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Objectives

You can watch the seminar [here](#).

Abstract: Central to how living systems function are molecular networks defining connections among different types of components such as mRNA, proteins and metabolites. Network-based approaches offer a powerful suite of tools to understand different disease and normal processes and can be grouped into two main classes: (a) methods for network reconstruction that aim to infer the structure of the network, (b) methods for network-based interpretation that use a network as a backbone for integrating and interpreting high-throughput omic datasets. In the first part of this talk, I will present some recent work from our group for the “network reconstruction” problem in the context of mammalian gene regulatory networks. Genome-scale regulatory network inference is a long-standing problem in gene regulation and is a key ingredient for building predictive models of organism state. I will present computational methods used to infer genome-scale regulatory networks by integrating publicly available gene expression datasets with other auxiliary datasets that provide prior support for a regulatory connection. Using our approaches we have inferred regulatory networks for early mammalian development and have used these networks to prioritize important regulatory nodes and edges that we experimentally validated. In the second part of the talk I will present network-based approaches for understanding three-dimensional organization of the genome and its role in phenotypic variation. I will present some case studies of how these approaches can be used to study genome organization in cancer as well as link regulatory variants identified in different genome-wide association studies to downstream pathways.



Short Bio: Sushmita Roy is an Associate Professor at the Biostatistics and

Medical Informatics Department and a faculty at the Wisconsin Institute for Discovery, University of Wisconsin, Madison. Her research lies at the intersection of machine learning and network-based methods

for tackling problems in regulatory genomics. Her group develops and applies computational methods for identifying regulatory networks that exist in living cells, examines their dynamics across different biological contexts. She works closely with biologists who study a variety of normal and disease processes including cancer, cell fate specification, host microbe interactions and evolution of gene regulation. Dr. Roy is a recipient of an Alfred P. Sloan Foundation Fellowship, an NSF CAREER award, a UW Vilas Foundation Fellow and a James McDonnell foundation scholar award.

Speakers

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Barcelona Supercomputing Center - Centro Nacional de Supercomputación

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