Although this general strategy is applicable across biological systems, its implementation must be adapted to the characteristics of the data. In human studies, ancestry matching and LD structure play a central role in interpretation, whereas in plant systems, environmental variation, genomic complexity, and gene copy number introduce additional challenges. These differences do not alter the overall framework but influence how individual steps are carried out and weighted.

Looking forward, advances in epigenomics, single-cell technologies, and multimodal datasets will enable the relationships between genetic variation and phenotypic outcomes to be examined across multiple biological layers. Integrating these data into existing analytical frameworks will allow regulatory pathways to be characterized with greater precision. Coupled with high-throughput experimental approaches, such developments have the potential to establish a more continuous link between data-driven inference and mechanistic validation, ultimately advancing the translation of statistical findings into actionable biological insights.

Author Contributions

Xuanjun Fang conducted this study, including literature review, data analysis, and the writing and revision of the manuscript. The author has read and approved the final version of the manuscript.

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