

# Enrichment Analysis Tutorial

This tutorial aims to explain the functionality of the “Enrichment Analysis” tool provided by GeneSetDB. GeneSetDB is available at <http://genesetdb.auckland.ac.nz/haeremai.html>.

## The web interface

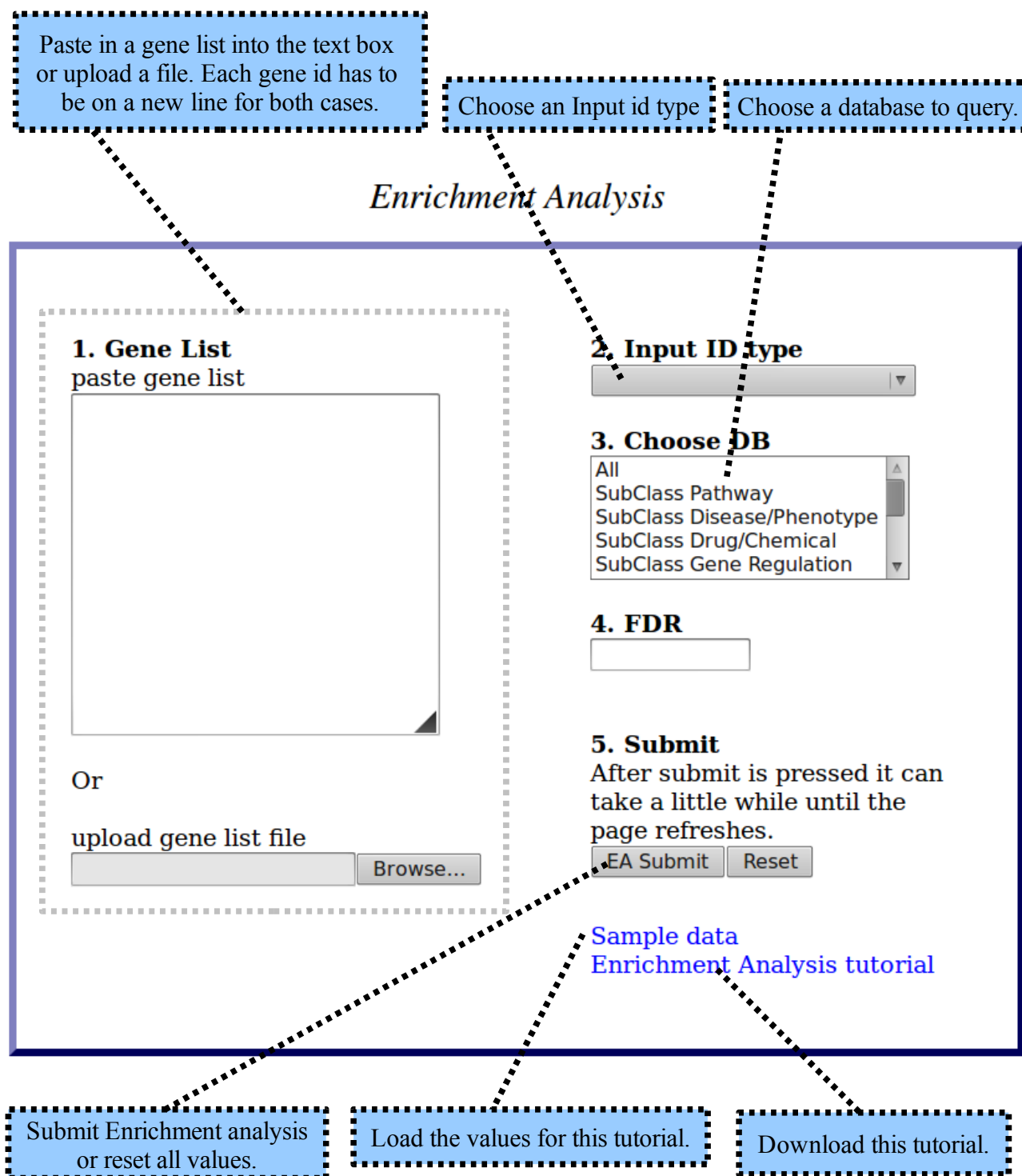


Fig. 1: Short explanation of the interface.

## 1. Gene List

Paste in a gene list or upload a file containing a gene list. Each ID needs to be on a new line in both cases (Fig.2).

### *Enrichment Analysis*

**1. Gene List**  
paste gene list

100132417  
100288675  
10170  
10346  
10384  
10561  
10673  
10800  
10906  
10964  
11262  
11274  
11277  
113730  
114908

Or

upload gene list file

Browse...

