## 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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 1–12.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 13-24.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 25-36.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 37-48.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 49-60.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 61-70.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 71-79.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 80-91.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 92-103.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 104–114.

- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 115–126.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 127-138.
- [13] F. Chhel, A. Goëffon, F. Lardeux, F. Saubion, G. Hunault, 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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 139–144.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 145-150.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 151–156.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 157–162.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 163–174.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 175–180.
- [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, ser. LNCS, C. Pizzuti, M. D. Ritchie, and M. Giacobini, Eds., vol. 6623. Turin, Italy: Springer Verlag, 27-29 April 2011, pp. 181–186.