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Research Article

Potential of Quantum Computing to Advance Psychiatry through Genetic Medicine, Gene Therapy, and Human-Centered Artificial Intelligence

George B Stefano*

Mind-Body Medicine Research Council, Institute for Integrative Health Care and Health Promotion (IGVF), Faculty of Health/School of Medicine, Witten/Herdecke University, Witten, Germany

More Information

***Corresponding author:** George B Stefano, Ph D, DR hc, Mind-Body Medicine Research Council, Institute for Integrative Health Care and Health Promotion (IGVF), Faculty of Health/School of Medicine, Witten/Herdecke University, Witten, Germany,
Email: gstefano@sunynri.org

https://orcid.org/0000-0002-8146-0740

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Abstract

Psychiatric disorders represent some of the most biologically complex challenges in medicine, arising from intricate interactions among genetic, epigenetic, environmental, developmental, and social factors. Advances in artificial intelligence (AI) have improved our ability to analyze large-scale biological datasets, identify biomarkers, and support precision medicine initiatives. However, the growing volume and complexity of genomic and multi-omic information increasingly challenge the capabilities of even the most advanced conventional supercomputers. Quantum computing offers a potential next step in biomedical discovery by enabling rapid analysis of multidimensional datasets, molecular simulations, and optimization problems relevant to genetic medicine and gene therapy. Extending these findings conceptually, we propose the forward-looking hypothesis that continued advances in quantum computing may eventually complement artificial intelligence and human expertise to facilitate increasingly sophisticated analyses relevant to psychiatric genetics and precision medicine. At present, no direct evidence of which we are aware demonstrates clinical implementation of quantum computing in psychiatric genomics. Accordingly, the concepts discussed in this Opinion should be viewed as a forward-looking scientific perspective that builds upon current advances in computational science and biomedicine while awaiting future experimental and clinical validation. Importantly, these advances should complement rather than replace human expertise. Human-in-the-loop systems remain essential for ensuring scientific rigor, ethical oversight, clinical judgment, and patient-centered care. The convergence of quantum computing, AI, genetic medicine, and human expertise may ultimately establish a transformative framework for future precision psychiatry and mental health therapeutics.

Introduction

Psychiatric disorders, including major depressive disorder, schizophrenia, bipolar disorder, autism spectrum disorder, and neurodegenerative diseases with psychiatric manifestations, remain among the most challenging conditions to understand and treat. Unlike monogenic disorders, psychiatric illnesses arise from the interaction of numerous genetic variants, epigenetic modifications, environmental influences, developmental trajectories, and psychosocial factors. As a result, identifying actionable molecular targets and effective personalized interventions has proven difficult.

Recent advances in artificial intelligence (AI) have significantly improved the analysis of biological and clinical datasets, enabling more sophisticated approaches to biomarker discovery, disease classification, drug development, and clinical decision support [1–6]. Nevertheless, the complexity of psychiatric disease biology continues to exceed the capabilities of many classical computational approaches.

Quantum computing may represent the next major advance in computational medicine. Unlike conventional computers that process information using binary bits, quantum computers utilize quantum bits (qubits), which can exist simultaneously in multiple states through superposition and entanglement. These properties permit exploration of extraordinarily large solution spaces and may provide substantial advantages for optimization, molecular simulation, and systems-level biological analyses [7].

In this regard, we propose the forward-looking hypothesis that continued advances in quantum computing may eventually complement artificial intelligence in addressing computational challenges associated with psychiatric genetics, systems biology, and precision medicine. While encouraging progress has been reported in computational chemistry, molecular simulation, and optimization algorithms, direct implementation of quantum computing within psychiatric genomics has not yet been established, and the concepts discussed throughout this Opinion should accordingly be viewed as a conceptual framework intended to stimulate future investigation rather than as established clinical practice.

Importantly, the future of psychiatric innovation may depend not only upon increasingly powerful computational systems but also upon maintaining meaningful human oversight throughout the discovery and therapeutic process. From this perspective, it can be surmised that future progress is most likely to arise through cooperative interactions among quantum computing, artificial intelligence, and Human-in-the-Loop (HITL) systems, thereby combining computational capability with scientific interpretation, ethical oversight, and clinical judgment.

