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MULTI-OMICS AI FOR PERSONALIZED CRITICAL CARE: A REVIEW OF DIGITAL TWINS, CRISPR, AND EXPLAINABLE SYSTEMS

Review article

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Abstract

Personalized medicine is changing the game, moving healthcare from one-size-fits-all treatments to strategies that fit each person’s unique biology. This shift really matters in intensive care, where patients are fragile, their bodies can change fast, and the stakes are high. Old school critical care leans on slow labs, scattered health records, and decisions based mostly on what doctors see and know in the moment. That leaves gaps and slows down care.

Now, with breakthroughs in multi-omics sciences like genomics, proteomics, metabolomics, and microbiomics — and the integration of powerful tools like AI, digital twins, CRISPR, explainable AI, and privacy-protecting technology — we’re looking at a new era. These innovations are turning critical care into something much smarter and more responsive, where doctors and systems can predict, adapt, and act before trouble hits.

This review pulls together all these advances, exploring how they come together for better predictions, smarter treatments, and clearer insights into what helps patients most. It covers how digital twin models can act as virtual patient copies, how CRISPR opens doors for targeted treatments, and how AI-driven drug recommender systems and explainable AI are boosting trust and transparency at the bedside. There’s also a deep dive into technologies like federated learning and blockchain, which make it possible to share knowledge without risking patient privacy.

Still, there are big questions—gaps in research, real-world hurdles, and ethical concerns that need real answers. The review wraps up by mapping out how to build personalized medicine frameworks for critical care that are practical, understandable, and ready for hospitals to use.

Keywords: personalized medicine, multi-omics, artificial intelligence, digital twins, CRISPR, explainable AI, federated learning, blockchain, precision genomics, critical care.

МУЛЬТИОМИЧЕСКИЙ ИИ ДЛЯ ПЕРСОНАЛИЗИРОВАННОЙ ИНТЕНСИВНОЙ ТЕРАПИИ: ОБЗОР ЦИФРОВЫХ ДВОЙНИКОВ, CRISPR И ОБЪЯСНИМЫХ СИСТЕМ

Обзор

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Аннотация

Персонализированная медицина меняет ситуацию, переходя от универсальных методов лечения к стратегиям, учитывающим уникальные биологические особенности каждого человека. Этот сдвиг имеет огромное значение в интенсивной терапии, где пациенты находятся в уязвимом состоянии, их организм может быстро меняться, а риски являются высокими. Традиционная интенсивная терапия опирается на длительные лабораторные исследования, разрозненные медицинские записи и решения, основанные в основном на том, что врачи видят и знают в данный момент. Это приводит к пробелам в лечении и замедляет оказание медицинской помощи.

Сегодня, благодаря прорывам в таких мультиомических науках, как геномика, протеомика, метаболомика и микробиомика, а также интеграции мощных инструментов — таких как искусственный интеллект, цифровые двойники, CRISPR, объяснимый ИИ и технологии защиты конфиденциальности — перед нами открывается новая эра. Эти инновации делают интенсивную терапию гораздо более «умной» и оперативной: врачи и системы могут прогнозировать, адаптироваться и принимать меры до того, как возникнут проблемы.

В данном обзоре обобщены все эти достижения и рассмотрено, как их сочетание позволяет улучшить прогнозы, сделать лечение более эффективным и получить более четкое представление о том, что приносит пациентам наибольшую пользу. Было рассмотрено, как модели «цифровых двойников» могут служить виртуальными копиями пациентов, как технология CRISPR открывает возможности для целевого лечения, а также то, как системы рекомендаций по лекарственным препаратам на базе искусственного интеллекта и объяснимый ИИ повышают уровень доверия и прозрачности при оказании медицинской помощи. Кроме того, в обзоре подробно рассматриваются такие технологии, как федеративное обучение и блокчейн, которые позволяют обмениваться знаниями без угрозы для конфиденциальности пациентов.

Тем не менее остаются серьезные вопросы — пробелы в исследованиях, практические препятствия и этические соображения, требующие реальных ответов. В заключение обзора предлагается план по созданию практичных, понятных и готовых к внедрению в больницах концепций персонализированной медицины для интенсивной терапии.

Ключевые слова: персонализированная медицина, мультиомика, искусственный интеллект, цифровые двойники, CRISPR, объяснимый ИИ, федеративное обучение, блокчейн, прецизионная геномика, интенсивная терапия.

