



Comparative analysis of protein interaction networks

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Received on April 8, 2002; accepted on June 15, 2002

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

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