Quantum computing beyond conventional super-computing

Modern supercomputers have enabled remarkable advances in systems biology, genomics, and precision medicine. However, psychiatric disorders frequently involve extraordinarily complex biological networks consisting of thousands of interacting genes, proteins, signaling pathways, and environmental modifiers. As these interactions increase, computational complexity often expands exponentially. Quantum computing offers the possibility of addressing problems that remain difficult or impractical for conventional computing systems. Quantum algorithms are particularly well suited for optimization, molecular simulation, and multidimensional pattern recognition. Such capabilities may allow researchers to analyze biological systems at scales previously inaccessible using classical approaches [7–9].

Recent advances suggest that quantum-enabled computational frameworks may accelerate analyses involving genome-wide association studies (GWAS), transcriptomics, epigenomics, proteomics, and multi-omic integration. Because psychiatric disorders are highly polygenic, involving numerous small-effect genetic variants distributed across biological networks, we propose the forward-looking hypothesis that future quantum-enabled computational approaches may eventually help identify higher-order molecular interactions that remain difficult to resolve using current methodologies, though this remains a hypothesis-generating possibility that awaits future experimental validation [8–10].

Importantly, we do not envision quantum computing as replacing conventional supercomputers. Rather, we anticipate that future biomedical discovery will increasingly rely upon complementary computational architectures in which classical high-performance computing, artificial intelligence, and quantum computing function cooperatively, each contributing unique computational strengths to increasingly sophisticated biological analyses. Such an integrated computational framework is particularly consistent with the Human-in-the-Loop philosophy advanced throughout this Opinion, in which technological innovation augments rather than replaces scientific reasoning, biological interpretation, and clinical judgment.

Quantum computing and genetic medicine

The emergence of precision medicine has shifted biomedical research toward individualized approaches based on genetic and molecular information. However, the translation of genomic discoveries into clinically actionable interventions remains a significant challenge. Quantum computing may help bridge this gap by enabling rapid analysis of vast genomic datasets and facilitating identification of disease-associated pathways. Continued advances in quantum computing may eventually complement existing computational approaches by enabling more sophisticated analyses of complex genomic datasets relevant to psychiatric disorders, including accelerated variant interpretation, enhanced biomarker discovery, and more comprehensive modeling of gene regulatory networks [8–10]. However, no direct evidence yet confirms routine implementation of these approaches within psychiatric genomics, and these concepts should therefore be regarded as hypothesis-generating perspectives requiring future experimental validation.

Particularly important may be the integration of quantum computing with systems biology approaches. Psychiatric disorders are increasingly recognized as network diseases involving interactions among genes, proteins, immune pathways, metabolic systems, mitochondrial function, and environmental influences. Building upon these established observations, we further propose that future quantum-enabled computational analyses may eventually facilitate a more comprehensive understanding of these multidimensional biological relationships, thereby supporting the continued evolution of individualized therapeutic strategies [8–10]. Whether quantum computing offers meaningful advantages over increasingly sophisticated classical computational approaches remains to be determined through future research. From this perspective, the greatest future contribution of quantum computing may not be computational speed alone, but rather its potential to complement artificial intelligence, systems biology, and Human-in-the-Loop scientific interpretation in developing increasingly integrated models of complex psychiatric disease biology.

Structural biology, alphafold, and psychiatric genomics

Artificial intelligence has already transformed structural biology through systems such as AlphaFold, which predict protein structures with remarkable accuracy. These advances have significantly accelerated biological discovery by linking genomic sequence information to protein function. Building on these advances, continued progress in quantum computing may eventually complement AI-driven structural biology by enabling more sophisticated modeling of protein folding, receptor interactions, molecular signaling pathways, and disease-associated conformational dynamics [11–14].

Such future computational capabilities could prove particularly valuable in psychiatry, where complex molecular interactions rather than single genetic abnormalities frequently contribute to disease susceptibility, progression, and therapeutic responsiveness. No direct evidence yet demonstrates the routine application of quantum computing to structural analyses within psychiatric genomics, so this perspective should be regarded as a conceptual extension of current advances in artificial intelligence, structural biology, and computational medicine that awaits future experimental and clinical validation.

