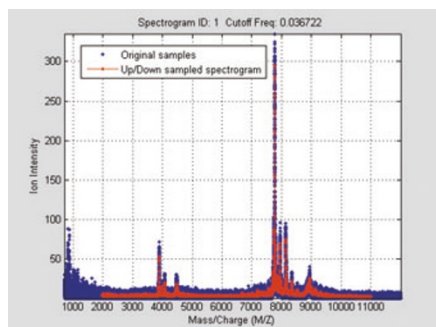# Bioinformatics

## Open environment

With the Bioinformatics Toolbox 2.0, researchers can perform mass-spectrometry data analysis, perform statistical inference and prediction, view graphs and conduct enhanced genomic and proteomic sequence analysis. Most functions are implemented in the open MATLAB language, enabling users to customize the algorithms or develop their own. The new mass-spectrometry data analysis feature is specifically designed for pre-processing data for performing customized analysis at a faster rate. Additional features include new classification functions and tools for identification of discriminating features and access to specialized visualization tools, ranging from sequence alignments and microarray principle component plots to building, viewing and manipulating phylogenetic trees.
**http://www.mathworks.com/**
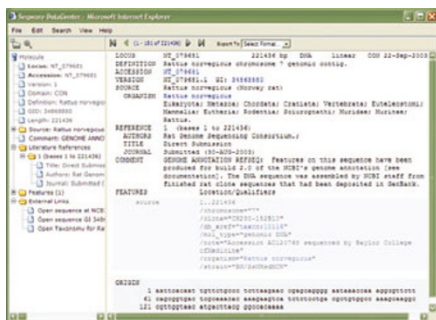


## Sequence data management

Ariadne Genomics' Seqware Data Center helps individuals, work groups and core facilities manage their proprietary DNA sequences along with public sequence collections on a local PC or a network. Seqware automatically updates GenBank from the NCBI data repository, and makes it easy to create, manage, update and annotate sequence sets, edit and annotate sequence records in the database, run flexible context searches, store, automatically update and reuse Blast results. Seqware Data Center installs seamlessly from a set of CD/DVD ROMs and requires no specific maintenance or database administration. No additional database licenses are required.
**http://www.ariadnegenomics.com/**
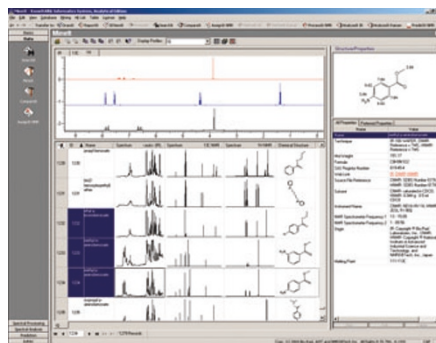


## Spectroscopy software

Bio-Rad Laboratories' KnowItAll Informatics System Version 5.0 features advanced multi-technique database searching, enabling the definition of searches in multiple spectral techniques concurrently in a single software platform—even across multiple databases—and viewing consolidated results. Searches may include substructures, properties, and a variety of experimental spectra, including NMR, MS, IR and Raman. The system also provides additional visualization and data mining tools along with special search tools to weight the importance of each data input and define how it factors into the final result.
**http://www.bio-rad.com/**

## Improved database

Applied Biosystems has updated its Panther system database of protein families, subfamilies, functions and pathways. Now consisting of a library of 6,683 protein families, divided into 31,750 functional subfamilies, and covering approximately 90% of mammalian protein coding genes, version 5.0 includes interactive resources for associating protein families with their biological pathways, as well as new tools for analyzing gene expression data in relation to molecular functions, biological processes and pathways. The Panther system database is publicly available online.
**http://panther.appliedbiosystems.com/**

## Working in a group

Causeway 1.2 sequence annotation software, from QbioCom, retains all of the sequence analysis functionality of the earlier version while allowing researchers to create 'annotations on the fly' that are immediately visible to all other researchers or managers within the organization—whether down the corridor or in a different time zone. Causeway uniquely integrates database-derived annotations from internal and external databases and the annotations derived from others users. A user can immediately see what is known about a sequence from public domain databases, from proprietary databases and from research conducted by others in the organization.
**http://www.qbiocom.com/**
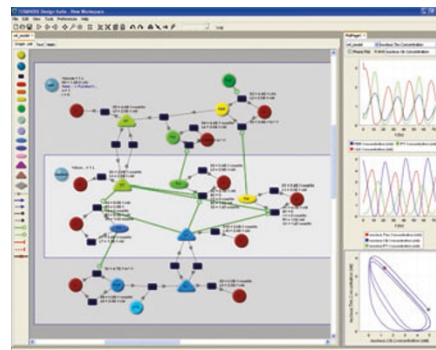


## Analytic design automation

The Teranode Design Suite 2.5 (TDS 2.5) is an enhanced closed-loop R&D platform used to integrate modeling into existing informatics infrastructures. It improves research productivity by giving scientists simplified, on-demand access to a comprehensive library of analytic models. TDS 2.5 enables users to predict and analyze experimental data using the comprehensive databases of pathway models from KEGG and simulations using MATLAB routines. In addition, users can leverage TDS 2.5's visual collaborative environment to simplify exchange and analysis across scientists and labs in complex research.
**http://www.teranode.com/**