

NPF□Network propagation for protein function prediction

CURRENT STATUS: UNDER REVIEW

BMC Bioinformatics  BMC Series

bihai zhao
Changsha University

✉ bihaizhao@163.com *Corresponding Author*
ORCID: <https://orcid.org/0000-0003-0870-7468>

Zhihong Zhang
Changsha uiversity

Meiping Jiang
Changsha University

Sai Hu
Changsha University

Yingchun Luo
Changsha University

Lei Wang
changsha university

DOI:

10.21203/rs.3.rs-16452/v1

SUBJECT AREAS

Bioinformatics

KEYWORDS

Network propagation, Protein-protein interaction, prediction of protein function Background

Abstract

Background: The accurate annotation of protein functions is of great significance in elucidating the phenomena of life, disease treatment and new drug development. Various methods have been developed to facilitate the prediction of functions by combining protein interaction networks (PINs) with multi-omics data. However, how to make full use of multiple biological data to improve the performance of functions annotation is still a dilemma.

Results: We presented NPF (Network Propagation for Functions prediction), an integrative protein function predicting framework assisted by network propagation and functional module detection, for discovering interacting partners with similar functions to target proteins. NPF leverages knowledge of the protein interaction network architecture and multi-omics data, such as domain annotation and protein complex information, to augment protein-protein functional similarity in a propagation manner. We have verified the great potential of NPF for accurately inferring protein functions. Comprehensive evaluation of NPF indicates that NPF archived higher performance than competing methods in terms of leave-one-out cross-validation and ten-fold cross validation.

Conclusions: We demonstrated that network propagation combined with multi-omics data can not only discover more partners with similar function, but also effectively free from the constraints of the "small-world" feature of protein interaction networks. We conclude that the performance of function prediction depends greatly on whether we can extract and exploit proper functional similarity information from protein correlations.

Full-text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed.

However, the manuscript can be downloaded and accessed as a PDF.

Tables

Due to technical limitations, tables are only available as a download in the supplemental files section.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

Tables.pdf

