

Project 4

Measuring the specificity of immune-cell cytokine signaling

Data overview

Cytokines are signaling molecules secreted and sensed by cells, including immune cells, which enables dynamic intercellular communication. ImmuneXpresso is an online resource that uses a text-mining engine to automatically infer directional immune-cell-cytokine interactions from PubMed abstracts [1].

From the main webpage (<http://immuneexpresso.org>), by clicking on the “Search immuneXpresso” button without specifying any search term, it is possible to access all immune-cell-cytokine interactions in once. Indeed, this will open a window named “Interactions”, containing all results. Using the “Export” button, results can be downloaded as a .csv file describing which cell types affect (e.g. secrete) or are affected by specific cytokines. The file contains info like the cell type (“Cell Ontology Label” column), cytokine name (“Cytokine”), actor/direction (“Actor”) and effect of the interaction (“Action Sentiment”).

Analysis to be performed

Consider only the following cell types:

- CD8-positive, alpha-beta T cell;
- CD4-positive, alpha-beta T cell;
- B cell;
- regulatory T cell;
- conventional dendritic cell;
- macrophage;
- T cell;
- monocyte;
- neutrophil;
- fibroblast.

For each cell type separately, compute:

- The number of *unique* cytokines with a *positive* interaction with that cell type, where the “Actor” is the *cytokine* (i.e. the cytokines affect the cell);
- The number of *unique* cytokines with a *positive* interaction with that cell type, where the “Actor” is the *cell* (i.e. the cell affects/secretates the cytokine).

Compute the same statistics, separately, also for *negative* and *unknown* effects.

Represent each of these six statistics with a barplot showing the differences between the ten cell types of interest.

Discuss the results putting in light which cell types affects/secretes more/fewer types of cytokines, and which ones are affected by more/fewer types of cytokines.

Report

The analysis above should be described in a short report that will be evaluated and considered for the final grade. The report should:

- Contain the **code** implemented to run the analysis above, together with the **results** (as tables, plots, or just numbers reported within the text) and their **description/discussion**.
- Be at **maximum 6 pages** long.
- Be saved in a Word doc named "**Surname_Name_Project4.doc**".
- Be sent by e-mail to Dr. Finotello not later than **June 03, 2019**, using "**RProject4_2019**" as e-mail object.

References

- [1] Kveler K, Starosvetsky E, Ziv-Kenet A, Kalugny Y, Gorelik Y, Shalev-Malul G, Aizenbud-Reshef N, Dubovik T, Briller M, Campbell J, Rieckmann JC, Asbeh N, Rimar D, Meissner F, Wiser J, Shen-Orr SS. ***Immune-centric network of cytokines and cells in disease context identified by computational mining of PubMed***. Nat Biotechnol. 2018 Aug;36(7):651-659. doi: 10.1038/nbt.4152. Epub 2018 Jun 18.