The School of Natural Sciences Presents

Applied Math Seminar:

SPAdes: A New Genome Assembly Algorithm and its Applications to Single-Cell Sequencing.

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3:30 PM – 4:30 PM
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ABSTRACT: The lion’s share of bacteria in various environments cannot be cloned in the laboratory and thus cannot be sequenced using existing technologies. A major goal of single-cell genomics is to complement gene-centric metagenomic data with whole-genome assemblies of uncultivated organisms. Assembly of single-cell data is challenging because of highly non-uniform read coverage as well as elevated levels of sequencing errors and chimeric reads. We describe SPAdes, a new assembler for both single-cell and standard (multicell) assembly, and demonstrate that it improves on the recently released E+V-SC and IDBA-UD assemblers (specialized for single-cell data) and on popular assemblers Velvet and SoapDeNovo (for multicell data). SPAdes generates single-cell assemblies, providing information about genomes of uncultivable bacteria that vastly exceeds what may be obtained via traditional metagenomics studies.

BIOGRAPHY: Dr. Tesler is an Associate Professor in the Department of Mathematics at the University of California, San Diego, a core faculty member in the interdisciplinary graduate and undergraduate programs in bioinformatics, and an Affiliate Faculty member of Computer Science and Engineering. He received his Ph.D. in Mathematics from the Massachusetts Institute of Technology in 1995 in the area of Algebraic Combinatorics. He studies computational and algorithmic aspects of comparative genomics, genome rearrangements, sequence assembly and genome-wide association studies. He was the conference chair and program chair of the RECOMB Satellite Workshop on Comparative Genomics 2007, and program chair of the RECOMB Satellite Workshop on Open Problems in Algorithmic Biology in 2012.

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