Список литературы

- [Asencio-Cortés et al.(2011)Asencio-Cortés, Aguilar-Ruiz and Márquez-Chamorro] Asencio-Cortés, G., Aguilar-Ruiz, J.S. and Márquez-Chamorro, A.E. (2011) 'A nearest neighbour-based approach for viral protein structure prediction'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBio 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 71–79.
- [Chhel et al.(2011)Chhel, Goëffon, Lardeux, Saubion, Hunault and Boureau] Chhel, F., Goëffon, A., Lardeux, F., Saubion, F., Hunault, G. and Boureau, T. (2011) 'Experimental approach for bacterial strains characterization'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 139–144.
- [Darabos et al.(2011)Darabos, Di Cunto, Tomassini, Moore, Provero and Giacobini] Darabos, C., Di Cunto, F., Tomassini, M., Moore, J.H., Provero, P. and Giacobini, M. (2011) 'Validating a threshold-based boolean model of regulatory networks on a biological organism'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 61–70.
- [Farinaccio et al.(2011)Farinaccio, Vanneschi, Provero, Mauri and Giacobini] Farinaccio, A., Vanneschi, L., Provero, P., Mauri, G. and Giacobini, M. (2011) 'A new evolutionary gene regulatory network reverse engineering tool'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBio 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 13–24.
- [Ferreri et al.(2011)Ferreri, Venturino and Giacobini] Ferreri, L., Venturino, E. and Giacobini, M. (2011) 'Do diseases spreading on bipartite networks have some evolutionary advantage?' In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 145–150.
- [González-Álvarez et al.(2011)González-Álvarez, Vega-Rodríguez, Gómez-Pulido and Sánchez-Pérez] González-Álvarez, D.L., Vega-Rodríguez, M.A., Gómez-Pulido, J.A. and Sánchez-Pérez, J.M. (2011) 'Finding motifs in DNA sequences applying a multiobjective artificial bee colony (MOABC) algorithm'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 92–103.
- [Hinselmann et al.(2011)Hinselmann, Jahn, Fechner, Rosenbaum and Zell] Hinselmann, G., Jahn, A., Fechner, N., Rosenbaum, L. and Zell, A. (2011) 'Approximation of graph kernel similarities for chemical graphs by kernel principal component analysis'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 127–138.
- [Holzinger et al.(2011)Holzinger, Dudek, Torstenson and Ritchie] Holzinger, E.R., Dudek, S.M., Torstenson, E.C. and Ritchie, M.D. (2011) 'ATHENA optimization: The effect of initial parameter settings across different genetic models'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 49–60.
- [Laroum et al.(2011)Laroum, Duval, Tessier and Hao] Laroum, S., Duval, B., Tessier, D. and Hao, J.K. (2011) 'Multi-neighborhood search for discrimination of signal peptides and transmembrane segments'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 115–126.

- [Leonarski et al.(2011)Leonarski, Trovato, Tozzini and Trylska] Leonarski, F., Trovato, F., Tozzini, V. and Trylska, J. (2011) 'Genetic algorithm optimization of force field parameters. application to a coarse-grained model of RNA'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 151–156.
- [Márquez-Chamorro et al.(2011)Márquez-Chamorro, Divina, Aguilar-Ruiz and Asencio-Cortés] Márquez-Chamorro, A.E., Divina, F., Aguilar-Ruiz, J.S. and Asencio-Cortés, G. (2011) 'An evolutionary approach for protein contact map prediction'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 104–114.
- [Qi et al.(2011)Qi, Michoel and Butler] Qi, J., Michoel, T. and Butler, G. (2011) 'Applying linear models to learn regulation programs in a transcription regulatory module network'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 37–48.
- [Quader et al.(2011)Quader, Snyder, Su, Mochan and Huang] Quader, S., Snyder, N., Su, K., Mochan, E. and Huang, C.H. (2011) 'ML-Consensus: a general consensus model for variable-length transcription factor binding sites'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBio 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 25–36.
- [Rezwan et al.(2011)Rezwan, Sun, Davey, Rust and Robinson] Rezwan, F., Sun, Y., Davey, N., Rust, A.G. and Robinson, M. (2011) 'Effect of using varying negative examples in transcription factor binding site predictions'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 1–12.
- [Sciacca et al.(2011)Sciacca, Spinella, Ienco and Giannini] Sciacca, E., Spinella, S., Ienco, D. and Giannini, P. (2011) 'Annotated stochastic context free grammars for analysis and synthesis of proteins'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 80–91.
- [Silva et al.(2011)Silva, Anunciao and Lotz] Silva, S., Anunciao, O. and Lotz, M. (2011) 'A comparison of machine learning methods for the prediction of breast cancer'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 163–174.
- [Toca et al.(2011)Toca, Márquez-Chamorro, Asencio-Cortés and Aguilar-Ruiz] Toca, C.E.S., Márquez-Chamorro, A.E., Asencio-Cortés, G. and Aguilar-Ruiz, J.S. (2011) 'A decision tree-based method for protein contact map prediction'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 157–162.
- [Toti et al.(2011)Toti, Atzeni and Polticelli] Toti, D., Atzeni, P. and Polticelli, F. (2011) 'An automatic identification and resolution system for protein-related abbreviations in scientific papers'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 175–180.
- [Yeu et al.(2011)Yeu, Ahn, Yoon and Park] Yeu, Y., Ahn, J., Yoon, Y. and Park, S. (2011) 'Protein complex discovery from protein interaction network with high false-positive rate'. In C. Pizzuti, M.D. Ritchie and M. Giacobini, (eds.) 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, LNCS, vol. 6623. Turin, Italy: Springer Verlag, pp. 181–186.