CellPhoneDB

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CellPhoneDB addresses the challenges of studying cell-cell communication in scRNA-seq and spatial data. It allows researchers to move beyond just measuring gene expression and delve into the complicated cellular communication world. By analyzing the scRNA-seq or spatial data through the lens of CellPhoneDB, researchers can identify potential signaling pathways and communication networks between different cell types within the sample. Partek Flo wrapped the statistical analysis pipeline (method 2) from CellPhoneDB v5 [1][2] for this purpose.

How to use CellPhoneDB in Partek Flow

Invoke the **CellPhoneDB** task in Partek Flow from a normalized counts data node using the *Exploratory analysis* section (Figure 1). We recommend running CellPhoneDB on the log normalized data directly.

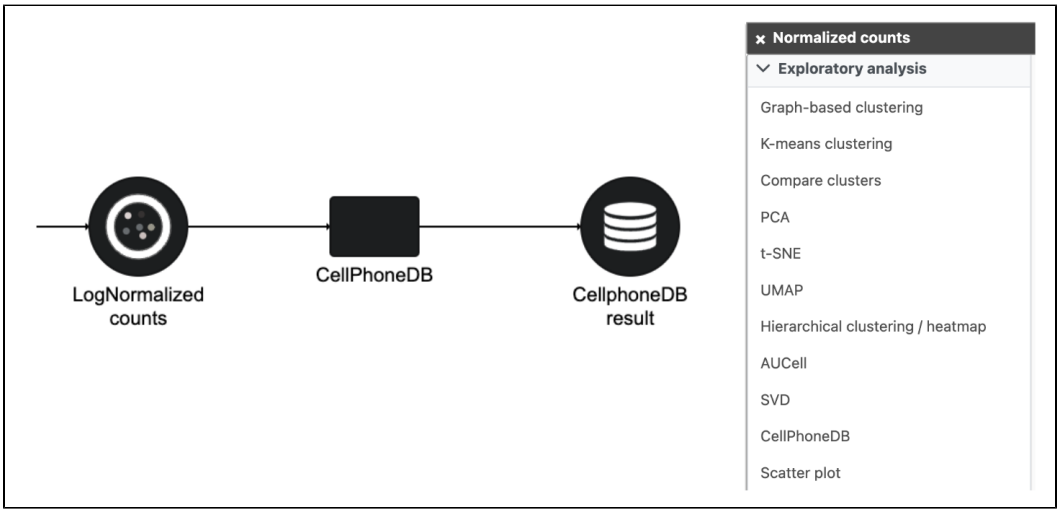

Figure 6. CellPhoneDB task in Flow.

To run **CellPhoneDB** task,

- Click a **Normalized counts** data node
- Click the **Exploratory analysis** section in the toolbox
- Click **CellPhoneDB**

The GUI is simple and easy to understand. For each option, the grey colored description explains more details (Figure 2). If the dataset working on is single cell RNA-Seq, it doesn't need the Micro environment file. However, if it is a spatial data, most likely you would like to provide the Micro environment file because of its spatial contents. By default, the value of 0.10 will be used as threshold to select which cells are used for the analysis in the cluster. However, the number could be adjusted manually or typed in directly. Simply click the **Finish** button if you want to run the task as default.

