Call for Papers
2nd International Conference on
Algorithms for Big Data
Palermo, Italy, 07-09 April 2014
http://algorithms-for-big-data.org/

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 intend 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. We invite submissions of unpublished original research articles dealing with new mathematical theories, methodologies, algorithms, and data structures for Big Data. Conference proceedings containing a short version of the papers will be published online by the CEUR-WS open-access publisher of the Technical University of Aachen (RWTH) and the full version of selected papers will be published in a special issue of Mathematics in Computer Science focusing on mathematical and computational aspects of molecular biology and genomics data to appears in August 2014.

Specific topics include, but are not limited to:

• Mathematical methods for sequence matching, sequence compression, and information retrieval
• Algorithms for sequence indexing, approximate indexing, and compressed indexing
• In place data structures, space conscious data structures, and external memory algorithms
• Mathematical results with applications in bioinformatics problems
• Combinatorial aspects of biological sequences and collections
• Algorithms and data structures for repetition discovery and motif recognition
• Mathematical methods for fragment assembly, reads reassembly, and genome alignment
• Mathematical methods for phylogenetic trees construction and comparison
• Combinatorial measures of sequence similarity

Important Dates

• Deadline for paper submission: 1 December 2013
• Notification of acceptance: 1 February 2014
• Final paper submission: 1 March 2014
• Proceedings publication: 7 April 2014
• Special Issue publication: Summer 2014
Programme Committee

- Anthony J. Cox, Illumina Cambridge Ltd., UK
- Maxime Crochemore, King’s College London, UK, and Université Paris-Est, France
- Raffaele Giancarlo, University of Palermo, Italy
- Roberto Grossi, University of Pisa, Italy
- Costas S. Iliopoulos, King’s College London, UK, and Curtin University, Australia (Chair)
- Juha Kärkkäinen, University of Helsinki, Finland
- Gregory Kucherov, CNRS and Université Paris-Est, France
- Alessio Langiu, King’s College London, UK, and University of Palermo, Italy (Co-Chair)
- Thierry Lecroq, Université de Rouen, France
- Moshe Lewenstein, Bar Ilan University, Israel
- Filippo Mignosi, University of L’Aquila, Italy
- Antonio Restivo, University of Palermo, Italy

Organising Committee

- Carl Barton, King’s College London, UK
- Alessio Langiu, King’s College London, UK, and University of Palermo, Italy
- Giovanna Rosone, University of Palermo, Italy

Proceeding Editors and Special Issue Guest Editors

Costas S. Iliopoulos, King’s College London, UK, and Curtin University, Australia
Alessio Langiu, King’s College London, UK, and University of Palermo, Italy

Submission Guidelines

Submitted (short) papers must contain an extended version within appendixes.

Short version must not exceed 6 single-spaced pages on A4 paper, including title, authors, affiliation, email addresses, abstract, images, and references. Accepted papers will be published in the conference proceedings and extended version will be considered for publication in the special issue of Mathematics in Computer Science. Author will be notified about the special issue together with the acceptance notification.

There are no page limits for extended versions and paper layout will need to be adapted to fit publisher rules. Authors must use single column page format, 11pt font size and reasonable margins. Referees will be provided for both the short and the extended version, so authors may feel free to leave any proof and auxiliary material into the extended version and to refer to that version.

Submission process is through the EasyChair conference system (for detailed instruction see the conference web site). Authors are encouraged to prepare submissions by using LaTeX. All submitted papers will be refereed by at least three reviews.

Conference Venue

The Conference will be held in Sala Gialla (Yellow Room) of Palazzo dei Normanni --- Piazza del Parlamento n.1, 90134 Palermo, Italy --- which is the house of Sicilian Regional Assembly. It is located in the historical centre of Palermo, Italy.