

IMCB/BII Invited Speaker



Speaker : Prof. Eugene Myers
*Director & Tschira Chair of Systems Biology,
MPI for Molecular Cell Biology and Genetics, Germany*

Date : 12 November 2013, Tuesday

Time : 2:00PM - 3:00PM

Venue : IMCB Seminar Room 3-46, Level 3, Proteos, Biopolis

Host : Dr. Weimiao Yu (IMCB) & Dr. Lee Hwee Kuan (BII)

Seminar :

Segmentation via Progressive Merging

We present a general framework for progressively merging 'super pixels' as an approach to segmenting an image. The idea is to merge regions in a series of passes leading to progressively larger and larger regions that ultimately are exactly the objects desired. Each pass is conservative in that it never merges two super-pixels from different objects. The power of this idea is that as the regions become larger, subsequent passes can use progressively more sophisticated characteristics of the regions, not possible on smaller super-pixels, to make merging decisions.

We illustrate the framework in two applications: separating colored neurons in a 3D stack, and segmenting cells in a 2D projection of a fly wing. For each problem we illustrate the distinctive, application specific, rule sequence that we developed. Statistics on the quality of the results will be presented.

About the Speaker :

In 2012 Gene Myers joined a growing group of computational biologists in Dresden as the founding director of a new Systems Biology Center that is being built as part of an extension of the Max-Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG). Previously Gene had been a group leader at the HHMI Janelia Farm Research Campus (JFRC) since its inception in 2005. Gene came to the JFRC from UC Berkeley where he was on the faculty of Computer Science from 2003 to 2005. He was formerly Vice President of Informatics Research at Celera Genomics for four years where he and his team determined the sequences of the Drosophila, Human, and Mouse genomes using the whole genome shotgun technique that he advocated in 1996. Prior to that Gene was on the faculty of the University of Arizona for 17 years and he received his Ph.D in Computer Science from the University of Colorado in 1981.

His research interests include the design and analysis of algorithms for problems in computational molecular biology, image analysis of bioimages, and light microscopy with a focus on building models of the cell and cellular systems from imaging data. He is best known for the development of BLAST -- the most widely used tool in bioinformatics, and for the paired-end whole genome shotgun sequencing protocol and the assembler he developed at Celera that delivered the fly, human, and mouse genomes in a three year period. He has also written many seminal papers on the theory of sequence comparison.