

Editorial

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To serve all our valuable contributors, reviewers, editors and readers more efficiently and promptly, we have launched the Journal of Computer Science and System Biology (JCSB)-Open Access. This journal is created in response to the NIH, Wellcome Trust and European Commission Public Access Policy. It is easily accessible, scientifically sound, and superior in article rapid review to generate confidence in you. You will see how attractive, profusely illustrated, interesting, informative and useful this, our new journal.

We need not repeat that in spite of cut-throat competition, we have been quite successful in promoting open access publishing. JCSB gives barrier-free access to the literature for research. It increases convenience, reach, and retrieval power. Free online literature and free online software facilitate full-text searching, indexing, mining, summarizing, translating, querying, linking, recommending, alerting, “mash-ups” and other forms of processing and analysis. **Open access is a property of individual works, not necessarily journals or publishers.**

JCSB provides rapid publication (monthly) of articles in the areas of computational biology and system biology. The Journal welcomes the submission of manuscripts that meet the general criteria of significance, scientific excellence and rapid review process makes JCSB is the choice for contributors. The academically sound Editorial Board members and well accomplished reviewers in respective subject areas facilitates the promotion of only significant research findings that would have high impact in years to come.

We thank all of our contributors for their continuous patronage and support, and hope you will enjoy the first issue of our new journal. In the first article Dr. Momiao Xiong et al., have shown the symmetrical nature of metabolic networks which leads to functional redundancy and increased robustness. Dr. Anil Kumar et al., have reviewed the latest findings in stress resistance by plants and PCR primer designing of DREB1A and DREB2A, drought resistant genes. Wang et al., reported that incorporating quantitative quality of data as weight, improves the reliability of *matarray*, a microarray image processing and data analysis package.

Dr.P.Shanmughavel et al have annotated 250 hypothetical proteins in *Mycobacterium tuberculosis* genome using BLAST, INTERPROSCAN, PFAM and COGs. Some these could have therapeutic nature. Dr. Lakshmi, P.T.V et al have carried out sequence – structure comparison of Phycocyanin using VAST and reported the number of structural neighbours. Dr. Oxana V. Galzitskaya et al have reported that evolution and ancestry between organisms can be estimated reliably from the analysis of loops in elongation factor EF1A. Dr. Chikhi abdelouahab et al have compared the docking and scoring algorithm of Arguslab and Surfex by applying it to 300 protein ligand complex. Dr. Sablok G et al have studied the distribution of Microsatellite markers and Single Nucleotide Polymorphisms in *Propolis spp.* Amnd report that A/T, AG/CT and AAG/CTT are abundant in putative unigenes. Dr. Shi Huang et al have reported that genetic equidistance and constant mutation cannot be directly correlated to explain molecular evolution. Dr. Pardasarathi et al have studied the differences and similarities in the virulence factors of four strains TIGR4, D39, G54 and nonencapsulated R6 in *Streptococcus pneumoniae*. Dr. J. Muthukumaran et al have predicted the three dimensional structure and active site analysis of inducible serine protease inhibitor-2, that is known to inhibit the activity of agriculturally important fungi. Dr. Dra Arlete A Martins et al have built the three dimensional structure model of hsp65 that has important role in vaccine design and modulation of immune response. Entropy plays a critical role in the long range structure of biopolymers. Dr. Ernest F. Retzel et al have reported a cross linking entropy model. This model links the two incompatible, lattice, and Gaussian polymer models into a single frame work and further elucidate their similarities and differences.

With a rigorous peer-review process, open access leads to a democratic way of publishing scientific results. For the first 30 submissions to JCSB, a healthy rejection rate of 53.8% was on record. With guidance and contributions from the editorial board members, we hope JCSB serves the exponential growth of research activities in applied computer science and system biology. We sincerely hope you would extend your full cooperation and support the open access publishing for significant scientific output.