

Chipster software

biologist-friendly microarray data analysis



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Chipster brings a comprehensive collection of up-to-date microarray data analysis methods within the reach of experimental biologists. Chipster's graphical client program runs on the user's computer, and the actual analyses are performed on central computing servers. Chipster is open source and installation package is available for local setups.

Analysis functionality

Chipster's rich analysis functionality is based on R/Bioconductor and other methods. Preprocessing, statistical tests, clustering, classification, and annotation are complemented with e.g. linear (mixed) models, and pathway and promoter analysis. Adding new analysis tools is easy, allowing institutes to customize the tool selection for their needs. Chipster supports Illumina, Affymetrix, Agilent and cDNA arrays. Being a generic platform, Chipster is not limited to microarrays but it has been also used for e.g. proteomics data.

Building and sharing workflows

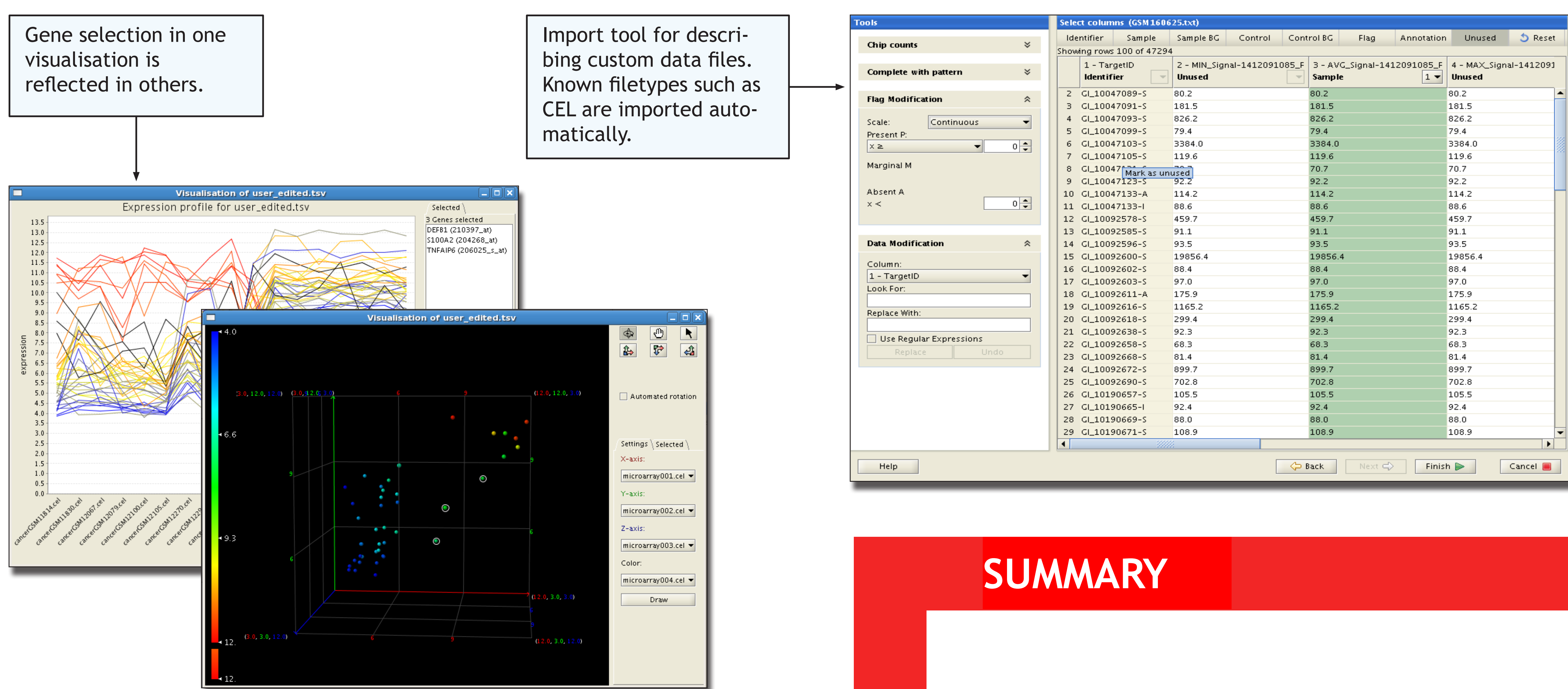
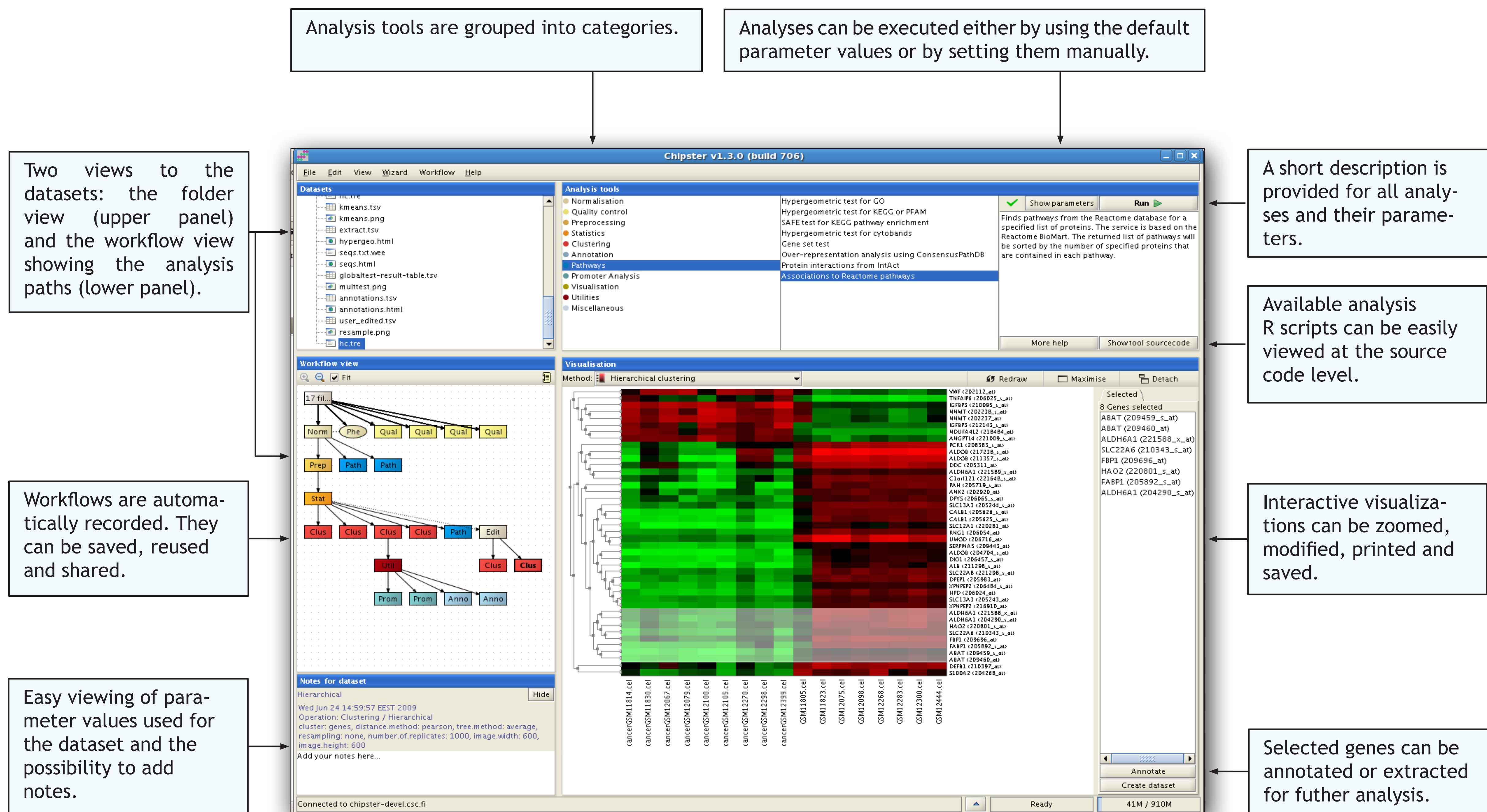
Chipster enables users to save their analysis pipelines as reusable workflows, which can be shared with others. The system keeps track of the analysis steps taken and displays them visually in a workflow graph. The user can experiment with different methods and parameters, and prune the resulting workflow tree by simply deleting the unwanted steps. The ability share workflows provides an easy way for bioinformaticians to collaborate with biologists.

Interactive data visualisations

Chipster's rich data visualisations include interactive scatter plots, expression profiles, volcano plot, heat-map, Venn diagram and histogram. In addition to tailoring these images, the user can create new gene lists by selecting data points visually.

System architecture

Graphical client software connects to the server environment via a message broker. Thanks to the message based architecture it is easy to run all components on a single server or distribute to multiple servers. It is also possible to connect external web services to the system. The fact that analysis packages and the associated databases are maintained and updated centrally makes it easy for the users and the bioinformatics core facilities supporting them.



SUMMARY

Microarray data analysis software with

- Intuitive graphical user interface
- Rich analysis functionality
- Possibility to reuse and share workflows
- Support for Illumina, Affymetrix, Agilent and cDNA chips
- Interactive data visualisation
- Runs on Windows, Linux and Mac OS X
- Open source (GPL)

<http://chipster.csc.fi>

<http://chipster.sourceforge.net>

