Message from the Editor-in-Chief

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The second half of the twentieth century was marked with great progresses in the sciences, most notably in the fields of Bioscience and Information Science. In the twenty-first century, it is highly expected that their strong collaboration leads to various developments and ultimately to understanding of the secrets of life. Bioinformatics should play the key role in this collaboration where many challenges remain. With the sheer amounts of data provided from DNA sequences, three-dimensional protein structures, chemical compounds, various kinds of biological networks and gene expression profiles, there is a dire need for the development of techniques which can effectively handle and process the increasing amount of data. Simple application of existing information processing techniques is far from enough. They must be changed and adapted to the differing needs of Bioinformatics. Furthermore, novel information processing techniques should be developed: breakthroughs are required.

This is the inaugural 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 goals. 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 is 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 ten original papers, whose range of topics covers from sequence analysis, prediction of structure, function and development, analysis of protein and metabolic networks, analysis of gene expression and CGH data, and cell simulation to drug design. Each paper was reviewed by two referees. Many of these papers are based on presentations at IPSJ-SIGBIO meetings. I thank all the authors of this issue and hope that readers enjoy reading these papers. TBIO is currently on a biannual schedule. The next issue is planned to be published in March, 2007. I look forward to receiving many submissions as well as seeing many presentations at IPSJ-SIGBIO meetings.

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