

Список литературы

- [1] Rezwan F, Sun Y, Davey N, Rust AG, Robinson M. 2011 Effect of using varying negative examples in transcription factor binding site predictions. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 1–12. Turin, Italy: Springer Verlag.
- [2] Farinaccio A, Vanneschi L, Provero P, Mauri G, Giacobini M. 2011 A new evolutionary gene regulatory network reverse engineering tool. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 13–24. Turin, Italy: Springer Verlag.
- [3] Quader S, Snyder N, Su K, Mochan E, Huang CH. 2011 ML-Consensus: a general consensus model for variable-length transcription factor binding sites. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 25–36. Turin, Italy: Springer Verlag.
- [4] Qi J, Michael T, Butler G. 2011 Applying linear models to learn regulation programs in a transcription regulatory module network. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 37–48. Turin, Italy: Springer Verlag.
- [5] Holzinger ER, Dudek SM, Torstenson EC, Ritchie MD. 2011 ATHENA optimization: The effect of initial parameter settings across different genetic models. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 49–60. Turin, Italy: Springer Verlag.
- [6] Darabos C, Di Cunto F, Tomassini M, Moore JH, Provero P, Giacobini M. 2011 Validating a threshold-based boolean model of regulatory networks on a biological organism. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 61–70. Turin, Italy: Springer Verlag.
- [7] Asencio-Cortés G, Aguilar-Ruiz JS, Márquez-Chamorro AE. 2011 A nearest neighbour-based approach for viral protein structure prediction. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 71–79. Turin, Italy: Springer Verlag.
- [8] Sciacca E, Spinella S, Ienco D, Giannini P. 2011 Annotated stochastic context free grammars for analysis and synthesis of proteins. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 80–91. Turin, Italy: Springer Verlag.
- [9] González-Álvarez DL, Vega-Rodríguez MA, Gómez-Pulido JA, Sánchez-Pérez JM. 2011 Finding motifs in DNA sequences applying a multiobjective artificial bee colony (MOABC) algorithm. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 92–103. Turin, Italy: Springer Verlag.
- [10] Márquez-Chamorro AE, Divina F, Aguilar-Ruiz JS, Asencio-Cortés G. 2011 An evolutionary approach for protein contact map prediction. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 104–114. Turin, Italy: Springer Verlag.
- [11] Laroum S, Duval B, Tessier D, Hao JK. 2011 Multi-neighborhood search for discrimination of signal peptides and transmembrane segments. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 115–126. Turin, Italy: Springer Verlag.

- [12] 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: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 127–138. Turin, Italy: Springer Verlag.
- [13] Chhel F, Goëffon A, Lardeux F, Saubion F, Hunault G, Boureau T. 2011 Experimental approach for bacterial strains characterization. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 139–144. Turin, Italy: Springer Verlag.
- [14] Ferreri L, Venturino E, Giacobini M. 2011 Do diseases spreading on bipartite networks have some evolutionary advantage? In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 145–150. Turin, Italy: Springer Verlag.
- [15] 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: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 151–156. Turin, Italy: Springer Verlag.
- [16] Toca CES, Márquez-Chamorro AE, Asencio-Cortés G, Aguilar-Ruiz JS. 2011 A decision tree-based method for protein contact map prediction. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 157–162. Turin, Italy: Springer Verlag.
- [17] Silva S, Anunciao O, Lotz M. 2011 A comparison of machine learning methods for the prediction of breast cancer. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 163–174. Turin, Italy: Springer Verlag.
- [18] Toti D, Atzeni P, Polticelli F. 2011 An automatic identification and resolution system for protein-related abbreviations in scientific papers. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 175–180. Turin, Italy: Springer Verlag.
- [19] Yeu Y, Ahn J, Yoon Y, Park S. 2011 Protein complex discovery from protein interaction network with high false-positive rate. In: Pizzuti C, Ritchie MD, Giacobini M (eds.), *9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011*, vol. 6623 of *LNCS*, pp. 181–186. Turin, Italy: Springer Verlag.