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Locating overlapping dense subgraphs in gene (protein) association networks and predicting novel protein functional groups among these subgraphs GERGELY PALLA, (a) Biological Physics Research Group of HAS and (b) Department of Biological Physics, Eotvos University, IMRE DERENYI, (b), ILLES J. FARKAS, (a,b), TAMAS VICSEK, (a,b) — Most tasks in a cell are performed not by individual proteins, but by functional groups of proteins (either physically interacting with each other or associated in other ways). In gene (protein) association networks these groups show up as sets of densely connected nodes. In the yeast, Saccharomyces cerevisiae, known physically interacting groups of proteins (called protein complexes) strongly overlap: the total number of proteins contained by these complexes by far underestimates the sum of their sizes (2750 vs. 8932). Thus, most functional groups of proteins, both physically interacting and other, are likely to share many of their members with other groups. However, current algorithms searching for dense groups of nodes in networks usually exclude overlaps. With the aim to discover both novel functions of individual proteins and novel protein functional groups we combine in protein association networks (i) a search for overlapping dense subgraphs based on the Clique Percolation Method (CPM) (Palla, G., et.al. Nature 435, 814-818 (2005), http://angel.elte.hu/clustering), which explicitly allows for overlaps among the groups, and (ii) a verification and characterization of the identified groups of nodes (proteins) with the help of standard annotation databases listing known functions.

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