Inferring signalling cascades from phosphoproteomic data
How to model changes in intracellular signalling networks

Identifying putative perturbed kinases
Footprint-based activity estimation

A footprint of a kinase is the collection of downstream phosphorylation sites regulated by it. These reflect the regulatory state of a kinase and can be used to robustly infer its activity. Prior knowledge is required to link phosphorylation sites to the respective kinase.

For the estimation of kinase activities, existing computational approaches summarise changes in abundance of phosphorylation sites into an activity score for each kinase. This allows the identification of deregulated kinases upon perturbation.

Case study: Elucidation of Metformin-Signalling in Heterogenous Colorectal Cancer Cells

Experimental setup
Kinase activity estimation
Input selection
AMPK-focused network contextualisation

12 colon cancer cell lines were treated with Metformin and phosphoproteomic data was generated

Differences between cell lines in response to metformin induced AMPK activation and downstream signal propagation

How to run PHONEMeS 2.0 with your data

All our tools are freely available on GitHub https://github.com/saezlab or bioconductor. We also provide a tutorial on how to run PHONEMeS: https://github.com/saezlab/PHONEMeS/blob/master/vignettes/tutorial.md. Feel free to contact us for support: sophia.mueller-dott@uni-heidelberg.de

Acknowledgment

We would like to thank our collaborators Barbara Salowitsch and Yanheg Liu from the Yale School of Medicine. This work is financed by the LiSyM-Cancer and the SIGNIT-CARE research cores supported by the German Federal Ministry of Education and Research.

References

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