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# $10^{th}$ Workshop on Biomedical and Bioinformatics Challenges for Computer Science – BBC2017

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**Abstract**
We present the $10^{th}$ Workshop on Biomedical and Bioinformatics Challenges for Computer Science – BBC2017, held in Zurich, 12 - 14 June 2017.

Peer-review under responsibility of the scientific committee of the International Conference on Computational Science

*Keywords:* Bioinformatics, Computational biology, Biomedical applications

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The huge amount of data produced by modern technologies has revolutionized several fields in life science, like proteomics, genomics, metagenomics, and phylogenetics. New sequencing technologies have played a fundamental role in this change of perspective, opening new challenges to bioinformatics. Bioinformatics researchers need to tackle these challenges by exploring, developing and applying novel computational concepts, methods, tools and systems. The new approaches are likely to involve advanced and large-scale computing techniques, computational approaches, technologies and infrastructures such as high-performance architectures and systems, distributed computing, computational simulation, algorithms design and engineering, applied bioinformatics, artificial and computational intelligence.

The tenth edition of the Workshop on *Biomedical and Bioinformatics Challenges for Computer Science* (BBC) took place at ETH Zurich, between 12-14 June 2017. The workshop goal is to involve researchers in computer science, bioinformatics and computational biology to present recent works that tackle these new challenges in bioinformatics and biomedicine. The workshop has been organized, as for the previous editions, in conjunction with the *International Conference on Computational Science* (ICCS). The workshop consists of two sessions.

The first session, *Bioinformatics Applications*, comprised five full papers. In the first paper *Orthology Correction for Gene Tree Reconstruction: Theoretical and Experimental Results*, Dondi et al. investigated the problem of correcting a relation graph that represents orthology/-paralogy relations among genes, providing theoretical as well as experimental results.

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In the paper *Rank miRNA: a web tool for identifying polymorphisms altering miRNA target sites*, Beretta et al provided a web application, called Rank miRNA for the aggregation of results of three known prediction tools, and to process and analyze new input miRNA sequences

In the paper *Higher accuracy protein multiple sequence alignments by genetic algorithm*, Behera et al. considered the Multiple Sequence Alignment (MSA) problem. The paper provided a new MSA method based on a stochastic approach, using evolutionary operators of a genetic algorithm to combine the results of two known sequence alignment tools.

In the paper *Machine learning models in error and variant detection in high-variation high-throughput sequencing datasets*, Krachunov et al. presented machine learning models to classify erroneous and rare variations. Moreover, a preselection phase is performed, selecting potential error candidates with a weighted frequency measure.

In the paper *Effect of Variations in Gap Junctional Coupling on the Frequency of Oscillatory Action Potentials*, Appukuttan et al. investigated the computational effects of differences in gap junctional properties on oscillating action potentials in electrically coupled tissues.

The second session *Medical Informatics Applications and Tools* comprised six full papers about medical application of informatics. In the first paper *Using Multi Network Alignment for Analysis of Connectomes*, Milano et al. considered the modeling of MRI connectomics with networks and applied multiple network alignment approaches to compare different networks.

In the second paper *Investigation of the visual attention role in clinical bioethics decision-making using machine learning algorithms*, Fernandes et al. proposed a machine learning approach to build predictive models using eye tracking data. The goal of the method is to provide results to support decision-making process in clinical bioethics, in particular in cases of euthanasia.

In the paper *Emotion recognition using facial expressions*, Tarnowski et al. considered the problem of recognizing emotional states by means of facial expressions. The proposed method relies on coefficients describing elements of facial expressions, based on six registered subjects, that were used as features.

In the paper *Accelerating the Diffusion-Weighted Imaging Biomarker in the clinical practice: Comparative study*, Borreguero Torro et al. presented implementations based on multicore (OpenMP) and GPU (CUDA) to speed up Diffusion Weighted Image (DWI) methods for the extraction of meaningful information about the microscopic motions of water of human tissues from MRI.

In the paper *Combining Grid Computing and Docker Containers for the Study and Parametrization of CT Image Reconstruction Methods*, Chillarn et al. studied the optimization of configurations and parameters on containers within a grid computing platform, in the context of computed tomography image reconstruction.

In the paper *Vocal signal analysis in patients affected by Multiple Sclerosis*, Vizza et al. presented a study of voice analysis for patients affected by Multiple Sclerosis (MS). The goal of the study is a better understanding of the disease: early detection, differential diagnosis, and monitoring.

These workshop proceedings include the final revised versions of the BBC papers, taking the feedback from reviewers and workshop audience into account. The program chairs sincerely thank the Program Committee members for the time and expertise they put into the reviewing work, the ICCS organization, for providing the opportunity to arrange the BBC workshop in conjunction with the ICCS 2017 conference, and all the workshop attendees.

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