on unequal outcomes. Numerous genomic datasets overrepresent individuals with European heritage; therefore, when algorithms built on such information are used for different populations, forecasts may lack accuracy. As an illustration, polygenic risk indicators for breast cancer show weaker performance among non-European communities - suggesting that AI-driven preventative measures could worsen current inequalities instead of addressing them (Liu et al., 2021; Roberts et al., 2023; Bianchi et al., 2024).

Another major risk arises from the interpretation of genetic test results. Precision medicine frequently encounters “variants of uncertain significance,” or VUS, which are difficult for clinicians to classify. A growing number of tools use artificial intelligence to determine if genetic changes are harmless or dangerous; however, poor training data can cause incorrect predictions. When a safe variation is incorrectly labeled risky, individuals may face avoidable operations; conversely, missing a dangerous change may delay appropriate care (Vears et al., 2022). Early BRCA1/2 interpretation models produced inconsistent outcomes, demonstrating that premature reliance on AI may weaken

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confidence and harm patients (Richards et al., 2015).

There are also dangers tied to transparency. Many AI systems used in oncology for therapy selection or resistance prediction operate as "black boxes." Without clear explanations, doctors might struggle to grasp why a tool suggests osimertinib for some patients but not others - even when their genetics look alike. Relying solely on opaque results could lead to wrong therapies; ignoring them completely, though, risks losing helpful clues. This tension complicates clinical decision-making while placing patients at risk of under- or overtreatment (Herzog, 2022; Bouderhem et al., 2024).

Genomic information carries unique privacy concerns since DNA is fixed for life, clearly traceable to one person, while exposing details not just about them - yet their family too. Such features cause harm greater than typical health data leaks when compromised. Instead of sharing full genetic records, modern precision medicine uses tools like decentralized learning - enabling joint research across centers without moving sensitive files - or secure computing approaches shielding data mid-process. Another method adjusts results slightly using intentional statistical noise, lowering chances someone gets identified later. Besides technology, reliable oversight structures, understandable permission steps, alongside open rules on how info is used help sustain confidence - especially within broad efforts including the British 100K Genomes effort (Turnbull et al., 2018; Parliamentary Science & Technology Committee, 2018).

The application of artificial intelligence in medical studies brings uncertainty. Programs like NCI-MATCH struggle to find sufficient qualified patients. While AI helps match people to trials, flawed algorithms or mismatched terms may exclude suitable applicants - or include unsuitable ones. Minor tech flaws, however, might grow into serious problems that impact data reliability and enrollment (Flaherty et al., 2020). Furthermore, questions around who is ethically or legally accountable stay unsettled. Because precision medicine often influences major choices - like deciding on chemo through a ctDNA result - it carries high stakes. When an AI wrongly assesses relapse likelihood, leading to flawed care plans, harm can follow. Still, it's uncertain if blame lies with doctors, hospitals, or the teams behind the algorithm (Habli et al., 2020). Without clear answers, confidence in these technologies - and the system using them - could weaken.

7. Potential Solutions

The use of AI in personalized medicine offers strong benefits - yet brings concerns like unfairness, unclear decisions, data safety, medical adoption, and responsibility. Ensuring AI supports - not weakens - patient-focused care requires clear, structured responses. Fixes must cover improved technology, better data rules, updates in treatment workflows, and stronger ethics monitoring (Habli et al., 2020).

A crucial first step is addressing bias in data sets. Rather than mainly using people of European background, artificial intelligence ought to learn from genetics and health records covering varied world populations. Projects like All of Us in the U.S., 100,000 Genomes in the UK, H3Africa on the African continent, and China Kadoorie Biobank help include groups previously left out (Bianchi et al., 2024; Turnbull et al., 2018; Mulder et al., 2018; Zhu et al., 2024). Creating shared global gene databases - through cross-border teamwork plus uniform rules for exchanging information - leads to fairer, more reliable tools for estimating cancer risks, judging medicine effects, or selecting patients for trials (National Human Genome Research Institute, 2022).

Creating explainable AI matters just as much for clarity and understanding. Since precision medicine affects critical medical choices, doctors need to see how algorithms reach conclusions. Instead of relying on hidden processes, tools in XAI point to main factors - like gene changes, scan results, or past health records - so providers can assess suggestions carefully (Herzog, 2022). When outcomes link to clear data, trust grows among both clinicians and patients using AI-assisted care (Bouderhem et al., 2024).

