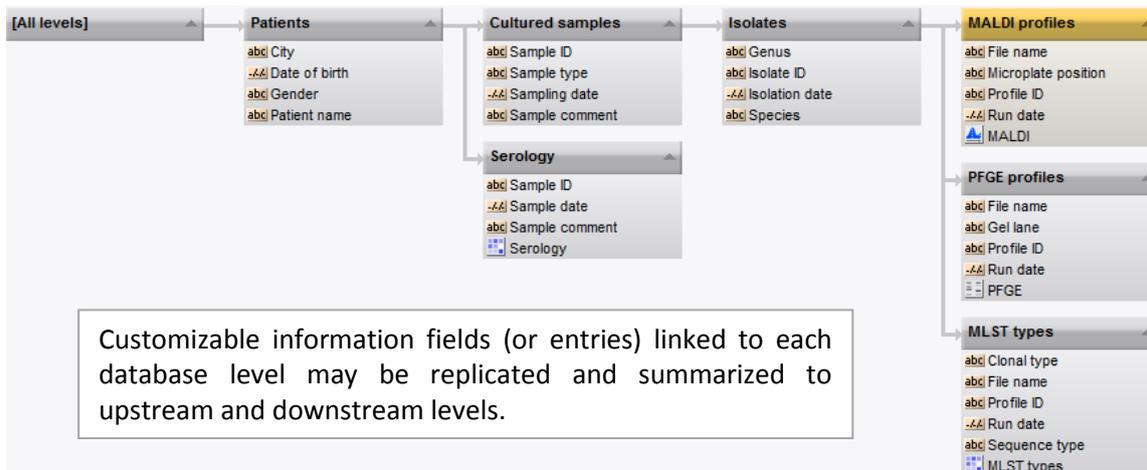


BioNumerics Seven comes with several fundamental improvements and a plethora of new analysis possibilities with a strong focus on user friendliness. Among the most important new features are the new database design for working with levels and dependencies, a new experiment type for analyzing spectrum data, an improved processing workflow for capillary sequencer data, new sequence analysis features for importing and processing sequence read sets, flexible metagenomics tools and aligning and clustering of whole genome maps. New state-of-the-art classifier algorithms have been added for setting up identification projects. On top of that, the software's overall performance has been further improved, resulting in a faster and more responsive package, ready to tackle vast amounts of data!

NEW FEATURES IN BIONUMERICS v7.1

GENERAL DATABASE FUNCTIONALITY

- New, highly adaptive database design for flexible working with levels and dependencies: advanced working with duplicates, replicates and multiple samplings of the same strain.



- A powerful Google-like search window enables you to rapidly find entries, experiment types, etc.

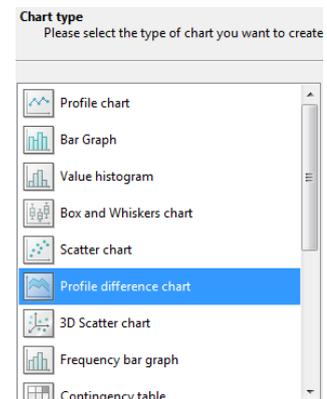
Search for:

