A COMPREHENSIVE COMPARISON OF METHODS FOR KINASE ACTIVITY INFERENCE

INTRODUCTION

In recent years, several methods have been developed to infer the activity of kinases from phosphoproteomic data. These methods rely on a fixed set of prior knowledge interactions and vary in the complexity of their algorithms. So far, a systematic comparison and evaluation is still missing.

KINASE PERTURBATION DATASETS

We estimated kinase activities for 103 manually curated perturbation experiments (Hernandez-Armenta, 2017).

In these experiments, 30 different kinases were perturbed, supposedly leading to an increase or decrease in activity.

SYSTEMATIC COMPARISON & EVALUATION

We compared the inferred activities by calculating the mean Pearson correlation between method and prior knowledge resource (left) and then evaluated the methods in terms of identifying the perturbed kinase in each experiment (right).

CONCLUSION & OUTLOOK

Overall, we observe that the prior knowledge resource has a greater impact on the inferred kinase activities, compared to the computational algorithms. For the future, we aim to incorporate the following points in assessing kinase activity inference methods:

- Inclusion of further computational methods/prior knowledge resources
- Combination of prior knowledge resources
- Extending the benchmark metric to validate the methods for more kinases

ACKNOWLEDGMENT

We would like to thank our collaborators Eric Jaeihng and Bing Zhang from the Baylor College of Medicine, with whom we are currently working on the extension of the benchmark metric. This work is financed by the LiSyM-Cancer research core supported by the German Federal Ministry of Education and Research.

METHOD OVERVIEW

The methods can be divided into two components:

A prior knowledge resource and a computational algorithm, which can be flexibly combined.

Prior knowledge resources

Computational algorithms

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