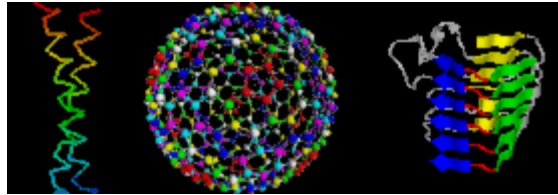


MIT
Department of Mathematics
& The Theory of
Computation Group
At CSAIL



Bioinformatics Seminar

Speaker: Dr. Manolis Kellis, Whitehead Institute

Title: Evolutionary Genomics: Complete genome duplication and fate of duplicated genes

Date: Monday, 3 November 2003

Time & Location

Refreshments: 11 am in the Applied Mathematics Common Room at MIT's Building 2, Room 349

Talk: 11:30 am to 1 pm in the Applied Mathematics Conference Room Building 2, Room 338

URL: <http://www-math.mit.edu/compbiosem/>

Abstract:

Whole-genome duplication has long been postulated as a powerful mechanism of evolutionary innovation. Recently, it has become possible to test this notion in complete genome sequence. We present direct proof that the yeast *S. cerevisiae* has undergone a complete duplication event by identifying a yeast species that descends from the pre-duplication ancestor. This enables us to study the fate of duplicated genes, including the nature of gene loss and rapid gene evolution. Genes that underwent accelerated evolution encode many kinases, transcription factors and regulatory proteins. Strikingly, 95% of cases of accelerated evolution involve only one member of a gene pair and thus allow one to distinguish ancestral and derived functions.

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For General Questions, please contact kvdickey@mit.edu