Our department, the first such department to be created within a School of Computer Science, emphasizes developing rigorous and theoretically sound computational approaches to building comprehensive models that address the fundamental problem of understanding how biological systems function. Computational methods will also be essential to translate this understanding into improved health care, and we have significant interest in developing clinical applications of the machine learning and analysis tools we are developing. Our approaches take advantage of the growing availability of genome-scale datasets to build comprehensive models, but they are also critically needed to decide what additional experiments should be done in order to optimally improve the models and lead as rapidly as possible to invaluable insights into possible means for treating or preventing disease.

Robert F. Murphy, Ph.D.
Head, Computational Biology Department
Ray and Stephanie Lane Professor of Computational Biology and Professor of Biological Sciences, Biomedical Engineering and Machine Learning

Ph.D. Program
- Joint Ph.D. in Computational Biology

Master’s Programs
- Joint M.S. in Computational Biology
- Joint M.S. in Biotechnology Innovation and Computation

Undergraduate Programs
- Joint B.S. in Computational Biology
- Minor in Computational Biology

Research Themes

Efficient Algorithms for Genome Sequence Analyses
Nucleic acid sequencing has become an inexpensive, commonplace tool for biologists and clinicians; however, analysis remains computationally slow, limiting its usability. We are developing fast, more memory-efficient algorithms for using sequencing for gene expression quantification, genome assembly, genomic variant detection, and other analyses so that they can be carried out at clinical or population scales. Current areas of focus include scaling sequence search up to petabyte-scale collections, faster and more accurate detection of genomic variants. We are also developing methods to learn how variants of many genes combine to affect the chances of acquiring complex diseases. This work will enable researchers, hospitals and sequencing centers to perform the analyses required to inform clinical decisions and to build better models of biological systems without enormous computational resources.

Spatiotemporal Network Learning
Networks of interacting molecules underlie all biological systems. Creation of computational models that can be combined to represent and simulate complex interacting networks is critical to understanding how cells, tissues and organisms function and how things can go wrong leading to disease. This area is a particular focus in the department, ranging from dynamic network models at the molecular level to spatiotemporal models of morphological changes at the cell and tissue level.
Gregory Johnson
Ph.D. student in Computational Biology

Gregory Johnson’s goal is to use machine learning and statistical modeling methods to learn how to put a cell together. He takes hundreds or thousands of images of cells in which particular components have been visualized by fluorescent labeling and constructs a model that captures the essence of the patterns the images contain. This has enabled the first-ever models of how the patterns of different organelles are related to each other.

Hao Wang
Ph.D. student in Computational Biology

The production of proteins is fundamental to all life. Proteins are produced from linear template transcripts by molecular machines called ribosomes that walk down these templates. Hao is studying the motion of these ribosomes. She is developing novel computational modeling and optimization techniques to detect ribosome traffic jams and stalling and to determine the “speed limit” at each point along a transcript from next-generation sequencing data. These are being used to create more sophisticated and more accurate models of protein production that will enable us to better predict how a cell responds to varying conditions and stresses by controlling levels of protein abundance.

“Beginning with its founding as the Lane Center for Computational Biology, the department’s unique computational approach to biological questions is a definitive advantage to our campus community and partners as we solve the most difficult biological questions that face our world.”
Andrew W. Moore
Dean, School of Computer Science

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Our alumni and friends are critical to enabling the experiences that change the lives of our faculty and students. YOU can help us by engaging with our faculty, advocating for our programs and supporting our shared vision that will transform the future.

We invite you to learn more about how you can help by contacting:

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