Special Issue

Advanced Statistical Computing in Medical Genomics: Emerging Techniques and Applications

Message from the Guest Editor

Key themes but are not limited to:

Multi-Omics Integration for Causal Inference: Developing methods to integrate genomics, transcriptomics, and epigenomics can deepen insights into complex traits. Tools like Mendelian Randomization and Bayesian networks can identify causal pathways behind genetic associations.

Machine Learning for Epistasis and Gene-Environment Interactions: advancing machine learning models (e.g., deep learning, random forests) to detect non-linear gene-gene and gene-environment interactions can improve understanding of complex genetic traits.

Polygenic Risk Scores for Diverse Populations: enhancing PRS methods to account for ancestry differences and linkage disequilibrium is critical to ensure predictive power across diverse populations, improving their clinical utility.

Efficient High-Dimensional Data Handling: developing methods like sparse modeling, regularization, and dimensionality reduction to manage large-scale genomic data can improve variant identification and reduce false positives in large-scale studies.

Guest Editor

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Deadline for manuscript submissions

closed (25 April 2025)

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Editor-in-Chief

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