RECOMB 2025 Special Issue

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Editorial

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The 29th International Conference on Research in Computational Molecular Biology (RECOMB 2025) took place from April 26 to 29, 2025, in Seoul, South Korea. This year, the conference received 339 full paper submissions, with 55 ultimately accepted after a rigorous peer-review process involving at least three reviewers per paper. Authors had the option to submit extended abstracts to the Conference proceedings, in lieu of full-length papers, while pursuing journal publication. *Genome Research*, a RECOMB partner journal, invited the revised versions of ~40% of the accepted papers for further review, ultimately leading to the publication of this Special Issue.

RECOMB is the leading international conference on algorithmic computational biology, bridging computational, mathematical, statistical, and biological sciences. It provides a scientific forum for cutting-edge theoretical advances in computational biology and their applications in molecular biology and medicine, emphasizing advancements in computational biology methodologies, including artificial intelligence (AI) and machine learning. *Genome Research* has been a leading journal in genomics for 30 years. The journal publishes high-impact studies on the structure, function, biology, and evolution of genomes, featuring novel computational algorithms that provide insight into biological processes, such as the functional effects of genetic variation. The partnership between RECOMB and *Genome Research* brings novel computational methodologies to a broader audience, encourages their application to significant genomic challenges, and demonstrates how new computational methods presented at RECOMB can drive discoveries in genomics and the broader field of molecular biology.

In this Special Issue of *Genome Research*, we introduce a diverse collection of 16 papers from RECOMB 2025. These include algorithmic and modeling innovations in the analysis of genomic, metagenomic, and transcriptomic data reflecting the breadth of recent developments in the field.

The first two papers in this Special Issue focus on new algorithms for analyzing genomic variation. Battistella et al. (2025) introduce Ralphi, a deep reinforcement learning framework to assemble parental haplotypes from sequencing reads. This paper received the "Best Paper Award" at RECOMB 2025. Dokmai et al. (2025) develop TX-Phase, a secure haplotype phasing method based on the framework of trusted execution environments.

The next two papers present advances in computational methods for metagenomic analyses. Shaw et al. (2025) present devider, a novel algorithm based on a positional de Bruijn graph for haplotyping small genomic sequences, such as those found in viruses, from long-read sequencing data. Ahmed et al. (2025) develop a new space-efficient full-text index, based on a method called cliff compression, for 16S rRNA classification.

The challenges posed by the need to analyze structural changes in the genome continue to motivate new methods. Chandra et al. (2025) introduce a pangenome graph-based alignment-free genotyping algorithm. Raeisi Dehkordi et al. (2025) propose OMKar, an efficient method that integrates structural and copy number variants within a breakpoint graph for computational karyotyping from optical genome mapping technology. Al-Abri and Gürsoy (2025) introduce ScatTR, a computational method to estimate the copy number of large tandem repeat (TR) expansions from short-read sequencing data, while Song et al. (2025) propose a tool, EquiRep, for accurate detection of TRs, which they apply to identify repeat units from satellite DNA and reconstruct circular RNAs from rolling-circular long-read sequencing data.

This issue also features new approaches to model the association of genomic variation to phenotype. Nappi et al. (2025) introduce BayesRVAT, a Bayesian framework for rare-variant association testing that can model multiple genomic annotations. Liu et al. (2025) propose ML-MAGES, a method that uses a neural network shrinkage and infinite mixture model to model shared and specific genetic effects across multiple traits.

New methods for the analysis of single-cell and spatial transcriptomic data remain an active area of research. Haber et al. (2025) propose LLOKI for integrating imaging-based spatial transcriptomic (ST) data sets by aligning features across technologies and correcting batches across data sets. Zheng et al. (2025) introduce SIID to impute and deconvolve gene expression across ST platforms using spatial alignment and a joint nonnegative matrix factorization (NMF) model. Lee et al. (2025) develop a supervised NMF model, called ALPINE, for data set integration and identifying condition-specific factors while removing batch effects. Robust methods for the selection of marker genes are the focus of two papers in this issue. Wang et al. (2025) introduce geneCover, a combinatorial, label-free, method to select an optimal panel of minimally correlated marker genes, whereas SepSolve from Borozan et al. (2025) seeks to find a small set of marker genes that lead to "*c*-separated cell types." The last paper in this issue focuses on the challenges arising from single-cell DNA sequencing data. Zhang et al. (2025) propose ScisTree2, an efficient local-search-based algorithm to infer cell lineage trees and call genotypes from large numbers of cells.

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Sussman, for their efforts and support for the RECOMB–*Genome Research* partnership. We trust that readers will appreciate the advances offered in these outstanding RECOMB 2025 papers and look forward to future submissions from the computational biology community to RECOMB in the years ahead.

Competing interest statement

S.S. served as Program Chair for RECOMB 2025 and had access to earlier versions of all papers included in this Special Issue of *Genome Research* prior to publication. B.B. is the Chair of the Steering Committee for the RECOMB series of conferences.

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