Found: 7 Highlight Select all Close

Hit column	Hit text	Key	AC - ACCESSION	Stx subtype	DE - DEFINITION
DE - DEFINITION	Escherichia coli stxA2 and stxB2	<input checked="" type="checkbox"/> AJ272135	Stx2a-026-126814	Stx2a	Escherichia coli stxA2 and stxB2
DE - DEFINITION	Escherichia coli stxA2d gene for shi...	<input checked="" type="checkbox"/> AJ567997	Stx2b-040-5293-98	Stx2b	Escherichia coli stxA2d gene for shi...
DE - DEFINITION	Escherichia coli stxA2d gene for shi...	<input checked="" type="checkbox"/> AJ567995	Stx2b-0128-24196-97	Stx2b	Escherichia coli stxA2d gene for shi...
DE - DEFINITION	Escherichia coli StxA2a, stxB2d	<input checked="" type="checkbox"/> AJ313015	Stx2b-022-3143-97	Stx2b	Escherichia coli StxA2a, stxB2d
AC - ACCESSION	Stx2d2-091-B2F1	<input checked="" type="checkbox"/> AF479829	Stx2d2-091-B2F1	Stx2d	Escherichia coli O91:H21 Shiga toxin
AC - ACCESSION	Stx2d1-091-B2F1	<input checked="" type="checkbox"/> AF479828	Stx2d1-091-B2F1	Stx2d	Escherichia coli O91:H21 Shiga toxin
DE - DEFINITION	Bacteriophage P27 stxA2e, stxB2e	<input checked="" type="checkbox"/> AJ249351	Stx2e-ONT-2771	Stx2e	Bacteriophage P27 stxA2e, stxB2e

- Redesigned import window with expanded functionality for new data types. A convenient wizard helps with the import of different types of data and data sources. Better control over which entries will be updated or added to the database.
- Improved import function for direct import of Microsoft Excel® files.

- Database storage capacity up to 10 GB with the default Microsoft SQL Express® database engine.
- Unlimited number of database entries in one view.
- Personalized dynamic views for all database objects, such as entry fields, experiment types, etc.
- Improved and universally integrated charts wizard with easy-to-use predefined templates and options to create, store and share custom templates.
- Database Sharing Tools are embedded in the general functionality. This makes sharing and exchanging data between databases, users and laboratories even more flexible.
- Easy-to-use back-up and restore options per database from the BioNumerics start-up window.
- Redesigned tab-based window for displaying plugins per functionality.
- Improved online help function is accessible from every window.

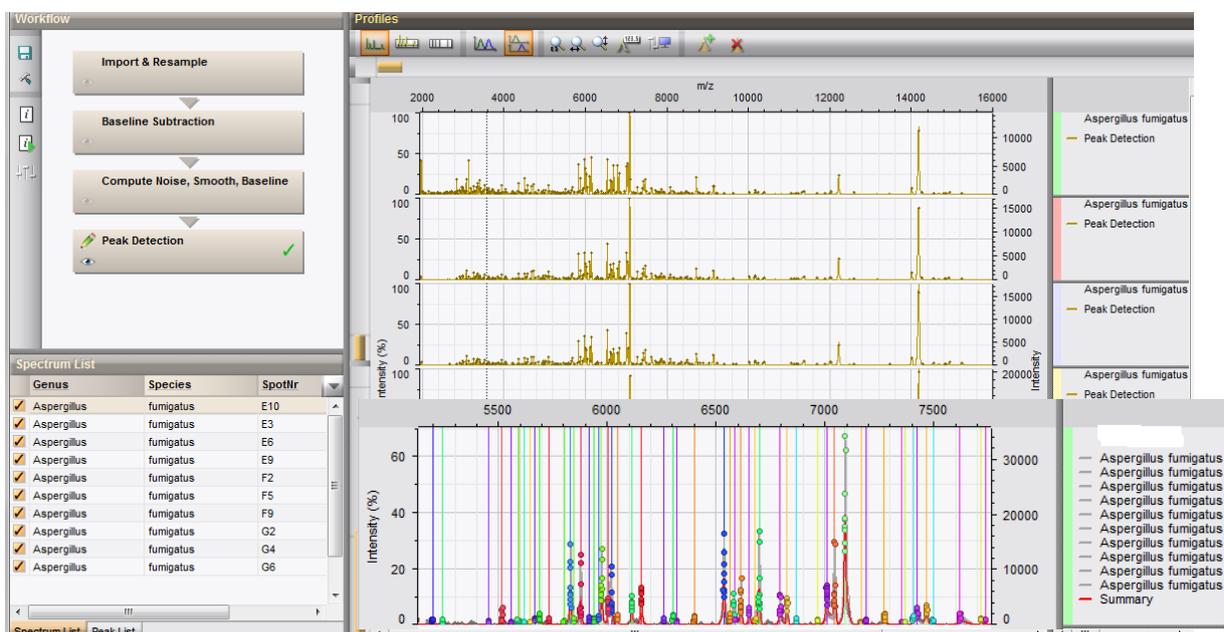


FINGERPRINT ANALYSIS

NEW SPECTRUM DATA TYPE

The new Spectrum data type enables comprehensive preprocessing, summarizing and follow-up analysis of e.g. MALDI-TOF, LCMS and ESI spectra.

