



HUMAN CELL ATLAS LATIN AMERICA

Questionnaire for Cell-Cell Communication Activities

This document is designed to be used together with the example jupyter notebooks available in:

<https://github.com/HCA-LatAm/Workshop-2021/blob/main/Cell-Cell-Communication/>

Ligand-receptor pairs (step 3 of the notebook CellChat-SingleDataset)

1. What elements or dataframes are in the object CellChatDB (as slots)? What information do they contain?
2. How many types of interactions (annotation column) are present in the list of ligand-receptor pairs? What do they represent?
3. List the top-10 signaling pathways with the highest number of ligand-receptor pairs. How many ligand-receptor pairs compose each of these pathways?

Cell-Cell Communication

Analysis of a single dataset

1. After running the function computeCommunProb (in step 5 of the notebook CellChat-SingleDataset), where can I find the p-values for each ligand-receptor pair given the interacting cells?
2. What are the top-10 interactions with lowest p-values?
3. Where can I find the communication scores computed with the function computeCommunProb?
4. What is the interaction with highest probability?
5. Using CellChat allows a smoothing approach of the gene expression values (in step 5 of the notebook CellChat-SingleDataset). Is there any difference in the significant ligand-receptor pairs computed after calculating the communication scores with and without the smoothing function?
6. An overall interaction score can be computed (function aggregateNet in CellChat). CellChat reports two different overall scores, counts and weights. What is the difference between these two scores?
7. List the top-5 pairs of interacting cells with the highest counts and highest weights.

8. Plot information about your favorite signaling pathway. If you don't have one, use the one associated with the ligand-receptor pair with the highest probability.

Comparison analysis of multiple datasets

1. After merging CellChat objects from independent runs on separate samples/conditions and running the respective analyses in the notebook CellChat-MultipleDatasets; which slots in the merged object allow us to obtain information about the comparison between conditions?
2. What is the main increase and decrease in the overall interactions?
3. What pathways are mostly associated to one condition and to the other?