Review

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# Integrating AI, CRISPR, and Multi-Omics for Predictive Longevity Research

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# Integrating AI, CRISPR, and Multi-Omics for Predictive Longevity Research

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**Abstract**

The pursuit of extending human healthspan and lifespan has become a central focus in modern biomedical research. Aging is a complex, multifactorial process influenced by genetics, epigenetics, environmental factors, and stochastic molecular events. Traditional approaches, relying on observational studies or single-omic analyses, have provided limited mechanistic insights into the determinants of longevity. Recent advances in multi-omics, genome editing, and artificial intelligence (AI) now offer a transformative framework for predictive and personalized longevity research [1]. In particular, the integration of AI-driven computational modeling, CRISPR-based genome engineering, and comprehensive multi-omic datasets holds the promise of elucidating key molecular drivers of aging and informing targeted interventions.

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## Introduction

Multi-omic technologies, including genomics, transcriptomics, proteomics, metabolomics, and epigenomics, provide a high-resolution view of cellular and organismal states across the lifespan. By capturing the dynamic interplay between genes, regulatory networks, metabolic pathways, and environmental influences, multi-omics enables the identification of biomarkers and molecular signatures associated with longevity. However, the scale and complexity of multi-omic data pose significant challenges for traditional statistical methods. This is where AI and machine learning (ML) approaches can make a substantial impact. Algorithms capable of handling high-dimensional data, detecting complex non-linear relationships, and generating predictive models allow researchers to identify critical nodes in aging networks, predict age-associated phenotypes, and prioritize potential therapeutic targets [2].

## Discussion

AI-driven analysis of multi-omic data can uncover previously unrecognized patterns that contribute to aging and longevity. For instance, machine learning can identify clusters of genes or proteins whose expression changes consistently with biological age, highlight metabolic signatures predictive of healthspan, and infer causal relationships within regulatory networks. Deep learning models, particularly graph neural networks, can model the intricate interactions between biomolecules, enabling in silico prediction of interventions that may modulate aging pathways [3]. Such predictive capabilities are essential for designing experimental strategies that are both efficient and targeted, reducing the time and cost associated with traditional trial-and-error approaches.

CRISPR-Cas genome editing technologies complement AI-guided predictions by providing a precise and scalable means to experimentally validate potential longevity targets. Genes identified through AI-driven multi-omic analyses can be selectively activated, silenced, or modified using CRISPR, enabling researchers to test their causal role in aging phenotypes. For example, CRISPR-mediated modulation of senescence-associated genes, telomere maintenance pathways, or mitochondrial regulators can provide functional evidence for their contributions to lifespan and healthspan [4]. Beyond single-gene editing, CRISPR-based screens can systematically perturb networks of genes to identify synergistic effects on cellular longevity. These screens, when guided by AI predictions, can dramatically increase the efficiency of discovering actionable interventions.

The integration of AI, CRISPR, and multi-omics is not only a powerful research strategy but also a foundation for personalized longevity interventions. Individuals exhibit significant heterogeneity in genetic background, epigenetic modifications, and environmental exposures, all of which influence aging trajectories. By combining personal multi-omic profiles with AI-based predictive modeling, it becomes possible to identify individualized targets for intervention. CRISPR can then be employed to design precise, patient-specific modifications or to guide the development of personalized therapeutics, such as gene therapies or targeted small molecules [5]. This convergence of computational prediction, high-resolution molecular profiling, and genome editing represents a paradigm shift toward precision geroscience.

Several practical considerations are critical for the successful integration of these approaches. First, the quality and standardization of multi-omic data are essential; batch effects, missing data, and technical variability can compromise AI model accuracy. Second, interpretability of AI predictions remains a challenge, particularly with deep learning models, and must be addressed to translate computational findings into actionable experimental designs. Third, ethical and safety considerations in applying CRISPR-based interventions for longevity require careful evaluation, including off-target effects, long-term consequences, and equitable access [6]. Finally, collaborative efforts across computational biology, molecular biology, and clinical research are vital to harness the full potential of this integrated approach.

Despite these challenges, early studies demonstrate the feasibility and promise of combining AI, CRISPR, and multi-omics for aging research. For instance, AI models trained on transcriptomic and epigenomic data have successfully predicted interventions that modulate senescence and extend lifespan in model organisms. Similarly, CRISPR-based functional screens informed by network analysis have identified novel regulators of cellular stress response, mitochondrial function, and proteostasis, whereby they are all key determinants of longevity [7]. As these technologies continue to mature, their integration is likely to accelerate the discovery of molecular interventions capable of extending healthspan in humans.

## Conclusion

In conclusion, predictive longevity research stands at the intersection of computational modeling, genome editing, and multi-omic profiling. By integrating AI to analyze complex molecular data, CRISPR to experimentally validate and manipulate targets [8,9], and multi-omics [10–12] to capture the full biological context, researchers are poised to uncover the mechanistic underpinnings of aging and design precise, personalized interventions. This convergence not only enhances our understanding of the biology of aging but also provides a roadmap for translating discoveries into actionable strategies for promoting healthspan and lifespan. The integration of AI, CRISPR, and multi-omics thus represents a powerful, forward-looking approach in biomedicine that has the potential to transform how we study, predict, and ultimately modulate human aging.

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