- Fast import of spectrum data from various formats (text files, *.btmsp files, mzML files).
- Customizable workflow templates allow easy preprocessing of raw spectra. Automated import & resampling actions. Clean-up your profiles using baseline subtraction, noise elimination and curve smoothing. Automatic peak calling with manual editing options.
- Creation of summary spectra based on peak matching and member averaging. Flexible settings can be applied to filter out spectra of low quality. Similarity values allow easy inspection of the coherence of included spectra.
- Powerful statistical tools enable the creation of comparisons and identification of discriminative peaks at a glance. Perform PCA analysis, matrix mining and create identification projects using state-of-the-art classifiers.



CAPILLARY SEQUENCER DATA ANALYSIS

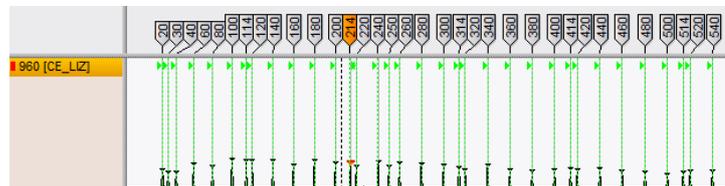
The improved Fingerprint Curve Processing window allows much faster pre-processing and reliable normalization of multichannel capillary electrophoresis data.

- Easy import of raw automated sequencers curves.

- Fast and flexible peak searching algorithms based on OD and curve range. Comprehensive options for removing curve noise, bleed through, stutter bands, etc.

Search thresholds		Band filters	
Peak detection	1	and	2
Gray zone	0	and	0
<input checked="" type="checkbox"/> Correct by peak intensity profile			
Minimum valley (% of peak height)	5		
Maximum number of peaks	200		
<input type="checkbox"/> Remove spikes on curve <input checked="" type="checkbox"/> Remove noise on curve <input type="checkbox"/> Filter by relative peak height <input type="checkbox"/> Filter by fragment length <input checked="" type="checkbox"/> Remove bleed through bands <input type="checkbox"/> Remove shadow bands <input type="checkbox"/> Remove doublets			

- New normalization algorithm with built-in predefined reference patterns enables reliable and fast normalization.



- Easy creation of comparisons and dendrograms using BioNumerics' impressive set of similarity coefficients and clustering algorithms.
- Fully backwards compatible with capillary fingerprint data from previous BioNumerics versions.



