

Список литературы

- [1] REZWAN, F. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 1–12, Turin, Italy, 2011, Springer Verlag.
- [2] FARINACCIO, A. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 13–24, Turin, Italy, 2011, Springer Verlag.
- [3] QUADER, S. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 25–36, Turin, Italy, 2011, Springer Verlag.
- [4] QI, J. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 37–48, Turin, Italy, 2011, Springer Verlag.
- [5] HOLZINGER, E. R. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 49–60, Turin, Italy, 2011, Springer Verlag.
- [6] DARABOS, C. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 61–70, Turin, Italy, 2011, Springer Verlag.
- [7] ASECIO-CORTÉS, G. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 71–79, Turin, Italy, 2011, Springer Verlag.
- [8] SCIACCA, E. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 80–91, Turin, Italy, 2011, Springer Verlag.
- [9] GONZÁLEZ-ÁLVAREZ, D. L. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 92–103, Turin, Italy, 2011, Springer Verlag.
- [10] MÁRQUEZ-CHAMORRO, A. E. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 104–114, Turin, Italy, 2011, Springer Verlag.
- [11] LAROUM, S. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 115–126, Turin, Italy, 2011, Springer Verlag.
- [12] HINSELMANN, G. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 127–138, Turin, Italy, 2011, Springer Verlag.

- [13] CHHEL, F. et al., Experimental approach for bacterial strains characterization, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, edited by PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 139–144, Turin, Italy, 2011, Springer Verlag.
- [14] FERRERI, L. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 145–150, Turin, Italy, 2011, Springer Verlag.
- [15] LEONARSKI, F. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 151–156, Turin, Italy, 2011, Springer Verlag.
- [16] TOCA, C. E. S. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 157–162, Turin, Italy, 2011, Springer Verlag.
- [17] SILVA, S. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 163–174, Turin, Italy, 2011, Springer Verlag.
- [18] TOTI, D. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 175–180, Turin, Italy, 2011, Springer Verlag.
- [19] YEU, Y. et al., 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 PIZZUTI, C. et al., volume 6623 of *LNCS*, pages 181–186, Turin, Italy, 2011, Springer Verlag.