

RELEASE NOTE: GELCOMPAN VERSION 6.5

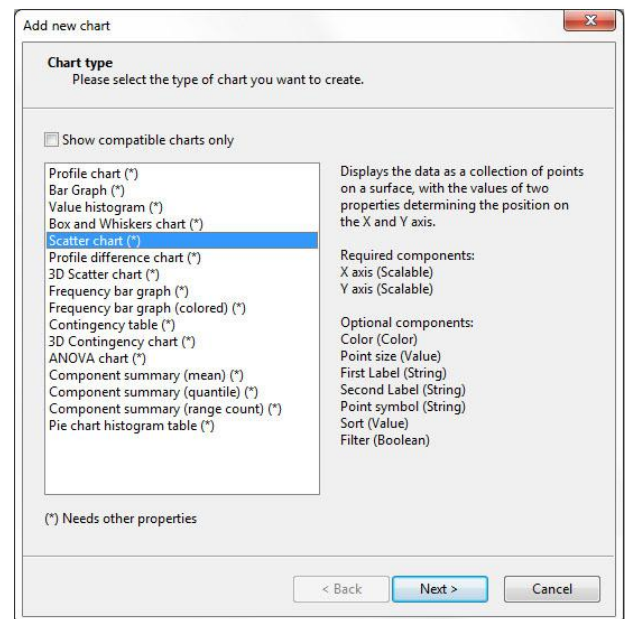
Charts and statistics

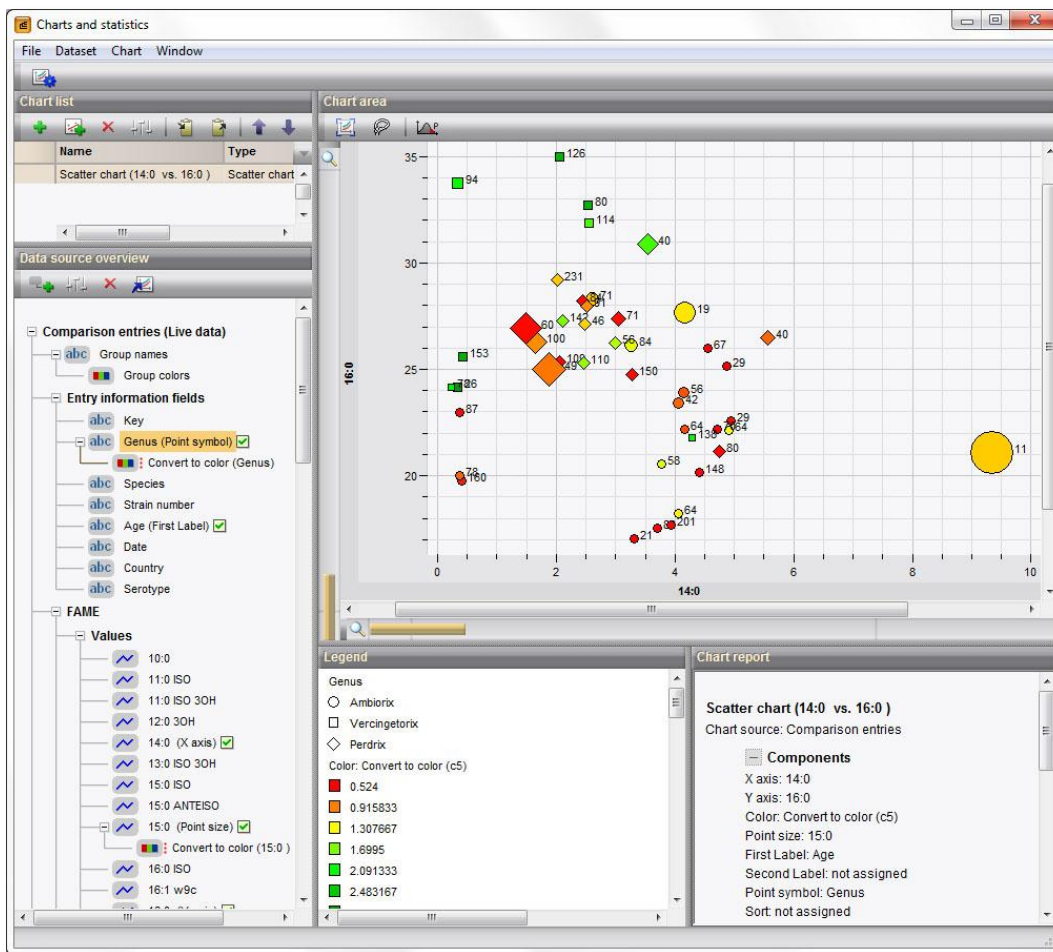
The new charts and statistics interface uses robust and logical concepts to guarantee that most if not all charting and plotting needs can be answered. The basis for every chart is the *data source*, which contains different *properties*. A property can e.g. be a string (information field) or a character value. For a selected combination of properties, all compatible chart types are listed by the software and the user can select the requested chart. Not less than 16 major types of charts are available. For each chart type, a number of optional properties can be used to provide additional information. For example, for a scatter chart, which is based on two numerical characters, the following additional information can be added:

- First label on each point in the chart (e.g. entry label)
- Second label on each point in the chart (can be any string property)
- Point symbol, which is assigned based upon the categories in a string property
- Point size, which is taken from another numerical property
- Point color, which can be derived from a string or numerical property.

