University of Stuttgart

Stuttgart Research Center Systems Biology (SRCSB)

Systems Biology Seminar Talk

„RNA Splicing analysis - How to get the signal out of the noise? “

Ass. Prof. Yoseph Barash

University of Pennsylvania, Philadelphia, USA

Thursday
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4 p.m. – 5 p.m.

Log in:
https://unistuttgart.webex.com/unistuttgart/j.php?MTID=m2445713e2d705e40f10e257064d51fa2

Abstract:

The growing awareness of the role of RNA splicing in human disease has led to many research works in diverse areas including some form of RNA splicing analysis. Similarly, a plethora of methods and tools for differential splicing analysis have been developed in recent years. In this talk I will cover some of the challenges in such analysis tasks, often overlooked in both tools and papers that employ them, and specific solutions we have been developing in the lab to address these challenges.

CV:

Yoseph Barash is a computational biologist who works on predictive models to understand RNA biogenesis, its regulation, and its role in human disease. His lab develops machine learning algorithms that integrate genomic and genetic data, followed by wet lab experimental verifications. Yoseph did his Ph.D. in machine learning under Prof. Nir Friedman at the Hebrew University, and his postdoctoral work with Prof. Ben Blencowe and Prof. Brendan Frey at the University of Toronto, focusing on alternative splicing of RNA. His work was the first to build predictive models for splicing variations as a function of the cellular condition (Barash et al Nature 2010), later extended to account for genetic variants (Xiong et al Science 2015). His lab was the first to offer tools mapping, quantifying, and visualizing complex splicing variations, showing these comprise over 30% of transcriptome variations in human and mouse (Vaquero et al, Elife 2016). The tools his lab develops to quantify and predict aberrant splicing has been applied to numerous disease studies and licensed by startup companies as well large companies such as Pfizer, GSK, and BioGen.

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