**2. Input ID type**

**3. Choose DB**

All  
SubClass Pathway  
SubClass Disease/Phenotype  
SubClass Drug/Chemical  
SubClass Gene Regulation

**4. FDR**

**5. Submit**  
After submit is pressed it can take a little while until the page refreshes.

EA Submit Reset

[Sample data](#)  
[Enrichment Analysis tutorial](#)

Fig. 2: Paste in a gene list or press “Browse” to upload a file.

## 2. Input ID Type

Choose the input ID type corresponding to the gene IDs you imported in step 1. For more information on identifiers, please consult the help page. For this tutorial we will select “Gene ID Human” (Fig.3).

### *Enrichment Analysis*

The screenshot displays the 'Enrichment Analysis' web interface. It is divided into several sections:

- 1. Gene List**: A text area labeled 'paste gene list' containing a list of gene IDs: 100132417, 100288675, 10170, 10346, 10384, 10561, 10673, 10800, 10906, 10964, 11262, 11274, 11277, 113730, and 114908.
- Or**: A section for uploading a file, with a text input field and a 'Browse...' button.
- 2. Input ID type**: A dropdown menu currently showing 'Gene ID Human'. This section is highlighted with a red dotted circle.
- 3. Choose DB**: A dropdown menu with options: All, SubClass Pathway, SubClass Disease/Phenotype, SubClass Drug/Chemical, and SubClass Gene Regulation.
- 4. FDR**: A text input field for entering the False Discovery Rate.
- 5. Submit**: A section with the text 'After submit is pressed it can take a little while until the page refreshes.' and two buttons: 'EA Submit' and 'Reset'.

At the bottom right, there are two blue links: 'Sample data' and 'Enrichment Analysis tutorial'.

Fig. 3: Choose the input ID type corresponding to the imported gene ids.

### 3. Choose DB

Specify which database to query (Fig.4). For more information on each of the databases please consult the help page and the “Source DB page. To select more than one press Ctrl and click on the databases to select or deselect them.

## *Enrichment Analysis*

The screenshot displays the 'Enrichment Analysis' web interface. It is divided into several sections:

- 1. Gene List**: A text area labeled 'paste gene list' containing a list of gene IDs: 100132417, 100288675, 10170, 10346, 10384, 10561, 10673, 10800, 10906, 10964, 11262, 11274, 11277, 113730, and 114908. Below this is an 'Or' section with an 'upload gene list file' text area and a 'Browse...' button.
- 2. Input ID type**: A dropdown menu currently set to 'Gene ID Human'.
- 3. Choose DB**: A multi-select dropdown menu with options: 'All', 'SubClass Pathway', 'SubClass Disease/Phenotype', 'SubClass Drug/Chemical', and 'SubClass Gene Regulation'. The last three options are highlighted with a red dashed oval.
- 4. FDR**: An empty text input field.
- 5. Submit**: A section with the text 'After submit is pressed it can take a little while until the page refreshes.' and two buttons: 'EA Submit' and 'Reset'.

At the bottom right, there are two blue links: 'Sample data' and 'Enrichment Analysis tutorial'.

**Fig. 4:** Select a set of databases to query.

## 4. FDR

Specify a value between 0 and 1 to filter the data according to the FDR (false discovery rate). For more information, please consult the help page. For this dataset we type in “0.00001” (Fig.5).

### *Enrichment Analysis*

**1. Gene List**  
paste gene list

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10561  
10673  
10800  
10906  
10964  
11262  
11274  
11277  
113730  
114908

Or

upload gene list file

Browse...

**2. Input ID type**  
Gene ID Human

**3. Choose DB**  
All  
SubClass Pathway  
SubClass Disease/Phenotype  
SubClass Drug/Chemical  
SubClass Gene Regulation

**4. FDR**  
0.00001

**5. Submit**  
After submit is pressed it can take a little while until the page refreshes.

EA Submit Reset

[Sample data](#)  
[Enrichment Analysis tutorial](#)

**Fig. 5: Specify FDR (False Discovery Rate)**

## **5. Submit**

Press the “EA Submit” button to submit this data to genesetdb (Fig.5).

## **6. Reset**

To reset all values press the “Reset” button next to the “EA Submit” button.

## **7. Load Enrichment analysis test data 1**

You can test if you did everything correctly by pressing this button (Fig. 1).

**If you have any questions or problems, please do not hesitate to contact us via**

**[bioinformatics@auckland.ac.nz](mailto:bioinformatics@auckland.ac.nz)**

**Happy analyzing!**