

MeV v4.6.2 bugfix release

November 23, 2010

- Hierarchical Clustering header trees now appear when HCL is auto-launched by another module.
- RHook default/cached prop loading and remote access and other Exception handling and forwarding.
- 64 Bit Java bypass added to TMEV.bat launch file.
- BN progress bar now updates properly when the module is run more than once.
- Added placeholder file to data/BN_files/kegg directory to ensure the folders always appear regardless of which unzip utility is used.
- Removed Cluster Analysis option for modules when Clusters have not been created.
- Several small fixes pertaining to loading and unloading data.
- Default setting changed in SAM when using R.
- Error handling in Non-Negative Matrix Factorization improved, Plotviewer label issues resolved.

MeV v4.6.1 bugfix release

August 12, 2010

- Errors fixed in selection of EASE file system.
- Default distance metric for HCL run after LIMMA is now Pearson Correlation.
- Loading annotation after expression data now stores organism and array data.
- Manually loaded of annotation files are now correctly flagged.
- Search function disabled when no data is loaded.
- MAGE-TAB file loader displays and processes files in preview window correctly.
- MeV manual link now redirects correctly.
- Toolbar resets to disabled correctly on clear data command.
- SAM default settings updated.
- Improvement to display of MeV banner in progress dialogs.
- Hierarchical tree view is no longer displayed for all nEASE sub-results.
- Improvement to "Save EASE table" menu options in EASE and nEASE results.
- State-saving improvements to EASE module.
- More compact, simpler nEASE results.
- Improvements to the Minet documentation.
- UI tweaks in BN dialog.

MeV v4.6 release

July 2, 2010

MeV v4.6 includes a large number of new features, including several new modules and large improvements to existing favorites.

Major additions

Attract Module

The Attract algorithm identifies the core gene expression modules that are differentially activated between cell types or different sample groups, and elucidates the set of expression profiles which describe the range of transcriptional behavior within each module.

Global Ancova Module

A technique for identifying differentially expressed gene sets based off of the calculation of an F-test between groups of samples. Analyses are typically run in a two-class format but may also be applied to additional groups. Global Ancova fits linear models to the data and compares them using the extra sum of squares principle. The result table includes p-values, permutation p-values and asymptotic p-values.

Minet Module

For a given dataset, minet infers the network in two steps. First, the mutual information between all pairs of variables in dataset is computed according to the estimator argument. Then the algorithm given by method considers the estimated mutual information in order to build the network.

SURV Module

The Survival (SURV) module contains two functions for the analysis of censored survival data. The first is a basic comparison of the survival curves of two groups of samples. The second feature of the module is the creation of a `cox` proportional hazards model based on the loaded gene expression data, using survival time as the reporting value.

EASE UI Rewrite

The EASE UI is simpler and easier to use now.

Updates to the BN module

Network Seed allows the user is to provide a file representing a network. Network seed can be used in one of the three ways:

1. Using the user network seed alone and bypassing literature based network seeding altogether.
2. Using the user network seed along with Literature mining seed.
3. User provided network is used as a complete network and the network structure is not learned, only the Conditional Probability Tables (CPTs) associated with the network is learned for downstream exploration.

A node by the name of “CLASS” shows up in the network which captures the effect of sample groups on the network. Once the network is displayed the “CLASS” node behaves and can be treated as any other node in the network.

Updates to the GSEA module

Two new viewers are now provided, including a p-value graph viewer and a gene set membership plot. Gene sets can now be automatically downloaded from GeneSigDB and MSigDb.

Updates to the SAM module

A new addition to the SAM module integrates RHook to make a newer version of SAM available to users. MeV’s SAM now makes use of serially correlated time-course data in the exploration of statistically significant gene expression.

Hierarchical Clustering Trees

MeV now displays hierarchical trees with meaningful and proportional node heights along with an optional scale tailored to the chosen distance metric used in constructing the tree.

Other Changes

Rama significance testing for spotted array data has been disabled, along with the Bridge module. These functions never worked properly and have been unsupported for some time. They are still available in older versions of MeV. The most recent version of MeV that contains these features is [MeV v4.5.1](#).

We have also retired the Single Array Viewer.

Minor Additions

- FDR calculation is displayed in the TTEST module.
- Annotation can now be auto-loaded by MeV after expression data has already been loaded.
- Agilent file loader has been updated to work with the latest file formats.
- Pearson correlation coefficients are now the default distance metric for most analysis modules.
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Known Issues

- MeV's R-driven modules (LIMMA, Attract, Surv, SAM, etc) will not be accessible when MeV is launched via Java Webstart. This is due to difficulty with including the required R libraries with the Webstart download. Until we identify a solution to this problem, the workaround is to download MeV and run it locally.

Questions? Comments?

Please let us know in the MeV forums.

https://sourceforge.net/forum/?group_id=110558