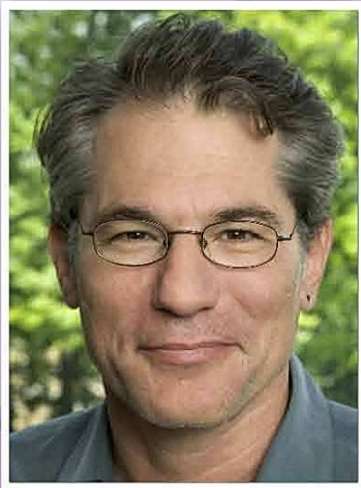


IMCB/BII Invited Speaker



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

Date : 12 November 2013, Tuesday

Time : 9:30AM - 10:30AM

Venue : BII, Level 7, Cysteine Room, Matrix, Biopolis

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

Seminar :

What's Behind Blast

While Blast is one of the most widely-used search engines for molecular biology, and there is a general understanding of how it works, few know the story of how it came about and the theoretical algorithmic result from which it was derived. I will tell the story and explain the theoretical algorithm --- an $O(DN^{\text{pow}(D/P)} \log N)$ expected-time algorithm for finding all D-matches to a query of length P in a database of length $N \gg P$. Surprisingly, this result, published in early 1994, has not been improved upon to this day.

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.

He was awarded the IEEE 3rd Millennium Achievement Award in 2000, the Newcomb Cleveland Best Paper in Science award in 2001, and the ACM Kanellakis Prize in 2002. He was voted the most influential in bioinformatics in 2001 by Genome Technology Magazine and was elected to the National Academy of Engineering in 2003. In 2004 he won the International Max-Planck Research Prize and in 2005 was selected as one of two distinguished alumni (with David Haussler) at his alma-mater, the University of Colorado. In 2006 Gene was inducted into Leopoldina, the German Academy of Science and awarded an honorary doctorate at ETH, Zurich.