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 *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 C. Pizzuti, M. D. Ritchie, and M. Giacobini, volume 6623 of *LNCS*, pp. 61–70, Turin, Italy, 2011, Springer Verlag.

[7] G. Asencio-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. Asencio-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 *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 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. Polticelli, 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.