

Postdoc Positions Available at Mount Sinai School of Medicine, NYC

Institute for Genomics and Multiscale Biology at Mount Sinai School of Medicine, NY

The Multiscale Institute faculty has backgrounds in Computer Science, Engineering, Statistics, Mathematics, Physics, Genetics, Molecular Biology, and related disciplines, and are looking for students from all of those fields. The essential requirement is an interest in and capability of thinking about real-world problems in quantitative terms. Additional desired (but not essential) characteristics will be (1) a background in biology, acquired through courses and/or research work and/or (2) experience with data-intensive real-world problems (from any domain) and/or (3) programming experience.

At the Multiscale Institute, you will have a chance to work with world class scientists and engineers tackling important and highly visible problems in computational biology, with an emphasis on translating such work into the medical domain. Some example targets of the Institute are identifying actionable biomarkers and therapeutics for complex human diseases.

Dr. Rui Chang's Lab

Research Interests

The researches in Dr. Chang's lab broadly cover the topics within the field of Systems Biology. In particular, we are focused on dissecting the gene regulatory networks and signaling pathways in human diseases, such as cancer and human developments, such as human embryonic, adult stem cells, by developing and integrating cutting-edge reverse engineering approaches and statistical models. Secondly, we are interested in reconstructing genome-wide and context-specific predictive network models of human cells to interrogate impact of underpinning biological process to the development of both physiological and pathological phenotypes and generate in-silico hypothesis in combination with laboratory validations towards next generation genetic therapy.

Current Projects

Dr. Chang's lab is interested in a variety of interdisciplinary themes covering machine learning, graphical models, Bayesian networks and the biological sciences, including:

- 1) Novel method development:
Developing novel reverse-engineering approaches and statistical models to reconstructing signaling pathways and predictive network model of human diseases which encompassing multi-scale molecule interactions, such as transcriptional regulations and protein-protein interactions. Based on the predictive model, to generate in-silico hypothesis and identify drug targets towards next generation genetic therapy.
- 2) Human disease modeling:
Integrating multi-scale -omics data in cancer and other human pathology by leveraging the cutting-edge network modeling approaches to dissect genome-wide and disease-specific molecular interaction network and identify dysregulated signaling pathways towards prediction and validate of novel drug targets. Current projects are extensively focusing on modeling various types of human cancer.
- 3) Human development and regenerative medicine:
Dissecting the genetic regulatory network in human embryonic stem cells, adult stem cells and cancer stem cells for stem cell pluripotency, self-renewal. Predict and validate high-

efficiency and high-safety recipes for disease-specific stem cell reprogramming and lineage-specific differentiation towards cell replacement therapy.

Postdoc Positions

Two postdoc positions are currently available in Dr. Rui Chang's lab:

General guideline

Prospective candidates should have a recent PhD degree in computer science, mathematics, bioinformatics/computational biology discipline and high motivation to pursue independent research in computational biology. Applicants are expected to have a solid background in programming and computational techniques, with a working knowledge of molecular biology and genetics being highly desirable.

Specific guideline

Position 1: Applicants who desired to focus on method developments and software development:

Prospective candidates should have a recent PhD degree in computer science specialized in machine learning, mathematics, statistics or physics. Strong working experiences in Bayesian networks and other graphical models is highly preferred. Candidate must have strong programming skills in C/C++/Java, Matlab and R. Programming skills in other language is a plus. Basic knowledge in biology and hands-on experience in computational biology is highly desired but not required. The candidate will be responsible for developing cutting-edge machine learning approaches based on graphical models and other mathematical models, and is expected to develop software platforms towards real-world human disease network modeling and drug target prediction by working closely with disease modeling team.

Position 2: Applicants who desired to focus on real-world disease modeling:

Prospective candidates should have a recent PhD degree in computer science, bioinformatics (computational biology) or biology science. Candidate must have strong knowledge in biology, genomics, and hands-on experience in computational biology projects involves analyzing and integrating omics data. Candidate should have a good programming skills in C/Java, Matlab or R. Programming skills in other language is a plus. Basic knowledge about graphical models, machine learning approaches is required. Strong understanding on Bayesian network is highly desired, but not required. The candidate will be responsible for integrating and analyzing multi-scale omics data and leverage cutting-edge method to reconstruct disease network and drug targets validation by working closely with method development team and laboratory collaborators.

Note:

Exceptional candidate have both strong machine learning background and biology knowledge can be considered to work cross projects and fields.

Contact:

Please send CV and three reference letters to rui.r.chang@mssm.edu