Genomics and Computational Biology lie at the center of a rapid convergence of biomedical research fields. Research in this graduate group focuses on the entire genome (as DNA) and the entire material determined by genes (as RNA or protein), and asks about the origins, function, and interactions of the system as a whole. Such questions and other developments in this field stimulate experimental laboratory work in genomics, as well as computational activities in bioinformatics.

Students and faculty in Penn's Genomics and Computational Biology Graduate Group bring diverse backgrounds and interests together from across the University of Pennsylvania. Members of this interdisciplinary group come from academic departments including Computer and Information Science, Bioengineering, Biology, Genetics, Medicine, Microbiology, Pathology and Laboratory Medicine, Pharmacology, and Statistics. Most are members of the Penn Genome Frontiers Institute or the Penn Center for Bioinformatics, which provide a focus for genomics and computational biology on the Penn campus (including the Children’s Hospital of Philadelphia and the Wistar Institute).

Genomics and Computational Biology at the University of Pennsylvania is in a unique position to facilitate collaborative research within Penn and across institutional boundaries. Our focus on thesis co-mentorship and balance between experimental and computational research enable our alumni to bring a multidisciplinary approach to their careers in academia and industry, as reflected in the selection of papers by GCB alumni highlighted here. In addition to the Wistar Institute and Children’s Hospital of Philadelphia, Philadelphia is home to many other research institutions creating a lively scientific community that fosters unique interactions.

Why Choose Penn?
Genomics and Computational Biology at the University of Pennsylvania is in a unique position to facilitate collaborative research within Penn and across institutional boundaries. Our focus on thesis co-mentorship and balance between experimental and computational research enable our alumni to bring a multidisciplinary approach to their careers in academia and industry, as reflected in the selection of papers by GCB alumni highlighted here. In addition to the Wistar Institute and Children’s Hospital of Philadelphia, Philadelphia is home to many other research institutions creating a lively scientific community that fosters unique interactions.

http://www.med.upenn.edu/gcb/index.shtml
Major areas of focus in Penn’s Genomics and Computational Biology Program

Genetic variation and genomics of human disease: High throughput technologies such as SNP arrays and exome/whole genome sequencing are being used at Penn to generate large cohorts of data for study of metabolic, neurodegenerative, and cancer related diseases.

Functional genomics: RNA-seq, ChIP-seq, and a variety of other sequence-based approaches are being used to study developmental, systemic, and behavioral processes. These studies are driving the development of new algorithms for aligning and analyzing sequence reads.

Chromatin Remodeling: The epigenome is being studied in the context of development and disease employing high throughput sequencing methods and computational methods.

Structural biology and proteomics: Algorithms are being developed for protein engineering and designing new molecular systems as well as understanding protein interactions.

Data integration: Databases, knowledge representation, and data mining are key bioinformatic approaches pursued at Penn to enable the management and understanding of the deluge of data coming from high-throughput technologies.

Algorithms and machine learning: Studies in this area include computational analysis and modeling of real-time, systems-level genomics, nanotechnology, and computational simulations of the evolutionary processes of cancer.

Statistics and Applied Math: Development of statistical methods and mathematical models is being pursued in association and support of the other areas of focus in GCB from genetics and genomics to disease.

Population genetics and evolutionary biology: The diversification of organisms from pathogens to people is being studied primarily using high throughput sequencing in association with the development of statistical and computational methods.

Contact us:
Genomics and Computational Biology
1420 Blockley Hall
423 Guardian Drive
Philadelphia, PA 19104
www.med.upenn.edu/gcb/index.shtml

Mukherjee et al. HIV Sequence Variation Associated With env Antisense Adoptive T-cell Therapy in the hNSG Mouse Mode Molecular Therapy 2010. 18 4: 803–811


