

Preface

The sequencing of the genomes of humans and other organisms is inspiring the development of new statistical and bioinformatics tools that we hope can modify the current understanding of human diseases and therapies. As our knowledge about the human genome increases so does our belief that to fully grasp the mechanisms of diseases we need to understand their genetic basis and the proteomics behind them and to integrate the knowledge generated in the laboratory in clinical settings. The new genetic and proteomic data has brought forth the possibility of developing new targets and therapies based on these findings, of implementing newly developed preventive measures, and also of discovering new research approaches to old problems.

To fully enhance our understanding of disease processes, to develop more and better therapies to combat and cure diseases, and to develop strategies to prevent them, there is a need for synergy of the disciplines involved, medicine, molecular biology, biochemistry and computer science, leading to more recent fields such as bioinformatics and biomedical informatics.

The 6th International Symposium on Biological and Medical Data Analysis aimed to become a place where researchers involved in these diverse but increasingly complementary areas could meet to present and discuss their scientific results.

The papers in this volume discuss issues from statistical models to architectures and applications to bioinformatics and biomedicine. They cover both practical experience and novel research ideas and concepts.

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