Applied Maths

BIONUMERICS VERSION 4.60: LIST OF NEW FEATURES

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BioNumerics version 4.60 is a minor upgrade with special emphasis on particular applications:

- 2D gel analysis
- SPA-typing
- CSCE analysis (= Heteroduplex Analysis)
- The script language has been further extended to make it possible to release powerful Plugin tools promptly upon the emergence of new techniques.

The following general software improvements were implemented:

Database

- A number of keyboard shortcuts are implemented:
  - Ctrl+T : bring selected entries to top
  - Ctrl+X : cut selection
  - Ctrl+C : copy selection
  - Ctrl+V : paste selection
  - Del : delete selection
- Option "Bring selected entries to top" causes the window to scroll to the top automatically.

Fingerprint types

Keyboard shortcut CTRL+R to mark reference lane in Normalization step.

Sequence types

- Tool with graphical preview window to export aligned sequences in formatted mode (rich text or plain text) in multiline layout

2D gel types

- Choice to display spots by contours or by semitransparent overlays
- New spot editing functions:
  - Fill internal spot holes
  - Smooth selected spots
  - Grow selected spots
  - Shrink selected spots
- Spot links can be marked as Confirmed and Unconfirmed
- Easy image displacement using right mouse button in 2D-gel Comparison window
- Easy selection fo query from drop-down menu in 2D-gel Comparison window

- Sort functions and more enhanced editing of Spreadsheet view in 2D-gel Comparison window
- Automated processing workflows using the 2D Gels Plugin

Comparisons

- A number of keyboard shortcuts are implemented:
  - Ctrl+T : bring selected entries to top
  - Shift + Arrow Up & Down: move entry up/down
  - Ctrl+S : save
  - Ctrl+X : cut selection
  - Ctrl+C : copy selection
  - Ctrl+V : paste selection
  - Del : delete selection
  - Ctrl+Page Up/Down : zoom in/out
  - Ctrl+Shift+Page Up/Down : zoom in/out in X dir
- Option "Bring selected entries to top" causes the window to scroll to the top automatically
- Bray-Curtis coefficient available for Composite data sets

Minimum Spanning trees

- Can be calculated on a similarity or distance matrix. MSTs can now be generated from any data set, including fingerprints, characters, sequences, etc.
- Keyboard shortcut Ctrl+Page Up/Down to zoom in/out

Chart & Statistics window

- Date intervals can be defined using new feature "Group by quarter".

Script language and script-based tools

- More than 270 new script functions in this release!
- New set of script functions for 2D gel processing and analysis
- New script functions for the Assembler

New Plugin tools

The following new Plugin tools are available and have their own manual. All plugins are free except the HDA plugin.

- *Spa-typing*: Plugin for Repeat Succession Analysis of the *Spa* gene of *Staphylococcus aureus*. This Plugin provides automated processing and analysis of Spa repeat sequences, with the following main features:
  - Automated batch import from a variety of sequencers (Applied Biosystems, Amersham, Beckman and other formats)
  - Automated batch processing and assembly of sequencer trace files with error and ambiguity reporting
  - Automated assignment of repeats and Spa types and search for most plausible repeats and Spa types in case of unresolved problems
  - Manual editing with History Recording and multilevel Undo/Redo
  - Automated download of updated repeat and Spa-types data from Spa-servers

- Comparison of Spa-types based upon the generalized 'DSI' model
- Cluster analysis and population genetics based upon Spa types by means of similarity based clustering techniques and Minimum Spanning Trees
- Fast identification and database comparison of new and unknown Spa types

NOTE: The Spa-typing Plugin requires the BioNumerics Sequence Types and the Cluster Analysis module.

– *2D gels*: Plugin for automated processing and analysis of 2D gels in various experimental setups. Deals with repeat experiments and multiplex gels such as DIGE staining.
  - Automated import, name parsing, spot finding, matching and spot linkage for multiple gels, each gel representing a new experiment condition
  - Automated import, name parsing, spot finding, matching and spot linkage of multiple gels in an experiment with repeats: spots of repeat gels are averaged and synthetic average gels are created and analyzed
  - Automated import, name parsing, spot finding, matching and spot linkage for multiplex experiments such as DIGE gels. Spots on all layers of a multiplex gel are identical and editing one layer causes all other layers to change accordingly

  NOTE: The 2D gels Plugin requires the BioNumerics 2D software, either standalone or as a module

A new version of the HDA (Heteroduplex Analysis) Plugin is available.