

Список литературы

- [1] Rezwan, F, Sun, Y, Davey, N, Rust, A. G, & Robinson, M. (2011) *Effect of Using Varying Negative Examples in Transcription Factor Binding Site Predictions*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 1–12.
- [2] Farinaccio, A, Vanneschi, L, Provero, P, Mauri, G, & Giacobini, M. (2011) *A New Evolutionary Gene Regulatory Network Reverse Engineering Tool*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 13–24.
- [3] Quader, S, Snyder, N, Su, K, Mochan, E, & Huang, C.-H. (2011) *ML-Consensus: A General Consensus Model for Variable-Length Transcription Factor Binding Sites*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 25–36.
- [4] Qi, J, Michoel, T, & Butler, G. (2011) *Applying linear models to learn regulation programs in a transcription regulatory module network*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 37–48.
- [5] Holzinger, E. R, Dudek, S. M, Torstenson, E. C, & Ritchie, M. D. (2011) *ATHENA Optimization: The Effect of Initial Parameter Settings Across Different Genetic Models*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 49–60.
- [6] Darabos, C, Di Cunto, F, Tomassini, M, Moore, J. H, Provero, P, & Giacobini, M. (2011) *Validating a Threshold-based Boolean Model of Regulatory Networks on a Biological Organism*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 61–70.
- [7] Asencio-Cortés, G, Aguilar-Ruiz, J. S, & Márquez-Chamorro, A. E. (2011) *A nearest neighbour-based approach for viral protein structure prediction*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 71–79.
- [8] Sciacca, E, Spinella, S, Ienco, D, & Giannini, P. (2011) *Annotated Stochastic Context Free Grammars for Analysis and Synthesis of Proteins*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 80–91.
- [9] González-Álvarez, D. L, Vega-Rodríguez, M. A, Gómez-Pulido, J. A, & Sánchez-Pérez, J. M. (2011) *Finding Motifs in DNA Sequences Applying a Multiobjective Artificial Bee Colony (MOABC) Algorithm*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 92–103.
- [10] Márquez-Chamorro, A. E, Divina, F, Aguilar-Ruiz, J. S, & Asencio-Cortés, G. (2011) *An Evolutionary Approach for Protein Contact Map Prediction*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 104–114.
- [11] Laroum, S, Duval, B, Tessier, D, & Hao, J.-K. (2011) *Multi-neighborhood search for discrimination of signal peptides and transmembrane segments*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 115–126.
- [12] Hinselmann, G, Jahn, A, Fechner, N, Rosenbaum, L, & Zell, A. (2011) *Approximation of Graph Kernel Similarities for Chemical Graphs by Kernel Principal Component Analysis*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 127–138.
- [13] Chhel, F, Goëffon, A, Lardeux, F, Saubion, F, Hunault, G, & Boureau, T. (2011) *Experimental Approach for Bacterial Strains Characterization*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 139–144.
- [14] Ferreri, L, Venturino, E, & Giacobini, M. (2011) *Do Diseases Spreading on Bipartite Networks Have Some Evolutionary Advantage?*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 145–150.

- [15] Leonarski, F, Trovato, F, Tozzini, V, & Trylska, J. (2011) *Genetic Algorithm Optimization of Force Field Parameters. Application to a Coarse-Grained Model of RNA*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 151–156.
- [16] Toca, C. E. S, Márquez-Chamorro, A. E, Asencio-Cortés, G, & Aguilar-Ruiz, J. S. (2011) *A decision tree-based method for protein contact map prediction*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 157–162.
- [17] Silva, S, Anunciao, O, & Lotz, M. (2011) *A Comparison of Machine Learning Methods for the Prediction of Breast Cancer*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 163–174.
- [18] Toti, D, Atzeni, P, & Polticelli, F. (2011) *An Automatic Identification and Resolution System for Protein-related Abbreviations in Scientific Papers*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 175–180.
- [19] Yeu, Y, Ahn, J, Yoon, Y, & Park, S. (2011) *Protein Complex Discovery from Protein Interaction Network with High False-Positive Rate*, LNCS eds. Pizzuti, C, Ritchie, M. D, & Giacobini, M. (Springer Verlag, Turin, Italy), Vol. 6623, pp. 181–186.