

Message from the Editor-in-Chief

TATSUYA AKUTSU†

This is the second issue of IPSJ Transactions on Bioinformatics (TBIO). TBIO aims on facilitating the exchange of knowledge between two differing fields (Bioscience and Information Science) toward reaching our common goal: understanding of the secrets of life. TBIO focuses on Bioinformatics and Computational Biology but also covers related fields including Information Science, Statistics, Mathematics and Bioscience. With the goal of incorporating a diverse range of perspectives as well as reaching an equally wide audience, this journal was started as an English journal. This publication is edited as well as financed by the Special interest group of Bioinformatics (SIGBIO), Information Processing Society of Japan (IPSJ).

One of the important features of TBIO is its evaluation criteria. Evaluation is done based upon the merits of the paper as opposed to the conventional point system. Papers which present either enough novelty or enough usefulness will be considered for publication though a competent level of English writing is required. Papers may also be evaluated on future potential. Another important feature of TBIO is its short review period, most articles being reviewed within one month of submission. In the shortest case, a paper was accepted 7 days after the submission. It is also worthy to mention that papers in TBIO are accessible online though IPSJ Digital Courier (<http://www.ipsj.or.jp/08editt/dc/index.html>). This facility is useful for the authors to widely circulate the results. The submission guidelines can be found at <http://www.ipsj.or.jp/katsudou/sig/sighp/bio/tob.html>.

TBIO accepts three kinds of papers: original papers, survey papers and database/software

papers. The topics covered by TBIO include, but not limited to: sequence analysis, evolutionary tree analysis, prediction and analysis of protein/RNA structures, analysis of proteomics/proteome data, analysis of gene expression data, inference and analysis of various kinds of biological networks, gene polymorphism data analysis, cell simulation, neuroinformatics, and systems biology.

This issue consists of five original papers and one database/software paper. The topics covered by these papers are: a statistical method for selecting important genes using gene expression data, inference of genetic networks using neural network models, software engineering for bioinformatics, computational complexity of a motif detection problem, a (bi)clustering method for gene expression data, and a system for clustering DNA sequence data. Each paper was reviewed by two referees. Some of these papers are based on presentations at IPSJ-SIGBIO meetings and the others will be presented at IPSJ-SIGBIO meetings, where information on IPSJ-SIGBIO is available from <http://www.ipsj.or.jp/katsudou/sig/sighp/bio/>. I thank all the authors of this issue and hope that readers enjoy reading these papers. From these papers, readers can see that wide range of papers are published in this journal: from theoretical papers to experience papers. Thus, I would like to invite potential authors to submit any types of papers once these are related to Bioinformatics and/or Computational Biology.

TBIO is currently on a biannual schedule. The next issue is planned to be published in September, 2007. I look forward to receiving many submissions as well as seeing many presentations at IPSJ-SIGBIO meetings.

† Editor in Chief
Bioinformatics Center, Institute for Chemical Research, Kyoto University