

Special Issue on
**Computational Systems Approaches to Elucidating
Mechanisms of Human Disease**

CALL FOR PAPERS

With the rapid development of genomic, transcriptomic, and proteomic technologies, there has been an explosion in the availability of systems-scale datasets. However, while we are data-rich, there is still a disconnection between the availability of data and the development of methods that can glean meaningful mechanistic insights from the data. This disconnect is especially pertinent in the context of human disease, where there is an extremely pronounced difference between the rate of data generation and the pace of rational drug development based on well-elucidated disease mechanisms.

The focus of this special issue is computational systems approaches that can be used to analyze genomic, transcriptomic, and proteomic datasets to obtain a holistic understanding of human disease processes. We welcome articles that apply analytical techniques to analyze high-dimensional data and learn complex patterns, which, when interpreted appropriately, enhance our understanding of the molecular bases of human disease.

Potential topics include but are not limited to the following:

- ▶ Computational methods for leveraging genome and exome sequencing datasets and genome-wide association studies to understand mechanisms of human disease
- ▶ Computational methods for analyzing transcriptomic datasets pertinent to human disease
- ▶ Systems analyses to infer human disease mechanisms from alterations in protein-protein interaction networks and related network inference approaches
- ▶ Integrative approaches to characterize molecular phenotypes relevant to disease (including high-throughput screens and perturbation-based techniques)
- ▶ Systems modeling of dysregulation of cellular signaling in human disease (with a special emphasis on alteration of signaling in cancer)
- ▶ Kinetic/thermodynamic modeling of processes/pathways relevant to human disease
- ▶ Energetic modeling of processes/pathways relevant to human disease (including molecular dynamic simulations)

Authors can submit their manuscripts through the Manuscript Tracking System at <https://mts.hindawi.com/submit/journals/scientifica/computational.biology/csad/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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