Introduction

Modern healthcare is shifting away from one-size-fits-all treatments and moving toward care that's truly personalized for each patient. The old methods worked alright when treating large groups, but they tend to ignore how each person's genetics, environment, immune system, metabolism, and other health issues can completely change how a disease progresses and how well a treatment actually works. That's where personalized medicine steps in, pulling together everything we know about a person — their unique biology, medical history, and environment — to make diagnoses, predictions, and treatment choices far more precise [2], [3], [6].

With the rise of DNA sequencing and biomedical sensors, we can now collect massive amounts of data. Scientists call this "multi-omics" data because it covers everything from genetic changes and protein activity to someone's metabolism. This paints a full picture of what's going on in the body. But here's the catch: the sheer amount and complexity of this information is just too much for traditional analysis. That's why researchers are turning to advanced tools like artificial intelligence and machine learning that can sift through the noise and find meaningful patterns [10], [11].

Critical care, especially in the ICU, really shows what's possible with personalized medicine. Why? Because ICU patients are in crisis — think severe infections, respiratory failure, cardiac arrest, or multiple organs shutting down. Doctors have to act fast, so every second and every detail counts. Even with the latest monitors, ICUs usually react to problems after the fact instead of foreseeing them.

Bringing together multi-omics data, AI-powered analysis, digital twin models, and tailored therapies can flip the script — turning critical care into something more proactive and predictive. But there are still plenty of hurdles: data is scattered across different systems, machines don't always talk to each other, AI models can be black boxes, and there are ongoing worries about privacy and security. This review takes a close look at these fast-moving innovations and examines how they're shaping the future of critical care that's personalized for every patient.

Multi-omics integration in personalized medicine

Multi-omics integration is at the heart of modern precision medicine. It lets researchers look at complex biological processes as a whole system instead of in isolated parts. Each "omics" layer brings something unique to the table. Genomics is all about changes in DNA — things like single nucleotide polymorphisms, insertions, deletions, or structural variations, which can set people up for certain diseases. Transcriptomics looks at which genes are turned on or off, showing how our bodies react to different environments or stresses. Proteomics dives into the world of proteins, measuring how many are present, how they're modified, and how they interact — basically, revealing what's happening in the cell right now. Metabolomics gives a snapshot of all the chemical intermediates and metabolic pathways, offering a direct peek into cellular activity. Epigenomics focuses on how gene expression is controlled, through mechanisms like DNA methylation and histone modification, without touching the DNA code itself [6], [7].

When you pull together all these different data types, you get more precise disease classification, discover new biomarkers, and target therapies more effectively. Cancer research, for instance, has used multi-omics to find molecular subtypes that plain histology just can't spot. Same thing with sepsis and inflammatory diseases — by analyzing transcriptomic and proteomic patterns, scientists have identified different immune response types, leading to more tailored treatments [8].

But integrating all this information isn't simple. Early on, researchers leaned on methods like principal component analysis or canonical correlation analysis. Now, they use deep learning too — autoencoders, graph neural networks, multimodal transformers — which can detect complicated patterns across all sorts of data. Still, there are some stubborn challenges. Missing data, batch effects, inconsistencies in how data is collected, and big computational costs all get in the way, making it tough to bring these techniques into everyday clinical practice.

Table 1 - Multi-Omics Data Comparison

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Omics Layer	Biological Insight	Clinical Relevance	Challenges
Genomics	DNA mutations	Disease risk prediction	Static, expensive
Transcriptomics	Gene expression	Disease activity	Temporal variability
Proteomics	Protein signaling	Functional pathways	Complex measurement
Metabolomics	Biochemical state	Real-time physiology	High variability
Epigenomics	Gene regulation	Environmental effects	Data complexity
Microbiomics	Host-microbe interaction	Immunity & gut health	Standardization issues

Artificial intelligence in critical care

Artificial intelligence has completely changed the way we analyze biomedical data. It's made it possible to pull real meaning out of massive, messy datasets that used to leave researchers stumped. Doctors and scientists now rely on machine learning tools like logistic regression, support vector machines, random forests, and gradient boosting for all sorts of clinical prediction tasks. Lately, deep learning has jumped ahead — models like convolutional neural networks, recurrent neural networks, and transformers are getting much better results, especially when working with everything from structured lab results to unstructured doctor notes [3], [10], [11].

In the ICU, AI is already at work. It helps spot trouble early — like a patient's condition is about to get much worse — even before the clinical team notices. These systems don't just hint at a problem; they can sometimes pick up on cases of sepsis, kidney injury, or respiratory failure hours in advance, looking at mountains of data from ICU databases such as MIMIC-III. That head start can make all the difference when time is critical [5], [12].

