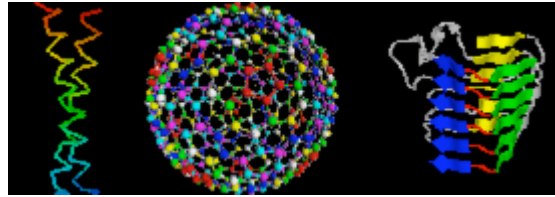


MIT
Department of Mathematics
& The Theory of
Computation Group
At CSAIL



Bioinformatics Seminar

Speakers: Joachim Theilhaber, Principal Scientist, Cambridge Genomics Center

Title: GECKO: a complete large-scale gene expression analysis platform

Date: Monday, 13 February 2006

Time & Location:

Refreshments: 11 am in the Theory of Computation Lab at MIT's Building 32, Stata Center Room G-575

Talk: 11:30 am the Theory of Computation Lab at MIT's Building 32, Stata Center, Room G-575

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

Abstract:

Gecko (Gene Expression: Computation and Knowledge Organization) is a complete, high-capacity centralized gene expression analysis system, developed in response to the needs of a distributed user community.

Based on a client-server architecture, with a centralized repository of typically many tens of thousands of Affymetrix scans, Gecko includes automatic processing pipelines for uploading data from remote sites, a data base, a computational engine implementing ~50 different analysis tools, and a client application. Among available analysis tools are clustering methods, principal component analysis, supervised classification including feature selection and cross-validation, multi-factorial ANOVA, statistical contrast calculations, and various post-processing tools for extracting data at given error rates or significance levels. A unique feature of the Gecko architecture is the concept of the Analysis Tree (actually, a directed acyclic graph), in which all successive results in ongoing analyses are saved. This approach has proven invaluable in allowing a large (~100 users) and distributed community to share results, and to repeatedly return over a span of years to older and potentially very complex analyses of gene expression data.

The Gecko system is publicly available as free software (<http://geckoe.sourceforge.net>). In totality or in parts, the Gecko framework should prove useful to users and system developers with a broad range of analysis needs.

The seminar is co-hosted by Professor Peter Clote of Boston College's Biology and Computer Science Departments and MIT Professor of Applied Math Bonnie Berger. Professor Berger is also affiliated with CSAIL & HST.

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