

Список литературы

- [Asencio-Cortés et al., 2011] Asencio-Cortés, G., Aguilar-Ruiz, J. S., & Márquez-Chamorro, A. E. (2011). A nearest neighbour-based approach for viral protein structure prediction. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 71–79
- [Chhel et al., 2011] Chhel, F., Goëffon, A., Lardeux, F., Saubion, F., Hunault, G., & Boureau, T. (2011). Experimental approach for bacterial strains characterization. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 139–144
- [Darabos et al., 2011] Darabos, C., Di Cunto, F., Tomassini, M., Moore, J. H., Provero, P., & Giacobini, M. (2011). Validating a threshold-based boolean model of regulatory networks on a biological organism. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 61–70
- [Farinaccio et al., 2011] Farinaccio, A., Vanneschi, L., Provero, P., Mauri, G., & Giacobini, M. (2011). A new evolutionary gene regulatory network reverse engineering tool. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 13–24
- [Ferreri et al., 2011] Ferreri, L., Venturino, E., & Giacobini, M. (2011). Do diseases spreading on bipartite networks have some evolutionary advantage? *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 145–150
- [González-Álvarez et al., 2011] González-Álvarez, D. L., Vega-Rodríguez, M. A., Gómez-Pulido, J. A., & Sánchez-Pérez, J. M. (2011). Finding motifs in DNA sequences applying a multiobjective artificial bee colony (MOABC) algorithm. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 92–103
- [Hinselmann et al., 2011] Hinselmann, G., Jahn, A., Fechner, N., Rosenbaum, L., & Zell, A. (2011). Approximation of graph kernel similarities for chemical graphs by kernel principal component analysis. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 127–138
- [Holzinger et al., 2011] Holzinger, E. R., Dudek, S. M., Torstenson, E. C., & Ritchie, M. D. (2011). ATHENA optimization: The effect of initial parameter settings across different genetic models. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 49–60
- [Laroum et al., 2011] Laroum, S., Duval, B., Tessier, D., & Hao, J.-K. (2011). Multi-neighborhood search for discrimination of signal peptides and transmembrane segments. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 115–126
- [Leonarski et al., 2011] Leonarski, F., Trovato, F., Tozzini, V., & Trylska, J. (2011). Genetic algorithm optimization of force field parameters. application to a coarse-grained model of RNA. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 151–156
- [Márquez-Chamorro et al., 2011] Márquez-Chamorro, A. E., Divina, F., Aguilar-Ruiz, J. S., & Asencio-Cortés, G. (2011). An evolutionary approach for protein contact map prediction. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 104–114
- [Qi et al., 2011] Qi, J., Michoel, T., & Butler, G. (2011). Applying linear models to learn regulation programs in a transcription regulatory module network. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 37–48

- [Quader et al., 2011] Quader, S., Snyder, N., Su, K., Mochan, E., & Huang, C.-H. (2011). ML-Consensus: a general consensus model for variable-length transcription factor binding sites. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 25–36
- [Rezwan et al., 2011] Rezwan, F., Sun, Y., Davey, N., Rust, A. G., & Robinson, M. (2011). Effect of using varying negative examples in transcription factor binding site predictions. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 1–12
- [Sciaccia et al., 2011] Sciaccia, E., Spinella, S., Ienco, D., & Giannini, P. (2011). Annotated stochastic context free grammars for analysis and synthesis of proteins. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 80–91
- [Silva et al., 2011] Silva, S., Anunciao, O., & Lotz, M. (2011). A comparison of machine learning methods for the prediction of breast cancer. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 163–174
- [Toca et al., 2011] Toca, C. E. S., Márquez-Chamorro, A. E., Asencio-Cortés, G., & Aguilar-Ruiz, J. S. (2011). A decision tree-based method for protein contact map prediction. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 157–162
- [Toti et al., 2011] Toti, D., Atzeni, P., & Polticelli, F. (2011). An automatic identification and resolution system for protein-related abbreviations in scientific papers. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 175–180
- [Yeu et al., 2011] Yeu, Y., Ahn, J., Yoon, Y., & Park, S. (2011). Protein complex discovery from protein interaction network with high false-positive rate. *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, volume 6623 of *LNCS*, 181–186