

Software Demonstrations

Sunday, August 4

15:00 – 16:00

Salon 3

BIOCAD for Constructing Gene Regulatory Networks

Kyushu Institute of Technology (Not-for-profit Track)

BIOCAD is a powerful software suit with GUI for constructing a large-scale map of complicated biochemical reaction networks, where chemical reaction equations with detailed attribute tags are employed in an XML-based common representation. Novel notation for designing the map is proposed by improving Kohn's method.

16:00 – 18:00

Salon 4

Issues in Modern Data Management

Tod Smith – 20 minutes

Geospiza

Geospiza's Finch(TM)-Suite of bioinformatics software components provides a highly scalable data management solution for laboratories engaged in DNA sequencing. Finch(TM)-Suite components provide for data entry and access through secure web-based interfaces. Finch-Servers reduce data collection costs through real time data analysis pipelines that can be configured for specialized needs.

Beowulf Computing in Bioinformatics

Tom Quinn – Director Business Development and Operations

Scyld

Beowulf was a concept conceived by Don Becker and Thomas Sterling at NASA Goddard to replace Super computers with COTS devices to achieve the same or similar results. Scyld Computing, a strategic HP partner, is the caretaker of Beowulf.org and are creators of the Scyld Beowulf Professional Edition cluster manager offering. This discussion will be a detailed description of Scyld Beowulf, its functions, features, operational characteristics and where we are taking clustered computing in the future.

HP's High Performance Technical Computing Overview and Strategy

Daniel Cox – Manager – Linux Cluster Programs HP Industry Standard Server Group
Hewlett-Packard Company

The new HP is an industry leader in high performance technical computing. With the merger of Compaq and HP, the product breadth and markets we choose to serve has been greatly enhanced. Furthermore, with the announcement of our Itanium 2 offering, July 10, greatly adds to our portfolio in bringing you the best price performance and overall performance in the industry. This topic will be to introduce you to our strategy and product portfolio for the next few years as we integrate as a company to provide our customers with the best products and services to meet their processing needs.

19:00 – 21:00

Salon 4

Catching Up With Data Growth

SGI (Corporate Track)

SGI is hosting a workshop where leading scientists will present the high-performance solutions they employ to solve the hard problems in life science research. Learn about how readily available, state-of-the art analysis, storage, and visualization technologies can be applied to your facility so that you can focus on answering the important research questions.

Monday, August 5

08:00 – 10:00

Salon 4

The Power Behind Bioinformatics Heroes: SRS Evolution

Lion bioscience (Corporate Track)

SRS Evolution provides you with the platform and tools you need to delivers all the functionality needed by your target identification and validation departments. You can seamlessly integrate your company's relational data with all the public and proprietary life science data, plus over 100 analysis tools, all through a unified interface.

Monday, August 5 continued

10:00 – 11:00

Salon 3

Probe Design And Proteomic Database at MGH

Massachusetts General Hospital (Not-for-profit Track)

In this demo, we will introduce microarray and proteomic tools developed at the Massachusetts General Hospital. They include oligo probe design for microarray; web-based proteomic database for protein expression; web-based sequence auto-annotation. All these tools are freely available at our web site.

11:00 – 13:00

Salon 4

ConSurf: A Server For The Identification Of Functional Regions In Proteins By Surface Mapping Of Phylogenetic Information

Tel-Aviv University (Not-for-profit Track)

ConSurf is a web server for the identification of functional regions in proteins of known 3D-structure. It uses advanced phylogenetic algorithms to estimate the evolutionary rate of each amino acid site; functional regions are usually comprised of slow evolving residues. ConSurf is available at <http://consurf.tau.ac.il>

12:00 – 14:00

Salon 3

GoSurfer, A Visualized Tool For Comparative Gene Analysis

Harvard School of Public Health (Not-for-profit Track)

GoSurfer software uses Gene Ontology (GO) structured vocabulary to perform comparative gene analysis. GoSurfer visualizes gene ontology information as a tree, with nodes and branches representing GO terms and paths. Different sets of genes can be mapped onto the tree with different colors. GoSurfer is available at <http://biosun1.harvard.edu/~szhong/GoSurfer.htm>

13:00 – 15:00

Salon 4

MacOSX on Xserve: An Ideal Platform for High-Throughput Informatics Research

Apple (Corporate Track)

Scientists utilize both UNIX analysis and desktop productivity applications, Bioinformaticists develop in an open, standards-based environment, and Administrators monitor/configure an industrial strength UNIX server with far less burden.

The power of UNIX combined with the Mac's legendary ease of use in a 1U rack mount enclosure is a winning combination for HTC clustering.

14:00 – 16:00

Salon 3

The Genesis Enterprise System: High Throughput Gene Expression Data Mining And Management

GeneLogic (Corporate Track)

Genesis: The GeneExpress Enterprise System is a powerful data management platform that lets researchers integrate, manage and analyze large amounts of gene expression and associated clinical data across an organization.

This live demonstration will explore how Genesis can be used to quickly identify key genomic targets across a wide range of disease and experimental states to help shorten the time to drug discovery.

15:00 – 16:00

Salon 4

LASER, PHASER, BLASTER: Protein Search Engines Eliminate Fake Homologs

Affini and Cold Spring Harbor Laboratory
(Not-for-profit Track)

Altschul's statistical theory tells us an alignment that is x PAM in evolutionary distance should score, under PAM x , the relative entropy of PAM x (for each aligned pair). We demonstrate graphically the practical significance of adding this consistency test to search algorithms such as Smith-Waterman and BLAST.

