

Talkmine, a workflow for the prediction of the interactions between secretome and surfaceome in the dialogue between cellular types

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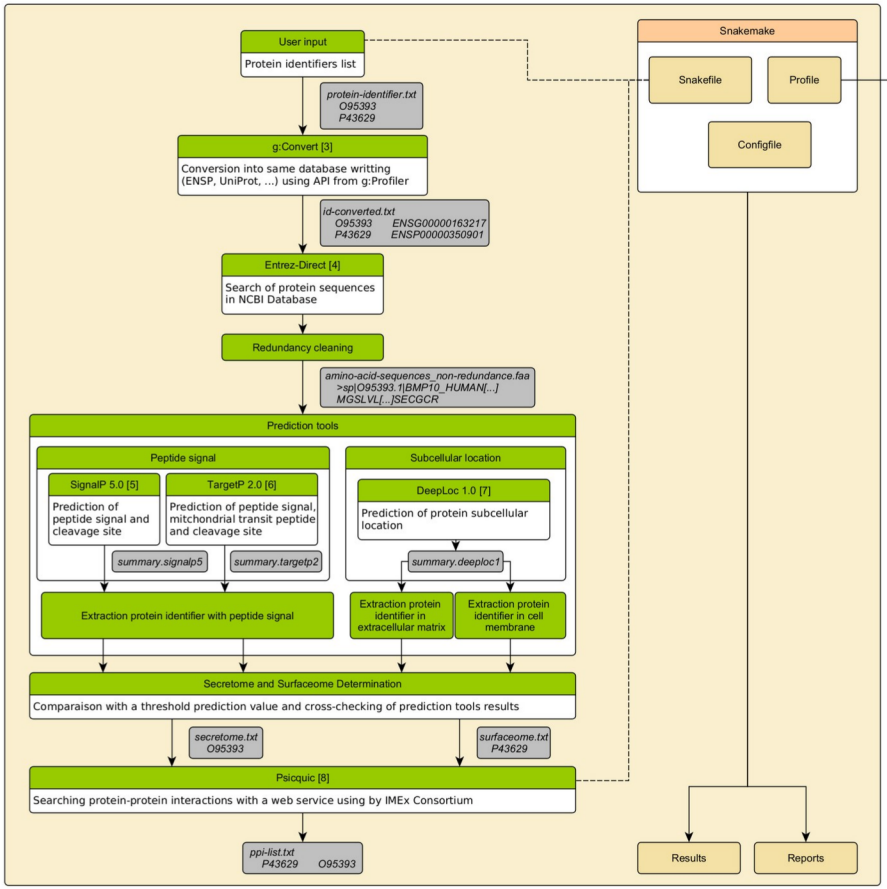
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Talkmine, a workflow for the prediction of the interactions between secretome and surfaceome in the dialogue between cellular types

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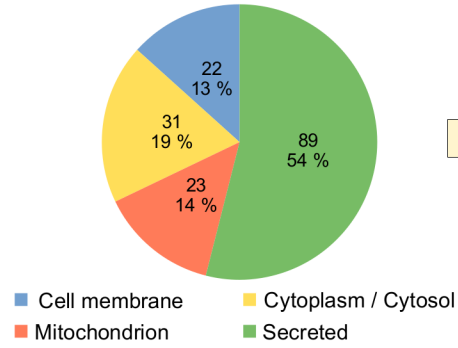
The prediction of the **protein-protein interactions** is studied in different domains, for example for their roles in the interplay between cellular types or tissues[1]. In particular, the interactions between **surfaceome** and **secretome** may strongly improved the understanding of **cellular crosstalk**. This project aims to develop a **Snakemake-based workflow**[2] named Talkmine for the identification of molecular dialogue between two biologic tissues resulting from protein-protein interactions.



The workflow Talkmine is developed to predict the interactions between the proteins from the secretome and the surfaceome. This work was initiated to be applied to *Bos taurus* to determine the interactions between muscle and fat tissue but it is possible to apply it to other tissues and to application fields such as biomedical or food research.

To test the generation of the secretome and surfaceome files : 165 UniProt identifiers

- 133 proteins from ProteINSIDE[9] dataset test (134 after update)
- 10 GPI-anchored proteins
- 10 proteins with an α-helical transmembrane domain
- 5 proteins with a β-barrel transmembrane domain
- 6 unconventionally secreted protein (including one located in the cell membrane)



Distribution of the dataset test within the subcellular compartments.
These distributions were established from UniProt data recorded on May 25th, 2021.

Talkmine

secretome.txt : 62 UniProt and Refseq identifiers
surfaceome.txt : 11 UniProt and Refseq identifiers

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