Comparative analysis of protein interaction networks
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ABSTRACT
Recent advances in proteomics and computational biology have lead to a flood of protein interaction data and resulting interaction networks (e.g. (Gavin et al., 2002)). Here I first analyse the status and quality of parts lists (genes and proteins), then comparatively assess large-scale protein interaction data (von Mering et al., 2002) and finally try to identify biological meaningful units (e.g. pathways, cellular processes) within interaction networks that are derived from the conservation of gene neighborhood (Snel et al., 2002). Possible extensions of gene neighborhood analysis to eukaryotes (von Mering and Bork, 2002) will be discussed.

REFERENCES