

## Jill P. Mesirov Appointed Associate Vice Chancellor for Computational Health Sciences

*UC San Diego School of Medicine recruits world leader in computational biology*

June 24, 2015 | Heather Buschman, PhD

Leading computational biologist Jill P. Mesirov, PhD, has been appointed associate vice chancellor for computational health sciences and professor of medicine at University of California, San Diego School of Medicine and Moores Cancer Center. Mesirov most recently served as associate director and chief informatics officer at the Broad Institute of MIT and Harvard, where she directed the Computational Biology and Bioinformatics Program.



Jill P. Mesirov, PhD, has been appointed associate vice chancellor for computational health sciences and professor of medicine at UC San Diego School of Medicine.

“We are pleased to announce Jill’s appointment,” said David A. Brenner, MD, vice chancellor for health sciences and dean of the UC San Diego School of Medicine. “As associate vice chancellor, she will help formulate an overarching strategy for computational health sciences and research computing, with the goal of building a world-leading hub for biomedical ‘big data’ research and technical advances in our School of Medicine.”

Mesirov’s research focuses on applying machine-learning methods to functional genomics data in two main areas: cancer and infectious disease. In cancer, Mesirov’s team is analyzing molecular data to determine the underlying biological mechanisms of specific tumor subtypes and to stratify patients according to their relative risks of relapse. In infectious disease, the team is using functional data to better

understand the host-pathogen relationship in malaria, as well as to identify biomarkers for differential diagnosis of viral and bacterial diseases and biomarkers of vaccine efficacy.

In addition to applying computational methods to biomedical research, Mesirov is committed to developing “biologist-friendly” software tools and making them freely accessible to the entire biomedical research community. To this end, her team has developed several popular analysis and visualization software packages, such as Gene Set Enrichment Analysis, GenePattern and the Integrative Genomics Viewer. These tools are used by tens of thousands of investigators worldwide to aid in their research.

Mesirov has extensive experience using high-performance computing to solve problems in science, engineering and business. Prior to joining the Broad Institute, she managed computational biology and bioinformatics in the Healthcare/Pharmaceutical Solutions Organization at IBM and served as director of research at Thinking Machines Corporation. She earned her PhD in mathematics at Brandeis University and was previously associate executive director of the American Mathematical Society.

Mesirov is a fellow of the American Association for the Advancement of Science, the American Mathematical Society and the International Society for Computational Biology. She is a member of the NCI Frederick Advisory Committee and previously served on the National Advisory Council for Human Genome Research and the Data and Informatics Working Group of the Advisory Committee to the Director of the NIH.

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## Media Contact

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Heather Buschman, PhD  
858-249-0456  
[hbuschman@health.ucsd.edu](mailto:hbuschman@health.ucsd.edu)

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