

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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [Chhel *et al.*(2011)Chhel, Goëffon, Lardeux, Saubion, Hunault & Boureau] CHHEL, F., GOËFFON, A., LARDEUX, F., SAUBION, F., HUNAUT, G. & BOUREAU, T. (2011). Experimental approach for bacterial strains characterization. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [Ferreri *et al.*(2011)Ferreri, Venturino & Giacobini] FERRERI, L., VENTURINO, E. & GIACOBINI, M. (2011). 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* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.

- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [Márquez-Chamorro *et al.*(2011)Márquez-Chamorro, Divina, Aguilar-Ruiz & Asencio-Cortés] MÁRQUEZ-CHAMORRO, A. E., DIVINA, F., AGUILAR-RUIZ, J. S. & ASECIO-CORTÉS, G. (2011). An evolutionary approach for protein contact map prediction. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [Qi *et al.*(2011)Qi, Michael & Butler] QI, J., MICHOEL, T. & BUTLER, G. (2011). 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* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [Toca *et al.*(2011)Toca, Márquez-Chamorro, Asencio-Cortés & Aguilar-Ruiz] TOCA, C. E. S., MÁRQUEZ-CHAMORRO, A. E., ASECIO-CORTÉS, G. & AGUILAR-RUIZ, J. S. (2011). 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* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.
- [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. In: *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (PIZZUTI, C., RITCHIE, M. D. & GIACOBINI, M., eds.), vol. 6623 of *LNCS*. Turin, Italy: Springer Verlag.