LAUFER CENTER
FOR PHYSICAL AND QUANTITATIVE BIOLOGY

Seminar 2016

PROGNOSTIX: A pipeline for personalized diagnostics and drug treatments

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How can one convert the plethora of information provided by Next Generation Sequencing into clinically actionable suggestions for diagnostics and drug treatments. We describe the key tools in the PROGNOSTIX methodology that begins to address these issues. We first describe and validate the ENTPRISE algorithm for predicting the likely disease association of missense variations. Compared to existing algorithms such as FATHMM whose false positive rate is 12.9%, the false positive rate of ENTPRISE is 5.4%. Moreover, unlikely many other approaches it does not assign variations based on the identity of the protein rather than the variations within the protein. We then describe a comprehensive proteome scale approach that predicts human protein targets and side effect of drugs. For drug-protein interaction prediction, FINDSITEcomb, whose average precision is ~30% and recall ~27%, is employed. Successful applications of the methodology to treat Chronic Fatigue Syndrome, to identify novel antibiotic leads and promising anti-seizure drugs are described.
For full abstract go to: http://laufercenter.stonybrook.edu/calendar

Friday October 21, 2016

2:30 PM

Laufer Center Lecture Hall 101

Host: Dima Kozakov

Stony Brook University

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