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	Nota di contenuto	CONTENTS; PREFACE; PROGRAM COMMITTEE; KINETIC MODELLING OF DNA REPLICATION INITIATION IN BUDDING YEAST; 1. Introduction; 2. ODE Model of the DNA Replication Initiation; 2.1. Model Construction; 2.2. Deriving Parameters from Experimental Data; 2.3. Fitting Parameters to Experimental Data; 3. Results; 3.1. Simulation Results and Network Properties; 3.2. DNA Replication Mutants; 4. Discussion; 5. Conclusion; Acknowledgments; Appendix A.; Appendix A.1. Detailed Description of the Replisome Activation; Appendix A.1.1. Assembly of the Pre-RC
		Appendix A.1.2. Assembly of the Pre-IC and Replisome Activation References; PREDICTING PROTEIN COMPLEX GEOMETRIES WITH LINEAR SCORING FUNCTIONS; 1. Introduction; 2. Methods; 2.1. Database of protein complexes and decoys; 2.2. Linear scoring function; 3. Results and Discussion; 3.1. Performance comparison; 4. Conclusions; Acknowledgments; References; CHARACTERIZING COMMON SUBSTRUCTURES OF LIGANDS FOR GPCR PROTEIN SUBFAMILIES; 1.

Introduction; 2. Methods; 2.1. Dataset; 2.2. Chemical structure comparison; 2.3. Extracting common substructures; 3. Results; 4. Discussion; Acknowledgments; References
A SYSTEMS BIOLOGY APPROACH: MODELLING OF AQUAPORIN-2 TRAFFICKING 1. Introduction; 1.1. Biological background; 1.2. Existing models; 1.3. Aims; 2. Methods; 2.1. Time course simulation, parameter estimation and time-dependent sensitivity analysis; 2.2. Cell surface biotinylation; 3. Results; 3.1. The model; 3.2. Time course simulation and parameter estimation; 3.3. Model variations and ranking; 3.4. Time-dependent sensitivity analysis; 3.5. Experiment: AQP2 transloeation after dDAVP stimulation; 3.6. Model predictions, analysis, and comparison with recent data; 4. Discussion; Acknowledgements References COMPARISON OF GENE EXPRESSION PROFILES PRODUCED BY CAGE, ILLUMINA MICRO-ARRAY AND REAL TIME RT-PCR; 1. Introduction; 2. Materials and Methods; 2.1. CAGE data summary; 2.2. Qualitative comparison between CAGE, illumina microarray and qRT-PCR; 2.3. Correlation analysis; 3. Results and Discussions; 3.1. Qualitative analysis; 3.2. Quantitative analysis; 4. Conclusions; Acknowledgements; References; ON THE PERFORMANCE OF METHODS FOR FINDING A SWITCHING MECHANISM IN GENE EXPRESSION; 1. Introduction; 2. Method; 2.1. Notations and preliminaries
2.2. Fast finding three-way gene interaction (FTGI)2.2.1. Logistic regression; 2.2.2. Log-likelihood test; 2.2.3. Mean-Co-variance (MC) test; 2.2.4. Procedure of FTGI; 2.3. The difference of correlation coefficients; 2.3.1. Pearson correlation coefficient; 2.3.2. Spearman correlation coefficient; 2.3.3. Biweight midcorrelation; 3. Experimental Result; 3.1. Data; 3.2. Computation time; 3.3. Top ranked gene combinations; 4. Discussion; Acknowledgements; References; GENE REGULATORY NETWORK CLUSTERING FOR GRAPH LAYOUT BASED ON MICROARRAY GENE EXPRESSION DATA; 1. Introduction; 2. Methods 2.1. Model setting

Sommario/riassunto	This volume contains 18 peer-reviewed papers based on the presentations at the 10th Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2010) held at Kyoto University from July 26 to July 28, 2010. This workshop started in 2001 as an event for doctoral students and young researchers to present and discuss their research results and approaches in bioinformatics and systems biology. It is part of a collaborative educational program involving leading institutions and leaders committed to the following programs: Boston - Graduate Program in Bioinformatics, Boston University;