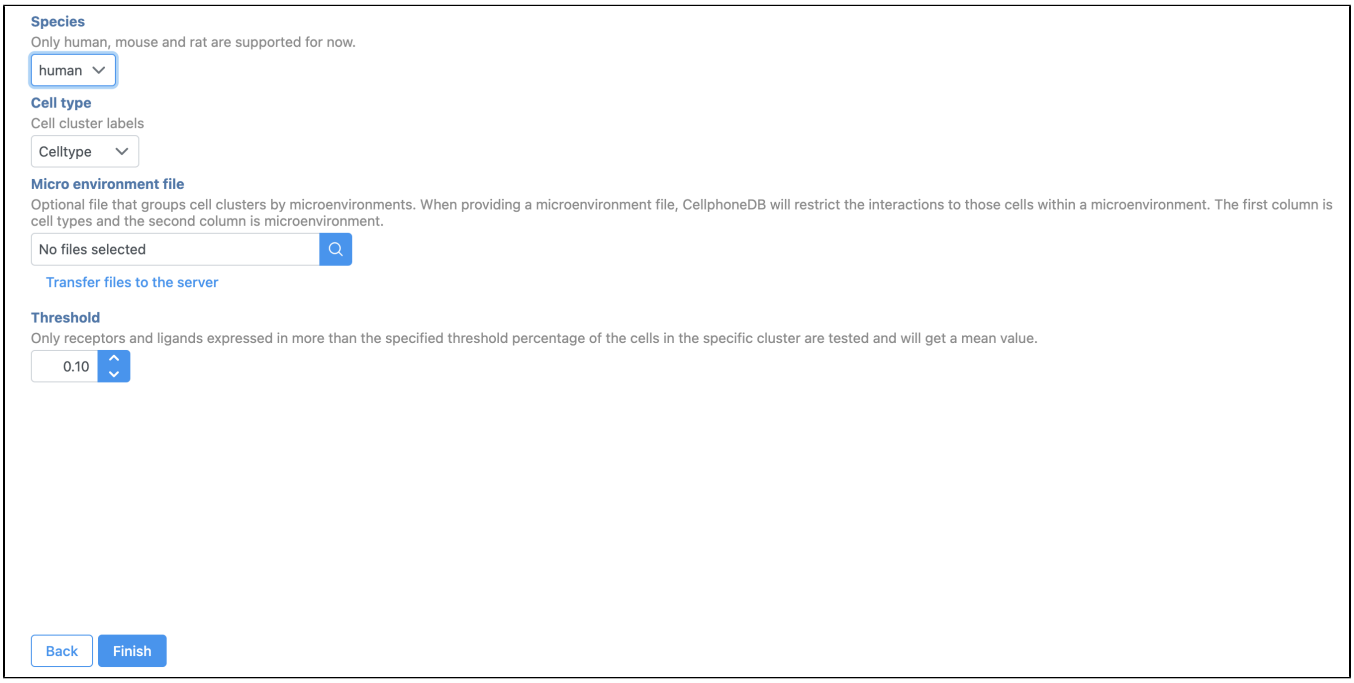

Figure 7. Interface of CellPhoneDB task in Partek Flow.

Double click the CellPhoneDB result data node will open the task report in Data Viewer. It is a heatmap that summarizes how many significant interactions identified in the cell type pairs (Figure 3).

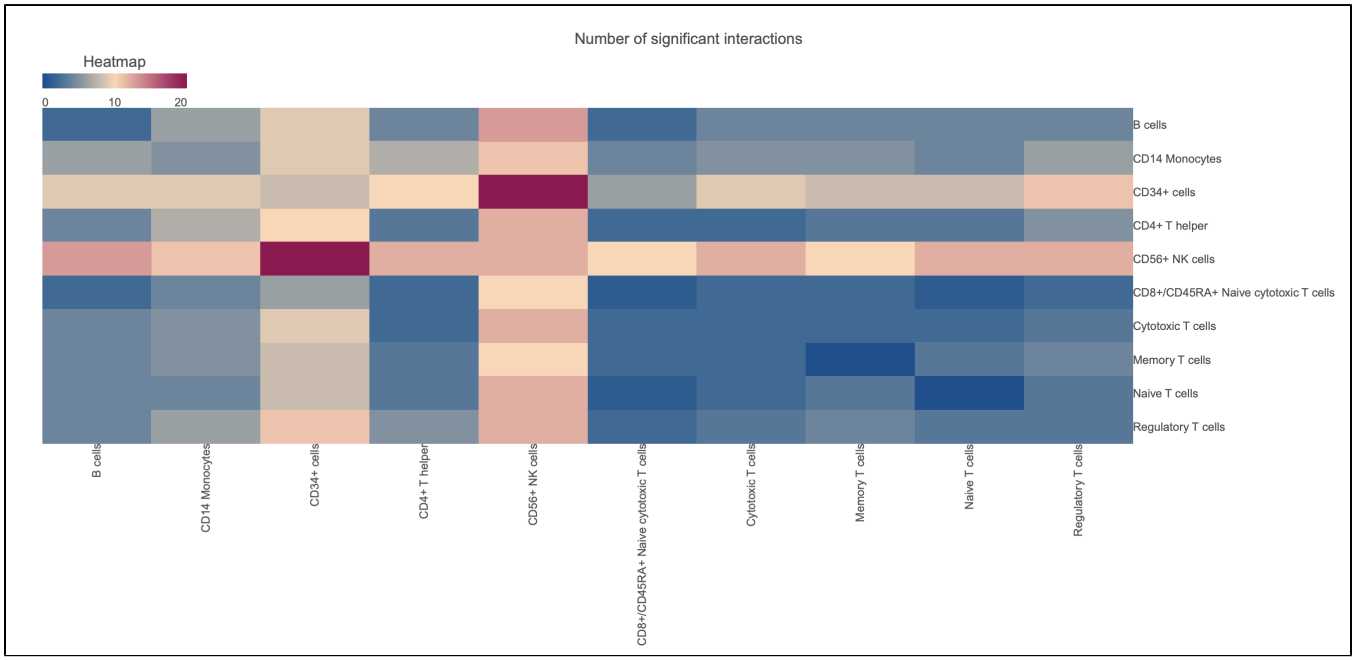

Figure 8. CellPhoneDB task report in Data Viewer.

