Comparative Interactomics

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Motivation

Motivation:Similar to what has been achieved by comparing genome structures and protein sequences, we hope to obtain valuable information about systems evolution by comparing the organization of interaction networks stored in protein interaction databases and by analyzing their variation and conservation. Equally significantly we can learn whether and how to extend the network information obtained experimentally in well-characterized model systems to different organisms.

Methods

Methods: MINT database(http://mint.bio.uniroma2.it/mint/) contains interactions described either in high throughput experiments (on yeast , Drosophila and nematode) or in low throughput experiments , involving about 17000 proteins. Approximately 50% of these have been mapped to the orthology groups created by using the Inparanoid algorithm (Remm, M., 2001). This mapping allowed us to compare the different interactomes stored in MINT on the basis of the orthology relationship and to generate the putative human interactome Homomint, implemented as a web available tool at http://mint.bio.uniroma2.it/mint/ with the aim to extend protein protein interactions experimentally verified in models organisms, to the orthologous proteins in Homo Sapiens. Moreover, graph theoretic algorithms implemented in the R package (http://www.r-project.org/, http://www.bioconductor.org/) provided us tools to perform a topological analysis of both the experimentally verified and putative protein interaction networks stored in the MINT database

Results

Results: From our analysis we conclude that, despite the recent completion of several high throughput experiments aimed at the description of complete interactomes, the coverage and quality of the available interaction information are not yet sufficient to draw any biologically meaningful conclusion from the comparison of different interactomes. Thus, the transfer of network information obtained from simpler organisms to evolutionary distant species should be carried out and considered with caution. By using smaller higher-confidence datasets, a larger fraction of interactions is shown to be conserved; this suggests that, with the development of more accurate experimental and informatic approaches, we will soon be in the position to study the evolution of protein networks.

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