MeV v4.8

November 18, 2011

New CLValid Module

A new module for cluster validation, CLVALID, has been added to MeV's existing clustering tools. CLVALID uses the R package "clValid" to compare the relative properties of 10 different clustering methods across a several different numbers of clusters. This module aims to help choose a method that is most compact, well-separated, connected, and stable. It also optionally makes use of bioconductor annotation packages to biologically validate the results.

New Annotation Support Files

The MeV team has built a new pipeline for producing the annotation files that are used to support modules like EASE and to display chromosomal location information and GO terms in the various gene table views throughout MeV. The new annotations are collected from Bioconductor v2.6, and are more complete than before. The files also include many new arrays, such as Affymetrix's Exon (ST) arrays.

For a complete list of supported arrays, please see:
ftp://occams.dfci.harvard.edu/pub/bio/MeV/annotation/bioconductor_2_6/supported_arrays.txt

In the future, we will be able to easily add new arrays as the Bioconductor team releases them, and to easily update these annotations when a new Bioconductor version is integrated into MeV. As a rule, MeV will provide annotation from the version of Bioconductor that is supported by MeV's currently-supported version of R. Currently, that version is R v2.11 and Bioconductor v2.6. This coordination is to ensure that annotation used internally by R modules is consistent with any annotation MeV displays.

Questions? Comments?

Please let us know in the MeV forums.
https://sourceforge.net/forum/?group_id=110558