The rapid development of the whole-genome sequencing methods and their reducing cost resulted in a huge number of sequenced genomes. Developing reliable methods for in-silico annotation of the expeditiously growing number of sequenced genomes is the next challenge of modern biology. We described a graph-theoretical approach for function prediction from the protein-protein interaction networks and outlined its strengths and weaknesses. We illustrate the principles of this approach on selected algorithms based on different ideas and provide their comparison and evaluation.