But putting AI into real clinical practice isn't simple [3], [11]. Models often don't work as well outside the hospitals where they were trained, mostly because patient populations, treatment routines, and even data collection can look pretty different from one place to another. And let's not forget: many of these models are still black boxes. They spit out answers with little clue why, which makes it tough for clinicians to trust or rely on them [23], [24]. To actually make AI a trustworthy partner in healthcare, the field needs deeper validation, more transparent models, and systems that fit naturally into how clinicians already work. Without those, AI's impact will hit a ceiling [1].

Digital twins in healthcare

Digital twin technology is changing how we model complex biological systems and personalize disease management. Picture a digital twin as a virtual copy of a real patient, always staying up-to-date thanks to live data. In healthcare, these digital twins pull together everything — physiological signals, images, lab tests, and molecular info — so doctors get a detailed picture of someone's health [14], [31].

There are different kinds of digital twins. Mechanistic models use math to mirror how the body works, like heart or lung functions. Data-driven models lean on machine learning to spot patterns in old data. Hybrid models blend both, aiming for sharper accuracy and clearer insights [35].

Critical care really benefits from these models. With digital twins, doctors can try out different treatments virtually and see what might happen. Take a respiratory twin — it can show how changes in ventilator settings affect oxygen levels and potential lung damage. Or a cardiovascular twin — it predicts what happens if you tweak fluids or give certain medicines [14]. Bringing in molecular data makes these models even smarter, helping tailor predictions down to the tiniest detail [32].

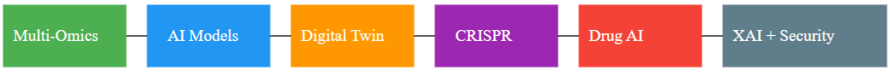

Figure 1 - Unified Precision Critical Care Framework

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Crispr and ai-driven precision therapeutics

CRISPR-Cas genome editing has changed the game in molecular medicine. Now, we can make precise, targeted changes to DNA — something that used to sound like science fiction. People see real hope for using this technology to treat things like genetic disorders, cancer, and some infectious diseases by going straight to the source and fixing harmful mutations. This whole shift started with Jennifer Doudna and Emmanuelle Charpentier, who helped turn CRISPR into the powerful tool it is today [17], [19].

Artificial intelligence is stepping in to make CRISPR even more powerful. Scientists use machine learning to predict which guide RNAs will work best, avoid unwanted DNA changes, and come up with smarter editing plans overall. Deep learning has really boosted the accuracy of CRISPR design, so therapies are getting safer and more effective [18].

There's another exciting layer to all this — combining CRISPR with digital twin systems. Basically, doctors can run simulations to see what might happen if they edit certain genes, allowing them to weigh benefits and risks before actually treating a patient. But there are still hurdles, like figuring out the best way to deliver CRISPR components, dealing with immune reactions, and sorting through the ethical issues. These challenges need answers before CRISPR becomes standard in clinics everywhere.

Ai-based drug recommendation systems

Doctors know that drug response can be unpredictable — what works perfectly for one person might not do much for another. That's a headache in clinics everywhere. AI drug recommendation systems try to tackle this problem head-on. They gather everything from a patient's genetics to medical history and even their basic health stats to help figure out which drug and what dose will actually work [20].

Pharmacogenomics — basically, using genetics to guide drug choices — has made big strides. Say someone needs warfarin. If they have certain changes in CYP2C9 or VKORC1 genes, their body handles the drug differently. Same goes for thiopurines and TPMT gene variants; those changes can make a treatment riskier or safer. AI can pull genetic info and real-world medical data together and use it to recommend better meds tailored to each patient [20], [21].

On top of that, reinforcement learning is starting to shape how doctors make decisions, especially in critical care. These AI methods "learn" by trying out treatment strategies in simulated situations and watching patient responses, adjusting as they go. Still, we're not fully there yet. Safety concerns, figuring out how AI thinks, and proving that it works in actual hospitals — those are big hurdles that haven't gone away [12], [22].

Table 2 - Drug Personalization Approaches

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Approach	Data Used	Example	Advantage
Pharmacogenomics	DNA variants	Warfarin dosing	Reduced toxicity
AI Prediction	Clinical + genomic	Cancer therapy	High accuracy
Reinforcement Learning	Time-series ICU	Sepsis treatment	Adaptive
Digital Twin Simulation	Full patient model	Drug response	Risk-free testing

Explainable ai in healthcare

Doctors don't just want AI to spit out answers — they need to know why a model came to a certain decision if they're going to trust and use it in healthcare. That's where explainable AI, or XAI, comes in. XAI methods actually show which factors led to a model's prediction, making things more transparent for clinicians [23], [24].

