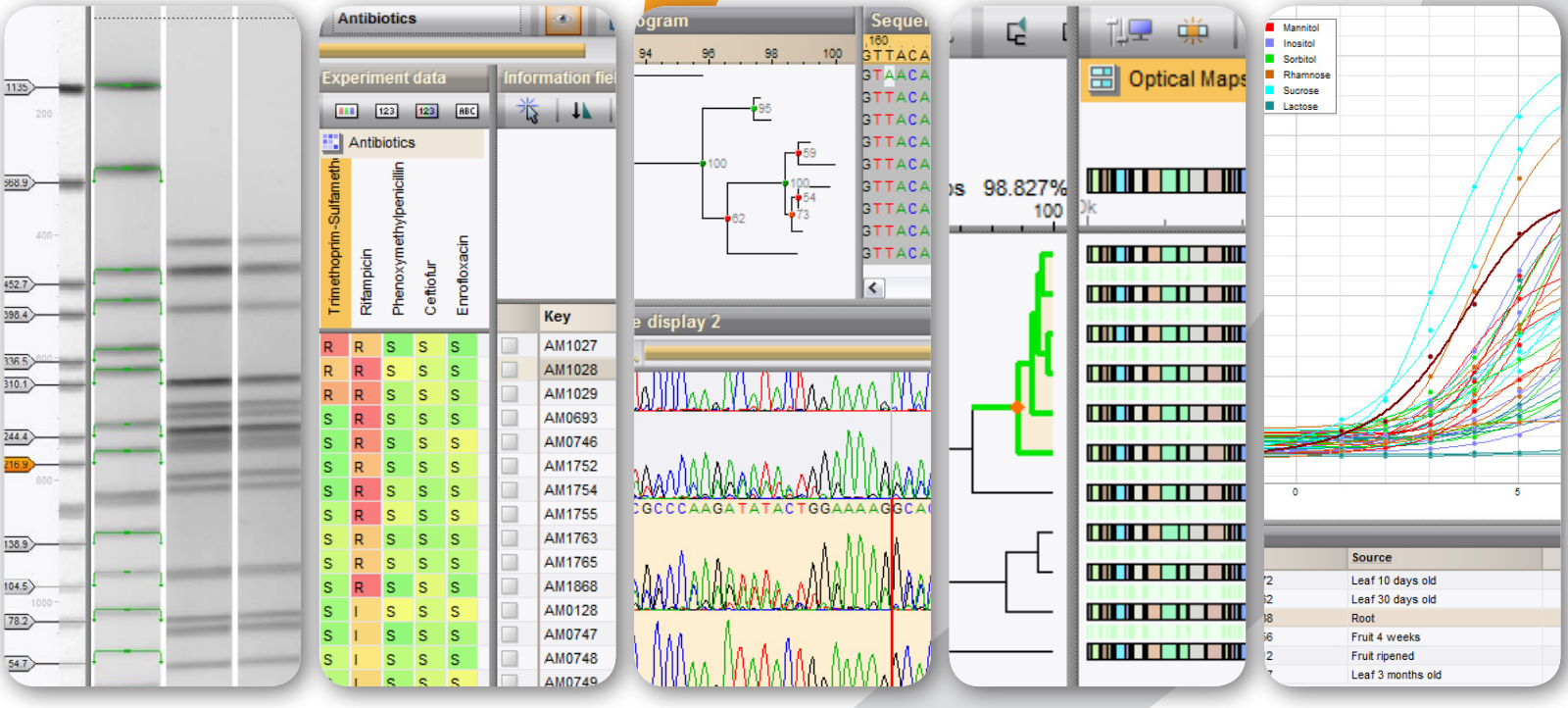
BioNumerics®

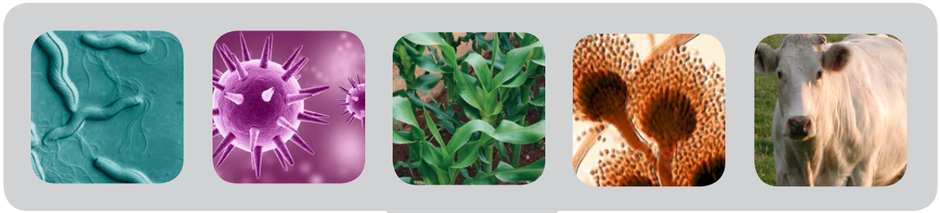
The Universal Platform for Databasing and Analysis of Biological Data



APPLIED MATHS

Manage. Analyze. Discover.

