

User Manual of IBDExplore October 2, 2023

IBDExplore is an interactive visualization web-tool with data summary, differential expressed gene analysis, gene signature analysis, enrichment analysis, and cell deconvolution analysis based on 34 IBD bulk-transcriptomic datasets.

Users begin IBDExplore by querying the datasets based on the disease, tissue, cell type, treatment and timepoint. Each attribute includes multiple options and users can select multiple options in each attribute (red box in Figure 1). The filtered data list will be shown in the right panel with detailed data information (blue box in Figure 1). Users can also search the keyword in the search box (black box in Figure 1). Clicking one dataset in the table can start the analysis page.

IBDExplore

Datasets

Developed by Immunology Computational Biology - GRC

The options presented below can be used to filter for datasets that match the specified criteria

Select diseases of interest

UC CD

Select tissues of interest

Colon

Select cell types of interest

Select treatments of interest

Infliximab

Select timepoints of interest

W0

To explore a dataset of interest, select the corresponding row from the table below.

Showing 1 to 4 of 4 entries

Search:

dataset_acc	title	disease	organism	experiment_type	source	cell_type	treat
GSE73661	The effect of vedolizumab and inflix...	UC;nonIBD	Human	Microarray	Colon		Vedo
GSE16879	Mucosal expression profiling in patie...	CD;UC;Healthy	Human	Microarray	Colon;ileum		Inflix
GSE23597	Expression data from colonic biopsy s...	UC	Human	Microarray	Colon		Inflix
GSE12251	A Predictive Response Signature to In...	UC	Human	Microarray	Colon		Inflix

Figure 1. Data query based on multiple attributes.

Data analysis page includes five tabs with five functions: Dataset Description, DGE Viewer, Signature Viewer, Enrichment Analysis, and Cell Deconvolution. “Data Description” tab includes the detailed information of the selected data set and PCA plot (Figure 2). Users can select the variable to color the dots in the PCA plot or select one or multiple conditions from one selected variable to filter the dots in the PCA plot (red box in Figure 2). Users can also select the PCs from PC1 to PC5 for x-axis and y-axis of PCA plot. Finally, users can plot the boxplot to compare the x-axis PCs of different conditions colored in the PCA plot (blue box).