Safeguarding personal health data requires strong methods that preserve privacy during machine learning. Instead of sharing actual patient details, federated learning lets various organizations jointly develop models while keeping information local - this lowers risk. To further secure genetic records, approaches like encrypted processing or noise-based anonymization can be applied across training phases (Santra et al., 2024). Beyond technology, transparent consent processes, structured oversight policies, and adherence to regulations help sustain confidence when using

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genomic data (United States Food & Drug Administration, 2025).

Good clinical integration works best if AI supports decisions instead of taking over from experts. Integrated properly into daily practice, AI results appear quickly in clear forms - helping care stay smooth. Working alongside doctors when designing systems ensures they fit actual medical demands while cutting confusion (Attia et al., 2020). Training staff on what AI can or cannot do leads to wiser, steadier use in various fields (Yagi et al., 2024).

Clear rules on who is responsible help keep medical AI use safe. If an AI suggestion causes harm to a patient, it should be clear if the doctor, hospital, or software creator is at fault. While some approval processes exist for medical AI, better protections are needed - particularly for systems that learn over time (United States Food & Drug Administration, 2023). Instead of relying only on current checks, independent ethics groups focused on AI in personalized care can support fair outcomes, openness, and patient choice (Santra et al., 2024).

Together, these methods show AI's risks in precise healthcare aren't certain. By using varied datasets, transparent models, solid privacy rules, smart medical use, also clear oversight, AI may be applied safely. Under close monitoring, tailored medicine powered by AI could shift from risky trial phase toward lasting, fair patient care (Habli et al., 2020).

8. Discussion

This review looked at how precision medicine is built differently from standard care while assessing AI's role in supporting its growth. Standard systems use group-level patterns, missing key differences between people. Instead, tailored approaches adjust prevention or treatments through genetics, biomarkers, or cellular details. Still, progress faces hurdles - like drug resistance, variable testing quality, unclear gene changes, high expenses, and combining varied health records.

The findings outlined here show AI starting to tackle several current challenges. Where therapy is monitored, machine learning identifies early heart-related side effects from treatments targeting HER2 - while also forecasting resistance changes like EGFR C797S. When it comes to diagnosis, refined algorithms boost how well liquid biopsies catch signals and lower incorrect alerts tied to uncommon DNA shifts. Rather than relying solely on tradition, AI aids prevention efforts by sorting unclear genetic variants and refining risk estimates for hereditary cancers. Additionally, systems powered by artificial intelligence streamline patient enrollment in targeted cancer trials; at the same time, integrated models combine genetic scans, medical images, and health records far beyond what humans alone could manage.

Even with progress, AI in precise healthcare carries serious risks. Because genomic data often contain bias, predictions may work less effectively for some groups, deepening gaps in care quality. Some AI models are hard to interpret, which makes doctors hesitant when using them for decisions about treatment. Issues around privacy stay relevant, particularly with massive gene-based records; a leak might expose someone's hereditary details forever. Getting AI into clinics is still inconsistent - as legal rules lag, medical staff face difficulty weighing automated advice against their own judgment.

The results here show AI-based precision medicine works best when applied thoughtfully. While technical, ethical, and policy protections need improvement, fairness and transparency in clinics depend on them. Instead of uniform data, diverse datasets help; similarly, interpretable systems matter more than opaque ones. Because privacy-safe analysis pairs with clear oversight, progress stays accountable. As these factors shape outcomes, equal access to AI's advantages becomes possible - so care grows personalized, reliable, and focused on patients.

9. Conclusion

Precision medicine shifts focus from wide-scale health strategies to personalized methods for prevention, diagnosis, or care. Although standard practices often use one-size-fits-all treatments, research shows combining genetic data with biological indicators helps doctors assess risks more accurately; it also supports choosing specific therapies while reducing unneeded procedures. Yet challenges remain - such as expense, complicated information handling, limited effectiveness over time, unclear meaning of some gene changes, and uneven integration into routine medical practice.

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Through these openings, AI acts as a key aid in every phase of tailored healthcare. Studies from clinics, genetics, and computing show it can sharpen diagnosis, foresee complications, refine therapy choices, streamline patient recruitment for trials, while linking diverse medical records. Still, such gains carry serious challenges - such as biased algorithms, poor explainability, threats to data security, uncertain accountability, also unequal access among groups.

Going forward, advancing AI in precision medicine responsibly means focusing on varied data sets along with transparent models. Secure systems for sharing information must be built alongside clinical processes supporting doctor decisions instead of undermining them. Regulations need to keep pace with learning algorithms while ethics rules protect fairness, responsibility, and patient choice. Collaboration between medical staff, tech experts, decision makers, plus worldwide health networks can help turn AI-powered care into a tool for earlier interventions, broader access, and tailored treatments.

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