

Chipster: A graphical user interface to DNA microarray data analysis using R and Bioconductor

Jarno Tuimala, Aleksi Kallio, Janne Käki, Taavi Hupponen, Petri Klemelä, Mikko Koski, Mika Rissanen, Eija Korpelainen

Alexi.Kallio@csc.fi, Jarno.Tuimala@csc.fi, Eija.Korpelainen@csc.fi

CSC, the Finnish IT Center for Science

In order to enable more researchers to benefit from the method development in the Bioconductor-project, we have created analysis software Chipster for microarray data. Chipster offers an intuitive graphical user interface to a comprehensive collection of up-to-date analysis methods.

Chipster supports all major DNA microarray platforms and, being a Java program, it is compatible with Windows, Linux and MacOS X. The basic analysis features such as preprocessing, statistical tests, clustering, and annotation are complemented with, e.g., linear (mixed) modeling, bootstrapping hierarchical clustering results, and finding periodically expressed genes from time series data. Analysis history is automatically recorded, and the analysis scripts can be viewed at the source code level.

Chipster can not only display images produced by R and Bioconductor, but also produce interactive visualizations for various clustering results, 2D and 3D scatter plots, histograms and time series plots. Users can freely choose different features of datasets to be plotted, such as log transformations of expression values.

Graphical client software runs on the user's computer, and connects to a remote server environment through a front-end server. Chipster can also connect to external Web Services. There is a possibility to set up a stand-alone version of the analysis environment on a Linux system, and an open source version will be available through SourceForge.

The technical implementation is designed to maximize flexibility and minimize memory usage and data transfer between components. New tools can be added using a simple annotation system, and no modifications or wrappers are needed. Analyzer instances are pooled so that analysis requests can be processed as fast as possible.

For more information about Chipster, please see:

<http://www.csc.fi/molbio/microarrays/nami>

<http://chipster.csc.fi>

<http://www.sourceforge.org/projects/chipster>