

Interaction Analyzer

Publication

Characterizing activating and inhibiting protein interactions based on a genome-wide siRNA cellular phenotyping screen

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Characterizing the activating and inhibiting effect of protein-protein interactions (PPI) is fundamental to gain insight into the complex signaling system of a human cell. A plethora of methods has been suggested to infer PPI from data, but none of them is able to characterize the effect of this interaction. We presented a novel computational development that employs mitotic phenotypes of a genome-wide RNAi knockdown screen and enables identifying the activating and inhibiting effects of PPIs (Suratane^e et al., submitted). This webpage contains the accompanying software for this study.

System requirements

- Linux
- R package (version 2.15.0 or higher) with installed libraries e1071, MASS and ROCR.
- GNU Linear Programming Kit (GLPK)

Downloads

- [Short manual](#)
- [InteractionAnalyzer.tar.gz](#)