User Manual of IBDIntegrate
October 2, 2023

IBDIntegrate is a data integration tool based on input gene/pathway list and selected data and comparisons.

Users began IBDIntegrate by selecting GENE or PATHWAY (redbox in Figure 1). If selecting GENE, two options for inputting interesting gene list are available (blue box). “Option 1” is to select the existing gene list from our database (we current provide three lists: chemokine, interleukin and TNF super family gene list). “Option 2” is to upload a txt file with gene symbol in each line. Then, users can query the datasets based on the disease, tissue, cell type, treatment and timepoint (green box). After clicking “CONFIRM SELECTIONS” button (black box), the selected datasets and all comparisons will be shown in the right panel (grey and darkblue boxes). Users can refine the datasets based on attributes and all comparisons related to the selected datasets. Finally, users should click “Run Integration” button to perform the data integration (brown box).

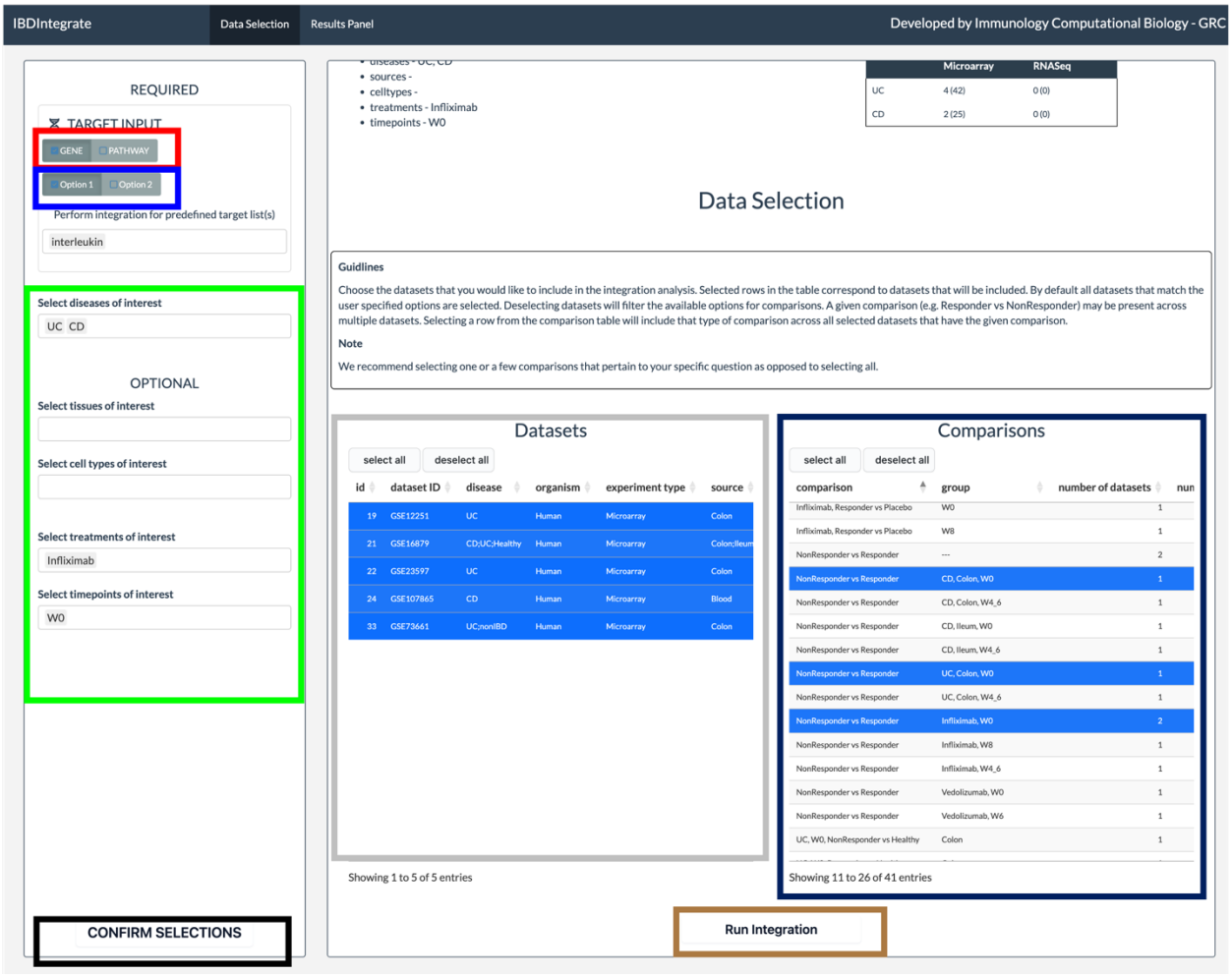

Figure 1. Data and comparison selection.

The integration results will be shown in the Results Panel. The gene list will be ranked based on the meta p values. Clicking on the triangle button in each row will show the details of this gene in all datasets.

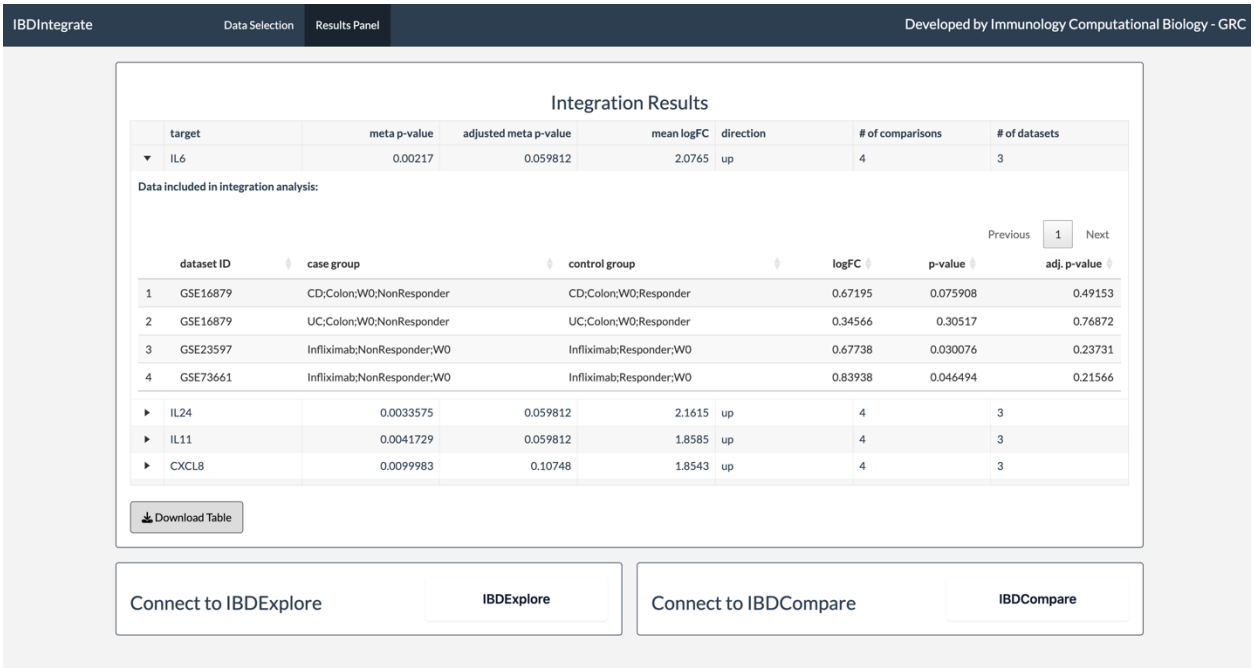

Figure 2. Results panel for data integration.