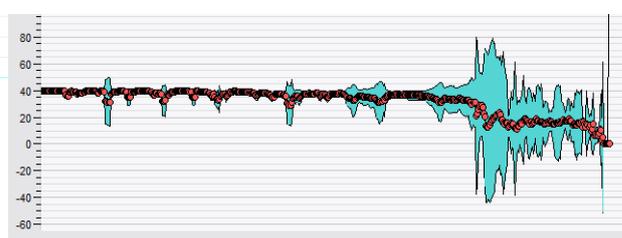
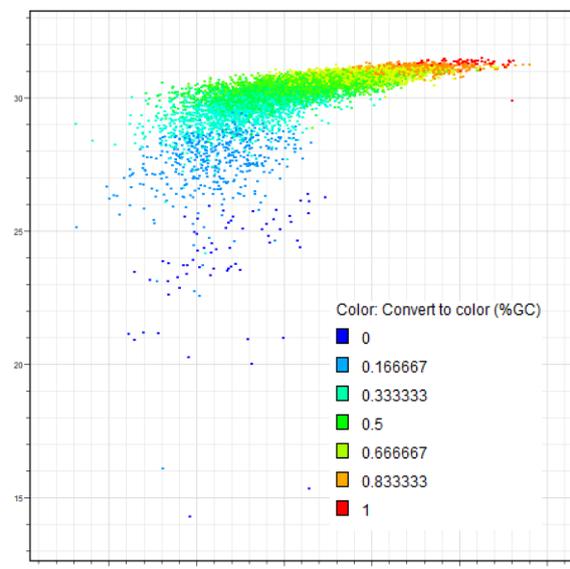
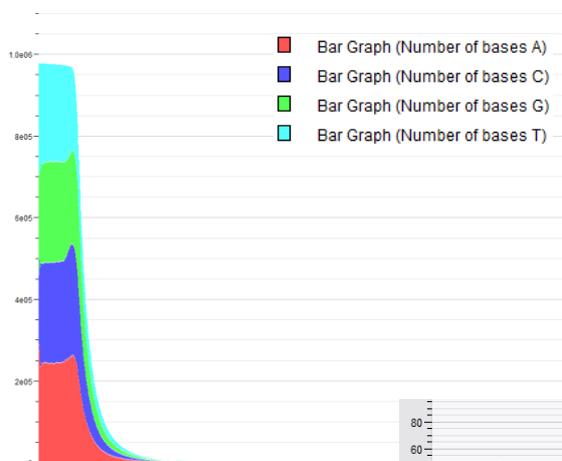
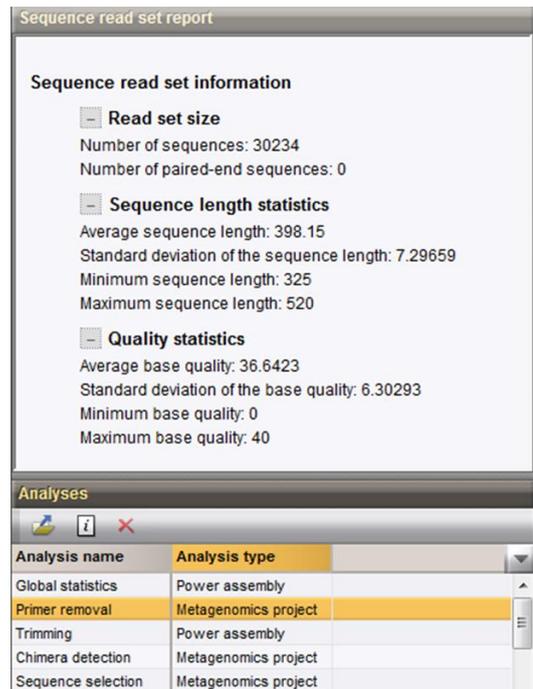
SEQUENCE ANALYSIS

This upgrade of BioNumerics brings new sequence analysis functionalities. The new Sequence read sets data type provides a complete software environment for analyzing Next-Gen Sequencer read sets. Perform comprehensive metagenomics studies with the new Genome Analysis Tools module.

NEW SEQUENCE READ SETS DATA TYPE

The new Sequence read sets offer a complete environment for importing, preprocessing and analyzing sets of reads from high-throughput sequencers or public repositories.

