The geneXplain platform:
An adaptable analysis pipeline for patient data

SysmedIBD

The geneXplain platform is an online toolbox and workflow management system for a broad range of statistical, bioinformatic and systems biology applications. The EU-funded SysmedIBD project aims at revealing oscillating biological processes associated with the inflammatory bowel disease, where the transcription factor NF-κB plays a key role. In the course of this project we have enhanced the platform with NF-κB-related workflows, opening up a broad spectrum of applicability, since NF-κB plays a pivotal role in a variety of central biological processes.

What you have

- Microarray data
- RNAseq data
- ChIPseq data
- Processed proteomics data

What we can do for you

- Perform a causal analysis of your differentially expressed genes (DEGs) by integrated promoter and pathway analysis ("upstream analysis")
- Define potential master regulators of the process under study, including:
  - o Data pre-processing
  - o Semi-automatic data quality assurance
  - o Identification of DEGs
  - o Highlighting of enhanced biological processes in your samples

What you will get from us

- A clearly arranged, detailed result report including publication-ready graphical summaries
- Free access to the geneXplain platform with all your data and results, and the option to continue your work, either by yourself or using one of our service offers

Our aim

- To support your work by a range of service and consulting offerings
- To provide you with maximum flexibility to decide on deepening your analysis at any time, either on your own or by employing our services

GeneXplain is a central SME partner in the EU-funded project SysmedIBD that brings together specialists from Europe, Israel and New Zealand. The main objective of SysmedIBD is to better understand chronic Inflammatory Bowel Disease and to find new approaches for therapies, especially to develop new biomarkers, to stratify patient cohorts and to suggest personalised treatments.

A systems medicine approach includes interdisciplinary research of systems biology, mathematics and medical practice. This includes extensive experimental data that is incorporated into mathematical models and allows the general practitioner, the specialist and the patient to better stratify and manage the disease.

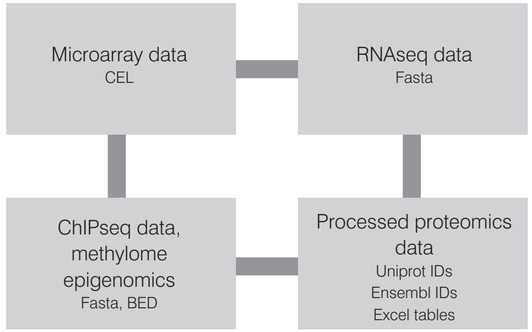
SysmedIBD is coordinated centrally by Prof. Werner Müller at the University of Manchester.

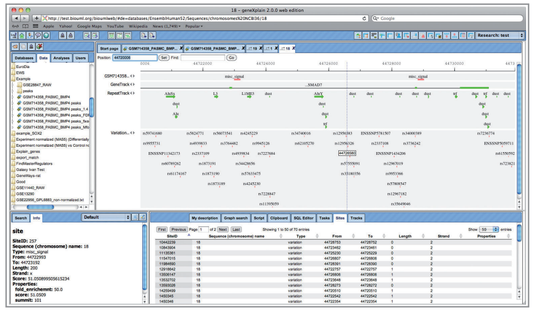
The geneXplain platform:
What you have

SysmedIBD

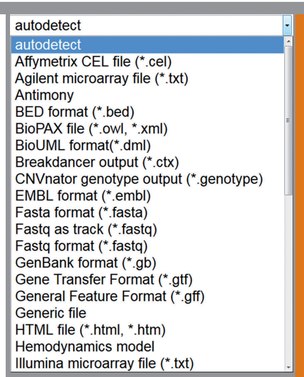
- You are a bench researcher **generating big data** and need assistance in your evaluation.
- You have different omics data; you wish to make a **comprehensive evaluation**, but have to deal with budget contraints.
- You are looking for a **user friendly interface** ready to tackle any analysis of key regulatory processes.
- You need a **fast and cost efficient management tool** to identify gene or protein mechanisms and interactions so you are able to suggest **personalised pharmacogenomics**.

- You have data from sources like:





Integrated genome browser and operations with tracks:
The geneXplain platform supports multiple operations with tracks. Tracks are files in BED, vcf, wig and more formats providing absolute genomic positions of the fragments or reads.



The geneXplain platform can work with many data sources

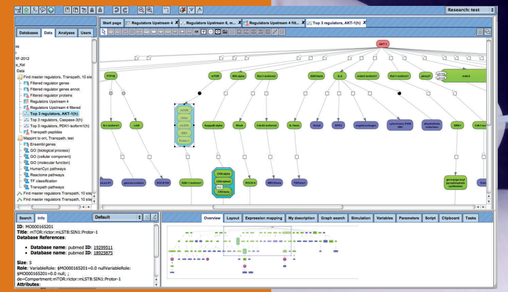
Prof. Werner Müller
Coordinator of SysmedIBD

One of our big challenges is to overcome the disease focused approach in medicine and get a more comprehensive view for an individual person and based on this view, try to prevent and/or treat diseases in the best possible way targeted for a given patient.

Systems medicine approaches build on "big data". To learn from experience from patient cohorts we need to be able to utilize this "big data" as detailed as possible.

The geneXplain platform:
What we can do for you

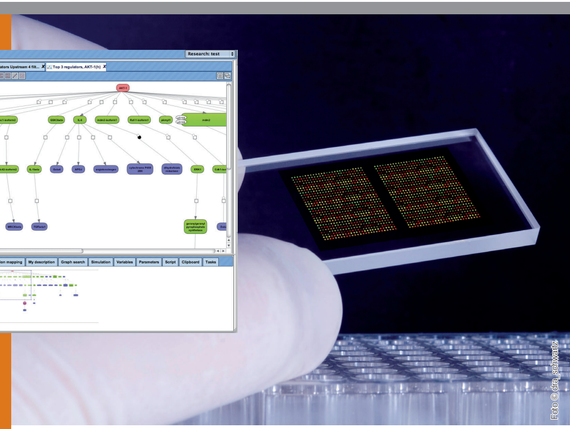
SysmedIBD



Identification of master regulators in the geneXplain platform using a pathway database

Prof. Edgar Wingender
CEO of geneXplain

This integrated promoter-pathway analysis approach uses a plethora of statistical, bioinformatic and systems biological computer tools. It has been proven in numerous applications to be capable of providing causal explanations of the phenomena observed and raising easily testable hypotheses about the biological process under study. We are therefore confident that our technology will also provide unprecedented opportunities to your project, as it does for the SysmedIBD consortium.



Causal analysis: The upstream analysis approach - an integrated promoter and pathway analysis. We offer you one platform for all standard formats.
Your benefit: All existing data bases can be used within one platform. A standard mask makes the handling of big data user-friendly.

Analyses of regulatory genome regions

- Most exact search for individual transcription factor binding sites (TFBS) with the TRANSFAC® PWM library
- Identification of tissue and disease specific enhancers via genetic algorithm by integration of NGS transcriptomic and epigenomic data

Analyses of pathways

- Most precise graph analyzing algorithm for finding master regulatory molecules with TRANSPATH®
- Identification of drug targets and causative biomarkers

Result: Potential master regulators of the process under study

Our algorithms reconstruct the pathways relevant in the system under study and identify convergence points. These are candidate master regulators of the investigated process.

The analyses are augmented by

- Identification of genes located near particular genome features, e.g. variation points or in vivo protein-binding fragments
- Identification of the enhanced biological processes and pathways in your samples
- Pre-processing of your raw data:
  - o A semi-automatic QA of your data
  - o Identification of differentially expressed genes (DEGs)