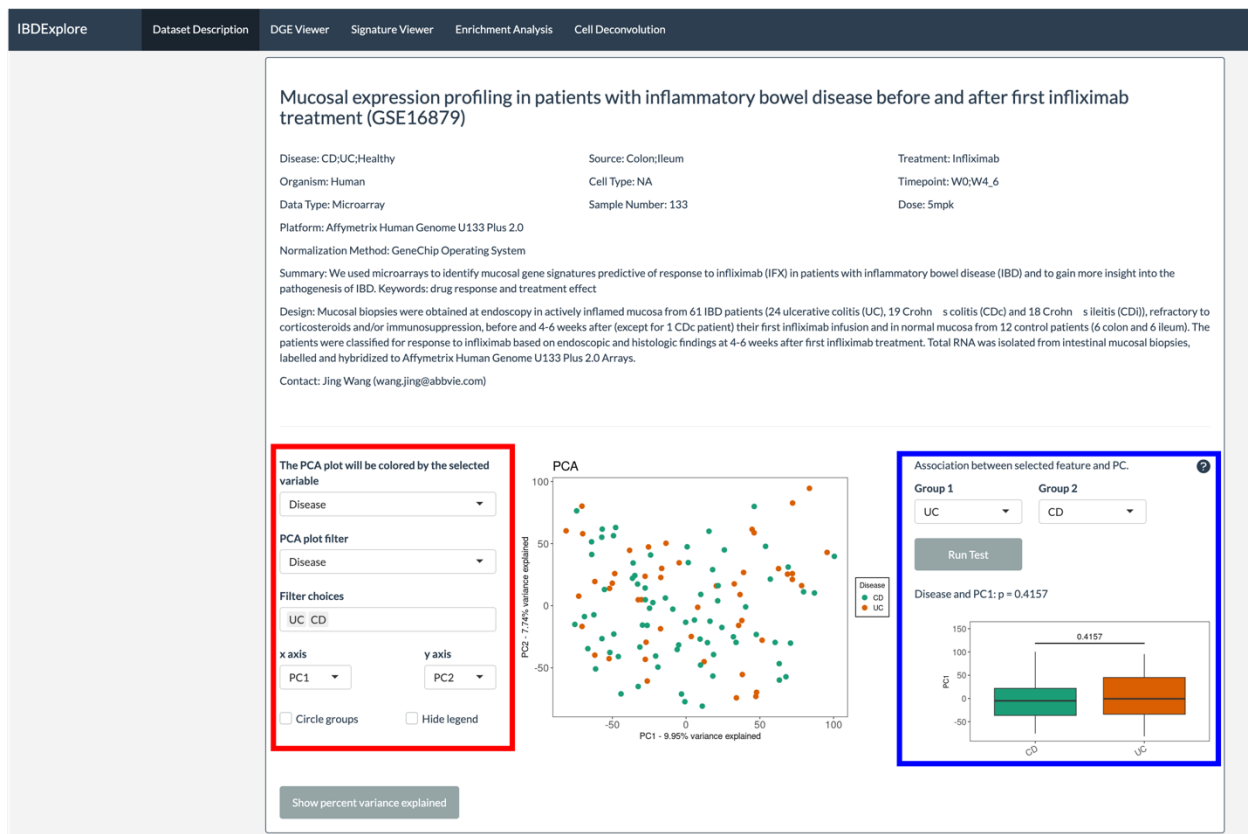


Figure 2. Data description tab

In the “DGE Viewer” tab, users need to select a comparison (red box in Figure 3) and input multiple genes (blue box). Then, the statistic values of these genes in the selected comparison will be shown in the table (orange box). A volcano plot will also be shown beside the table to highlight the significant genes based on defined threshold. Users can change the threshold or y-axis value by clicking the button on the top-left of the volcano plot (black box). Users can also select genes in the table to highlight them in the volcano plot and plot the boxplots based on the selected comparison.

