

The geneXplain platform

Based on the BioUML technology developed by the Institute of Systems Biology, a platform has been developed that allows to integrate a number of individual modules, "bricks", each of which provides as well-defined function in the field of bioinformatics, systems biology or cheminformatics. Altogether, the whole system will provide a toolbox suitable to establish complete pipelines from transcriptomics and proteomics data to new drugs.

The central platform is open source, so that any community member can contribute own modules.

In addition, geneXplain GmbH provides a number of state-of-the-art bricks on a commercial basis, implying a thorough quality control and maintenance guarantee.

Services

Making use of the expertise acquired during the past 20 years of development and applying own tools onto a range of biological problems, geneXplain also offers tailor-made data analysis services and collaborations on joint projects. These projects may refer to biomarker discovery, drug target identification and search for new drugs or new drug applications.

About geneXplain

GeneXplain's mission is to provide a comprehensive platform for bioinformatic, systems biological and cheminformatic tools. The raison d'être of this platform is to assist translational research in the life sciences, mainly in the context of personalized medicine and pharmacogenomics. We intend to make our expertise available to academic and commercial partners in collaborative research projects.

To achieve this, geneXplain offers:

- The geneXplain platform to provide an integrated and comprehensive workflow management of a large number of "bricks", each providing a specific function in analyzing biological data
- In Silico Molecular Cloning (IMC) for handling large-scale genome data
- GenomeTraveler (GT) for handling next generation sequencing (NGS) data
- PASS and PharmaExpert for predicting biological activities of compounds qualitatively
- GUSAR for QSAR model building and quantitative activity prediction

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geneXplain Platform

*The toolbox for
bioinformatics,
systems biology and
cheminformatics*



geneXplain

geneXplain platform™: an integrated data analysis pipeline

Key features

- Collection, storage and analysis of experimental data
- Loading raw microarray data and statistical processing
- Comfortable work with tabulated data: comparison, joining, subtracting, sorting, etc.
- Comprehensive analysis of regulatory sites with the TRANSFAC® database
- Mapping to Gene Ontology terms, gene enrichment analysis
- Network clustering and search for master regulator molecules
- Dynamic simulations
- Possibility to graphically program a specific pipeline (workflow), and add new scripts

Site & promoter analysis

Sequence analysis for potential transcription factor binding sites is done using the rich library of positional weight matrices of the TRANSFAC® database, but a limited set of matrices derived from high-throughput data is also freely available.

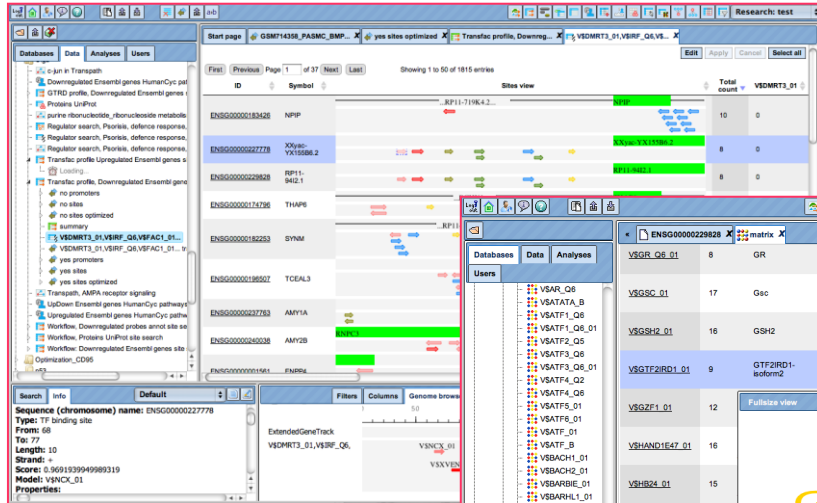
The platform also offers more complex promoter analyses by identifying combinations of sites that are specific for sets of co-regulated genes.

Dynamic simulations

The geneXplain platform provides visual modeling including a comprehensive simulation engine and parameter fitting option.

Standards in system biology

The geneXplain platform supports all main standards in systems biology: SBML, SBN, CellML, OBO.



Statistical processing

The geneXplain software provides a user-friendly way to statistically process raw microarray data, e.g. by correlation analysis, hypergeometric analysis, meta analysis, and polynomial regression. As a result, up- and down-regulated genes are reliably identified.

Network analysis

Network analysis is done with a proprietary algorithm that identifies statistically significant clusters of genes in any list (green nodes), which may be under control of a master regulator (red node).

One of the underlying databases, GeneWays, has been generated by A. Rzhetsky by text mining of more than 360,000 full text papers and of more than eight million publication abstracts [Iossifov et al., PLoS Comput. Biol. 5:e1000559, 2009].

Another possibility is to employ the TRANSPATH® database from BIOBASE with its more than 226,000 manually curated reactions [Krull et al., Nucleic Acids Res. 34:D546-D551, 2006]

Workflow management

Subsequent performance of particular analysis modules can be saved as a graphically represented workflow. Modules are shown as blue rectangles, and outputs of each step, displayed as yellow rhombs, serve as inputs into the next analysis step. A workflow that is specific for a given data set can be easily constructed by drag and drop of the required analysis modules. In addition, Java scripts can be added directly within the platform, for more specific requirements of the analysis.

A slide show demonstrating one pre-defined workflow ("Identify Master Regulators in Networks") can be found on our Facebook site (www.facebook.com/genexplain).

