

RELEASE NOTE: BIONUMERICS VERSION

6.6.4

The main improvement in this upgrade is an increased performance of data import and database actions. A number of database actions such as importing fields and/or characters, adding or deleting entries, renaming entries etc. will perform significantly faster on large databases. Furthermore, a number of improvements have been made to the [Import plugin](#), and a number of bugs reported in the [BioNumerics main program](#) have been resolved.

BIONUMERICS PROGRAM

DATABASE

- Improved performance of import and database actions on large databases.

ADVANCED CLUSTERING

- Enabled menu item “Materialize” for MST’s with hypothetical nodes.
- Added a script function for performing the “Materialize” command on an existing network that can be materialized.
- Added a script function to check whether a node is hypothetical.
- Added a script function to retrieve the data from a hypothetical node.
- Solved a bug concerning the enabling of the node label drop-down box.

PRIMER DESIGN

- On starting up the primer design module, the standard zoom modus is now 'full zoom in' (base-level).
- Starting up the primer design module now automatically selects a locus (target for primer design):
 - If no selection is defined, the full sequence is taken as target.
 - If a feature is selected in the sequence viewer, this feature will be taken as target region.
 - If a sequence selection is defined within the sequence viewer or alignment window (discriminative primer design), this selection will be taken as target region. Of course, a locus can be re-edited within the primer design window.
- The button "Add/edit locus" is consequently changed into "Edit locus" and is placed at second position (after "Run"-button).
- Within the primer design settings dialog, two items have been added:

- A checkbox "*Write reverse primers in conformance with the minus strand*". This means that all reverse primers are written in the reverse-complement direction (with respect to the leading (plus) DNA-strand). This option is by default enabled: all reverse primers will be shown, printed, exported in the reverse-complement orientation. If this option is disabled, reverse primers are written in conformance with the leader (plus) DNA strand.
- Primer settings can now be saved. A priority set can be appointed.
- Within the PCR listing, two buttons have been added for selecting respectively the forward and reverse primer within the view window.
- When primer design is started from a multiple alignment, primers are now displayed with 'base-difference'-indications with respect to the negative selection of sequences. This feature is enabled within sequence viewer, primer listing and PCR listing.
- The export format of primers to the clipboard is now explained by an additional information header (tab-delimited format).
- Title of the locus settings dialog box has changed from "primer target definition" into "Edit locus definition".
- Bug fix: "minimal discrimination"

ALIGNMENT WINDOW

- A sequence alignment can now be exported from the Alignment window to an open or newly created comparison.

IMPORT PLUGIN

New version of the import plugin: 2.23.

NEW FEATURES

- Speed-up of multiple character creation.
- Improved handling of 'duplicate' errors while importing data.
- Improved fetching sequences from internet:
 - Import of FASTA files exported from KODON software.
 - Import of CLC Bio annotated sequences.
 - Import of RefSeq sequences.
 - Import of a whole-genome project as one annotated sequence.
 - Added download site NIG (DDBJ - Japan).

OTHER PLUGINS

- Import sequencer fingerprint plugin v1.61:
now with new option "Invert curves" to invert the X-axis of the curves.
Bug fix: message "You are about to perform..." is now only shown when needed.
- HIV drug resistance plugin v1.40: adapted to reflect the new download location of the Stanford HIVDB resistance algorithms.
- Spa-plugin v2.15 and TRST-plugin v1.12:
Updated repeat search algorithm: repeats can be subsequences of other repeats
Repeat search will no longer automatically re-trim the assembly
Assign types : improved validation of correct start & stop patterns
- Added Alignment Tools plugin (always active)
- Added Annotation Tools plugin (always active)
- SmartFinder v1.00:
Import and analysis of SmartFinder data (PathoFinder BV) (Licensed plugin)