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 different type of data (transcriptomics, proteomics, epigenomics, and metabolomics) to new drugs and biomarkers.

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.

Recent publications

Kel A et al. (2019) Walking pathways with positive feedback loops reveal DNA methylation biomarkers of colorectal cancer. BMC Bioinformatics. **20** (Suppl 4), 119.

Blazquez R et al. (2018) PI3K: A masterregulator of brain metastasis-promoting macrophages/ microglia. Glia. **66,** 2438.

Niehof M et al. (2017) RNA isolation from precision-cut lung slices (PCLS) from different species. BMC Res Notes. **10**, 121.

Mandić AD, et al. (2017) c-Jun N-terminal kinase 2 promotes enterocyte survival and goblet cell differentiation in the inflamed intestine. Mucosal Immunol. **10**, 1211.

Pietrzyńska M et al. (2016) Experimental and in silico investigations of organic phosphates and phosphonates sorption on polymer-ceramic monolithic materials and hydroxyapatite. Eur J Pharm Sci. **93**, 295.

More publications can be found on our web page.

geneXplain Platform

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 cancer research, 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:

- TRANSFAC®, the most comprehensive database on eukaryotic transcription regulation. TRANSFAC® is now also available under the geneXplain platform, providing the most comprehensive collection of TF DNA-binding profiles.
- TRANSPATH®, one of the largest pathway/network databases presently available, particularly well suited for geneXplain's proprietary *Upstream Analysis*.
- HumanPSD, a rich information resource connecting pathways with targets, drugs and clinical trials.
- PASS and PharmaExpert for predicting biological activities of compounds qualitatively.
- GUSAR for QSAR model building and quantitative activity prediction.

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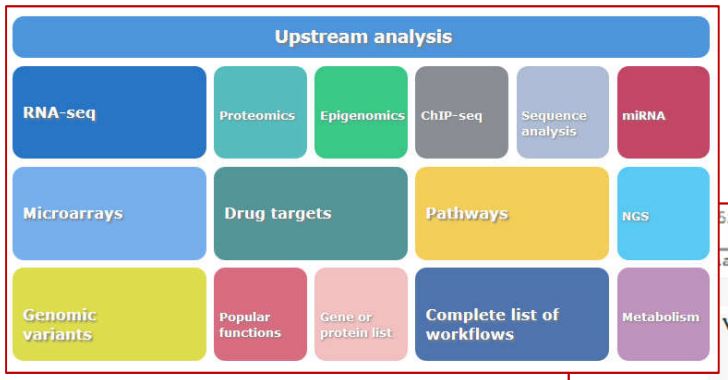
geneXplain Platform

The toolbox for bioinformatics, systems biology and multi-omics

geneXplain



geneXplain platform™: an integrated data analysis pipeline

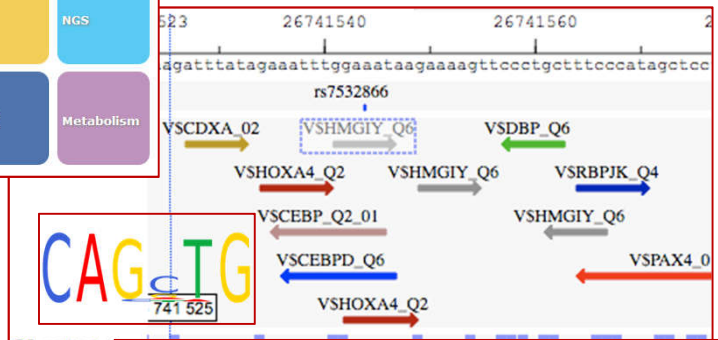
Key features

- Collection, storage and analysis of experimental data
- Analysis of microarray, ChIP-seq, proteomics, GWAS data and more
- Comprehensive analysis of regulatory genome regions with the TRANSFAC® database
- Mapping to ontologies and gene set enrichment analysis (GSEA)
- Network clustering, master regulator molecules, potential biomarkers and drug targets with the TRANSPATH® database
- Dynamic simulations
- Nearly 100 predefined workflows (specific pipelines)
- Make your own workflow by graphical programming
- Add your own JavaScript and R scripts; API available

Analysis of regulatory genome regions for TFBSs

Sequence analysis for potential transcription factor binding sites is done using the rich library of positional weight matrices of the TRANSFAC® database.

The platform also offers identification of composite modules specific for sets of co-regulated genes.

