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## Editorial

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**Biographical notes:** Rubem P. Mondaini is a Professor of Optimisation and Mathematical Biology at the Federal University of Rio de Janeiro, RJ. He is the founder of the BIOMAT Consortium – BIOMAT Institute for Advanced Studies of Biosystems – <http://www.biomat.org> – a non-profit association of scientists from universities and research centres of many countries which has been responsible for the organisation of the annual series of BIOMAT Symposia since the year 2001.

Panos M. Pardalos is Distinguished Professor of Industrial and Systems Engineering at the University of Florida. He is also affiliated faculty member of the Computer Science Department, the Hellenic Studies Center, and the Biomedical Engineering Department. He is also the Director of the Center for Applied Optimization. He received the degrees of Honorary Doctor from Lobachevski University (Russia) and the V.M. Glushkov Institute of Cybernetics, Ukraine. He is a fellow of AAAS, a fellow of INFORMS, and in 2001 he was awarded the Greek National Award and Gold Medal for Operations Research. His recent research interests include network problems, global optimisation and applications, energy, data mining, biomedical applications, and massive computing.

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The present issue of the *International Journal of Bioinformatics Research and Applications* contains some selected papers from BIOMAT 2007, the *Seventh International Symposium on Mathematical and Computational Biology*, which was held

at Armação dos Búzios, RJ, Brazil, in November 2007. There were 150 submitted papers and about 120 participants with 15 Keynote Speakers and 32 contributed papers with authors coming from Europe, USA, Asia and Africa. The level of acceptance for the two publication vehicles of the BIOMAT 2007 Symposium was of 25% and this is the tradition of the BIOMAT series.

The first BIOMAT Symposium – BIOMAT 2001, was held in Rio de Janeiro on April 2001 with 273 participants. The BIOMAT Consortium was then founded in order to organise a series of international interdisciplinary symposia on Mathematical and Computational Biology. The BIOMAT 2002 and BIOMAT 2003 symposia were held in Rio de Janeiro on September 2002 and November 2003, respectively. The BIOMAT 2004 symposium was held in Ilhéus, state of Bahia, Brazil. The BIOMAT 2005 was held in Petrópolis, RJ, Brazil, on December 2005 and the BIOMAT 2006 was held in Manaus, state of Amazonas, Brazil, on November 2006. The BIOMAT 2008 Symposium was held in Campos do Jordão, state of S. Paulo, Brazil, on November 2008. The BIOMAT 2009 Symposium is scheduled to be held in Brasília, DF, Brazil, on September 2009. The BIOMAT 2010 Symposium will be a joint meeting with the prestigious SMB 2010 annual meeting, to be held at Rio de Janeiro, RJ, on July 2010, by decision of the SMB Board of Directors.

This issue has eight selected papers. Two of these papers, the first and the seventh, by A. Goriely et al. and R.P. Mondaini, respectively, are theoretical essays about helical and coil curves and other possibilities for modelling the characteristic sequences of atom sites in proteins and biomacromolecules in general. The second paper is a computational study of the causal agent of “witches broom disease” – *Moniliophthora perniciosa* (Stahel) (Singer) which can infect *Theobroma cacao*. The design of new inhibitors can be realised by targets as the potential enzymes of *M. perniciosa* like pyrophosphorylase. Its 3D structure was obtained by comparative modelling approach. Methods of Molecular Dynamics have provided the necessary calculation and the Ramachandran plot was used to validate the resulting model.

The third paper is the description of a molecular model for the 3-dimensional structure of the key enzyme Purine Nucleoside Phosphorylase (PNP) from *Toxoplasma gondii*, where the PNP from *Plasmodium falciparum* is used as a template. The stability of the model has been tested by Molecular Dynamics.

The fourth paper selected paper of this issue is an introduction of an approach to solve the phylogeny problem. An algorithmic representation of a phylogenetic tree is introduced with the computational of total parsimony and the description of the proposed heuristic.

In the fifth paper, the statistical properties of time variation in profiles of global gene expression are studied on the model organism *Saccharomyces cerevisiae*. A relation between connectivity of transcriptional regulatory gene networks and the relative fluctuations of mean expression of temporal transcription noise is then emphasised as a conjecture. This is then confirmed for two samples of a 93 genes set of the regulatory network: randomly selected genes and subsets of connecting genes forming a percolating cluster.

The sixth paper is an essay on the screening of epileptic patients through optimisation and data mining techniques as an alternative to the neurophysiological signals used by neurologists. This study is essentially based on a multidimensional time series to identify abnormal brain patterns with epileptic configurations. This multidimensional data mining framework is then proposed to revolutionise the diagnosis of epilepsy.

The eighth paper is an approach for dealing with missing values through fuzzy clustering and resampling by considering the missing values to be at random completely. Relevant partitions with high level of missing values can be identified by this method.