Machine learning-based methods for protein-protein interaction prediction

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Abstract

The long awaited challenge of post-genomic ear and systems biology research is computational prediction of protein-protein interactions that ultimately lead to protein functions prediction. The main motivation is i) how protein complexes with known 3D structure be used to identify and classify protein binding sites? ii) how can we infer knowledge from these classification such that protein-protein interaction can be predicted for protein with unknown structure? In this pilot project, we have done a) critical survey in this domain – background study, computational approaches for finding protein-protein interactions, protein features extraction, feature representation, training a classifiers and evaluation, protein interaction databases and their classifications, software tools, benchmark datasets, performance metrics, and identification of open research challenges in this area, and b) application of mRNA expression for finding protein-protein interactions based on different machine learning techniques.