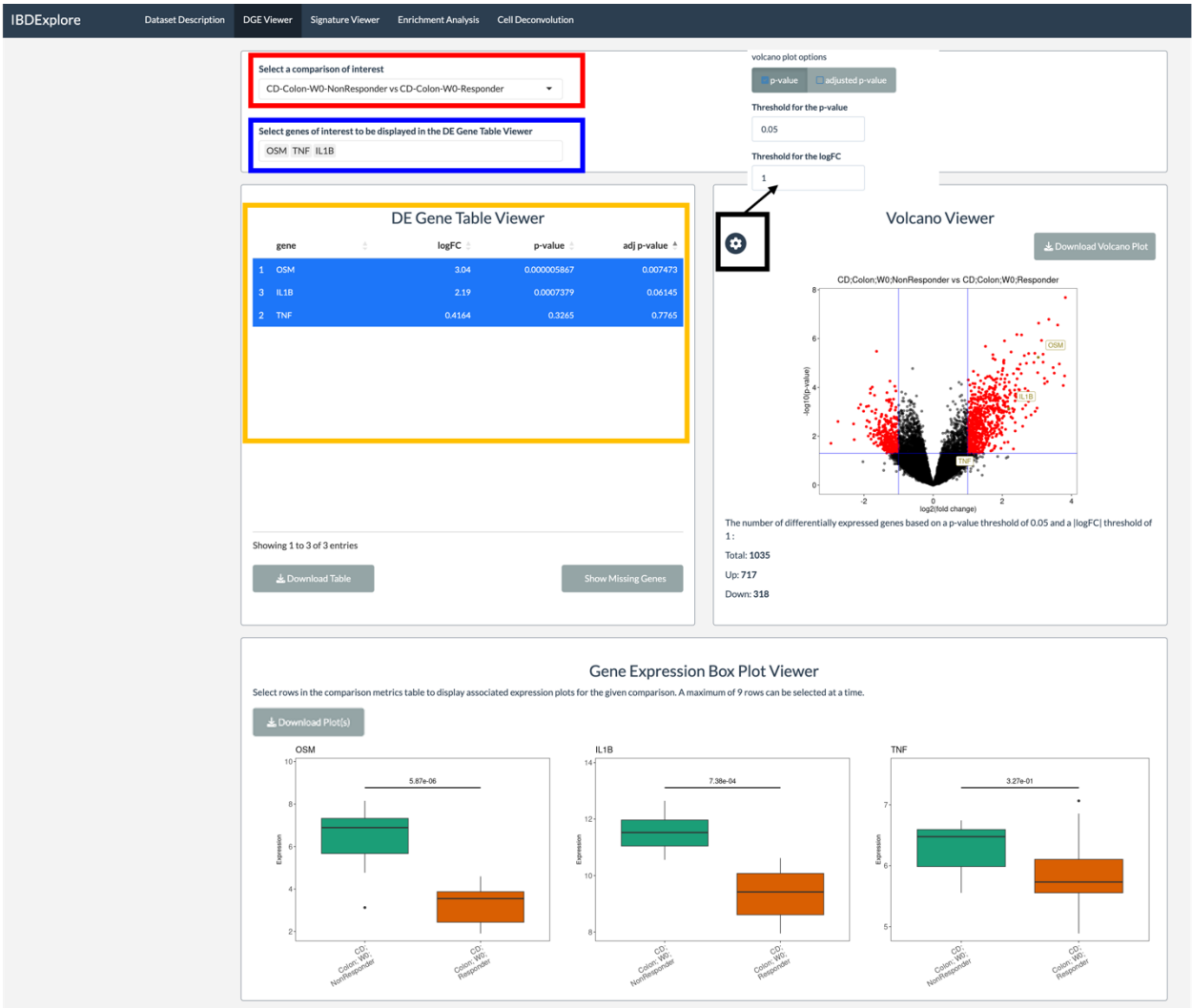


Figure 3. DGE Viewer tab

In the “Signature Viewer” tab, users can select multiple comparisons (red box in Figure 4) and input multiple genes (one gene each line, orange box). Clicking the “Generate Plot(s)” button, multiple boxplots related to the selected comparisons will be plotted (black box). The y-axis of each boxplot is the mean expression of the input genes. Users can also select the conditions included in the dataset (blue box) and the mean expression of each condition will be plotted together in one boxplot (yellow box). The details of all comparisons related to the selected conditions will be shown in the table.