In order to achieve maximal flexibility, properties can be converted into new *derived properties* using *operators*. For example, strings can be concatenated or combined, strings can be converted into values and vice versa, numerical and statistical operations can be performed on values, etc.

Charts can be generated from different sources, such as the main window, the comparison window, the entry edit window, the pairwise comparison window, and plugin applications. In the comparison window, it is possible to create charts from entries, characters, similarity/distance values and dendrogram branch data.





In case of scatter charts, a large number of regressions can be fitted. For each chart type, appropriate statistics can be calculated and exported as text or rich text.

A chart window along with all its charts, derived components, chart settings and regressions can be saved as a template. Saved templates are very useful to generate specific charts that need to be viewed routinely on different sets of entries or characters.

Interface

- Inverted “arrange entries by field” possible in main window and comparison window.
- The Main window status bar shows the number of selected entries.
- Mouse wheel enabled for experiment list in entry window.

Database

- Times in date/time strings are now stored in ISO standard format (same for time zones). This makes the exchange of date/time data between BioNumerics and other software easier.
- Optionally a regular expression can be entered in the "Field properties" to validate field content.
- Optional default content can be filled in for entry information fields. Special tokens can be used:
 - General: [CurrentDate], [CurrentDateTime], [CurrentYear], [CurrentMonth], [CurrentDay]
 - Connected DB only: [DbUser], [OSUser], [UniqueNr], [UniqueNr:7]
- A template for automatic generation of new keys can be specified ("Database > Set new key template..."). The same tokens can be used as for default entry field information.

Fingerprint types

- A new option to show only the "active zones" for fingerprints. The option is accessible in the Fingerprint window with "Layout > Hide inactive zones" and in the Comparison window with "Fingerprints > Settings > Set active zone" (also available as button). This feature can be used to line up the edges of normalized fingerprints.
- New quick way to change the active zone directly within a comparison using the above tool (for single zone only!).
- Color marking of bleed-through regions (spectral overlap) on fingerprint patterns from automated sequencers.

Comparison window

- Advanced clustering window contains the following new features:
 - Node colors are now shown in the Entry panel and the Entry selection panel.
 - New parameters for partitioning (creation of complexes):
 - Minimum number of nodes in a group
 - Option to use selected nodes only.
- Option "Create groups from database field" now optionally allows suppressing the creation of groups from empty fields.
- The tree name is displayed in the status bar.

Dimensioning techniques and statistics

- 3D PCA or MDS view: the "Show tree" function always displays the active tree (=the one currently displayed in the comparison window). Now any other tree than the default can be mapped on a PCA or MDS.
- Standard deviation is calculated on Simpson's index of diversity in the Chart tool.

Libraries and identification

- Library window: new command to sort units alphabetically.

Plugins

- *Import plugin:*
 - Redesigned, more general and more flexible, wizard-driven import plugin. Possibility to save import templates.
- *Import/Export as XML:*
 - The plugin is now "flexible field" aware.

Scripting

- New manual for Python scripting.
- The Python editor contains the following new features:
 - Possibility to drag and drop variables from the variables tree. Holding the SHIFT key while dropping writes the full path.
 - New feature "Edit > Check bracket".
 - More categories in the Python tree: S for static function, μ for member function.
- Colored regions can be defined on fingerprints. The colors appear on gel images.
- Custom info fields for band classes can be created (scripts or object query window).

Bug fixes

- Improved behaviour of comparison print (preview) in the absence of a default printer.
- Previously, entries could not be deleted if they were member of a subset. Now they are automatically removed from the subset first and then deleted.
- When calculating a band-based similarity coefficient between 2 fingerprints, if one or both is not present in the database, an "absent" result is now correctly reported. Previously, zero similarity was reported.
- Normalization now works correctly for fingerprint patterns with curve resolutions of higher than 22,000 values.
- GCStart returns an informative error when trying to run setlic without proper privileges.

Administration

- New InstallShield-based setup that enables easier setup, maintenance and upgrading of GelCompar II:
 - Instance-aware so that previous installs can be modified, repaired or updated.
 - Upgrades can be installed over previous versions or as separate new instances. This facilitates the installation and use of beta versions and upgrades as separate instances from the production version, for example for testing and validation.
 - The full installation procedure with all parameters and choices is recorded as an INI XML file.
 - The INI XML template can be applied for automated silent installation, e.g. for server-based deployment of BioNumerics in large sites.
- In case of network license, improved session logging for Netkey+.
- Check SN tool to display the software serial number can be run from startup window (in the Settings menu).
- When the table structure is updated, "BUILDREPORT.TXT" now also contains a time stamp (useful for support purposes).
- New approach to loading BXT's: they are now loaded from a subdirectory "BXT" and have extension ".dll".
- A new setting available in Database system settings: "Include time zones in time stamps".