BITS 2016 Call for Abstracts

http://bits2016.bioinformatics.it/

Submissions are invited for poster and oral contributions to the **annual meeting of the Bioinformatics Italian Society (BITS)**, which will be held at the **Aula Magna of the University of Salerno, campus of Fisciano, on June 15-17, 2016.**

The following traditional topics are covered during the conference (but are not limited to):

- **Algorithms for Bioinformatics**
- **Biobanks**
- **Biological Databases**
- **Comparative Genomics**
- **Epigenetics**
- **Genomics**
- **Genomics of Disease**
- **Molecular Evolution**
- **Next Generation Sequencing**
- **Pharmacogenomics**
- **Protein structure and function**
- **Proteomics**
- **Systems Biology**
- **Transcriptomics**

In addition to the traditional panels, this year the Call includes topics for two **Special Sessions** proposed by members of the Society:

- **Big Data Management, Modeling and Computing**
- **Clinical bioinformatics: from computational models to clinical answers**

A detailed description of the Special Sessions is available at the end of this Call.

Abstracts will be reviewed by the Scientific Committee and accepted for oral communication and poster presentation or rejected in case they do not match the scientific standards of the conference. Two or three anonymous referees will evaluate each abstract. We encourage the authors to use the maximum space available in the submission form in order to describe at the best their work and results.

Accepted abstracts will be collected in the conference proceedings. Negotiations are ongoing for the publication of a Supplement in an international journal with full articles dedicated to the subjects presented at the conference as poster or oral communications

Abstract submission requires early registration to the conference of the presenting author after the acceptance notification. Participants may submit up to a maximum of one oral communication and one poster, or two posters.

IMPORTANT DATES:

April 7, 2016: Deadline for Abstract submission for oral communications and posters

April 4, 2016: Deadline for Travel Grant requests

April 29, 2016: Abstract acceptance notification (Oral communications and posters)

May 2, 2016: Communication of decisions on Travel Grant assignments

May 9, 2016: Deadline for early registration to the conference (required for authors of accepted abstracts)

June 15–17, 2016: BITS2016 meeting

Special Sessions

In addition to the traditional panels, this year the Call includes the following topics for Special Sessions proposed by members of the Society:

1) Big Data Management, Modeling and Computing.

Modern genomics promises to answer fundamental questions for biological and clinical research, e.g., how cancer develops, how driving mutations occur. Unprecedented efforts in genomics are made possible by Next Generation Sequencing (NGS), a family of technologies that is progressively reducing the cost and time of reading the DNA.

So far, the bioinformatics research community has been mostly challenged by primary analysis (production of sequences in the form of short DNA segments, or "reads") and secondary analysis (alignment of reads to a reference genome and search for specific genomic features on the reads, such as variants/mutations and peaks of expression); the most important emerging problem is the so-called tertiary analysis, concerned with sense making, e.g., discovering how heterogeneous regions interact with each other, by integrating heterogeneous DNA features, such as variants or mutations in a DNA position, or signals and peaks of expression, or structural properties of the DNA, e.g., break points (where the DNA is damaged) or junctions (where DNA creates loops). According to many biologists, answers to crucial genomic questions are hidden within genomic data already available in public repositories, but suitable tools for processing them are lacking.

BITS 2016 is an ideal forum for discussing the current status and perspectives of the NGS tertiary analysis as well as the results of the Data-Driven Genomic Computing (GenData 2020) PRIN

project, which includes 9 top-quality research groups throughout Italy, and focuses on tertiary analysis. Accordingly, we propose a Special Session that covers the challenging aspects of genomic big data modeling and computing, and involves both bioinformatics and computer science expertise. Special session topics can include (a) Challenging aspects and current status of genomic big data management, (b) Leveraging genomic repositories through their integrated access, (c) Semantic methods for genomic data, (d) New methods for integrated biomedical data processing and analysis, (e) Genomic questions and relevant biological problems on big NGS data, and new data management methods for their solution.

2) Clinical bioinformatics: from computational models to clinical answers.

Prognostic marker identification is one of the most pressing issues in clinical research. Therapeutic stratification, based on clinical and molecular risk factors, is essential for supplying the most appropriate treatment. However, patients receiving the same treatment can have markedly different clinical courses and thus, the identification of new prognostic markers for improved risk estimation at the time of diagnosis is critical for increasing treatment efficacy and ultimately patients' survival. Increasing awareness and advances in bioinformatics research has stimulated the development and the application of new intelligible, reliable, robust and flexible mining methods.

Innovative solutions to the problem are coming from the exosomal miRNA extracted from patients' biological fluids. The analysis of data coming from this kind of experiments is made arduous by the difficulty of gathering technical replicates and suitable data normalization methods. Recent advances in bioinformatics provided new tools for dealing with data coming from different sources and technologies.

Next-generation sequencing data require novel paradigms for metadata management and file tracking for adequate storage and computational units. Scientific studies in the fields are evolving towards global scale collaborations at multi-disciplinary levels, involving scientists located in different geographical regions. Moreover, it is increasingly important to integrate data coming from different disciplines, such as patient clinical history/record, biological/genomic data, and structural/functional images (tomography, histological images, etc...).

This session aims at evaluating the state of the art, recent approaches, open challenges, and the potential future developments of the clinical bioinformatics with particular emphasis at the translational implications of the research findings.