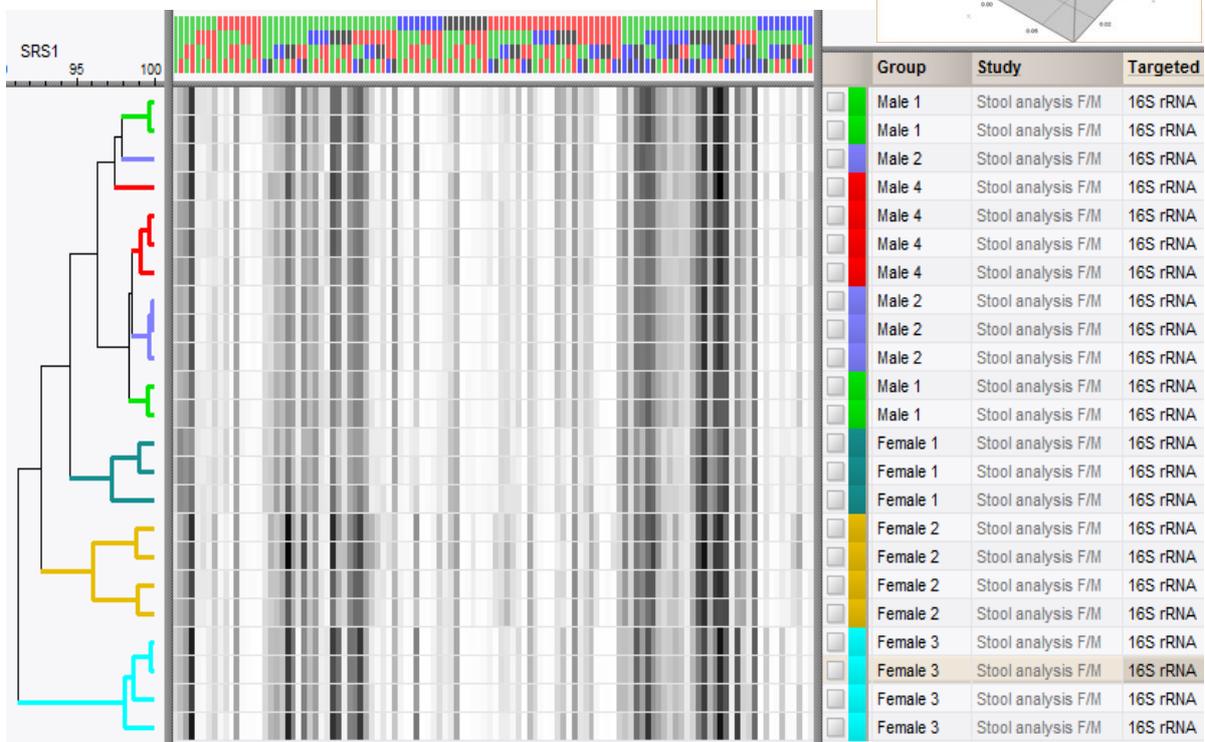
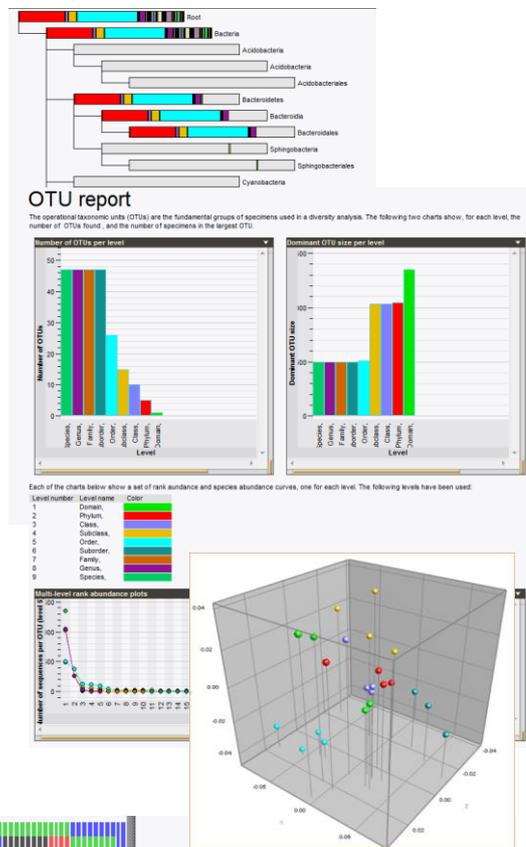
- Storage of large amounts of short sequences (including paired-ends and quality scores).
- Fast import of sequence read sets from various high-throughput sequencer platforms (e.g. Roche/454, Illumina, IonTorrent ...).
- Comprehensive data preprocessing and quality control settings for demultiplexing, splitting paired-ends reads, primer removal, structural and quality trimming, chimera detection using Chimera.Slayer and cleaning up sequence read sets.
- Global statistics calculation of sequence reads: creation of read length histograms, revision of base distribution and quality score distribution. Generation of reports in various text, table and chart formats.
- Creation of comparisons using all available similarity coefficients and hierarchical clustering methods, PCA, MDS, etc.