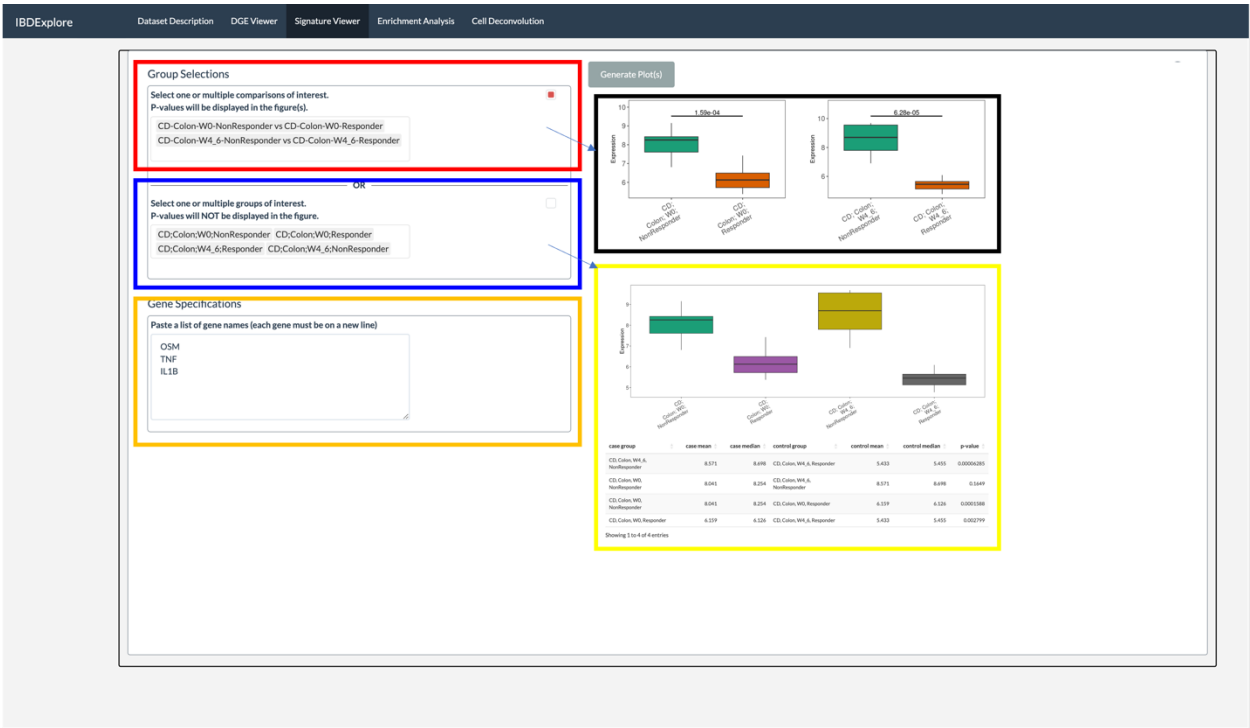


Figure 4. Signature Viewer tab

IBDExplore integrates WebGestaltR package (<https://cran.r-project.org/web/packages/WebGestaltR/index.html>) to perform the enrichment analysis. Users need to select one method from ORA and GSEA (default is ORA, red box in Figure 5) and select one comparison (blue box). If users select ORA method, they need to input the threshold of p value and log fold change and the directionality (green box). After selecting the database from dropdown menu (black box) and clicking “Run ORA” button, IBDExplore will return a comprehensive report for the enrichment analysis. Details of the report can be found in <https://academic.oup.com/nar/article/47/W1/W199/5494758?login=true>.

IBDExplore
Dataset Description
DGE Viewer
Signature Viewer
Enrichment Analysis
Cell Deconvolution

Enrichment Analysis

ORA
GSEA

This enrichment analysis option uses WebGestalt to perform Over-Representation Analysis on the genes pertaining to the selected comparison.

Select a comparison of interest for the enrichment analysis
CD-Colon-W0-NonResponder vs CD-Colon-W0-Responder

p-value
adjusted p-value

p-value cutoff
0.05


logFC cutoff
1

up
down

Select a type of database (changing this selection will alter available options on the right)
pathway

Select a database to use
KEGG

Run ORA


WEB-based GENE SeT Analysis Toolkit
Translating gene lists into biological insights...

Summary

[Result Download](#)

Job summary

GO Slim summary for the user uploaded IDs

Enrichment Results

Redundancy reduction: ☒ All ☐ Affinity propagation ☐ Weighted set cover

Table
Bar chart
Volcano plot

FDR ≤ 0.05
FDR > 0.05

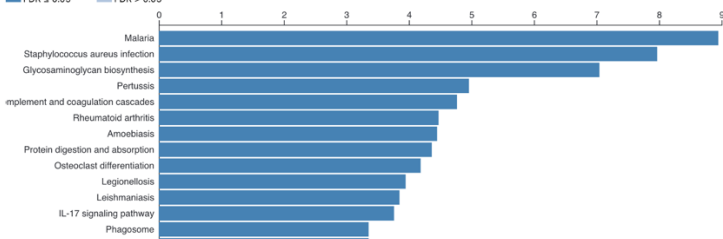


Figure 5. Enrichment Analysis tab

In the “Cell Deconvolution” tab, users should click the “Perform Cell Deconvolution” button first (red box in Figure 6) and then select the comparison and threshold of p-value and minimum cell fraction (blue box). Then, the boxplots related to the significant cell types will be plotted. X-axis of each boxplot is the conditions related to the selected comparison and y-axis is the cell fractions. Detailed of cell deconvolution algorithm can be found in the IBDTransDB paper.

