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Editorial

Editorial of the Special Issue of the 10th Workshop on Biomedical and Bioinformatics Challenges for Computer Science—BBC 2017

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Abstract: In this special issue, we present two of the papers presented at the 10th Workshop on Biomedical and Bioinformatics Challenges for Computer Science—BBC2017, held in Zurich, 12–14 June 2017.

Keywords: bioinformatics; computational biology; biomedical applications

Modern technologies, in particular new sequencing technologies, produce a huge amount of data that has lead to a great impact in several fields in life science, notable example being proteomics, genomics, metagenomics, and phylogenetics.

This increase in available data leads to new challenges for researchers in bioinformatics, in particular for the development of new computational tools, based on different approaches, such as large-scale computing techniques, high-performance architectures and systems, distributed computing, computational simulation, algorithms design and engineering, 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 and 14 June 2017. The workshop aimed at involving researchers in different fields, from computer science to bioinformatics and computational biology, in order to present recent development in these fields.

The workshop, as for the previous editions, was organized in conjunction with the *International Conference on Computational Science* (ICCS). After the workshop, the best papers were invited to submit an extended version to the "Computers" journal, and the following two documents were accepted after the review procedure: "On the Use of Voice Signals for Studying Sclerosis Disease" by Patrizia Vizza, Giuseppe Tradigo, Domenico Mirarchi, Roberto Bruno Bossio and Pierangelo Veltri, and "Application of Machine Learning Models in Error and Variant Detection in High-Variation Genomics Datasets" by Milko Krachunov, Maria Nisheva and Dimitar Vassilev.

In the first paper, the authors present an analysis for the identification of dysarthria, that is impaired speech related to Multiple Sclerosis (MS). The paper, through the analysis of vocal signals, aims at finding relevant patterns related to impaired speech.

In the second paper, the authors deal with the identification of erroneous and rare variations in genomics datasets. The paper presents a machine learning approach, based on four different models, for the classification of bases into erroneous and rare variations. Data are preprocessed

with a preselection of potential errors through a weighted frequency measure, based on a pairwise comparison of the considered sequences.

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