

Список литературы

- [1] F. REZWAN, Y. SUN, N. DAVEY, A. G. RUST, and M. ROBINSON, Effect of Using Varying Negative Examples in Transcription Factor Binding Site Predictions, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 1–12, Turin, Italy, 2011, Springer Verlag.
- [2] A. FARINACCIO, L. VANNESCHI, P. PROVERO, G. MAURI, and M. GIACOBINI, A New Evolutionary Gene Regulatory Network Reverse Engineering Tool, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 13–24, Turin, Italy, 2011, Springer Verlag.
- [3] S. QUADER, N. SNYDER, K. SU, E. MOCHAN, and C.-H. HUANG, ML-Consensus: A General Consensus Model for Variable-Length Transcription Factor Binding Sites, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 25–36, Turin, Italy, 2011, Springer Verlag.
- [4] J. QI, T. MICHOEL, and G. BUTLER, Applying linear models to learn regulation programs in a transcription regulatory module network, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 37–48, Turin, Italy, 2011, Springer Verlag.
- [5] E. R. HOLZINGER, S. M. DUDEK, E. C. TORSTENSON, and M. D. RITCHIE, ATHENA Optimization: The Effect of Initial Parameter Settings Across Different Genetic Models, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 49–60, Turin, Italy, 2011, Springer Verlag.
- [6] C. DARABOS, F. DI CUNTO, M. TOMASSINI, J. H. MOORE, P. PROVERO, and M. GIACOBINI, Validating a Threshold-based Boolean Model of Regulatory Networks on a Biological Organism, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 61–70, Turin, Italy, 2011, Springer Verlag.
- [7] G. ASECIO-CORTÉS, J. S. AGUILAR-RUIZ, and A. E. MÁRQUEZ-CHAMORRO, A nearest neighbour-based approach for viral protein structure prediction, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 71–79, Turin, Italy, 2011, Springer Verlag.
- [8] E. SCIACCA, S. SPINELLA, D. IENCO, and P. GIANNINI, Annotated Stochastic Context Free Grammars for Analysis and Synthesis of Proteins, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 80–91, Turin, Italy, 2011, Springer Verlag.
- [9] D. L. GONZÁLEZ-ÁLVAREZ, M. A. VEGA-RODRÍGUEZ, J. A. GÓMEZ-PULIDO, and J. M. SÁNCHEZ-PÉREZ, Finding Motifs in DNA Sequences Applying a Multiobjective Artificial Bee Colony (MOABC) Algorithm, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 92–103, Turin, Italy, 2011, Springer Verlag.
- [10] A. E. MÁRQUEZ-CHAMORRO, F. DIVINA, J. S. AGUILAR-RUIZ, and G. ASECIO-CORTÉS, An Evolutionary Approach for Protein Contact Map Prediction, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO*

- 2011, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 104–114, Turin, Italy, 2011, Springer Verlag.
- [11] S. LAROUM, B. DUVAL, D. TESSIER, and J.-K. HAO, Multi-neighborhood search for discrimination of signal peptides and transmembrane segments, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 115–126, Turin, Italy, 2011, Springer Verlag.
 - [12] G. HINSELMANN, A. JAHN, N. FECHNER, L. ROSENBAUM, and A. ZELL, Approximation of Graph Kernel Similarities for Chemical Graphs by Kernel Principal Component Analysis, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 127–138, Turin, Italy, 2011, Springer Verlag.
 - [13] F. CHHEL, A. GOËFFON, F. LARDEUX, F. SAUBION, G. HUNAUT, and T. BOUREAU, Experimental Approach for Bacterial Strains Characterization, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 139–144, Turin, Italy, 2011, Springer Verlag.
 - [14] L. FERRERI, E. VENTURINO, and M. GIACOBINI, Do Diseases Spreading on Bipartite Networks Have Some Evolutionary Advantage?, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 145–150, Turin, Italy, 2011, Springer Verlag.
 - [15] F. LEONARSKI, F. TROVATO, V. TOZZINI, and J. TRYLSKA, Genetic Algorithm Optimization of Force Field Parameters. Application to a Coarse-Grained Model of RNA, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 151–156, Turin, Italy, 2011, Springer Verlag.
 - [16] C. E. S. TOCA, A. E. MÁRQUEZ-CHAMORRO, G. ASENCIO-CORTÉS, and J. S. AGUILAR-RUIZ, A decision tree-based method for protein contact map prediction, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 157–162, Turin, Italy, 2011, Springer Verlag.
 - [17] S. SILVA, O. ANUNCIAO, and M. LOTZ, A Comparison of Machine Learning Methods for the Prediction of Breast Cancer, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 163–174, Turin, Italy, 2011, Springer Verlag.
 - [18] D. TOTI, P. ATZENI, and F. POLITICELLI, An Automatic Identification and Resolution System for Protein-related Abbreviations in Scientific Papers, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 175–180, Turin, Italy, 2011, Springer Verlag.
 - [19] Y. YEU, J. AHN, Y. YOON, and S. PARK, Protein Complex Discovery from Protein Interaction Network with High False-Positive Rate, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by C. PIZZUTI, M. D. RITCHIE, and M. GIACOBINI, volume 6623 of *LNCS*, pp. 181–186, Turin, Italy, 2011, Springer Verlag.