

Keynote title:

Understanding Etiology of Complex Neurodevelopmental Disorders: Two Approaches

Keynote Speaker:

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Abstract:

Complex human phenotypes, such as autism, schizophrenia, and anxiety, undoubtedly partially overlap in genomic variations that predispose to or protect against these maladies. (Genetic overlap of complex phenotypes has gained increasing experimental support and is no longer just an ungrounded scientific hypothesis.) Furthermore, as yet largely unknown shared environmental factors likely tend to trigger the manifestation of more than one phenotype. Although it may seem overly ambitious to target multiple phenotypes jointly, we believe we can obtain much more information from existing data and gain new insights into individual phenotypes by modeling phenotypes jointly. My talk sketches two distinct computational approaches to this problem.

Short Bio:

Andrey Rzhetsky is a computational biologist at the University of Chicago. He has worked on mathematical modeling for evolutionary biology, approaches to the analysis of large molecular networks and massive mining of biomedical literature.