



Code of Life:

Unraveling biological mysteries through computational innovation

In recent years, computational biology has revolutionized our understanding of biological systems, propelling significant advancements in personalized medicine, genomics, and biotechnology. The integration of machine learning algorithms with genome sequencing has enabled the prediction of protein structures and functions, advancing drug discovery at an unprecedented pace. Systems biology, empowered by computational tools, now

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provides intricate models of cellular processes, enhancing our ability to manipulate and engineer biological systems for therapeutic applications. Moreover, computational simulations have become pivotal in unraveling complex networks of genetic interactions, leading to insights into disease mechanisms and the development of targeted treatment strategies. These computational advancements are not just accelerating basic biological research, but are also directly impacting clinical outcomes, marking a new era of biologically integrated computing.

Data management, another critical contribution, goes beyond mere storage solutions. Here, computer scientists develop advanced frameworks capable of organizing, indexing, and retrieving biological data with a level of sophistication that facilitates complex queries and data relationships. This infrastructure is vital for the curation of databases like GenBank, ensuring the data remains not only accessible, but also actionable, for researchers worldwide.

Moreover, computer scientists are instrumental in modeling and simu-

lation efforts that allow biologists the opportunity to test hypotheses in silico before they are investigated in vitro or in vivo. These computational models serve as virtual laboratories,

providing a testbed for experiments that would be otherwise impractical or impossible. From cellular processes to ecosystem dynamics, the ability to simulate biological systems offers a powerful means to explore theoretical and practical questions.

I hope this issue of *XRDS* will give you a deeper understanding of computational biology, both as a field and as a community. As the volume and complexity of biological data continue to increase, the role of computer science will only become more central, solidifying its status as a cornerstone of modern biological research. I invite you to appreciate the advancements made in computational biology and, if you would like to go further, reflect on what multifaceted and integral roles you can play in advancing biological sciences in the digital age.

Our two guest editors for this are Dr. Xinzhou Ge and Meng Wang. Dr. Ge's main area of research is biological statistics. His research involves false discovery rate control in omics

data analysis, analysis of quantitative trait loci associated with transcriptome, and statistical methods in single-cell data. He is now an assistant professor at Oregon State University. Wang is Ph.D. student at Caltech, working at the interface between machine learning and neuroscience, particularly in framing the learning behavior in biology into rigorous computation. The combination of her knowledge, experience, and interest in the concept of community with her co-editor's in-depth understanding of computational methods was a perfect fit for this issue. They have done outstanding work in bringing together an interesting mix of authors addressing key aspects of the computational biology community. A big thank you to them for bringing together this eclectic and thought-provoking ensemble of articles.

—Jiayi Li

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