

Targets

Hands-on-training

Part 1: Upstream analysis workflow in geneXplain platform

Part 2: Look and feel of Genome Enhancer software

Part 1

Run a complete upstream analysis with the geneXplain platform.

Part 1 – Run a complete upstream analysis with the geneXplain platform.

Open the **Upstream analysis (TRANSFAC(R))** and TRANSPATH® workflow as shown below.

The screenshot displays the geneXplain platform interface. On the left, a sidebar menu shows the navigation structure: Databases, Data, and Analyses (highlighted with a red circle). Under Analyses, the Workflows section is expanded, showing a list of workflows. The 'Upstream analysis (TRANSFAC(R) and TRANSPATH(R))' workflow is highlighted with a red circle. A red dashed arrow points from this workflow to the main configuration panel on the right.

The main panel, titled 'Upstream analysis (TRANSFAC(R) and TRANSPATH(R))', contains a table of configuration options:

Parameter	Value
Input Yes gene set	(select element)
Species	Human (Homo sapiens)
Annotation source	databases/EnsemblHuman100/Data/gen...
Input No gene set	...ata/Housekeeping genes (Human) 300
Profile	...s/vertebrate_non_redundant_minSUM
Start of promoter	-1000
End of promoter	100
Results Folder	(select element)

Below the table, there are two buttons: 'Run workflow' and 'Edit workflow'.

Part 1 – Run a complete upstream analysis with the geneXplain platform.

Navigate to the *GSM558469_E2F1_hg19 filtered exp1000 dist1000 L<600* track and drag-and-drop it to the **Input Yes track** field of the workflow input mask. Navigate to the *Housekeeping genes (Human) track -100000 to -98000 filtered chr 1* track and drag-and-drop it to the **Input No track** field of the workflow input mask. The field **Sequence source** should be set to Ensembl Human 75 genome build. Click **Run workflow** when parameters are set as shown below.

The screenshot displays the geneXplain platform interface. On the left, a sidebar shows a tree view of data sources under 'Databases' and 'Data'. The 'Data' section is expanded, showing a list of folders and files. A red dashed line indicates a drag-and-drop action from the file 'TNF_upregulated_Ensembl_genes (Upstream analysis)' to the 'Input Yes gene set' field in the workflow configuration. Another red dashed line indicates a drag-and-drop action from the file 'TNF_non_changed_Ensembl_genes' to the 'Input No gene set' field. A red oval highlights the 'TNF_non_changed_Ensembl_genes' file in the sidebar. A red arrow points to the 'Run workflow' button, with the word 'RUN' in red text below it.

Upstream analysis (TRANSFAC(R) and TRANSPATH(R))