Improved structural modeling may ultimately facilitate identification of novel therapeutic targets and enhance understanding of pathogenic mechanisms underlying psychiatric and neurodegenerative disorders. From this perspective, future integration of artificial intelligence, quantum computing, and Human-in-the-Loop scientific interpretation may provide a more comprehensive framework for translating structural biological discoveries into precision psychiatric medicine.

Gene therapy and quantum-enhanced optimization

Gene therapy has emerged as one of the most promising approaches in modern medicine. Technologies such as CRISPR-Cas systems offer unprecedented opportunities to modify disease-associated genes and biological pathways. However, significant challenges remain regarding target selection, off-target effects, vector optimization, delivery mechanisms, and long-term safety.

Building on these advances in gene editing, continued developments in quantum computing may eventually complement existing methodologies by optimizing gene-editing strategies—assisting in evaluating large numbers of potential guide RNA configurations, optimizing therapeutic target selection, modeling complex gene regulatory interactions, and improving prediction of unintended genomic modifications [8,9,15,16].

To date, no direct evidence confirms the application of quantum computing to clinical gene-editing optimization within psychiatric disorders. Accordingly, these concepts should be regarded as a conceptual extension of current advances in quantum computing, artificial intelligence, and genetic medicine that will require future experimental and clinical validation.

Thus, as gene therapy continues to evolve, computational advances may become increasingly important **for** improving therapeutic precision, safety, and biological understanding. From this perspective, future integration of quantum computing, artificial intelligence, and Human-in-the-Loop scientific interpretation may ultimately provide a more comprehensive framework for optimizing increasingly complex gene-based therapeutic strategies. Such developments may be particularly relevant for psychiatric disorders, where therapeutic targets often involve highly interconnected biological networks rather than single genes.

Polygenic risk scores and precision psychiatry

Polygenic risk scores (PRS) have emerged as important tools for estimating genetic susceptibility to complex psychiatric disorders by integrating the cumulative effects of numerous common genetic variants. Although PRS continue to improve risk stratification and contribute to precision medicine initiatives, their predictive performance remains limited by the biological complexity of psychiatric disorders, gene-gene interactions, epigenetic regulation, environmental influences, and population-specific genetic diversity.

Building on these observations, continued advances in quantum computing may eventually complement existing computational approaches used for PRS development by enabling analyses of increasingly complex, multidimensional genomic datasets—potentially improving identification of higher-order genetic interactions, optimizing multidimensional predictive modeling, and enhancing integration of genomic, transcriptomic, epigenomic, proteomic, and clinical datasets relevant to psychiatric disease [17,18].

No direct evidence currently demonstrates that quantum computing improves polygenic risk prediction or clinical decision-making within psychiatric genomics; these concepts should therefore be regarded as a forward-looking conceptual framework that extends current advances in computational biology, artificial intelligence, and precision medicine while awaiting future experimental validation.

Importantly, the future clinical utility of PRS will likely depend not only upon increasingly sophisticated computational methodologies but also upon continued improvements in biological understanding, data quality, population diversity, and clinical interpretation. From this perspective, future integration of quantum computing, artificial intelligence, and Human-in-the-Loop scientific interpretation may ultimately contribute to more comprehensive and biologically informed precision psychiatry, though whether these computational advances yield clinically meaningful improvements beyond increasingly sophisticated classical approaches is an open question for future study.

Human-in-the-Loop: Preserving Scientific Judgment in the Era of Quantum Computing

Although advances in artificial intelligence and quantum computing have the potential to transform biomedical research, computational capability alone cannot replace scientific reasoning, biological insight, ethical judgment, or clinical experience. Throughout the history of medicine, major technological advances have served to augment rather than replace human expertise. Therefore, we propose that the continued evolution of quantum computing should likewise be viewed as an enabling technology that complements, rather than supplants, human scientific and clinical decision-making.

Human-in-the-Loop systems provide an essential framework in which computational analyses remain subject to continuous scientific interpretation, validation, and ethical oversight. By integrating computational efficiency with human expertise, HITL approaches help ensure that increasingly sophisticated algorithms remain transparent, biologically meaningful, clinically relevant, and aligned with patient-centered care [19–23].