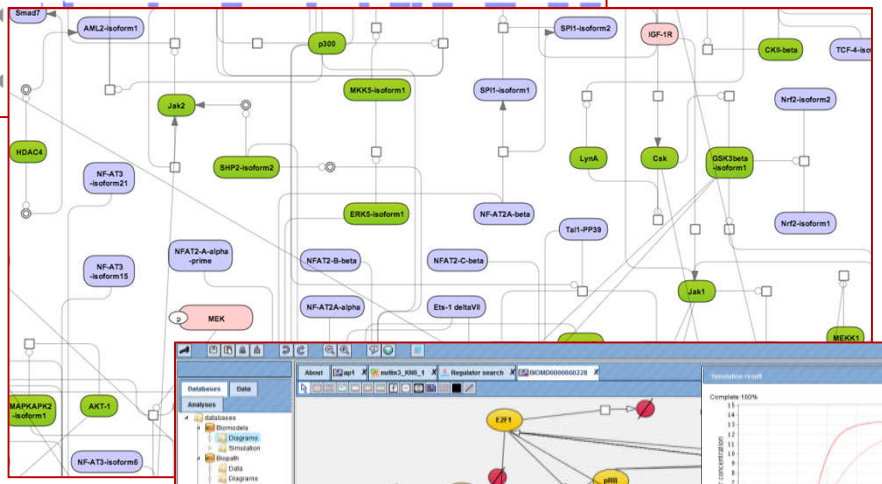


Network analysis

Networks are analyzed with a proprietary algorithm that identifies statistically significant clusters of genes (green nodes) that 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 700,000 manually curated reactions and 1,720 pathways in the release 2019.2 [Krull et al., Nucleic Acids Res. 34:D546-D551, 2006]

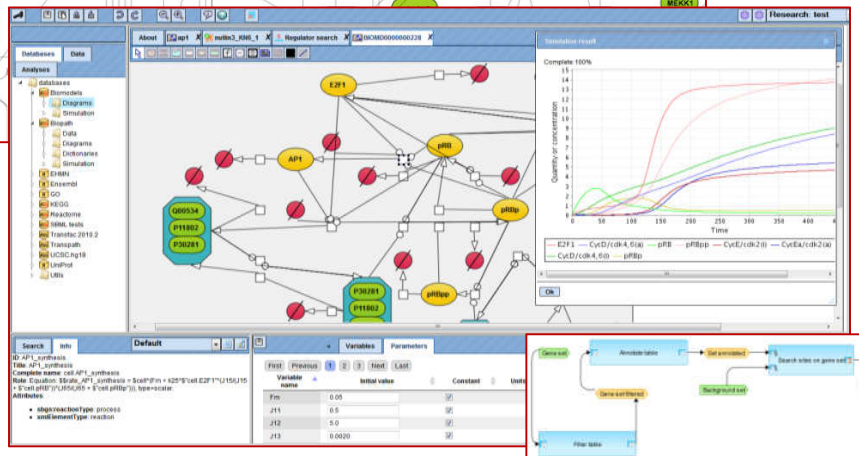


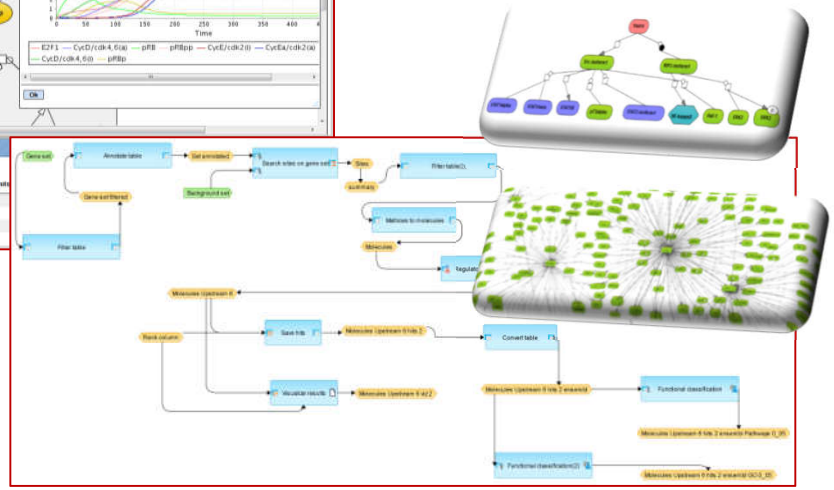
Functional analysis of genome variations

This workflow maps SNPs onto genes and evaluates their biological impact on the coding or regulatory potential of a gene. Regulatory SNPs are associated with nearby transcription factor binding sites. Results can be easily visualized with the built-in genome browser and exported in several formats.

Dynamic simulations

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





Workflow management

Subsequent performances 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, own Java scripts can be added to the workflow as required.