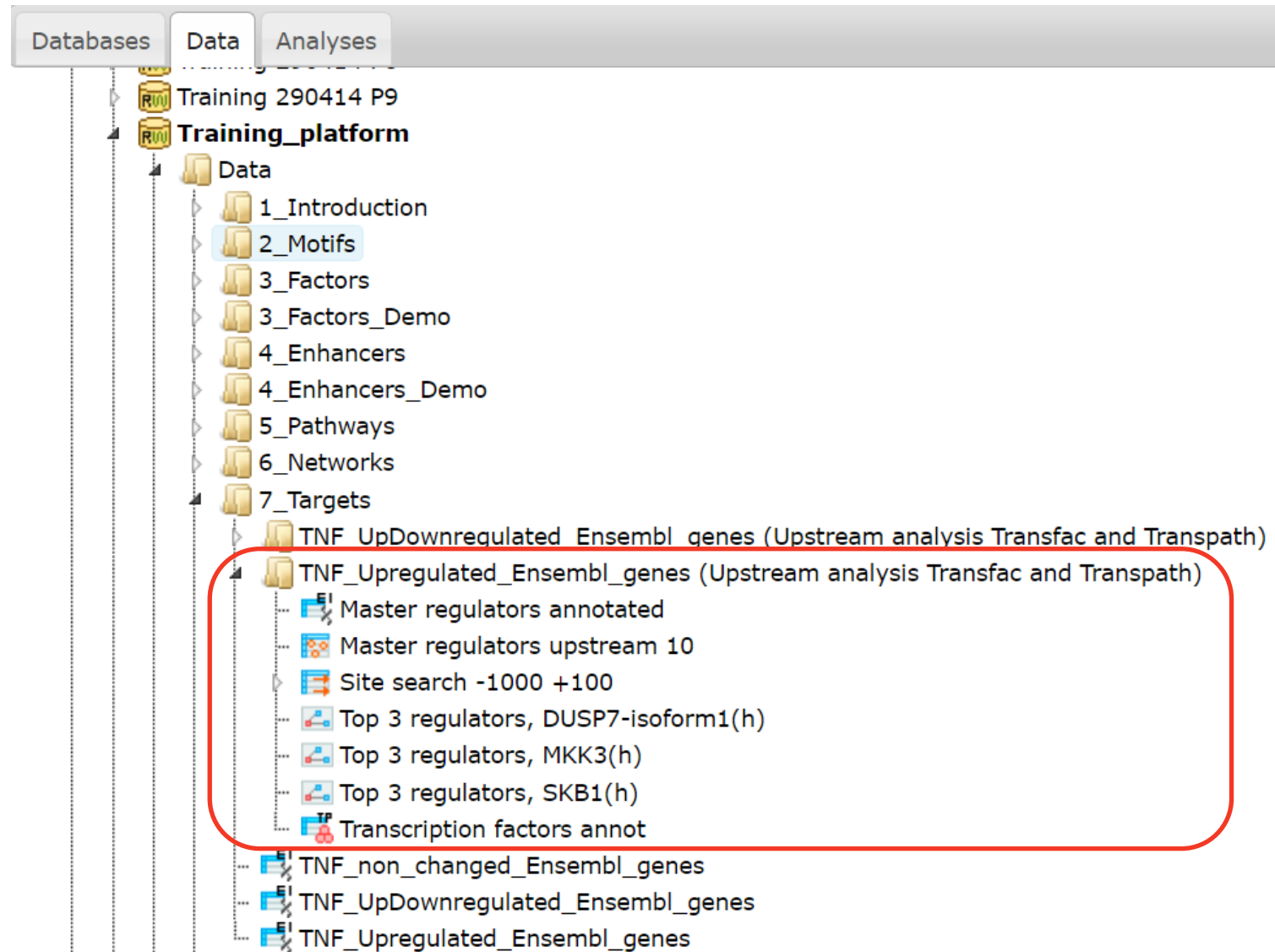
Input Yes gene set	...ets/TNF_Upregulated_Ensembl_genes
Species	Human (Homo sapiens)
Annotation source	databases/EnsemblHuman100/Data/geni
Input No gene set	...ts/TNF_non_changed_Ensembl_genes Auto
Profile	...s/vertebrate_non_redundant_minSUM
Start of promoter	-1000
End of promoter	100
Results Folder	...ream analysis Transfac and Transpath)

Run workflow Edit workflow

RUN

Part 1 – Run a complete upstream analysis with the geneXplain platform.

