



Bioinformatics for Plant genome

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Abstract: Large amounts of genome sequence data are available and much more will become available in the near future. A DNA sequence alone has, however, limited use. Genome annotation is required to assign biological interpretation to the DNA sequence. The aim of genome annotation is to describe the biological function of every single nucleotide during the life span of an organism. This requires the help of bioinformatics. Bioinformatics is a multidisciplinary approach that combines several areas of expertise in the automated analysis of bio-molecular data. To achieve the goal of proper annotation of a genome, close cooperation between bioinformaticians and biologists is required at several levels. Communication in bioinformatics for genome annotation is a major challenge on several levels: communication between computers and communication between researchers are both at stake, as well as the communication between computers and human beings. The global bioinformatics community is moving towards a web infrastructure. The second major issue in bioinformatics and genome annotation is the quality of annotation data. Most annotation depends in some way or another on previous annotations. Obviously the quality of such prediction relies on the quality of the underlying data. The issue of error propagation is an important issue in the field of genome annotation and needs much future attention.

Key words: bioinformatics; genom ; DNA sequence

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