



III Brazilian Workshop on Bioinformatics

Brasília, Brazil, October 20-22, 2004

The year 2004 marked the celebration of the 50th anniversary of Watson and Crick's elucidation of the DNA double helix structure, a real mark in the history of science. Since that time auspicious moment in 1954, there were several key advances in biology that contributed to the beginning of the genomics era, marked by the sequencing of a complete genome for the first time in 1995, for the bacterium *Haemophilus influenzae*. Since then, there has been an explosion of information; currently a new organism is sequenced nearly every week. At this time, there are 1543 genome projects, among which 285 have complete genomes, 740 are ongoing prokaryotic genome projects and 517 are ongoing eukaryotic genomes (<http://www.genome-online.org/>).

As a consequence of the tremendous amount of information generated by these projects, modern research requires much more sophisticated algorithms, software tools for data storage and retrieval, data integration, information extraction, exploratory data analysis, and discovery. Such algorithms and tools must be able to deal with heterogeneous biological data sources, databases, knowledge bases, and ontologies.

Bioinformatics encompasses the development and use of tools and techniques for genetics and molecular biology, as well as computer science. The development of new algorithms to process information to understand life through molecular interactions strictly defines bioinformatics. Bioinformatics and computational biology are also a means to expand our knowledge of genomic-based information and diseases, link genotypes to phenotypes, unravel polygenic causalities, and identify new therapeutic targets. Design and development of such tools is a major goal of bioinformatics/computational molecular biology.

The III Brazilian Workshop on Bioinformatics (WOB 2004) provided a forum for discussions of emerging bioinformatics concepts and methods, concomitant with recent advances in theory and knowledge across the biological studies. The emphasis of this meeting was algorithms and tools that address important problems in molecular biology, genomics and proteomics that are computationally efficient, could be implemented or tested and that could provide new biological results and insights. Original research on computational aspects of computational biology and genome informatics was also included.

Thirty-five full papers were submitted to WOB 2004 and were revised by a team of 65 researchers. Twelve of these were accepted for technical sessions in the Workshop. This col-

lection of papers, put together through an initiative of the editors of *Genetics and Molecular Research* and the WOB 2004 organizing committee, is a natural follow-up of the III Brazilian Workshop on Bioinformatics. The papers deal with innovative features of Molecular Sequence Analysis, Motifs, Genetic Algorithms, Functional Genomics Annotation, Protein Structure, Molecular Evolution and Phylogenetics, and Software Tools for Computational Molecular Biology, considered important for the understanding of the workings of free-living organisms.

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