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Editorial

Digital epigenetics: At the crossroads of data, the epigenome, and artificial intelligence

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In recent decades, traditional epidemiology, which emphasizes the systematic collection of clinical and questionnaire-based data, has significantly transformed in response to a remarkable influx of large-scale digital data, social network analytics, and sensor-based information.[1,2] This transformation, known as digital epidemiology, has changed the landscape of identifying disease trends and tracking public health.

In parallel, epigenetics— a field that combines molecular biology and epidemiology to elucidate the impact of environmental factors on gene expression—has become increasingly important in the realms of public health research and precision medicine.[3] Population-based epigenetic studies, or epigenetic epidemiology, offer a profound understanding of how environmental, social, and behavioral exposures shape disease risk. Advanced molecular techniques such as epigenome-wide association studies (EWAS) have been established to assess and interpret epigenetic markers at scale.[4-6]

In this editorial, we present a forward-looking vision for epigenetics, drawing upon a synthesis of significant literature in digital epidemiology, epigenetics, and artificial intelligence (AI). Our central thesis is that the field must move beyond isolated approaches and explicitly promote the integration of large-scale digital data with population-level epigenetic profiles via advanced AI. We assert that this is not solely an incremental step, but an essential convergence to unveil previously unattainable insights into gene–environment interactions and evolving exposure patterns, influencing the future direction of this emerging field.

The convergence of these two domains—scalable digital data and molecular epigenetic signals—promises the advent of a novel discipline that we may call digital epigenetics. This emerging field seeks to generate large data sets that encompass environmental, neurobiological, and epigenetic data, collected from a wide variety of digital sources including electronic health records, real-time monitoring via wearable devices such as smartwatches, and large omics databases, all analyzed through advanced computational models.[7] Such integration could uncover novel behavioral and environmental drivers of epigenetic changes, while simultaneously advancing predictive applications in precision medicine.[2]

Author's Biosketch

Morteza Ghojazadeh is a distinguished epidemiologist and a leading figure in the emerging field of Digital Epidemiology. His interdisciplinary research program sits at the intersection of artificial intelligence, evidence-based medicine, and neurosciences, with a specialized focus on fMRI applications. A prolific scholar, Ghojazadeh has authored over 300 peer-reviewed articles and is consistently ranked among the world's top 2% most-cited scientists (Stanford University/Elsevier). His work is characterized by a rigorous methodological approach, heavily utilizing systematic reviews and meta-analyses to synthesize complex evidence and drive the field forward.

AI plays a crucial role in this transformation. Machine learning and deep learning models have demonstrated their capacity to utilize epigenome-centered data for disease risk prediction, molecular status classification, and the discovery of complex gene–environment interaction patterns.[8] Recent studies and systematic reviews suggest that applying AI to epigenetic data not only enhances predictive accuracy but also facilitates the identification of new biomarkers and the interpretation of multidimensional datasets.[9]

Several key opportunities define the landscape of digital epigenetics:

1. Integrating wearable, environmental, and electronic health data digitally recorded enables dynamic modeling of temporal relationships between exposures and epigenetic modifications [2].
2. AI models trained on multimodal datasets (clinical, behavioral, and epigenetic) can guide earlier and more targeted interventions.[10]
3. Large-scale digital data can reveal fine-grained environmental or behavioral patterns (e.g., sleep

disruption or urban exposure) often missed by traditional studies, thus supporting hypothesis generation in molecular epidemiology.[11]

However, the promise of digital epigenetics is accompanied by considerable challenges that must not be overlooked: ensuring the quality and interoperability of digital data; safeguarding genomic and health privacy; preventing population-level algorithmic bias; and maintaining biological interpretability of complex AI models [12]. In order for digital epigenetics to deliver trustworthy and ethically sound benefits to public health, it is crucial to establish transparent frameworks for data governance, standardized model evaluation, and robust ethical and legal oversight.[13]

Finally, advancing this vision requires a coordinated scientific and policy agenda involving investment in privacy-preserving data-sharing infrastructures, the promotion of longitudinal studies that combine digital and molecular data collection, and the formation of multidisciplinary teams that bridge the fields of epigenetics, data science, and bioethics.[14] Equally important is educating researchers and policymakers regarding both the potentials and limitations of AI in epigenetic research. Once these prerequisites have been met, digital epigenetics may well represent the next frontier of data-driven health science, poised to transform both biomedical research and clinical practice.[15]

Competing Interests

None declared.

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