
Preface

In recent years, there is a growing interest in applying mathematical theories and methods (algorithms, combinatorics, codes, etc.) to describe and analyse scientific regularities of massive, complex, and fast changing data produced via Next-Generation-Sequencing technology. Various algorithms and data structures were devised to efficiently solve bioinformatics problems concerning comparing, searching, analysing, storing, compressing, and modelling this kind of data. These sequences are characterised in being massive and high-repetitive collections of nucleotides or amino acid sequences plus some metadata like quality score values.

Following the success of the Royal Society meeting on the Storage and Indexing of Massive Data, held last year in Chicheley Hall, UK, this second meeting intended to gather international researchers mainly from the fields of bioinformatics, computer science, and mathematical as well as R&D industry fellows in order to present scientific papers or survey articles on the algorithmic advancements in Big Data technology.

In this edition, sponsored by the the Algorithms and Bioinformatics Group at the Informatics Department of King's College London, UK, and the Words and Automata Research Group at Mathematics and Informatics Department of University of Palermo, Italy, 9 original research papers have been accepted for presentation and an invited talk has been given by Prof Filippo Mignosi, dealing with new mathematical theories, methodologies, algorithms, and data structures for Big Data.

We thanks all the participants and also we wish to thank all the members of the Program Committee for their collaboration in the reviewing process of the papers, and the colleagues of the Organizing Committee for their resourceful cooperation.

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