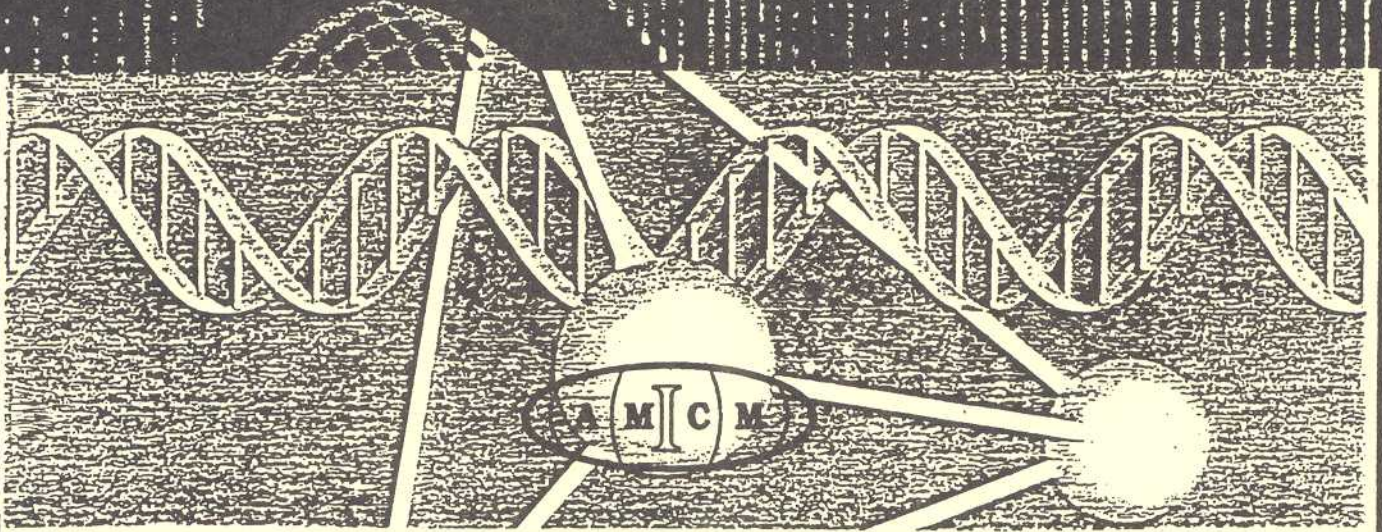


# BOOK OF ABSTRACTS



## Eleventh International Conference on Mathematical and Computer Modelling and Scientific Computing

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Washington, DC, U.S.A.

$$\rho \frac{\partial V_\alpha}{\partial t} + \rho \left( V_R \frac{\partial V_R}{\partial R} + \frac{V_\alpha}{R} \frac{\partial V_\alpha}{\partial \alpha} + \frac{V_\alpha V_R}{R} + \frac{V_\theta}{R \sin \alpha} \frac{\partial V_\alpha}{\partial \theta} - \frac{V_\theta^2 \cot \alpha}{R} \right)$$

Modelling

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## A FRAMEWORK FOR AUTOMATED COMPARISON OF COMPLETE PROKARYOTIC GENOMES

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An automated pair-wise cross-species comparison of complete genome will provide a cost-effective and time-efficient computational tool to derive the functions of genes, gene conservation, mechanism of evolution, metabolic pathways and their variations within various organisms. In this paper, we describe a framework for an automated comparison of complete prokaryotic genomes to derive putative orthologues, paralogues, gene-groups, fused genes, and gene-replications. The framework has three stages: blast comparison to filter gene-pairs with high similarity, matching of filtered gene-pairs using Smith-Waterman's algorithm for pair-wise alignment, and graph matching and fuzzy logic techniques to resolve ambiguities in identifying orthologues and paralogues, gene-groups, fused-genes, and gene-replications. The application of graph matching technique is the novel contribution in the paper. The graph matching stage represents pair of complete genomes as bipartite graphs with each gene as a node, and develops variations of stable marriage techniques in a bipartite graph to identify gene-groups, and resolve ambiguities in gene-pair matching to identify orthologues and paralogues. Algorithms and a general purpose software has been described. The results derived from automatic comparison describing the presence of putative orthologues and gene-groups and fused-genes and gene-replication have been discussed briefly.