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C.W. Li, W.C. Chang, & B.S. Chen. System Identification and Robustness Analysis of the Circadian Regulatory Network via Microarray Data in Arabidopsis Thaliana 1 Introduction; 2 Dynamic System Description of Circadian Regulatory Model; 3. Assay of the Model; 3.1. Assay of ARX System Model; 3.1.1. Determination of system order; 3.2. Sensitivity Analysis of Circadian System; 3.2.1. Circadian clock frequency assay; 3.2.2. Trans-perturbation assay; 3.2.2.1. Trans-sensitivity rate Y simulation of gene; 3.2.2.2 Trans-expression threshold M1 simulation of gene; 4. Results; 5. Discussion

Acknowledgments References; P. Horton, K.-J. Park, T. Obayashi, & K. Nakai. Protein Subcellular Localization Prediction with WoLF PSORT; 1. Introduction; 2. Methods; 2.1. Dataset; 2.1.1. Site Definition; 2.2. WoLF PSORT system; 2.3. Classification; 2.3.1. Candidate Features; 2.3.2. Classification Algorithm; 2.3.3. Extensions for Dual Localization Prediction; 2.3.4. Feature Selection and Weighting; 2.3.5. Reducing Over-reliance on Sequence Similarity; 2.3.6. Evaluation of WoLF PSORT Accuracy; 3. Results; 3.1. Effect of Feature Weighting; 3.2. WoLF PSORT Combined with BLAST

3.3. WoLF PSORT Server 4. Discussion; 4.1. Interpretable Results; 4.2. Evaluation in the Presence of Similar Sequences; 4.3. Predicting Dual Localization; 5. Conclusion; 6. Acknowledgement; References; P.-H. Chi & C.-R. Shyu. Predicting Ranked SCOP Domains by Mining Associations of Visual Contents in Distance Matrices; 1. Introduction; 2. Preliminaries; 3. Method; 3.1. Space Partition Algorithm Using C4.5 Decision Tree; 3.2. Mining Training Data and Prediction Model; 4. Experiment; 5. Conclusion; References; D. Ruths & L. Nakhleh. RECOMP: A Parsimony-Based Method for Detecting Recombination

1. Introduction

## Sommario/riassunto

High-throughput sequencing and functional genomics technologies have given us a draft human genome sequence and have enabled large-scale genotyping and gene expression profiling of human populations. Databases containing large numbers of sequences, polymorphisms, and gene expression profiles of normal and diseased tissues in different clinical states are rapidly being generated for human and model organisms. Bioinformatics is thus rapidly growing in importance in the annotation of genomic sequences, in the understanding of the interplay between genes and proteins, in the analysis of the genetics