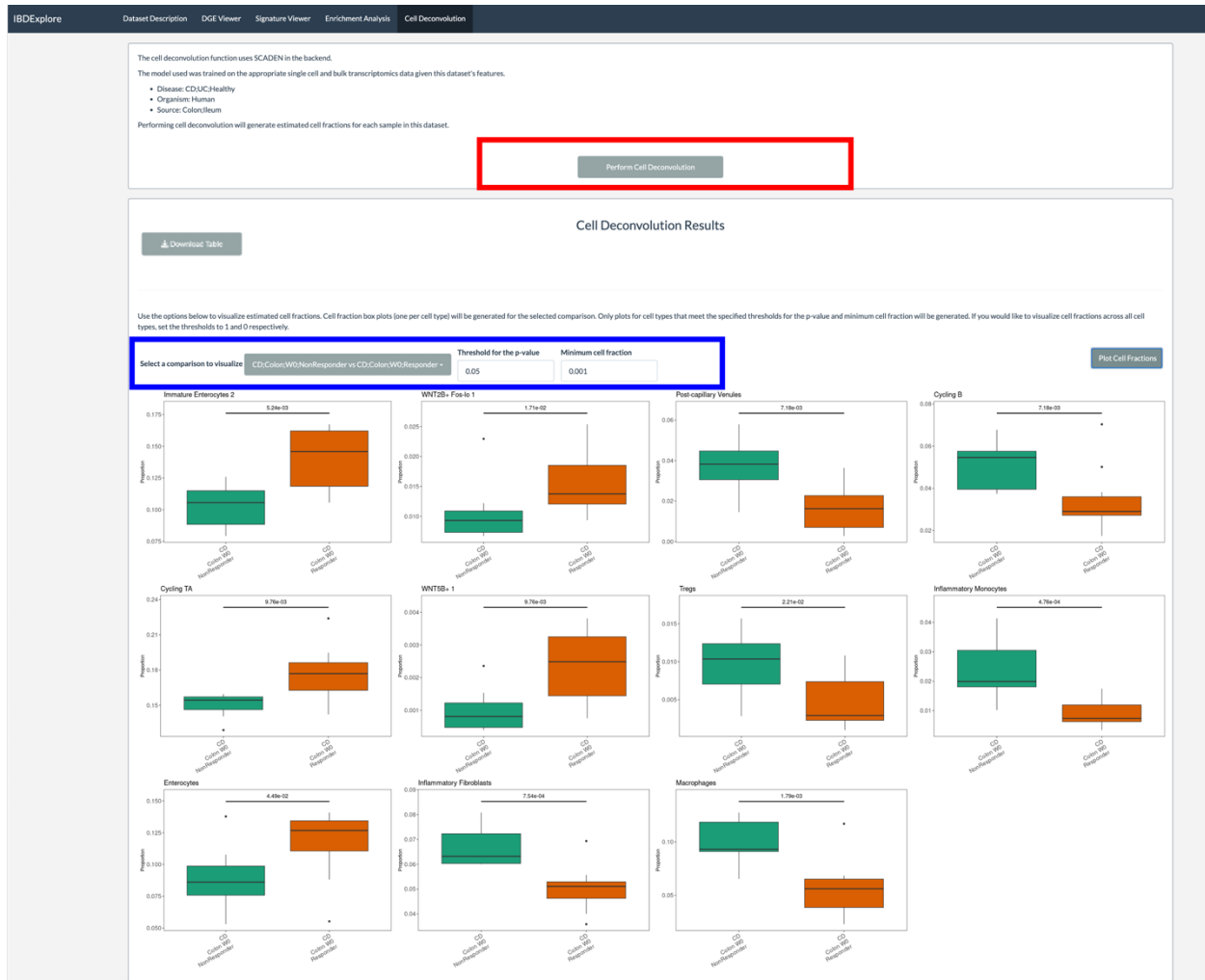


Figure 6. Cell Deconvolution tab