

Список литературы

- [1] F. Rezwan, Y. Sun, N. Davey, A. G. Rust and M. Robinson, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 1–12, Springer Verlag, 27-29 April, 2011.
- [2] A. Farinaccio, L. Vanneschi, P. Provero, G. Mauri and M. Giacobini, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 13–24, Springer Verlag, 27-29 April, 2011.
- [3] S. Quader, N. Snyder, K. Su, E. Mochan and C.-H. Huang, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 25–36, Springer Verlag, 27-29 April, 2011.
- [4] J. Qi, T. Michoel and G. Butler, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 37–48, Springer Verlag, 27-29 April, 2011.
- [5] E. R. Holzinger, S. M. Dudek, E. C. Torstenson and M. D. Ritchie, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 49–60, Springer Verlag, 27-29 April, 2011.
- [6] C. Darabos, F. Di Cunto, M. Tomassini, J. H. Moore, P. Provero and M. Giacobini, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 61–70, Springer Verlag, 27-29 April, 2011.
- [7] G. Asencio-Cortés, J. S. Aguilar-Ruiz and A. E. Márquez-Chamorro, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 71–79, Springer Verlag, 27-29 April, 2011.
- [8] E. Sciacca, S. Spinella, D. Ienco and P. Giannini, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 80–91, Springer Verlag, 27-29 April, 2011.
- [9] D. L. González-Álvarez, M. A. Vega-Rodríguez, J. A. Gómez-Pulido and J. M. Sánchez-Pérez, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 92–103, Springer Verlag, 27-29 April, 2011.
- [10] A. E. Márquez-Chamorro, F. Divina, J. S. Aguilar-Ruiz and G. Asencio-Cortés, *An evolutionary approach for protein contact map prediction*, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 104–114, Springer Verlag, 27-29 April, 2011.

- [11] S. Laroum, B. Duval, D. Tessier and J.-K. Hao, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 115–126, Springer Verlag, 27-29 April, 2011.
- [12] G. Hinselmann, A. Jahn, N. Fechner, L. Rosenbaum and A. Zell, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 127–138, Springer Verlag, 27-29 April, 2011.
- [13] F. Chhel, A. Goëffon, F. Lardeux, F. Saubion, G. Hunault and T. Boureau, *Experimental approach for bacterial strains characterization*, in *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 139–144, Springer Verlag, 27-29 April, 2011.
- [14] L. Ferreri, E. Venturino and M. Giacobini, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 145–150, Springer Verlag, 27-29 April, 2011.
- [15] F. Leonarski, F. Trovato, V. Tozzini and J. Trylska, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 151–156, Springer Verlag, 27-29 April, 2011.
- [16] C. E. S. Toca, A. E. Márquez-Chamorro, G. Asencio-Cortés and J. S. Aguilar-Ruiz, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 157–162, Springer Verlag, 27-29 April, 2011.
- [17] S. Silva, O. Anunciao and M. Lotz, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 163–174, Springer Verlag, 27-29 April, 2011.
- [18] D. Toti, P. Atzeni and F. Polticelli, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 175–180, Springer Verlag, 27-29 April, 2011.
- [19] Y. Yeu, J. Ahn, Y. Yoon and S. Park, *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* (C. Pizzuti, M. D. Ritchie and M. Giacobini, eds.), vol. 6623 of *LNCS*, (Turin, Italy), pp. 181–186, Springer Verlag, 27-29 April, 2011.