BioNumerics: one powerful platform for databasing, analyzing, and sharing all your biological data



Today, the ability to generate massive amounts of biological data has heightened the challenge of managing information and extracting meaning from it. Ever more techniques allow us to produce millions of raw data points in a single experiment: next generation sequencing, microarrays, SNP arrays, MALDI, just to name a few. An even bigger challenge is attempting to combine the results from different experimental techniques in order to address more complex questions and enhance our understanding of the underlying biology. The BioNumerics software platform addresses these challenges with its four cornerstones:

1 Import and, where appropriate, automated preprocessing of any kind of experimental data, ranging from electrophoresis and MALDI profiles to whole-genome and metagenome sequence data, microarrays, or phenotype characters.

2 A relational multi-user database environment for lab-wide storage and easy and intelligent retrieval of experimental and descriptive information.

3 Powerful querying, data mining and exploration, analysis, comparison, visualization, and reporting using predefined, script-based or user-defined procedures.

4 Integrated networking, data exchange, cloud and Internet-connectivity in a peer-to-peer or client-server environment.

BioNumerics is the most complete and powerful solution for databasing and comparative analysis of biological data. The software has gained worldwide recognition as an invaluable tool for bioresearch and has been cited in more than 8,000 peer-reviewed research papers. It is the daily workhorse in thousands of research and testing labs, including universities, hospitals and public health centers, food, drug and pharmaceutical industries, and a wide range of federal and private laboratories involved in typing, quality control, screening, testing, breeding, etc.

Manage

- Sequences
  - Assemble data from Sanger-based sequencers in batch
  - Preprocess and assemble NGS sequence reads using adaptable pipelines
- Character sets
  - Import and preprocess character data from a wide range of sources including phenotype panels, antibiotic resistance profiles, microarrays, etc.
- 1-D fingerprints
  - Import and normalize all types of gel and sequencer based electrophoresis patterns
- Spectral profiles
  - Import and preprocess mass spectrometry (MALDI, SELDI), gas chromatography, HPLC and other spectra
- Trend data
  - Import sequential measurements of one parameter in function of another (e.g. growth or enzymatic activity in function of time)
- Metadata
  - Store metadata for experiments, samples, organisms, patients
  - Create rich and object-oriented databases using levels and dependencies

Analyze

- Clustering
  - Wide array of tree and network inference algorithms
  - Integrated tree reliability and significance analysis
- Identification
  - Powerful classifiers including Naive Bayesian, SVM, Shrunken Centroids
  - Consensus results on multiple data sets and classifiers
- Statistics
  - Ordination, partitioning, and group validation techniques, powerful plotting
  - Numerous statistical tests including ANOVA and MANOVA
- Sequence analysis
  - Multiple alignment and SNP analysis with powerful quality assessment tools
  - Primer design, RE analysis, frame determination, oligo databasing,...
- Genome comparison
  - Whole genome alignment, annotation, and SNP analysis: gene-by-gene k-mer based comparison for in-silico extraction of traditional typing info
- Metagenomics
  - In depth metagenomics analysis based on deep sequencing of marker genes

Discover

- Report
  - Powerful and comprehensive graph and chart creation tools
  - Professional printing and exporting of reports and analyses
  - Customized reporting using BioNumerics' Python script language
- Share
- Publish
  - Peer-to-peer data exchange and database sharing
  - Client-server based data sharing networks
  - Access to public databases (MLST-net, pubTRST, EMBL, Genbank,...)

Available modules

The modular structure of BioNumerics allows you to choose a configuration that matches exactly your research needs, now and in the future.

Data modules

Fingerprint Data. Normalization and analysis of electrophoresis fingerprints from slab gels, automated sequencers, and lab–on–a chip systems. Preprocessing and analysis of spectral data such as MALDI.