To explore more, the task of **Explore CellPhoneDB results** allows users to filter CellPhoneDB results by specifying the cell type pairs and genes of interest. After clicking the CellPhoneDB data node (Figure 4a), one will find there's only task triggered under Exploratory analysis menu (Figure 4b). Its GUI is also simple and easy to understand (Figure 4c). Genes of interest are data dependent and usually come from the published results of similar studies or the differential gene analysis between different conditions (eg, cancer patient vs healthy controls). Once set up, click the **Finish** button to submit the job.

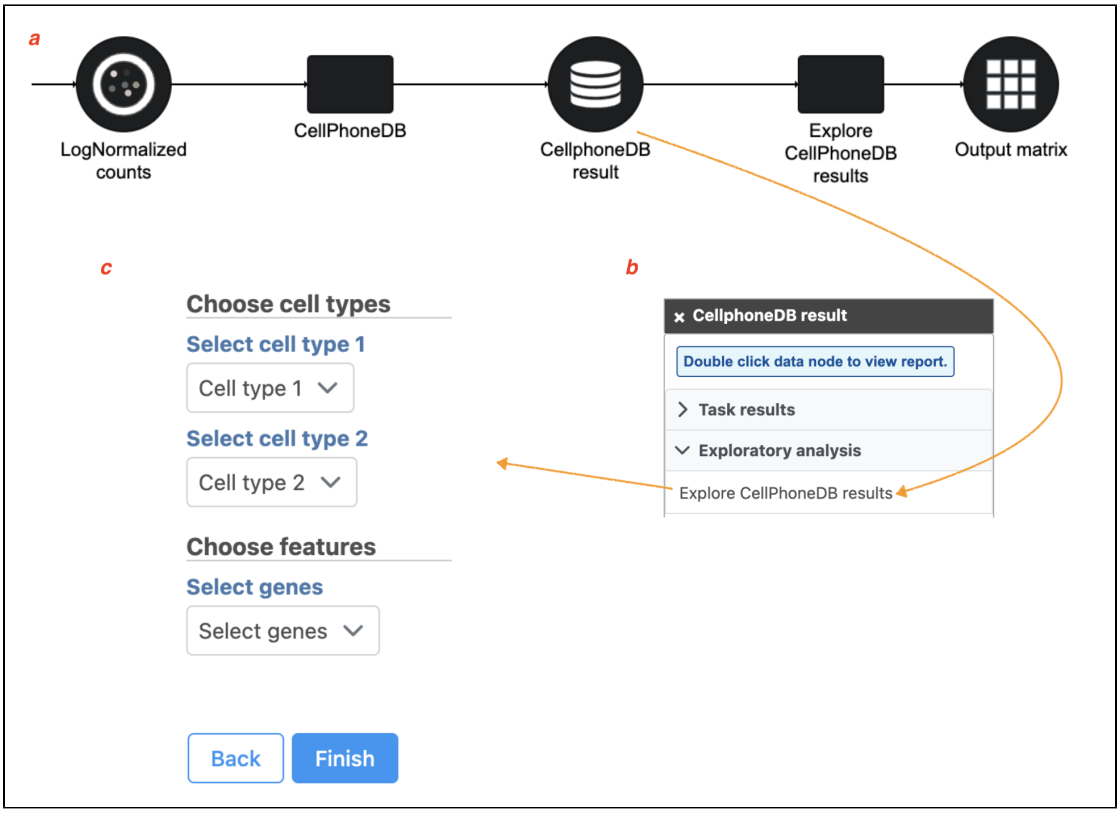

Figure 9. Task of Explore CellPhoneDB results in Partek Flow.

Double click the Output matrix data node will open the task report in Data Viewer. It is another variant of heatmap that displays how genes of your interest interact in the defined cell type pairs (Figure 5). The exampled plot also indicates the data are from two environments. For instructions on setting up the Micro environment file for your spatial study, refer to Figure 2. CellPhoneDB analysis classifies signaling pathways for genes of interest. These classifications are then used to annotate the heatmap within the task report.

