

MATHEMATICS AND MOLECULAR BIOLOGY VII: MODELING ACROSS THE SCALES — ATOMS TO ORGANISMS

*January 5–10, 2002
La Fonda Hotel, Santa Fe, NM*

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Analysis of Topological properties of closed curves in confined volumes: Applications to DNA packing

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Role of Conformational Entropy in Increased Rates of Intramo

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Time-resolved X-ray Crystallography of the Photosynthetic Reaction Center of *Rhodospseudomonas viridis*

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The Molecular Xerox machine caught in action: Visualization of DNA Polymerase Activity at the Single Molecule Level

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Working with noisy microarray data

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Globally coupled oscillator networks

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Correlating Sequence Motifs with Transcriptional Regulation

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Towards a Model of the Cell Cycle Protein Network

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ELECTROKINETIC ANALYSIS OF THREE-DIMENSIONAL CELLULAR MICROA

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K*SYNC: throwing everything at sequence to structure alignme

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Barnacle: An Assembly Algorithm for Clone-based Sequences of Whole Genomes

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molecular dynamics modeling of endothelial differentiation gene receptors

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Rate Based or Spike-Time Based Learning Rule?

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Computational studies on an unusual amidase antibody

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Transitional States in Double Helical DNA

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Influence of DNA intrinsic curvature on binding cooperativity of intercalating agents

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Topology of Spiral Waves in Excitable Media

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Spindle Pole Separation During Prophase: A Quantitative Model

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Isothermal Compressibility and the Intraprotein and Protein-water Interaction in Globular Proteins

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Structural studies of prokaryotic transcription

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Resolution of DNA knots in *E. coli*

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Mathematical structures for description and manipulation of

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pKa VALUES OF BURIED IONIZABLE RESIDUES: STRINGENT BENCHMARK

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Mechanical Unfolding of Individual *T. Thermophila* Ribozymes (Onoa *et al.*)
Experimental Test of Jarzynski's Equality (Liphardt *et al.*)

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Evolution as a thermodynamic process

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Artificial Networks and Noise

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Linkage Parameters for Clustering Complete Proteins

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Methods for inference of genetic regulatory networks

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The Molecular Control of Cell Movements in the Early Vertebrate

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Statistical Methods for the Analysis of Comparative Genomic Hybridization (CGH) data

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Evaluating metabolic pathways through gene expression data

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The Human STAGA: more than just a Histone Acetyltransferase

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Simple Motor Gestures for Birdsong

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MULTIPLE TESTING IN MICROARRAY DATA ANALYSIS

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Simultaneous Gene Clustering and Subset Selection for Classification via MDL

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The Origins of Symmetry Breaking in the Folding of Proteins

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EXPERIMENTAL DESIGN AND STATISTICAL INFERENCE FOR GENE EXPRESSION

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Stochastically gated diffusion: ligand escape out of a protein

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Rhythms in the nervous system: themes and variations

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The Classification of Rational Knots and Tangles — A Combinatorial Proof

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The New Frontier: Modeling The Impact of Human Activities in the Amazonian Forest

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Large-scale Distributed Docking Using AutoDock

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A Genetic Algorithm for Structure-Based De Novo Design

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The antigenic evolution of influenza A

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Global cis-regulatory motif identification through comparative genomic analysis of regulatory regions in hemiascomycetous yeast

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COMPUTATIONAL IDENTIFICATION OF REGULATORY "MODULES" IN THE GENOME OF DROSOPHILA MELANOGASTER

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Singular Value Decomposition for Gene Expression Data Analysis

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Neuronal Responses to Aperiodic Stimuli

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Fluorescent microscopy, microarrays and circadian rhythms

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Stability of Intracellular Calcium Waves

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The probability of topological concordance of gene trees

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Understanding the function of a photosensory protein based on gas-phase spectroscopy of its chromophore

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Representing target range and texture in the auditory system

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Removing DNA-bound Proteins by Stretching, Twisting, and Unzipping DNA

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Polymerase beta opening motion explored by dynamic simulation

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Discovering the mechanical functions of proteins and DNA

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GenePath: A SYSTEM FOR AUTOMATED EXPLORATION OF GENETIC PATH

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Microarray Analysis of Dictyostelium Development

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The Form of Shapes and How We Learn to See Them

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Reversible and irreversible unfolding of single RNA molecule

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WEIGHBOR: AN IMPROVED LIKELIHOOD-LIKE METHOD FOR PHYLOGENETIC RECONSTRUCTION

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Differential phosphorylation of Pho4 leads to differential

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Mechanism of acetylcholinesterase inhibition by fasciculin

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Structure, Function and Localization of PKA: An Interdisciplinary Approach

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FIRST-PRINCIPLES MOLECULAR DYNAMICS STUDY OF THE ACTIVE SITE

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Probabilistic clustering of sequences: Inferring bacterial

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THE PROTEIN FOLDING KINETICS FOR THE DIFFUSION-COLLISION MODEL

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Recombination Preserves Protein Building Blocks

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Precise timing in early response to electric stimulation in dense cultures of cortical neurons

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DNA Hybridization Modeling and its Application to the Design

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Regulatory networks revealed by transcriptional profiling in the yeast

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BALSA: A Bayesian Algorithm for Local Sequence Alignment

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Spontaneous calcium release in ventricular myocytes: mechanisms and implications

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The Challenge of Building Responsive Bioinformatics Support in a Rapidly Evolving World

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Review & discuss recent progress related to several important issues in microarray analysis—Joint analysis of match & mismatch probes in Affymetrix arrays—How to handle signal saturation—Methods to incorporate more bio. info. into the analysis

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Rate Based or Spike-Time Based Learning Rule? A Model

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TOWARDS COMPREHENSIVE ANALYSIS OF SYNTHETIC LETHAL GENETIC I

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The entropic benefit of a cross-link in protein association

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The evolution of DNA regulatory regions for proteo-gamma

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