

Master project 2020-2021

Personal Information

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Project

Computational systems biology

Project Title:

Computational Prediction of Host-pathogen Protein-protein Interactions in Human

Keywords:

Microbiology, Protein-protein interactions, Machine learning, Biomedical databases

Summary:

Protein-protein interactions (PPIs) define the complexity of biological processes in healthy and disease states. Intra-species PPIs describe partially this complexity but symbiotic and pathogenic interactions contribute as well by either benefiting or harming the host. The study of inter-species PPIs are of special interest in the case of pathogens since knowledge extracted from these interactions can lead to new therapeutic targets to avoid their negative effects on the host. There exists an extensive collection of intra-species PPIs enabled by the rapid development of high-throughput experimental technologies. However, experimental identification of inter-species interactions is not simple and computational prediction becomes then necessary (Cuesta-Astroz et al 2018). For instance, we proposed a homology-based prediction method to obtain human-parasite PPIs in 15 parasitic species (Cuesta-Astroz and Santos et al 2019). Additionally, this method incorporated biological context relevant in the parasites' life cycles to obtain accurate spatially-resolved interactions. Here, we want to implement a method that benefits from features derived from intra-species interactions to predict inter-species interactions focusing on human-pathogen interactions. The vast amount of intra-species interactions compiled in publicly available databases can be used to train sequence-based classification algorithms that can then be tested in both intra- and inter-species interactions also available in several resources. Furthermore, this method can be improved by annotating the predicted interactions with known biological context such as infection, survival and pathogenic mechanisms. This project will be carried out in close collaboration with Dr. Yesid Cuesta-Astroz from the University of Antioquia and the Colombian Institute of Tropical Medicine (Medellin, Colombia).

References:

Computational and Experimental Approaches to Predict Host-Parasite Protein-Protein Interactions. Cuesta-Astroz Y, Oliveira G
Analysis of Predicted Host-Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism Cuesta-Astroz Y, Santos A, Oliveira G, and Jensen LJ Comparing two deep learning sequence-based models for protein-protein interaction prediction Richoux F, Servantie C, Borès C, and Télatchéa S

Expected skills::

Python, Machine learning, Fast.ai, PyTorch

Possibility of funding::

No

Possible continuity with PhD: :

To be discussed
