# Part 1 : Introduction to geneXplain platform



Wolfenbüttel

info@genexplain.com

# **Topics:**

1. In this part we will learn how to navigate in the platform, how to search for information and how to load:

- gene tables,
- GEO database
- 2. We will learn how to filter tables & annotate genes
- 3. Data Normalization
- 4. Principal Component Analysis
- 5. Performing LIMMA Differential Gene expression
- 6. geneXplain Methods convert different database identifiers.

#### **1.1 Login into the geneXplain platform**

Open the geneXplain platform page in your browser: <u>https://platform.genexplain.com/</u>

Specify your credentials and click Login.

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		Login Register								



#### 1.2 Copy a gene list to your data project in geneXplain platform

Navigate to the file <u>IFN 6h vs Control DEGs adj p-val<0.05 genes</u> from the Training\_Input\_Data directory. Double-click on the table name to open it in the Workspace. **Save a copy** of the example table (with right mouse click). Choose your **Data** folder of your user project as copy location, which is named with **First name** and **Last name** from registration process. Click the **Ok** button for copying process.

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#### 1.3 Filtering a table in geneXplain platform

Open the copied file <u>IFN 6h vs Control DEGs adj p-val<0.05 genes</u> from your user **project**. Double-click on the table name in your **Data** folder to open it in the Workspace. Navigate to the **Filters** tab in the Operation field. Select the template **Above threshold**, the column **logFC**, and type threshold **1.0.** Click on the **Apply filters** button in the low menu bar. Click the **Export filtered table** button in the low menu bar. Give the name of the output table and click **OK**. The new filtered table will be stored in your **Data** folder in the Tree Area.



You can also use predefined templates for easy creation of the filtering expressions.

**1.4** *Exercise:* More operations with tables

- Create table with down-regulated (DN) genes by filtering the table in geneXplain platform;
- Import a new table with NC genes from your computer;

#### **1.8 Loading microarray data from Gene Expression Omnibus (GEO) into geneXplain platform**

Navigate to the **Data** folder of the project and click on **Import** button in menu bar. Select **Cweb/FTP** in the Import file menu. With right click copy the link address in GEO (<u>http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11440</u>) Past URL and click **OK** and after upload **Import**.



#### 1.9 Exercise: "Make notes on the imported data from GEO"





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## 1.11 Exercise: "Do Principle Component Analysis (PCA)" (Home work)



### 1.12 Compute differentially expressed genes (DEG) using Limma package. (Home work)

Navigate to the **Microarrays** section in **Start page** and click on **Compute differentially expressed genes with Limma** link. Drag-and-drop **Normalized (RMA)** into **Input table** filed in the form. Select column names corresponding to different conditions. Click **Run workflow**.



#### 1.13 Filtering genes LogFC>1 (Home work)

Double-click on the table name and open it in the Work space. Navigate to the **Filters** tab in the Operation field. Select a template **Above threshold**, column **LogFC**, threshould **1**. Click on **Apply filters** button in the low menu bar. Click **Export filtered table** button in the low menu bar. Give the name of the output table. And click **OK**. The new filtered table will be stored in your folder in Tree aria.

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··· 📑 Non-changed genes Ensembl	ENSG0000001036	<u>223120_at</u>	alpha-L-fucosidase 2	FUCA2	Homo sapiens	0.51798	0.32523	0.71074	
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