Systems biology is the term used, in the biomedical field, to discuss the new direction taken, in carrying out research. The holistic approach is undertaken instead of the previously reduction approach. Systems biology is facilitated enormously by the high throughput technologies generating enormous amount of data. It still remains an unsolved challenge to analyze and interpret the enormous volumes of ‘omics’ data. Bioinformatics and biostatistics play crucial roles to this endeavour. This journal presents innovative research in Systems Biology applications and other biomedical technologies aiming in general at the promotion of the health care. Its target audience includes Medical Doctors, Computer Scientists, Informaticians, Bioinformaticians, Biomedical Informaticians, Biologists, Bioengineers, Pharmaceutical Industry people, Public Health people and Epidemiologists.

Specifically, the first article argues that the rapid accumulation of biological data and the corresponding enormous growth in the number of published research papers have rendered data annotation and literature searching immensely laborious tasks. To this end, the authors have developed MINOTAUR, a Web-based assistant tool that helps biologists and biocurators to find relevant facts in online databases and biomedical literature abstracts. The suite is available for interactive use at: http://www.bioinf.manchester.ac.uk/dbbrowser/minotaur/about.html.

The second article presents a methodology for-patient stratification by analyzing clinical and molecular information on a per-patient level represented as a data graph. This approach rests on linking patient specific clinical data and biomarker profiles with molecular functional units being derived by segmenting a human proteome interaction network. As a result patient strata are built holding sets of affected functional molecular units as common denominator. Annotation of such functional units on the level of associated diseases biomarkers and drug targets allows reconciliation with respective clinical data for further improving the assignment of patients to specific strata.

The third article presents, as most of the bacterial chromosomes contain a circular DNA molecule, a simple, yet efficient, sensitive and accurate algorithm, specifically designed for mapping millions of short reads to a genomic sequence with circular structure.

The fourth article discusses that modeling of the tomographic weights usually incorporates angle of view, decay and attenuation. A usual assumption is that the gamma camera is a long way from the object, this leads to the approxi-
formation that the angle of view subtending the front of the collimator tube is the same as that subtending the back. If, however, the distance between camera and subject is small then this approximation may not be good enough and artifacts may be produced. A comparison between exact solid angle and the approximate solid angle formula of Weir and Green (1994) is presented.

Finally, the fifth article reports on a Web 2.0 tool that adopts an incremental formalization approach, whereby a set of loosely coupled resources are gradually transformed into argumentative discourse out of which decisions emerge. The overall idea of the proposed tool is to function as a collective electronic logbook (serving all members of the collaborating group), which captures important discussions about the evaluation and assessment of related resources, the design rationale of the associated experiments and the justification of the decisions made. Through a particular collaboration scenario, various possibilities and challenges are exploited for managing biomedical collaboration with the use of the proposed tool. The proposed tool is being developed in the context of an FP7 EU project, namely Dicode (http://dicode-project.eu/), which aims at facilitating and augmenting collaboration and decision making in diverse data-intensive and cognitively-complex settings.

In conclusion, the inaugural issue forebodes the journal’s impact, which could be summarized as presenting original contributions to the creation of knowledge for both Systems Biology and Biomedical Technologies.

Sophia Kossida
Anastasia Kastania
Editors-in-Chief
IJSBBT

Sophia Kossida received her BSc degree in Biology from the University of Crete in Greece in 1995. She was awarded the free-mover Erasmus scholarship and spent a year in Trinity College of Dublin, in Ireland within the Genetics Department, Bioinformatics Unit, where she worked on the genome of Saccharomyces cerevisiae. She received the full MRC scholarship to carry out her DPhil, which she was awarded in 1998 from Oxford University, Merton College in the UK. She did extensive work on sequence analysis of viral genomes (DNA viruses and retroviruses) and deciphered their evolutionary history. She carried out a post-doc at Harvard University, USA at the Molecular & Cellular Biology Department within the FlyBase group, holding a NIH fellowship. She was employed as Senior Scientist within the Target Discovery Group of Lion Bioscience Research Inc. (LBRI) in Cambridge, MA, USA where she worked on the human genome mining project. She was the co-ordinator between LBRI and the Bayer Diabetes group in the US and in Germany as well as the scientist in charge for the patent applications. She moved over to Toulouse, in France where she was appointed Director of Bioinformatics of Endocube, a start up company focusing in endothelial cells. In parallel, she was appointed Associate Professor of Bioinformatics at the University of Paul Sebatier in Toulouse, France. She joined Novartis in Switzerland in 2002 as Lab head within the Functional Genomics Group. She worked on a few different sequence analysis projects with main focus on proteases. She joined BRF in July 2004 as tenure track research Bioinformatician, Center of Basic Research II, Biotechnology Division. Sophia holds 11 published patent applications. Her team within BRF was appointed the National Contact Point for Bioinformatics for the EMBnet.
Anastasia N. Kastania received her BS in Mathematics and her PhD degree in Medical Informatics from the National & Kapodistrian University of Athens, Greece. She works in the Athens University of Economics and Business, Greece since 1987. Research productivity is summarized in various articles (monographs or in collaboration with other researchers) in international journals, international conferences proceedings, international book series and international books chapters. She has more than twenty years teaching experience in University programs and she is the writer of many didactic books. She also has ten years experience as Researcher in National and European Research Projects. Research interests are telemedicine and e-health, e-learning, bioinformatics, biomedical engineering, tele-epidemiology, mathematical modeling and statistics, web engineering, quality engineering and reliability engineering.