## Contents

### Papers

1. **A systematic evaluation of normalization methods in quantitative label-free proteomics**
   Tommi Välikangas, Tomi Suomi and Laura L. Elo

2. **Inter-kingdom prediction certainty evaluation of protein subcellular localization tools: microbial pathogenesis approach for deciphering host-microbe interaction**
   Abul A. Khan, Zahir Khan, Mohd. Abdul Kalam and Azmat Ali Khan

23. **The present and future of de novo whole-genome assembly**
    Jang-il Sohn and Jin-Wu Nam

41. **A bioimage informatics platform for high-throughput embryo phenotyping**

52. **Combinatorial epigenetic regulation of non-coding RNAs has profound effects on oncogenic pathways in breast cancer subtypes**
    Juan Xu, Zishan Wang, Changjie Xiang, Zheng Zhao, Jing Li, Yongdong Li and Xin Li

65. **Synthetic data sets for the identification of key ingredients for RNA-seq differential analysis**
    Guillem Rigaill, Sandrine Balzergue, Véronique Brunaud, Eddy Blondet, Andrea Rau, Odile Rogier, José Caua, Cathy Maugis-Rabusseau, Ludovic Neveux-Massicot, Sébastien Aubourg, Claire Lune, Marie-Laure Martin-Mauger and Etienne Berannoy

77. **Notions of similarity for systems biology models**
    Ron Henkel, Robert Merkerlof, Tim Kacprowski, Christian Knapler, Wolfram Liebermeister and Dagmar Waltemath

89. **The framework for population epigenetic study**
    Linna Zhao, Di Liu, Jing Xu, Zhaoyang Wang, Yang Chen, Changgui Lei, Ying Li, Guiyou Liu and Yongshuai Jiang

101. **Genome-wide DNA methylation analysis identifies candidate epigenetic markers and drivers of hepatocellular carcinoma**
    Yongchang Zheng, Qianqian Huang, Zijian Ding, Tingting Liu, Chenghai Xue, Xinting Sang and Jin Gu

109. **An empirical likelihood ratio test robust to individual heterogeneity for differential expression analysis of RNA-seq**
    Maoqi Xu and Liang Chen

118. **Computational pan-genomics: status, promises and challenges**
    The Computational Pan-Genomics Consortium

136. **Transferring entropy to the realm of GxG interactions**
    Pablo A. Ferrando and Shih-Chieh Huang

148. **Comprehensive assessment and performance improvement of effector protein predictors for bacterial secretion systems III, IV and VI**
    Yi Ao, Jianwei Wang, Chen Li, Andre Lopes, Tatiana Marques-Correa, Jonathan Wilke, Yang Zhang, Ute Schleyer, Industrious Wang, Jiangning Song and Pierre Allemand

162. **A graphical model approach visualizes regulatory relationships between genome-wide transcription factor binding profiles**
    Haris S. Yag, David Faruqi, Lauren Weersch and Berthold Giagkios

174. **A review of validation strategies for computational drug repositioning**
    Adam S. Brown and Dingjiong J. Patel
Aims

The aim of Briefings in Bioinformatics is to provide an indispensable resource for the experimental practitioner seeking awareness of the disparate sources of data and analytical tools of contemporary biology, biotechnology and medicine based on the molecular level. This includes all areas of genomics, proteomics, metabolomics, interactomics and network biology, imaging, systems biology, chemo-informatics, computational biology and clinical/medical informatics that have a molecular foundation to the study. Large-scale instrumentation and computerisation is reducing the time that needs to be spent in the laboratory. Instead, the rate-limiting step is the analysis and interpretation of data. The journal provides topical reviews of new methodologies as they become established.

The Editors, Martin Bishop and Russ Altman, welcome the submission of review papers and case studies for publication. Essential criteria for the publication of papers are that they provide practical guidance to the users of bioinformatics software and databases to supplement available manuals and tutorials, providing a brief conceptual review and overview of the problem addressed, its solution, dynamic range and limitations. We publish reviews of clearly defined subject areas for both experimental biologists and bioinformatics specialists. Reviews may be broader or more narrowly focussed but must cover a variety of approaches to a very well-specified biological problem or research area. We do not publish work on new methods that have not yet been described elsewhere. Please do not submit manuscripts concerning original research as they will be immediately rejected.

Some areas that members of the Editorial Board have identified as important and presently underrepresented in the pages of the Journal include the complex fields of epigenetics and the construction of evolutionary models and the elucidation of evolutionary relationships. Methodological approaches of interest include software comparison and benchmarking, data cleaning and curation, accuracy of predicted and extracted information, ontologies and text-mining, solutions that allow for the large-scale analysis of biological data in reasonable time (high performance computing solutions and cloud systems), standards, training and change management.

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Types of Submission

Submissions of the following types are accepted for review in the Journal:

- Review articles (2000–7000 words)
- Protocols for solving a specific problem using different sets of programs (2000–5000 words)
- Opinion articles: topical or controversial areas that do not warrant a full review (500–1000 words)
- Letters to the Editor (relating to a topic previously published in the Journal) (500–1000 words)
- Software and website reviews (by authors other than the originators) (500–1000 words)
- Book reviews (500–3000 words)