Lu et al. Cilia 2015, 4(Suppl 1):P90
http://www.ciliajournal.com/content/4/S1/P90

Cilia

POSTER PRESENTATION Open Access

From proteomic data to networks: statistics and methods reveal ciliary protein interaction landscape

Q Lu[1*], K Koutroumpas[2], K Boldt[3], J Van Reeuwijk[4], N Katsanis[5], F Képès[2], R Roepman[4], M Ueffing[3], RB Russell[1]

From Cilia 2014 - Second International Conference
Paris, France. 18-21 November 2014

Objective:

The assembly of protein interaction networks (PIN) is an important step to understand the biological function of proteins. Affinity purification coupled to mass spectrometry (AP-MS) has become the technique of choice for the assembly and analysis of PINs. However, most current studies, especially in human cells, are focused on specific biological systems (*e.g.* the cilium) resulting in datasets of a small to intermediate scale. In such cases, methods that developed for genome-scale datasets are of limited utility. We propose here a framework that is specifically designed for the analysis of incomplete proteomic data focused on ciliary function and ciliopathies.

Methods:

The proposed framework consists of three steps. Initially, a revised Socio-Affinity algorithm [1] is applied to quantify the pairwise protein interaction affinities. After filtering hits from noise the constructed PIN is mined for protein clusters using a novel graph-clustering algorithm. Finally, Principle Component Analysis (PCA) is used to assess the quality of detected complexes.

Results:

We applied our algorithm to data from more than 400 TAP-MS experiments, using over 200 ciliary genes as baits. Weighted PINs consisting of low, medium and high confidence interactions were extracted from the data, and for each network a set of protein complexes is reported. Several known ciliary complexes have been successfully identified, while novel ciliary complexes are predicted.

Conclusion:

We demonstrate a computational framework that can deal with context specific proteomic data. Application to experimental data focusing on cilia provides a ciliary protein interaction landscape with the ciliary biological processes/functions in the centre.

Equal contribution by Q. Lu and K. Koutroumpas

Authors' details
[1]Cell Networks, Bioquant, University of Heidelberg, Heidelberg, Germany. [2]Institute of Systems and Synthetic Biology, Genopole, CNRS, Université d'Evry, Evry, France. [3]Division of Experimental Ophthalmology and Medical Proteome Center, Eberhard-Karls Universität Tübingen, Tübingen, Germany. [4]Department of Human Genetics and Radboud Institute for Molecular Life Sciences, Radboud University Medical Center, Nijmegen, The Netherlands. [5]Center for Human Disease Modeling, Department of Cell Biology, Duke University, Durham, NC, USA.

Published: 13 July 2015

Reference

1. Gavin AC, Aloy P, Grandi P, Krause R, Boesche M, Marzioch M, *et al*: **Proteome survey reveals modularity of the yeast cell machinery.** *Nature* 2006, **440(7084)**:631-636.

doi:10.1186/2046-2530-4-S1-P90
Cite this article as: Lu *et al.*: From proteomic data to networks: statistics and methods reveal ciliary protein interaction landscape. *Cilia* 2015 **4** (Suppl 1):P90.

[1]Cell Networks, Bioquant, University of Heidelberg, Heidelberg, Germany
Full list of author information is available at the end of the article