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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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1 Contexte

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.

2 Materials and Methods

First objective was to identify and test some opensource tools known to predict proteins that belong to secretome or surfaceome. Publically available tools were classified according to three classes, i.e. peptide signal, subcellular location or topology prediction, and have been tested with a dataset of 164 UniProt protein entries whose subcellular location are known.

Secondly, we developed a workflow to connect the selected tools. In brief, user sends a gene or protein identifiers list to a python tool, g:Convert^[3] which converts identifiers to a same format, according to a defined database. Then, Entrez-Direct tool^[4] generates a multi-fasta file with all protein sequences listed in the NCBI database, injected to secretome and surfaceome tools. Finally, proteins tagged to secretome and surfaceome classes are send to PSICQUIC tool^[5], which determines the interactions between proteins from these two classes.

3 Results

The resulting protein-protein interactions prediction from Talkmine is available both in standard output and in flat file. The user has access to the list of protein-protein interactions between the two tissues but also to the intermediate results.

4 Conclusion and perspectives

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.

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