NEW GENOME ANALYSIS TOOLS MODULE

Perform metagenomics analysis based on deep sequencing of marker genes. Quantification, visualization and comparison of microbial communities starting from the raw sequence reads.

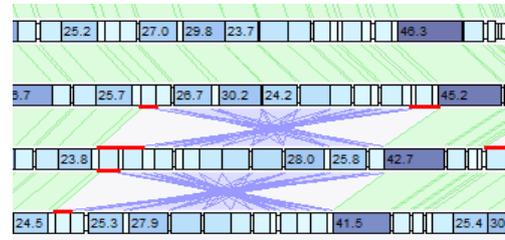
- Import, assemble and process high-throughput sequencer data using customizable automated workflows with built-in trimming and quality control actions.
- Generate OTU reports after identification of metagenomics sample sequences against a taxonomic reference database.
- Evaluate single sample diversity for the different taxonomic levels using several within-sample and community diversity indices and curves (Inverse Simpson index, Collector curves, Rarefaction curve, etc.).
- Use BioNumerics' wide range of data mining, clustering, identification and statistical tools for sequence clustering, visualizing OTU abundances and evaluation of α - and β -diversity.
- Display your data using rich charts and dimensioning methods: MDS, PCA, etc.



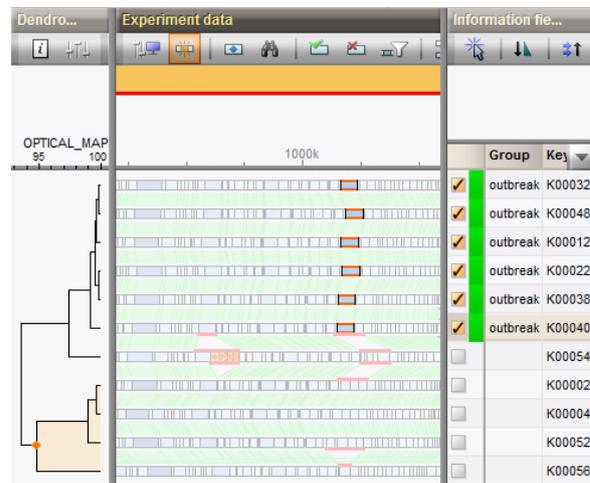
WHOLE GENOME MAPS ANALYSIS MODULE

The new Whole Genome Maps module is designed to analyze high resolution, ordered whole genome restriction maps. As whole genome mapping provides highly detailed strain information, its analysis in BioNumerics is mainly focused on (epidemiological) strain typing and characterization.

