

## Список литературы

- [1] REZWAN, F., SUN, Y., DAVEY, N., RUST, A. G., and ROBINSON, M., Effect of using varying negative examples in transcription factor binding site predictions, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 1–12, Turin, Italy, 2011, Springer Verlag.
- [2] FARINACCIO, A., VANNESCHI, L., PROVERO, P., MAURI, G., and GIACOBINI, M., A new evolutionary gene regulatory network reverse engineering tool, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 13–24, Turin, Italy, 2011, Springer Verlag.
- [3] QUADER, S., SNYDER, N., SU, K., MOCHAN, E., and HUANG, C.-H., ML-Consensus: a general consensus model for variable-length transcription factor binding sites, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 25–36, Turin, Italy, 2011, Springer Verlag.
- [4] QI, J., MICHOEL, T., and BUTLER, G., Applying linear models to learn regulation programs in a transcription regulatory module network, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 37–48, Turin, Italy, 2011, Springer Verlag.
- [5] HOLZINGER, E. R., DUDEK, S. M., TORSTENSON, E. C., and RITCHIE, M. D., ATHENA optimization: The effect of initial parameter settings across different genetic models, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 49–60, Turin, Italy, 2011, Springer Verlag.
- [6] DARABOS, C., Di Cunto, F., TOMASSINI, M., MOORE, J. H., PROVERO, P., et al., Validating a threshold-based boolean model of regulatory networks on a biological organism, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 61–70, Turin, Italy, 2011, Springer Verlag.
- [7] ASECIO-CORTÉS, G., AGUILAR-RUIZ, J. S., and MÁRQUEZ-CHAMORRO, A. E., A nearest neighbour-based approach for viral protein structure prediction, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 71–79, Turin, Italy, 2011, Springer Verlag.
- [8] SCIACCA, E., SPINELLA, S., IENCO, D., and GIANNINI, P., Annotated stochastic context free grammars for analysis and synthesis of proteins, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 80–91, Turin, Italy, 2011, Springer Verlag.
- [9] GONZÁLEZ-ÁLVAREZ, D. L., VEGA-RODRÍGUEZ, M. A., GÓMEZ-PULIDO, J. A., and SÁNCHEZ-PÉREZ, J. M., Finding motifs in DNA sequences applying a multiobjective artificial bee colony (MOABC) algorithm, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 92–103, Turin, Italy, 2011, Springer Verlag.
- [10] MÁRQUEZ-CHAMORRO, A. E., DIVINA, F., AGUILAR-RUIZ, J. S., and ASECIO-CORTÉS, G., An evolutionary approach for protein contact map prediction, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on*

*Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 104–114, Turin, Italy, 2011, Springer Verlag.

- [11] LAROUM, S., DUVAL, B., TESSIER, D., and HAO, J.-K., Multi-neighborhood search for discrimination of signal peptides and transmembrane segments, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 115–126, Turin, Italy, 2011, Springer Verlag.
- [12] HINSELMANN, G., JAHN, A., FECHNER, N., ROSENBAUM, L., and ZELL, A., Approximation of graph kernel similarities for chemical graphs by kernel principal component analysis, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 127–138, Turin, Italy, 2011, Springer Verlag.
- [13] CHHEL, F., GOËFFON, A., LARDEUX, F., SAUBION, F., HUNAULT, G., et al., Experimental approach for bacterial strains characterization, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 139–144, Turin, Italy, 2011, Springer Verlag.
- [14] FERRERI, L., VENTURINO, E., and GIACOBINI, M., Do diseases spreading on bipartite networks have some evolutionary advantage?, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 145–150, Turin, Italy, 2011, Springer Verlag.
- [15] LEONARSKI, F., TROVATO, F., TOZZINI, V., and TRYLSKA, J., Genetic algorithm optimization of force field parameters. application to a coarse-grained model of RNA, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 151–156, Turin, Italy, 2011, Springer Verlag.
- [16] TOCA, C. E. S., MÁRQUEZ-CHAMORRO, A. E., ASENCIO-CORTÉS, G., and AGUILAR-RUIZ, J. S., A decision tree-based method for protein contact map prediction, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 157–162, Turin, Italy, 2011, Springer Verlag.
- [17] SILVA, S., ANUNCIAO, O., and LOTZ, M., A comparison of machine learning methods for the prediction of breast cancer, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 163–174, Turin, Italy, 2011, Springer Verlag.
- [18] TOTI, D., ATZENI, P., and POLITICELLI, F., An automatic identification and resolution system for protein-related abbreviations in scientific papers, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 175–180, Turin, Italy, 2011, Springer Verlag.
- [19] YEU, Y., AHN, J., YOON, Y., and PARK, S., Protein complex discovery from protein interaction network with high false-positive rate, in PIZZUTI, C., RITCHIE, M. D., and GIACOBINI, M., editors, *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, pp. 181–186, Turin, Italy, 2011, Springer Verlag.