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***IEEE Transactions on IEEE/ACM Transactions on Computational Biology and Bioinformatics***

**Special Issue/Section on Deep Learning and Graph Embeddings for Network Biology**

**GUEST EDITORS:**

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**TOPIC SUMMARY:**

Biological Networks are powerful resources for modelling, analysis, and discovery in biological systems, ranging from molecular to epidemiological levels. In recent years, network models and algorithms have been used to represent and analyse the whole set of associations and interactions among biologically relevant molecules inside cells, (*e.g.,* proteins, genes, transcription factors and more recently the big class of non-coding genes), supporting the elucidation of the molecular mechanisms as well as the development of precision medicine for many relevant diseases (*e.g.,* cancers or brain disorders).

Mathematical machinery that is central to this area of research is graph theory and machine learning on graph-structured data. Recent research efforts have introduced methods and tools that can model biological phenomena and learn and reason about them through networks. Such data and models are typically stored in various databases of experimental data and repositories of biomedical knowledge. Network data extracted from these databases are often mined for knowledge about a biological system of interest (*e.g.,* using network statistics or community detection algorithms) and to compare two or more networks (*e.g.,* using network alignment algorithms). Current approaches may present limitations in some applications since they can fail to generalize from observed network structure to new biological phenomena, are unable to include prior knowledge in the analysis, rely on user-defined heuristics and painstaking manual feature engineering to extract features from biological networks, or fail to support researchers when limited biological data is available (*e.g.,* small datasets with low coverage).

Recent years have seen a surge in approaches, such as deep learning, that have shown broad utility in uncovering new biology and contributing to new discoveries in wet laboratory experiments. In particular, in biological and biomedical area, deep learning have evidenced an efficient way to deal with data generated from modern high-throughput technologies.

In parallel, the field of network science has been influenced by the development of methods that automatically learn to encode network structure into low-dimensional embeddings, using data transformation techniques based on matrix factorization, deep learning, nonlinear dimensionality reduction, and complex non-linear models. The key idea of these methods (or graph representation learning) is to automatically learn a function able to map nodes in the graph (or other graph structures) to points in a compact vector space, whose geometry is optimized to reflect topology of the input graph. The relevance and potential of graph representation learning are evidenced by the rise of approaches that are beginning to effect on the way network biology is performed today at the fundamental level. Therefore, there is strong need to discuss and foster these advances in a systematic way to give support both to researchers and practitioners.

The goal of this special issue is to collect both surveys and papers describing novel methods and applications in computational biology and bioinformatics. Papers presenting applications in medicine and healthcare are also welcome.

The topics of interest for this special issue include, but are not limited to:

* Deep learning and graph neural networks for network biology
* Learning meaningful representations for biomedical networks
* Learning node, edge, higher-order, and graph-level embeddings for biological networks
* Next-generation graph embedding techniques for important problems, including node classification, link prediction, graph classification, network alignment and beyond
* Graph representation learning for visualizing and interpreting interaction data
* Next-generation network science through network embeddings
* Relevant benchmark datasets, initial solutions for new challenges and new directions in network biology
* Applications of network embeddings broadly in computational biology, genomics, medicine, and health

**IMPORTANT DATES:**

Abstract submission: Jan-Feb 2020

Open for submissions in ScholarOne Manuscripts: February 28 2020

Closed for submissions: July 30, 2020

Results of first round of reviews: September 15, 2020

Submission of revised manuscripts: October 15, 2020

Results of second round of reviews: November 15, 2020

Publication materials due: December 15, 2020

**SUBMISSION GUIDELINES:**

Prospective authors are invited to submit their manuscripts electronically after the “open for submissions” date, adhering to the *IEEE/ACM Transactions in Computational Biology and Bioinformatics* guidelines (http://www.computer.org/portal/web/tcbb-cs/author). Please submit your papers through the online system (https://mc.manuscriptcentral.com/tcbb-cs) and be sure to select the special issue or special section name. *Manuscripts should not be published or currently submitted for publication elsewhere.* Please submit only full papers intended for review, not abstracts, to the ScholarOne portal. If requested, abstracts should be sent by e-mail to the Guest Editors directly.

**GUEST EDITORS BIOGRAPHIES:**

**Pietro Hiram Guzzi**

**Pietro H. Guzzi** is an Associate Professor of Computer Science and Bioinformatics at the University ‘Magna Græcia’ of Catanzaro, Italy, since 2008. He received his PhD in Biomedical Engineering in 2008, from Magna Græcia University of Catanzaro. He received his Laurea degree in Computer Engineering in 2004 from the University of Calabria, Rende, Italy. His research interests comprise bioinformatics, network analysis. In network analysis, in particular, Pietro has worked on local alignment of biological networks providong some tools for network alignment. Actually is working on novel approaches of alignment that merge together both local and global alignment and on the development of novel methods of analysis based on the integration of heterogeneous networks thorugh embedding. Pietro is an ACM member and serves the scientific community as reviewer for many conferences. He is associate editor of IEEE/ACM TCBB, and of SIGBioinformatics Record.

**Marinka Zitnik**

Marinka Zitnik is an Assistant Professor at Harvard University. Her research investigates artificial intelligence and machine learning to advance science, medicine, and health. Her methods have had a tangible impact in biology, genomics, and drug discovery, and are used by major biomedical institutions, including Baylor College of Medicine, Karolinska Institute, Stanford Medical School, and Massachusetts General Hospital. Before Harvard, she was a postdoctoral scholar in Computer Science at Stanford University and a member of the Chan Zuckerberg Biohub at Stanford. She received her Ph.D. in Computer Science from University of Ljubljana while also researching at Imperial College London, University of Toronto, Baylor College of Medicine, and Stanford University. Her work received several best paper, poster, and research awards from the International Society for Computational Biology. She has recently been named a Rising Star in EECS by MIT and also a Next Generation in Biomedicine by The Broad Institute of Harvard and MIT, being the only young scientist who received such recognition in both EECS and Biomedicine.