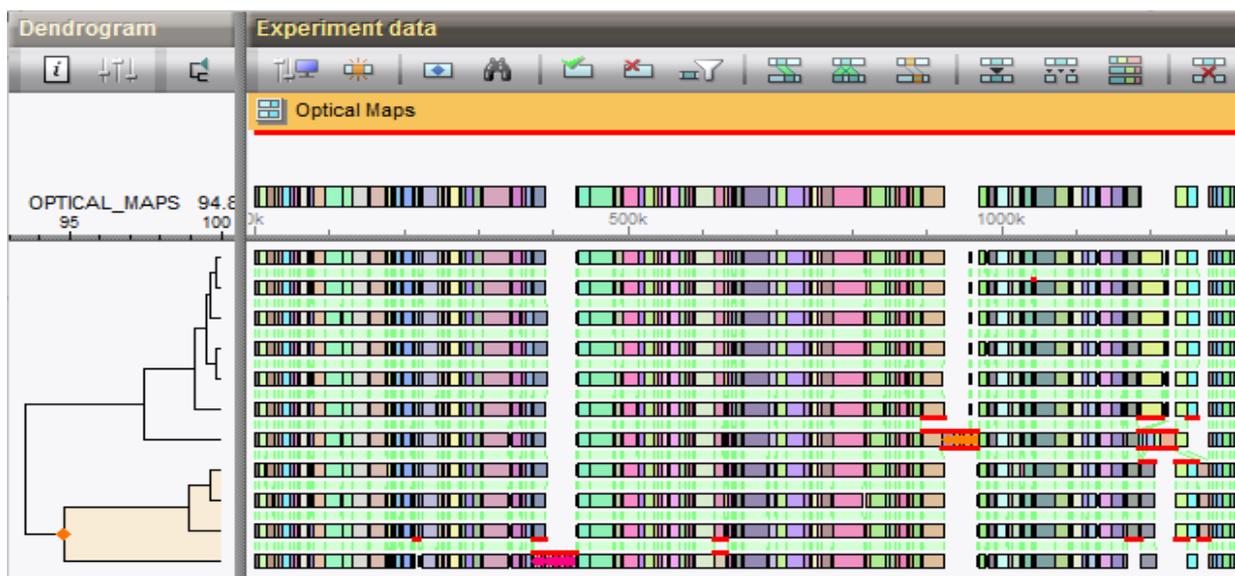
- Straightforward XML import of whole genome map data (OpGen, Inc.).
- Comprehensive viewing and search tools for at-a-glance recognition, selection and annotation of fragments.
- Accurate map-based clustering allows distinguishing of highly related strains using new and fast tolerance- and pattern-based algorithms.



- Exclusive tools for finding and highlighting discriminating fragments between groups of isolates.



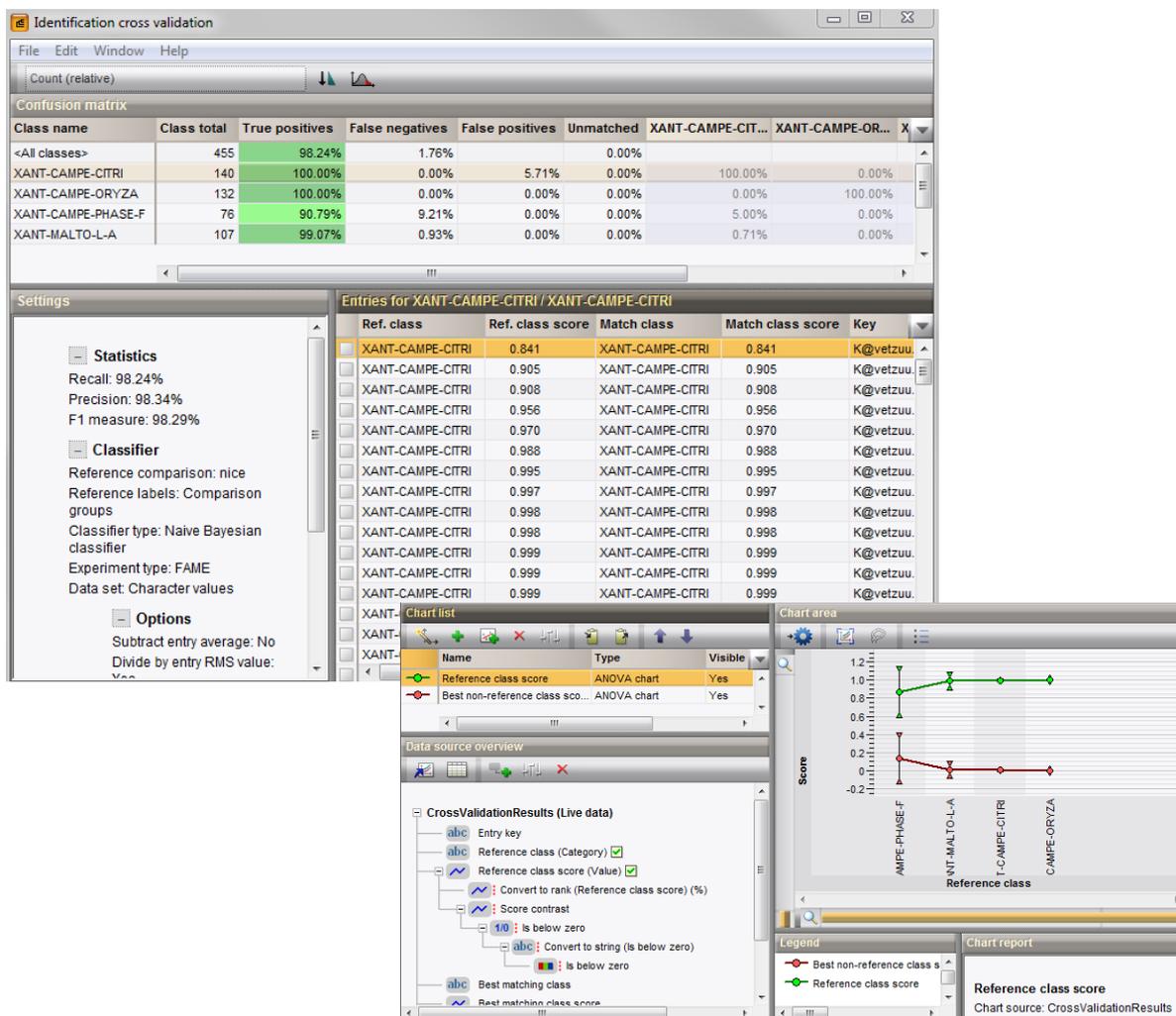
- Pattern-based and multiple alignment options allow to accentuate genomic differences at a glance.



