Title: A review of software for predicting gene function

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Abstract: A rich resource of information on functional genomics data can be applied to annotating the thousands of unknown gene functions that can be retrieved from most sequenced. High-throughput sequencing can lead to increased understanding of proteins and genes. We can infer networks of functional couplings from direct and indirect interactions. The development of gene function prediction is one of the major recent advances in the bioinformatics fields. These methods explore genomic context by major recent advances in the bioinformatics fields rather than by sequence alignment. This paper reviews software related to predicting gene function. Most of these programs are freely available online. The advantages and disadvantages of each program are stated clearly in order for the reader to understand them in a simple way. Web links to the software are provided as well.