16:00 – 18:00

Salon 3

BioCoRE: A Biological Collaborative Research Environment

University of Illinois at Urbana-Champaign (Not-for-profit Track)

BioCoRE, a free web-based collaborative environment, enhances biomedical research, training. BioCoRE submits jobs to remote sites, shares images across distance, creates input files. BioCoRE features synchronous and asynchronous chat, project-wide "bookmarks," shared web-based filesystem. Summary pages report progress, sessions are auto-recorded and reviewed. Secure data accessible to project team only.



Intelligent Systems for Molecular Biology

Edmonton, Alberta, Canada • August 3 – 7, 2002

17:00 – 18:00

Salon 4

Sun Powers The Grid For Life Sciences

SUN Microsystems (Corporate Track)

Grid computing will be presented & discussed from a technical and business perspective. The concepts covered will include job submissions, load & resource distribution, scheduling and scaling. Options for establishing local computer to global grids will be discussed. Examples will be presented in the context of high-throughput bioinformatics.

Tuesday, August 6

10:00 – 12:00

Salon 3

Expressionist Refiner: Genedata's Solution For Microarray Data Quality Assessment And Reporting

GeneData (Corporate Track)

GeneData will demonstrate Expressionist Refiner, our quality control software for automated, high throughput assessment of microarray data quality. Flawed data can be flagged or eliminated prior to statistical analysis. The software is user-configurable, enabling QC criteria of varying stringency, and includes facilities for correcting errors such as gradients and distortions.

10:00 – 12:00

Salon 4

An Integrated and Distributed Bioinformatics Platform for Genome Canada

Genome Prairie (Not-for-profit Track)

On April 2nd 2002, Genome Canada funded the Bioinformatics platform project to a total amount of 10 million dollars (5 million dollars from Genome Canada, to be matched by 5 million dollars of industrial and provincial contributions) over three years. The main scientific research goals of the project focus on data standardization (BioMOBY) and the visualization of complex genomic features (Bluejay and Genquire). A computing GRID, in which networked computers from many sites in Canada will appear to function as a single computer, will provide user-friendly access to the complex networked Bioinformatics infrastructure in Canada. A help desk and custom programming facility will assist other genomics research projects in Canada on a cost-recovery basis.

12:00 – 14:00

Salon 3

Data and Knowledge Management

IBM Life Sciences (Corporate Track)

Come join IBM Life Sciences in a stimulating forum on issues relevant to the explosion of data in drug discovery. Progress within the life sciences depends upon the ability to access, manage, and analyze massive amounts of data. Researchers need solutions that allow them to work with distributed data sources and diverse data formats via single query access. IBM is uniquely positioned to bring together a comprehensive set of technology solutions enabling the transformation of data into knowledge. We will discuss concepts to facilitate the interoperability of Life Science applications, data, & tools.

14:00 – 15:00

Salon 3

Proteome Analyst — A Web-Based Tool For High-Throughput Proteome Function Prediction

University of Alberta (Not-for-profit Track)

Proteome Analyst (PA) is a web-based tool for predicting the functions of each sequence in a proteome. For example, one or more classification-based function predictors can be applied to any sequence. More importantly, PA users can easily train their own custom classification-based predictors and apply them to their sequences — www.cs.ualberta.ca/~bioinfo/PA

14:00 – 16:00

Salon 4

New Advances from Market Leader

InforMax Inc. (Corporate Track)

Powerful yet user-friendly bioinformatics tools remain a key need of biologists. InforMax will demonstrate our leading desktop and workgroup applications which support emerging scientific paradigms in functional and systems biology. In use by over 2100 organizations, InforMax's recently upgraded and rapidly-advancing tools deliver advanced capabilities without expensive infrastructure or training.



Wednesday, August 7

10:00 – 11:00

Salon 3

The Pathway Tools Software

SRI International (Not-for-profit Track)

A pathway/genome database (DB) integrates information about the genes, gene products, and biochemical pathways of an organism. The Pathway Tools software developed in conjunction with EcoCyc includes algorithms for interrogation, visualization, editing, and WWW publishing of pathway/genome DBs. It also includes tools for pathway visualization of gene-expression data, for comparative analysis of metabolic networks, and for prediction of the metabolic network of an organism.

10:00 – 11:00

Salon 4

PROTONET — Automatic Classification of Proteins

Hebrew University (Not-for-profit Track)

ProtoNet provides an automatic hierarchical clustering of the Swissprot protein database. The clustering is based on an all-against-all BLAST similarity search. It provides a classification of the input proteins into a hierarchy of clusters of varying degrees of granularity. Possible applications are: function prediction, defining superfamilies and subfamilies, and large-scale protein annotation.

11:00 – 12:00

Salon 4

Mining Genomic Data: Systems, Corg, Genenest, Splicenest, GHMM and HMMEd

Max Planck Institute for Molecular Genetics Berlin (Not-for-profit Track)

We provide a wide range of WWW-accessible services to mine genomic data: Systems, Genenest and Splicenest integrate clusters of proteins, EST sequences and genomic DNA. This is extended by Corg, the database of conserved non-coding blocks. GHMM and HMMEd provide an interactive environment to hand-craft HMMs for highly sensitive searches.