CLASSIFIERS AND IDENTIFICATION MODULE

New state-of-the-art classifier algorithms based on similarity values, numerical data, binary data or categorical data matrices. Comprehensive parameter optimization and cross-validation.

- A wide array of classifier algorithms such as Naïve Bayesian, Support Vector Machine, and Shrunken Centroids.
- Extensive framework for cross-validation analysis of reference sets.
- Easy optimization of identification parameters.
- Conveniently view multiple classifiers and consensus results in one window.
- Comprehensive visualization options.



ABOUT THE BIONUMERICS PROGRAM

The BioNumerics platform is a modular software environment for the integrated analysis of all your biological data. BioNumerics can be configured exactly to match your research needs!

APPLICATION MODULES

- **Fingerprint Types:** This module enables gel image analysis and contains new functionalities for processing automated sequencer fingerprints and spectrum data types.
- **Character Types:** Define any array of characters, import similarity or distance matrices.
- **Sequence Types:** Analyze both Sanger sequence data as well as Next-Gen Sequencing reads. The functionality of this module is expanded with the Sequence Molecular Analysis Tools.
- **Whole Genome Map Types:** Fast visualization and clustering of whole genome maps (OpGen, Inc.) for epidemiological strain typing and characterization.
- **Trend Data Types:** Process all types of sequential readings that express an evolution of one parameter in function of another (e.g. enzymatic activity, growth curves, real-time PCR, etc.).

ANALYSIS MODULES

- **Tree and Network Inference:** Create comparisons and cluster analyses using a wide range of similarity coefficients and clustering algorithms.
- **Dimensioning and Matrix Mining:** Perform MDS and PCA, geo plotting ... Identify differentiating characters and perform two-way clustering of any matrix table of characters and entries.
- **Genome Analysis Tools:** Perform side-by-side comparisons of genomes and chromosomes, integrated metagenomics analysis and chromosome comparison and annotation tools. The Chromosome Comparison and Annotation Tools are included in this module.
- **Classifiers and Identification:** Set up identification projects using new state-of-the-art classifiers, with automated parameter optimization and comprehensive cross-validation tools.
- **Versioning & Audit Trails:** Record all changes to any database object, user logging, export XML reports, digital signatures, etc.

New Softlock software protection: no physical dongle needed anymore for new network licenses.

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