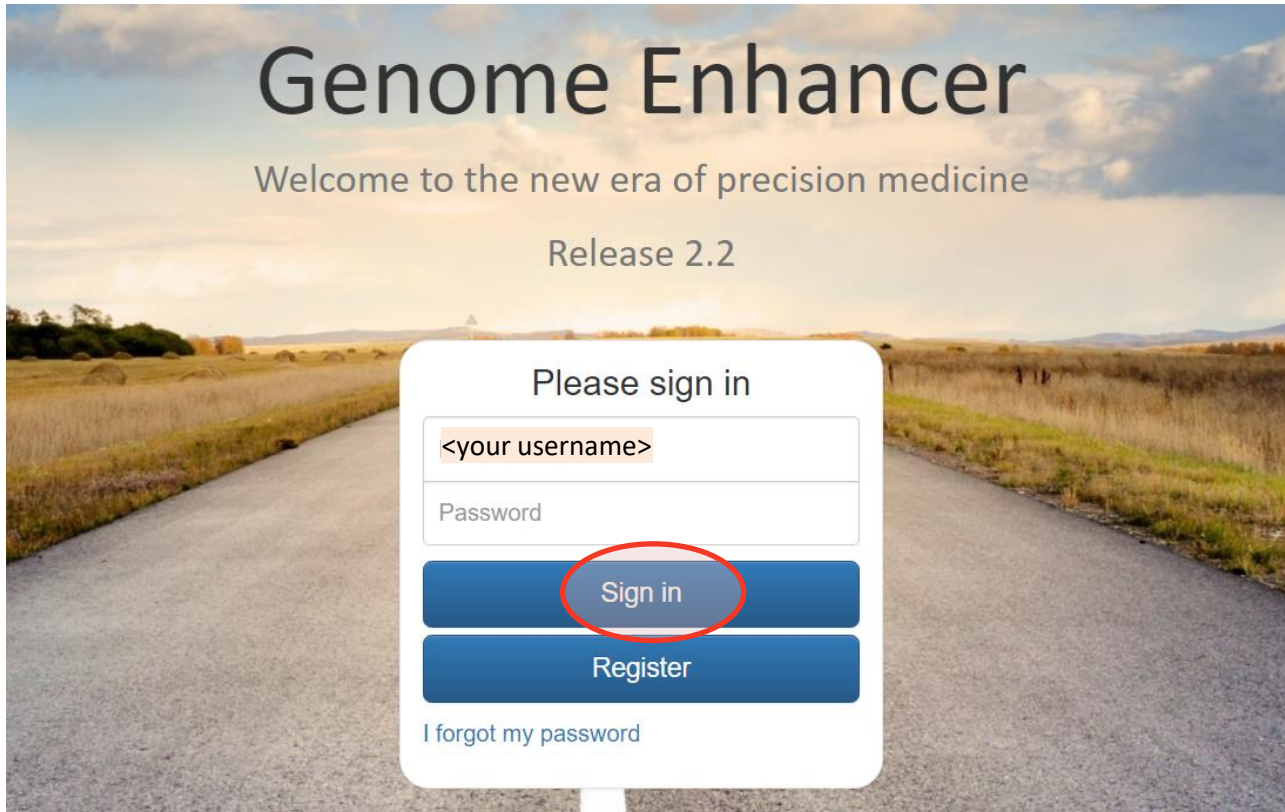
Have a look to the results folder and corresponding files.



Part 2 – Genome Enhancer tour

Genome Enhancer page in your browser: <https://genexplain-platform.com/bioutilweb/>

Specify your credentials and click **Login**.



Genome Enhancer

Welcome to the new era of precision medicine

Release 2.2

Please sign in

<your username>

Password

Sign in


Register

[I forgot my password](#)

Welcome




Welcome to Genome Enhancer!

For operating instructions on how to use the system please click on the  button at the top menu panel. Guidance will be given in accordance with the current step of the wizard.

☐ Don't show this again

Ok



< Prev

Next >

Genome Enhancer

Wizard

Enhance your genome

Demo projects

Colorectal Cancer (Personalized patient data) --- Genomics, VCF	PDF	HTML
Esophageal Squamous Cell Carcinoma (GSE32424) --- Transcriptomics, FASTQ	PDF	HTML

Show more ▾

+ Start New Project

Delete Project

Your projects

000001	<input type="checkbox"/>
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< Prev

Select project

Upload my data

Prepare my data

Describe my data

Start analysis

See report

Next >

Project: IFN-alpha induction (GSE31193) --- Transcriptomics, LogFC Table

Enhance your genome

Demo projects

Colorectal Cancer (Personalized patient data) --- Genomics, VCF	PDF	HTML
Esophageal Squamous Cell Carcinoma (GSE32424) --- Transcriptomics, FASTQ	PDF	HTML
IFN-alpha induction (GSE31193) --- Transcriptomics, LogFC Table	PDF	HTML
Lung cancer, treatment by TGF (ST000010) --- Metabolomics, Table	PDF	HTML
Osteosarcoma, neoplasm metastasis (GSE66789) --- Transcriptome + Proteome, RNA-seq + Mass-spec proteomics	PDF	HTML
Ovarian cancer, cisplatin-resistance (GSE15709) --- Transcriptomics +	PDF	HTML

< Prev

Select
project

Upload
my data

Prepare
my data

Describe
my data

Start
analysis

See
report

Next >

Project: IFN-alpha induction (GSE31193) — Transcriptomics, LogFC Table

Enhance your genome

Name	Size	Target folder	Progress	Delete
Drop files here				Acceptable file formats
				Table data templates
+ Add files...				Upload from URL
Next >				

