# Preface

Phenomenal increase in both speeds of computation and amounts of biological data which require processing have led to the emergence of a new field of study which has been called *Computational Biology*. The term includes computations of two kinds largely. The first involves simulating biological phenomena on a computer. The second involves using computation to process and interpret biological data resulting from experiments. There has much work in recent years on both kinds of problems, justifying a special issue of this journal on Computational Biology.

This special issue features papers on both the above kinds of computational biology. There are 5 papers in all. The first paper titled "Computational Molecular Biology: A survey of problems and tools", by L. Parida deals with computational problems motivated by the *Human Genome Project*, which aims at sequencing the genomes of various organisms. The next two papers, namely "Protein Dynamics: Molecular simulations of RNase A and related proteins" by G. Nadig, R. Varadarajan and S. Vishveshwara, and 'Design of rapidly folding protein-like heteroploymer chains and their cell dynamics: A Lattice Model study" by S. Vishveshwara, I. Shrivastava, M. Cieplak and J. R. Banawar, describe computer simulation studies concerning *Protein Folding and Dynamics*. The fourth paper, "Consensus of Trees – Desirable Properties and Computational Methods" by S. Kannan and Z. Sweedyk deals with such consensus structures as *Evolutionary Trees* in a rather general setting. The fifth paper "The spatial organization of plant communities in a deciduous forest: A computational geometry based analysis" by N. V. Joshi, H. S. Suresh, H. S. Dattaraj and R. Sukumar uses *Computational Geometry* tools to analyze spatial organizations of plant communities. It is hoped that the 5 papers together provide a flavour of the various issues and problems in Computational Biology.

I would like to thank Prof. M. S. Shaila and Prof. V. S. Borkar for asking me to guest-edit this issue. Thanks also to Mr. N. M. Malwad, Mr. K. Sreenivasa Rao and Ms. R. Geetha for their help in processing the submissions and coordinating the editing and printing process.

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