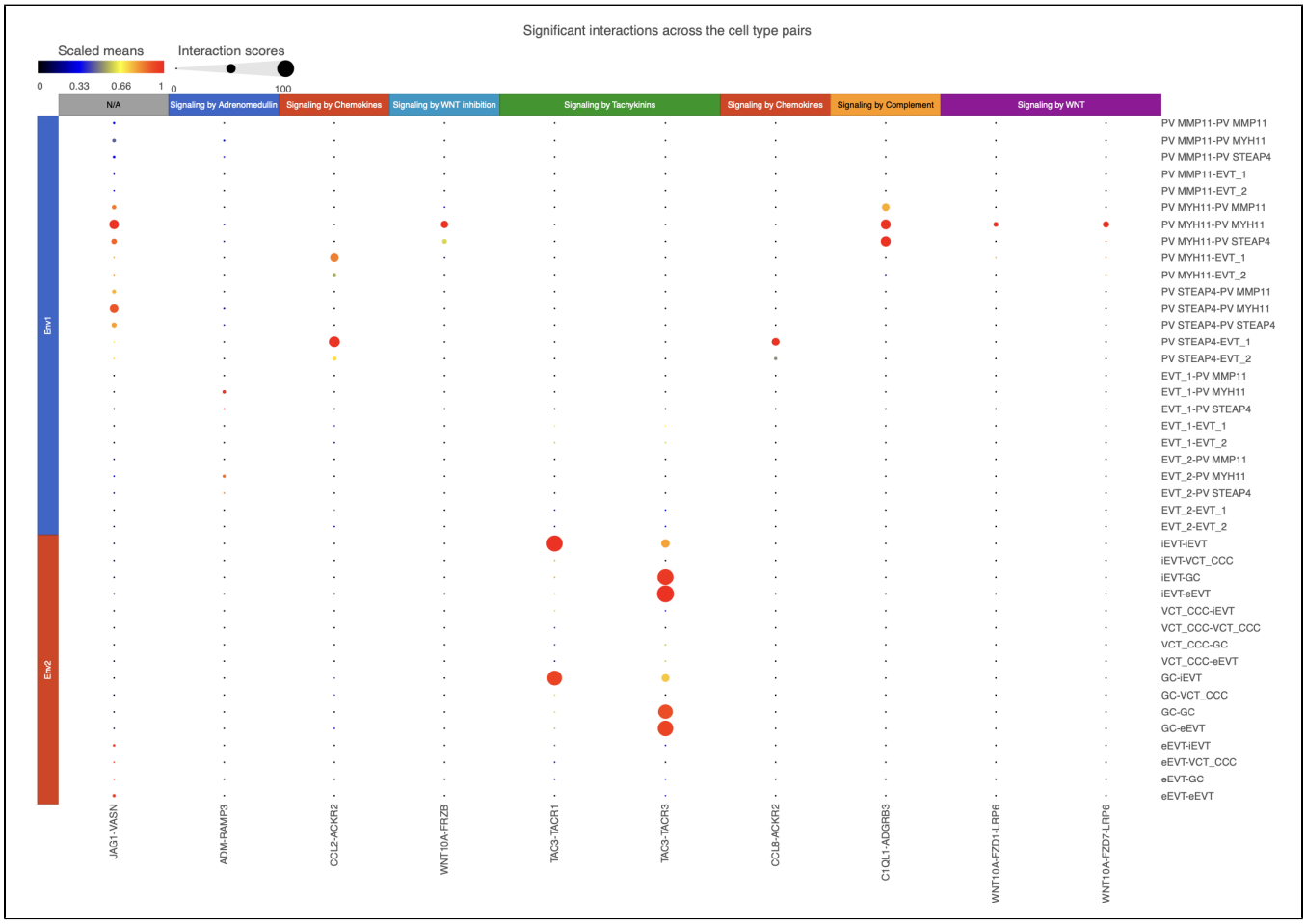

Figure 10. Task report of Explore CellPhoneDB results in Data Viewer.

Why are the values of clusterA-clusterB different to the values of clusterB-clusterA?

It is important to note that the interactions are not symmetric. The authors state that, "Partner A expression is considered for the first cluster/cell type (clusterA), and partner B expression is considered on the second cluster/cell type (clusterB). Thus, *IL12-IL12 receptor* for clusterA-clusterB (i.e. the receptor is in clusterB) is not the same as *IL-12-IL-12 receptor* for clusterB-clusterA (i.e. the receptor is in clusterA), and will have different values." [3][4]

Where do the interactions come from?

The interactions come from the CellphoneDB database. It is manually curated repository using reviewed molecular interactions with demonstrated evidence for a role in cellular communication. [5]

References

1. *Troule, etc (2023)*. CellPhoneDB v5: Inferring cell-cell communication from single cell multiomics data. https://arxiv.org/pdf/2311.04567.pdf
2. https://github.com/ventolab/CellphoneDB
3. https://github.com/ventolab/CellphoneDB/blob/master/docs/RESULTS-DOCUMENTATION.md
4. https://cellphonedb.readthedocs.io/en/latest/RESULTS-DOCUMENTATION.html#why-values-of-clustera-clusterb-are-different-to-the-values-of-clusterb-clustera
5. https://github.com/ventolab/cellphonedb-data

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.