Editorial

Ralf Hofestädt[1] / Falk Schreiber[2] / Björn Sommer[2] / Jens Allmer[3]

Computational miRNomics – Integrative Approaches

[1] Bioinformatics and Medical Informatics, University of Bielefeld, Bielefeld, Germany
[2] Computational Life Sciences, University of Konstanz, Konstanz, Germany
[3] Molecular Biology and Genetics, Izmir Institute of Technology, Urla, Izmir, Turkey, E-mail: jens@allmer.de

Message from the Editors-in-Chief

With this special issue on Computational miRNomics, we would like to start a new generation of publications in the *Journal of Integrative Bioinformatics (JIB)*. From 2017 onwards, JIB will be published by De *Gruyter* which is one of the largest Open Access publishers in Germany with a long history. Established in 1918 with roots reaching even further back, the JIB editorial board decided that De Gruyter is the perfect partner to increase the level of professionalism for our publication processing and journal development.

While De Gruyter has a strong tradition in scientific publishing, JIB is one of the longest-running Bioinformatics journals. Established in Germany, it published more than 300 peer-reviewed articles since its inauguration in 2004. The publication archive, as well as new papers, can be found and downloaded from https://www.degruyter.com/view/j/jib.

From the beginning, JIB has been supported by IMBio – Information management in Biotechnology, which is a working group of the German Informatics Society (Gesellschaft für Informatik e.V.). More information regarding our activities as well as the previous JIB website (up to December 2016) is available from http://www.imbio.de.

We publish proceedings papers, like the one from the *Integrative Bioinformatics* conference series, special issues like the one introduced below, as well as original research articles submitted to our journal.

Whereas the issues in the past were published based on events and the cumulative number of submitted manuscripts, we are now following a new scheme, publishing each quarter of the year one issue, containing issue-related articles as well as free ones. Every article will be available online "ahead-of-print" before the compilation of the issues.

In contrast to the previous publishing system which was developed more than a decade ago, the new ScholarOne-based system is up-to-date and provides a reliable and comfortable environment for our authors, reviewers, and the editorial team.

We are looking forward to a new era of publications for the Journal of Integrative Bioinformatics. For this purpose, we extended our portfolio – we are now welcoming manuscripts covering the following Integrative Bioinformatics-related topics:

- Computational Systems Biology

- Databases and data integration

- Big data and data mining

- Precision Medicine and Biomedical Informatics

- Semantic web, standards, and ontologies

- Tool integration and workflow systems

- Network simulation and analysis

- Computational infrastructure and frameworks

- Integrative, whole cell, and molecular modeling

- Visualization and animation

Moreover, we are working on the establishment of JIBtools, a list of computational tools associated with the journals' topics: http://www.imbio.de/journal/JIBtools.

To further promote the success of JIBtools, we are welcoming new editors who are willing to oversee a tool list within their area of expertise!

If you are interested in suggesting a new special/conference issue, a new JIB tool list or you would like to give feedback of any kind, please do not hesitate to contact the editorial office: jib.editorial@degruyter.com.

Computational miRNomics

MicroRNAs (miRNAs), discovered more than 2 decades ago [1], are generated following a relatively well-defined molecular pathway [2]. Hairpin-like structures (pre-miRNAs) are excised from RNA. These are further processed into short single-stranded RNAs. These mature microRNAs are short non-coding RNA sequences involved in post transcriptional regulation of protein abundance. Thereby, they have a direct impact on the phenotype [3].

Hassani-Pak and Rawlings are giving an overview of knowledge discovery from federated databases for linking genes and phenotypes. Such methods represent basic tools for computational miRNomics today and in the future [4]. Their discourse does not include miRNAs, but Suluyayla et al. [5] describe a new database containing miRNAs and their target interactions which can be queried using VANESA [6] to enrich gene regulatory pathways with miRNA interactions. Genes and their interactions are evolutionary conserved and Yazbeck et al. analyze and quantify miRNA evolution [7]. Their analysis is complemented by an analysis of mutations in mature miRNA sequences by Bhattacharya and Cui [8]. Finally, Goswami et al. analyze the practical impact of differential miRNA regulation for salt tolerance in rice [9].

This concludes the two volume special assessment of miRNomics where the first volume [10] concentrated on computational aspects of miRNA and target discovery. This second volume focuses on evolutionary and integrative aspects of miRNA analyses while both provide practical applications.

Conflict of interest statement: Authors state no conflict of interest. All authors have read the journal's Publication ethics and publication malpractice statement available at the journal's website and hereby confirm that they comply with all its parts applicable to the present scientific work.

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