< Prev

Select project

Upload my data

Prepare my data

Describe my data

Start analysis

See report

Next >

GenomeEnhancer

Wizard Description X

GenomeEnhancer

Projects

- 000001
- 000002
- 00001
- 00001t
- 00005
- 0001_test
- 0001_test22
- 0007
- 001_test2
- 002_test2
- 00_test1
- 1
- 123
- 200716
- 200818
- 201508G1A_01
- 201508G1A_02
- 201508G1A_03
- 201508G1A_04
- 201508G1A_1
- 201508G1A_2
- 201508G1A_3
- 201508G1A_4
- 202015
- 222
- 331
- 361
- 555
- 826_Samples_GBM
- A549 IAV DI and IA
- ACE2

Drag and drop all files you want to analyze into this box

E01_Transcriptomics_LogFC-Table

ID

LogFoldChange

Drag and drop all files you want to analyze into this box

E01_Transcriptomics_LogFC-Table
ID
LogFoldChange

Experiment

LogFoldChange
E01_Transcriptomics_LogFC-Table

Control

Enhance your genome

Disease:

Tissue:
(optional)

Select one or more diseases you are studying

Choose your data for analysis:

Select the conditions you want to compare in your analysis.

If only one condition will be analyzed, remove the unnecessary *Condition 2* by clicking on *Less conditions* button.

If two or more conditions will be analyzed, specify the condition which refers to the baseline (control/background set).

Baseline

Condition 1: ☐

Condition 2: ☒

[+ More conditions](#)

[- Less conditions](#)

[Start analysis](#)

[< Prev](#)

Select
project

Upload
my data

Prepare
my data

Describe
my data

**Start
analysis**

See
report

[Next >](#)

Part 1 – Genome Enhancer tour

Have a look to the results with clicking **Brief Tale** and **Full Story**.

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Genome Enhancer

Wizard

Project: IFN-alpha induction (GSE31193) --- Transcriptomics, LogFC Table

Enhance your genome

Reports

Name	Parameters	Status
2020.10.26-16:20:53-25	Project: IFN-alpha induction (GSE31193) --- Transcriptomics, LogFC Table; Conditions: Experiment; Tissue: 54) liver -- normal; Disease: Hepatitis C	Completed <div>Brief TaleFull Story</div>

< Prev

Select project

Upload my data

Prepare my data

Describe my data

Start analysis

See report

Next >

Report on promising druggable targets and drugs for treating Hepatitis C that are identified on the basis of analysis of differentially expressed genes in liver tissue

Demo User

geneXplain GmbH

info@genexplain.com

Project IFN-alpha induction (GSE31193) --- Transcriptomics, LogFC Table

Data received on 13/08/2019; Run on 26/10/2020; Report generated on 26/10/2020

Based on the performed analysis, the following drugs were proposed as most promising candidates for treating the pathology under study: **Naloxone, Tofacitinib and Perindopril.**

These drugs were selected for acting on the following targets: TLR4, JAK2 and ITGA2B. The targets were identified by analysis of molecular mechanism of the pathology under study.

Proposed drugs are top ranked drug candidates, that were found to be active on the identified targets and were selected from 4 categories:

1. FDA approved drugs or used in clinical trials drugs for the studied pathology;
2. Repurposing drugs used in clinical trials for other pathologies;
3. Drugs, predicted by PASS to be active against identified drug targets and against the studied pathology;
4. Drugs, predicted by PASS to be active against identified drug targets but for other pathologies.

Proposed drugs were selected on the basis of Drug rank which was computed from two scores:

Wizard BriefReport X Report X

Sequence and Pathway analysis

TLR4 and CCND3 are promising druggable targets for treating Hepatitis C that control activity of IRF7, EP300 and E2F1 transcription factors on promoters of differentially expressed genes in liver tissue

Demo User
geneXplain GmbH
info@genexplain.com
Data received on 13/08/2019 ; Run on 26/10/2020 ; Report generated on 26/10/2020
Genome Enhancer release 2.2 (TRANSFAC®, TRANSPATH® and HumanPSD™ release 2020.3)

Part 1 – Genome Enhancer Help page

Click the link below and read through the description of the Genome Enhancer Software.

<https://ge.genexplain.com/bioulweb/ge/help/step-project.shtml>

Practical session completed