

MeV v4.2.02 bugfix release

September 30th, 2008

Bugfixes

- Mac and Linux: "Save" dialogs allow input of a new filename.
- Improved sample datafiles are included in the download.
- Added auto color selection to cluster operations selection dialog.
- Fixed One-Way ANOVA saving bug.
- Improved cluster operations in Cluster Manager.
- Cytoscape can now be launched via Java WebStart from the BN module in the absence of an internet connection, provided that the application has been cached. The application is launched using cached web properties, if Cytoscape webstart jars exist from previous downloads.
- Changed default number of BN bootstrap iterations to 20.

MeV v4.2.01 bugfix release

August 20th, 2008

Bugfixes

- When the data source was changed using the "Set as Datasource" option in the result tree, the Gaggle broadcast functions would send the wrong data, or occasionally throw an exception. This has now been fixed.
- Initialization dialog of t-Test and ANOVA required an existing cluster repository to run analyses, even when using button selection. This has now been fixed.
- The Cluster Selection tool failed when clusters had been previously selected using different clustering sources. This has now been fixed.

New Bayesian Networks & Literature Mining Network Format for Cytoscape

- Uses XGMML format for creating graphs when gene annotation is available.
- Uses MeV Annotation model to provide node annotation as attributes in XGMML format.
- When gene annotation is not available, it resorts to SIF format for Cytoscape networks.

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Major additions

Main Toolbar Redesign

A new main toolbar utilizing drop-down menus was designed to accommodate a growing number of MeV functions and replaces a long list of module buttons. Modules are now

grouped into seven categories on the main toolbar – Clustering, Statistics, Classification, Data Reduction, Meta Analysis, Visualization and Miscellaneous.

Bayesian Networks & Literature Mining Module Updates

- ❖ Addition of KEGG pathway based interactions as priors in generating complex interaction networks.
- ❖ Cytoscape is no longer included as part of the release to display networks. Instead Cytoscape is launched via Java Webstart and networks are loaded as files or as broadcasts through Gaggle.
- ❖ New viewers to display network files that are created.
- ❖ New viewers support right-click pop-up menu to launch Cytoscape with networks listed in the viewers. Earlier, once Cytoscape was closed the networks could not be viewed anymore.
- ❖ After state saving there was no way to view the networks in Cytoscape. Now that feature is added to launch Cytoscape from the viewers after state saved data is loaded back to MeV.
- ❖ Improved User Interface with lot of validtions.
- ❖ Improved error and exception handling for following situations:
 - No interactions found.
 - Too many interactions found.
 - Cluster Size to big to support.
 - Out of Memory Error.
 - Miscellaneous previously un-handled exceptions.

Clustering interface improvements

New cluster creation tool, rework of cluster displays, multi-cluster display, cluster ordering

- ❖ Multi-cluster display and rearrangement
- ❖ Automatic cluster assignment based on annotation
- ❖ Cluster selection feature added to t-Test, ANOVA and 2-factor ANOVA
- ❖ Removal of dependence on config directory and included files
- ❖ New properties file storage

Gaggle Interface

MeV now implements the Gaggle interface. The Gaggle is a bioinformatics data-sharing protocol developed at the Institute for Systems Biology in Seattle, Washington. The purpose of the Gaggle is to allow the movement of biological data between applications on a desktop computer and between the desktop and various websites. More information about the Gaggle is available from the ISB Gaggle website, <http://gaggle.systemsbiology.net/>.

MeV can now accept broadcasts of data matrices from other Gaggle-enabled applications, and can broadcast expression matrices and gene lists from module result viewers, such as the expression viewer. Also, Gaggle is used by the Relevance Networks and Bayesian Networks modules to broadcast network data to Cytoscape.

Bug Fixes/Minor Additions

- ❖ Addition of full-length PCA calculation, in addition to current estimation
- ❖ HCL optimal leaf-node ordering
- ❖ Module nodes in the result tree can now be renamed
- ❖ NonpaR init dialogs open file choosers to the MeV data directory by default.
- ❖ NonpaR init dialog calls new HCL dialog instead of old one.
- ❖ PCA dialog now has "median" centering selected as default
- ❖ Refactoring of viewer classes
- ❖ Improvements to EASE initialization dialog
- ❖ Integration of EASE with new annotation model
- ❖ Default location set for browsing annotation files from the file loaders
- ❖ Cluster-creation dialog now auto-selects an unused color for new clusters
- ❖ HCL memory assessment tool predetermines user's system capabilities and displays a warning if they do not have enough memory