

A survey of current trends in computational predictions of protein-protein interactions

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Main work

- In this review, we focus on computational methods for PPIs detection and show recent advancements in this critical areas from three aspects: PPIs data source, protein feature representation and prediction strategy. At the end of the paper, we also discuss the prospect of deep learning technology in computational proteomics and the opportunities of quantum mechanics in this field.

Survey different method in predict PPIs

Table Comparison of several state-of-the-art PPIs prediction approaches

Methods	Type of information	Characters
Sprinzak and Margali	experimental binding data structural domains	good interpretability but poor generalization ability
Bock and Gough	sequence information physicochemical properties	good interpretability but poor accuracy
Martin et al	experimental data sequence information	does not require physio-chemical information prior knowledge of domains
Ben and Noble	various information including homologous interactions, GO annotations, protein sequence et.	can integrate kinds of knowledge, but not very efficient.
Shen et al	only protein primary sequence	good generalization ability does not require any knowledge
Guo et al	protein primary sequence physicochemical properties	good performance but sensitive to data sources
Chou et al	protein primary sequence physicochemical properties	does not require prior knowledge but sensitive to physicochemical properties
You et al	only protein primary sequence	excellent performance but not very efficient.