Список литературы

[Asencio-Cortés *et al.*(2011)Asencio-Cortés, Aguilar-Ruiz & Márquez-Chamorro] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 71–79, Springer Verlag, Turin, Italy.

[Chhel *et al.*(2011)Chhel, Goëffon, Lardeux, Saubion, Hunault & Boureau] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 139–144, Springer Verlag, Turin, Italy.

[Darabos *et al.*(2011)Darabos, Di Cunto, Tomassini, Moore, Provero & Giacobini] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 61–70, Springer Verlag, Turin, Italy.

[Farinaccio *et al.*(2011)Farinaccio, Vanneschi, Provero, Mauri & Giacobini] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 13–24, Springer Verlag, Turin, Italy.

[Ferreri *et al.*(2011)Ferreri, Venturino & Giacobini] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 145–150, Springer Verlag, Turin, Italy.

[González-Álvarez *et al.*(2011)González-Álvarez, Vega-Rodríguez, Gómez-Pulido & Sánchez-Pérez] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 92–103, Springer Verlag, Turin, Italy.

[Hinselmann *et al.*(2011)Hinselmann, Jahn, Fechner, Rosenbaum & Zell] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 127–138, Springer Verlag, Turin, Italy.

[Holzinger *et al.*(2011)Holzinger, Dudek, Torstenson & Ritchie] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 49–60, Springer Verlag, Turin, Italy.

[Laroum *et al.*(2011)Laroum, Duval, Tessier & Hao] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 115–126, Springer Verlag, Turin, Italy.

[Leonarski *et al.*(2011)Leonarski, Trovato, Tozzini & Trylska] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 151–156, Springer Verlag, Turin, Italy.

[Márquez-Chamorro *et al.*(2011)Márquez-Chamorro, Divina, Aguilar-Ruiz & Asencio-Cortés] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 104–114, Springer Verlag, Turin, Italy.

[Qi *et al.*(2011)Qi, Michoel & Butler] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 37–48, Springer Verlag, Turin, Italy.

[Quader *et al.*(2011)Quader, Snyder, Su, Mochan & Huang] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 25–36, Springer Verlag, Turin, Italy.

[Rezwan *et al.*(2011)Rezwan, Sun, Davey, Rust & Robinson] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 1–12, Springer Verlag, Turin, Italy.

[Sciacca *et al.*(2011)Sciacca, Spinella, Ienco & Giannini] Sciacca, 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 80–91, Springer Verlag, Turin, Italy.

[Silva *et al.*(2011)Silva, Anunciao & Lotz] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 163–174, Springer Verlag, Turin, Italy.

[Toca *et al.*(2011)Toca, Márquez-Chamorro, Asencio-Cortés & Aguilar-Ruiz] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 157–162, Springer Verlag, Turin, Italy.

[Toti *et al.*(2011)Toti, Atzeni & Polticelli] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 175–180, Springer Verlag, Turin, Italy.

[Yeu *et al.*(2011)Yeu, Ahn, Yoon & Park] 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* (eds. C. Pizzuti, M.D. Ritchie & M. Giacobini), vol. 6623 of *LNCS*, pp. 181–186, Springer Verlag, Turin, Italy.