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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 71–79.
- [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. In C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 139–144.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 61–70.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 13–24.
- [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 C. Pizzuti,
 M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 145–150.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 92–103.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 127–138.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 49–60.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 115–126.

- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 151–156.
- [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. In C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 104–114.
- [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. In C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 37–48.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 25–36.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 1–12.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 80–91.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 163–174.
- [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. In C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 157–162.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 175–180.
- [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 C. Pizzuti, M. D. Ritchie, & M. Giacobini (Eds.), 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011. Turin, Italy: Springer Verlag, vol. 6623 of LNCS, 181–186.