Character Data. Import and analyze character data from a wide range of sources including phenotype panels, antibiotic resistance profiles, microarrays, etc.

Sequence Data. Assemble and analyze Sanger sequence data and NGS sequence reads. Access a wide variety of sequence analysis, search and alignment, and comparison tools.

Whole Genome Map Data. Align and cluster whole genome maps for bacterial strain typing and identification.

Trend Data. Analyze sequential measurements that express an evolution of one parameter in function of another, e.g., enzymatic activity, growth curves, rt–PCR, etc.

Analysis modules

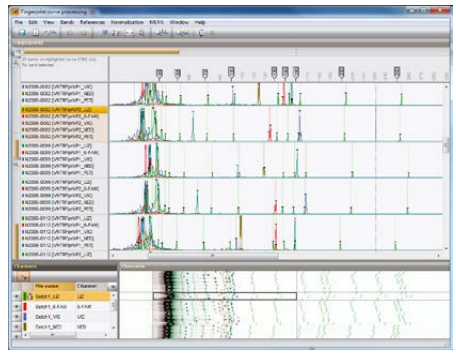
Tree and Network Inference. Select from an impressive range of clustering algorithms to calculate evolutionary trees and relationship networks. Display confidence levels on clusters and branches.

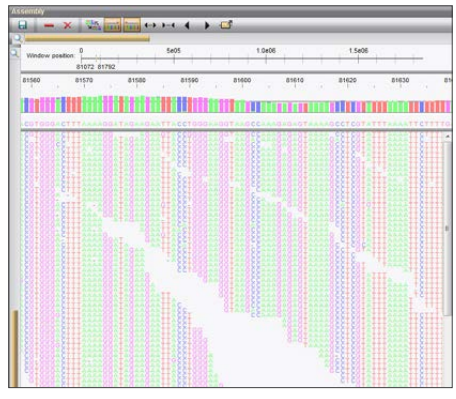
Dimensioning and Matrix Mining. Create non–hierarchical groupings using various ordination techniques such as principal components analysis, multidimensional scaling, discriminant analysis, and identify discriminating features between groups. Perform in–depth analysis of character matrices.

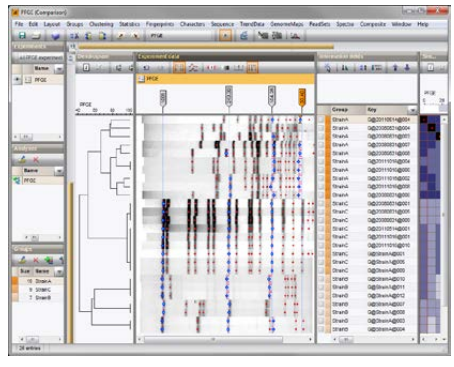
Genome Analysis Tools. Align and compare chromosomes side–by–side or calculate multiple chromosome alignments. Calculate SNPs and mutations on multi–chromosome alignments and annotate new chromosomes. Perform microbial metagenomics diversity analysis.

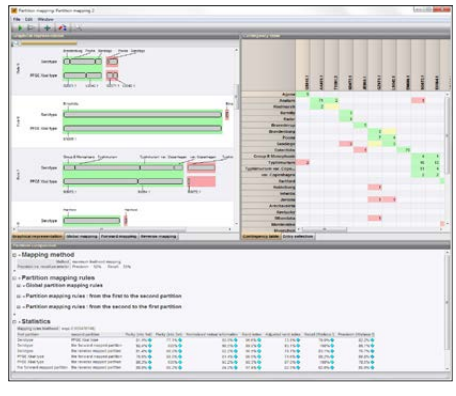
Classifiers and Identification. Identify unknown samples against reference data sets using state–of–the–art classifiers such as Naive Bayesian, SVM, Shrunken Centroids, and a range of similarity coefficients. Enhance your identification projects with parameter optimization and comprehensive cross–validation tools. Compare and validate different techniques or procedures.

Versioning and Audit Trails. Create audited databases (fully FDA Title 21 CFR Part 11 compliant) by recording all changes and keeping all versions of selected database objects. Compare and restore versions. Log user activity, create digital signing privileges.









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