Evolutive constraints for wiring and characterizing human subproteomes

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Motivation

Interest in the 'proteome wiring' of model organisms has been motivation to numerous large scale efforts to map protein-protein interactions. However, it is unclear if the integration of existing experimental and computational protein interaction maps into one 'unique hypothetical and averaged' human interactome can be of biological relevance. The two main concerns are data quality, which remains to be critically assessed, but more importantly, the existing variety of tissue and temporally specific interactomes in human, also referred to as subinteractomes.

Here, we focus on the attempt to wire well studied decomposable proteomes or subproteomes, which underly different biological processes, by using biologically relevant predictors in a statistical modeling framework. Particular attention is given to the evaluation of the impact that evolutionary constraints have posed on interacting proteins in the different subinteractomes.

Methods

Based on the assumption that interacting pairs of proteins should co-evolve to maintain functional and structural complementarity, we set up predictors based on the correlation between the similarity of the phylogenetic trees, and on the co-occurrence of specific domains of interacting proteins.

We employed data sets from manually curated databases and text mining approaches as goldstandard references in the context of statistical modeling-machine learning frameworks.

Results

Preliminary results indicate that the evolutionary constraints operating on the interacting proteins specifically characterize the different subinteractomes. For example, the SH2/SH3-ome and other domain-specific subinteractomes, the plasma proteome, show different degree of co-evolution. As a consequence, the predictive power of the descriptors based on the evolutionary constraints shows biological context dependence.

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