BITS 2017

Call for Abstracts

http://bioinformatics.it/bits2017

Submissions are invited for **poster and oral contributions** to the ***annual meeting of the Bioinformatics Italian Society (BITS)***, *on* ***July 5-7, 2017***.

The **main conference location** will be at **"Teatro Massimo"** (**M2** room), Viale Trento 9**,** 09122, Cagliari, Italy (http://www.sardegnateatro.it/location/m2)

Topics of interest include, but are not limited to, the following:

- **Algorithms for Bioinformatics**
- **Biological Databases**
- **Comparative Genomics**
- **Epigenetics**
- **Precision Medicine**
- **Genomics of Disease**
- **Molecular Evolution**
- **Next Generation Sequencing**
- **Pharmacogenomics**
- **Protein structure and function**
- **Proteomics**
- **Systems Biology**
- **Database and Big Data application in Bioinformatics**
- **Trascriptomics, RNA-Seq, Chip-Seq, mRNA, piRNA**
- **Gene Network**

The Call also consider topics deemed relevant for the following special sessions, proposed by BITS members:

- **Predictive modeling of diseases and Personalized Medicine**
- **Genome variations and their impact on biomedicine**
- **Genome 3D: Bioinformatics, computing infrastructure and opportunities for Chromatin Conformation Analysis**

Abstracts will be peer reviewed by the Program Committee members of BITS 2017. The accepted abstracts will be selected for oral communication or poster presentation.

Accepted abstracts will be included in the BITS2017 conference proceedings.

Negotiations are ongoing for the publication of a Supplement of BMC Bioinformatics and BMC Medical Genomics with full articles dedicated to the subjects presented at the conference as poster or oral communications.

Please visit the conference website at http://bioinformatics.it/bits2017 for precise formatting and submission instructions.

Upon acceptance notification, each presenting author is expected to perform early registration to the conference.

IMPORTANT DATES

~~**Friday, April 28, 2017:** Deadline for abstract submission for oral communications and posters~~

Tuesday, May 16, 2017: Extended deadline for abstract submission for oral communications and posters

Friday, May 5, 2017: Deadline for travel grant requests

Monday, May 22, 2017: Abstract acceptance notification (oral communications and posters)

Tuesday, May 23, 2017: Communication of decisions on travel grants

Friday, June 2, 2017: Deadline for early registration to the conference (*)

July 5–7, 2017: BITS 2017 annual meeting

TUTORIALS

In collaboration with BITS 2017, the **tutorials** will be given:

July 3, 2017:	GPU applications in Bioinformatics
July 3–5, 2017:	Galaxy for Bioinformatics tool developers (in collaboration with ELIXIR)
July 8, 2017:	Modeling transcription regulation for system medicine of common human diseases
	Workflow management of bioinformatics data using Orange

More information on the tutorials will be made available soon on the web site of the conference.

(*) Required for authors of accepted abstracts.

SPECIAL SESSIONS

In addition to the traditional panels, this year the following special sessions will take place, proposed by BITS members and selected by the steering committee of the association.

1 - Predictive modeling of diseases and Personalized Medicine

Predictive modeling of diseases is a generic concept that spans over several fields of biomedicine. Infectious disease management, drug resistance prediction/assessment, as well as short- and long-term prognosis are all examples of fields in which predictive modeling actually takes place. Notably, modeling activities can be targeted to deal with a population of individuals or a single individual. The former perspective typically ensures statistical significance, whereas the latter yields personalized predictions. No matter which underlying assumptions hold, predictive models are typically derived from the analysis and assessment of heterogeneous data. Significant cases occur when the output of clinical evaluation and trials, also concerning the interactions between drugs and target molecules, is used to generate models aimed at investigating life expectancy for the disease at hand, the resistance to infectious diseases, and/or healthcare needs according to a personalized perspective.

2 - Genome variations and their impact on biomedicine

Genetic variations among human individuals may occur in different ways. The most acknowledged type of variation, i.e., single-nucleotide polymorphisms (SNPs), occurs when a single nucleotide differs between different individuals. Small insertions/deletions (INDELs) are insertions or deletions of up to 1K bp. Further variations include insertions, inversions, deletions, and duplications of DNA segments larger than 1K bp, as well as segmental duplications. In addition, copy number variations refer to the duplication or deletion of a segment of DNA sequence compared to a reference genome assembly. The largest types of genome variation are chromosomal changes, such as modifications of large portions of chromosomes and translocation events. Although all these genomic variants are not necessarily disease-causing, it is well known that many SNPs, INDELs, structural variants, and chromosomal aberrations are in fact associated with one or more diseases. For this reason, the study of the underlying mechanisms are deemed very important in the task of making a diagnosis and/or a prognosis on a statistical or personalized basis.

3 - GENOME 3D: Bioinformatics, computing infrastructure and opportunities for Chromatin Conformation Analysis

During the last decade, a technology called “chromosome conformation capture” has been developed to stabilize the DNA conformation, allowing the identification of sequences that are close to each other in the 3D space of the nucleus. Since this approach has been coupled with Next-Generation Sequencing, evidences of the 3D genome conformation role in regulating and maintaining cellular functions are continuously emerging. These data provide a better understanding of the changes in the three-dimensional genome architecture that influence the regulations of the cellular function. Genome conformation data can be used to correlate gene co-localization, co-expression and co-regulation, providing a common ground for multi-omics data integration. However, generating a unified view of spatial, temporal, genetic and epigenetic properties poses various challenges of data analysis, visualization, integration and mining, as well as of high performance computing and big data management. In this session we want to present some issues and perspectives of this new branch of bioinformatics, oriented at the comprehension of the three-dimensional genome architecture.