Moreover, we propose the forward-looking hypothesis that the greatest future contribution of quantum computing may arise not from computational power alone, but from its integration with artificial intelligence and HITL systems capable of interpreting increasingly complex biological information. Such cooperative computational frameworks may ultimately facilitate more comprehensive analyses of multidimensional psychiatric datasets while preserving the scientific judgment necessary for responsible biomedical discovery and clinical translation. The complexity of psychiatric disorders further emphasizes the importance of maintaining human oversight throughout the investigative and therapeutic process. Interpretation of genomic findings, assessment of biological plausibility, evaluation of therapeutic risk, and integration of psychosocial and environmental factors require scientific reasoning that extends beyond computational prediction alone.

Accordingly, we envision a future computational ecosystem in which classical high-performance computing, artificial intelligence, quantum computing, and Human-in-the-Loop scientific expertise function cooperatively, each contributing complementary strengths to precision psychiatry. Within this framework, technological innovation serves to augment human intelligence rather than replace it, thereby supporting more rigorous scientific investigation, improved clinical decision-making, and ultimately more personalized patient care.

Future perspectives

Psychiatry is entering an era in which increasingly sophisticated computational technologies are converging with advances in genomics, molecular biology, structural biology, artificial intelligence, and precision medicine. Continued progress in these complementary disciplines has the potential to reshape our understanding of complex psychiatric disorders and to facilitate increasingly individualized therapeutic strategies.

Conceptually, we further propose that quantum computing may ultimately become an important component of future computational psychiatry. Rather than functioning as an isolated technology, its greatest contribution may arise through integration with artificial intelligence, systems biology, genetic medicine, and HITL scientific interpretation [7–10,15–23]. Such a multidisciplinary computational framework could facilitate increasingly comprehensive analyses of multidimensional biological datasets while supporting more biologically informed approaches to precision psychiatry.

As noted throughout this Opinion, no direct evidence currently demonstrates routine implementation of quantum computing within psychiatric genomics or precision psychiatric medicine. The concepts presented here should therefore be viewed as a conceptual extension of current advances in computational science, molecular biology, and psychiatric genetics that will require continued technological development, experimental investigation, and clinical validation.

Future advances in quantum hardware, error-correction strategies, hybrid quantum-classical algorithms, and computational biology will ultimately determine the extent to which these technologies become integrated into biomedical research and clinical practice. Whether quantum computing ultimately provides clinically meaningful advantages beyond increasingly sophisticated classical computational approaches is a question that future research will need to address.

From this perspective, the future of precision psychiatry is unlikely to depend upon any single technological innovation. Rather, we envision an integrated scientific ecosystem in which classical high-performance computing, artificial intelligence, quantum computing, systems biology, and HITL scientific expertise function cooperatively to advance biological discovery, improve therapeutic precision, and enhance patient-centered psychiatric care.

Conclusion

Psychiatric disorders represent some of the most biologically complex challenges in contemporary medicine, reflecting intricate interactions among genetic, epigenetic, molecular, environmental, developmental, and psychosocial factors. Continued advances in artificial intelligence, systems biology, computational medicine, and genetic technologies are already transforming our understanding of these disorders and creating new opportunities for precision psychiatry. It may be surmised that continued developments in quantum computing may ultimately complement existing computational methodologies by facilitating increasingly sophisticated analyses of complex biological systems relevant to psychiatric disease [7–10]. Rather than representing a replacement for conventional computational approaches, quantum computing is envisioned as one component of an integrated computational ecosystem that includes classical high-performance computing, artificial intelligence, systems biology, and HITL scientific expertise [19–23]. Accordingly, the concepts presented here should be regarded as a hypothesis-generating conceptual framework. Whether quantum computing ultimately fulfills the potential proposed in this Opinion remains an important question for future investigation. Nevertheless, continued progress in computational science provides a strong foundation for exploring how emerging technologies may contribute to increasingly personalized, biologically informed, and patient-centered psychiatric care.

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Author contributions

George B. Stefano conceived the conceptual framework of this Opinion, performed the literature review, interpreted the scientific evidence, prepared and revised the manuscript, and approved the final version for submission.

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