Take SHAP, created by Scott Lundberg, or LIME. Both of these tools break down how much each feature mattered in a given prediction. This helps doctors see the reasoning behind a model's output, so they can check its logic and feel more comfortable relying on it.

But it doesn't stop at just listing important features. Some newer XAI methods dive deeper — they look at cause and effect, and even test "what if" scenarios (that's known as counterfactual reasoning). This kind of analysis is especially valuable in critical care, where even a small decision can mean a lot for a patient's health. With these tools, clinicians aren't just guessing — they're seeing real evidence behind AI recommendations [25].

Table 3 - Explainable AI Techniques

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Method	Type	Use Case	Limitation
SHAP	Global + Local	Feature importance	Computational cost
LIME	Local	Model explanation	Instability
Attention Maps	Deep learning	Sequence models	Not fully interpretable
Counterfactuals	Causal	Clinical decisions	Complex generation

Privacy-preserving AI

Sharing sensitive healthcare data — especially things like your genetic info — always stirs up worries about privacy and security. That's where federated learning comes in. Instead of shipping raw data between hospitals or research groups, everyone trains AI models together, separately, keeping their own data safe. It's a smarter way to collaborate without risking privacy [26].

Now, blockchain adds another layer of security. It creates clear, tamper-proof records of who accessed what and when, and it spreads control out, so no one person or group holds all the power. Big organizations like the National Institutes of Health regularly stress how key secure data sharing is for stuff like precision medicine [27].

Other tech tools help too. Things like differential privacy [28], homomorphic encryption, and secure multiparty computation — all those mouthfuls — keep sensitive details locked down, but still let researchers pull out useful insights. That means we get the benefits of big data without putting anyone's personal info on the line.

Table 4 - Security Techniques Comparison

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Technique	Purpose	Strength	Limitation
Federated Learning	Distributed training	Data privacy	Communication cost
Blockchain	Data integrity	Tamper-proof	Scalability
Differential Privacy	Noise addition	Strong privacy	Accuracy loss
Homomorphic Encryption	Secure computation	High security	Very slow

Challenges and future directions

Personalized medicine holds a lot of promise in critical care, but there are still some big hurdles. Multi-omics data is expensive to gather, and it's tough to bring together all those different data sources. Standardized datasets don't really exist yet, plus nobody's quite sure how regulations will shake out [6], [7]. Then there's the tricky stuff — like the ethical issues with genomic editing and letting AI make tough decisions [17].

Researchers need to focus on making systems that scale up easily and work well with each other. It's important to make models that doctors can actually understand and use in real time [36]. And some new tech — like quantum computing, foundation models, or neuromorphic hardware — could push predictive accuracy and speed even further [33].

Table 5 - Research Gap Matrix

DOI: https://doi.org/10.60797/BMED.2026.9.8.6

Area	Current State	Gap	Opportunity
Multi-Omics	Separate analysis	Lack of integration	Unified models
AI Models	High accuracy	Low interpretability	Explainable AI
Digital Twins	Experimental	Not real-time	ICU deployment
CRISPR	Lab success	Clinical integration missing	AI-driven therapy
Drug Systems	Static rules	No personalization	RL-based systems
Security	Basic encryption	No unified framework	Blockchain + Federated Learning

Conclusion

Personalized medicine in critical care is on the edge of a huge leap forward. Multi-omics technologies, artificial intelligence, digital twins, CRISPR therapeutics, and secure data systems all come together to make it possible. With these tools, doctors can predict problems, adapt treatments, and truly tailor care to each patient. That means better outcomes, fewer deaths — real progress. But none of this happens alone. Experts from different fields have to work together, validate these approaches, and make sure everything stays ethical. If we want these breakthroughs in actual hospitals, we need clear, unified, and secure systems that people can trust and understand.

Конфликт интересов

Не указан.

Рецензия

Все статьи проходят рецензирование. Но рецензент или автор статьи предпочли не публиковать рецензию к этой статье в открытом доступе. Рецензия может быть предоставлена компетентным органам по запросу.

Conflict of Interest

None declared.

Review

All articles are peer-reviewed. But the reviewer or the author of the article chose not to publish a review of this article in the public domain. The review can be provided to the competent authorities upon request.

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