

## Список литературы

- [1] M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012.
- [2] T. Manning and P. Walsh, “Automatic task decomposition for the neuroevolution of augmenting topologies (NEAT) algorithm,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 1–12.
- [3] L. Manzoni, M. Castelli, and L. Vanneschi, “Evolutionary reaction systems,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 13–24.
- [4] L. Rosenbaum, A. Jahn, and A. Zell, “Optimizing the edge weights in optimal assignment methods for virtual screening with particle swarm optimization,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 25–36.
- [5] C. Darabos, M. Giacobini, T. Hu, and J. H. Moore, “Lévy-flight GP: towards a new mutation paradigm,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 37–48.
- [6] S. Marini and A. Conversi, “Understanding zooplankton long term variability through genetic programming,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 49–60.
- [7] H. Franken, A. Seitz, R. Lehmann, H.-U. Häring, N. Stefan, and A. Zell, “Inferring disease-related metabolite dependencies with a bayesian optimization algorithm,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 61–72.
- [8] M. Nobile, D. Besozzi, P. Cazzaniga, G. Mauri, and D. Pescini, “A GPU-based multi-swarm PSO method for parameter estimation in stochastic biological systems exploiting discrete-time target series,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 73–84.
- [9] F. Pinheiro, F. Santos, and J. Pacheco, “Tracking the evolution of cooperation in complex networked populations,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 85–95.
- [10] L. Vanneschi, M. Mondini, M. Bertoni, A. Ronchi, and M. Stefano, “GeNet: A graph-based genetic programming framework for the reverse engineering of gene regulatory networks,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 96–107.
- [11] 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 *10th European Conference on Evolutionary Computation, Machine Learning and*

- Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 108–119.
- [12] Q. Pan, C. Darabos, and J. H. Moore, “The role of mutations in whole genome duplication,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 120–131.
  - [13] “Comparison of methods for meta-dimensional data analysis using in silico and biological data sets,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 132–143.
  - [14] S. Santander-Jiménez, M. A. Vega-Rodríguez, J. A. Gómez-Pulido, and J. M. Sánchez-Pérez, “Inferring phylogenetic trees using a multiobjective artificial bee colony algorithm,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 144–155.
  - [15] G. Asencio-Cortés, J. S. Aguilar-Ruiz, A. E. Márquez-Chamorro, R. Ruiz, and C. E. Santiesteban-Toca, “Prediction of mitochondrial matrix protein structures based on feature selection and fragment assembly,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 156–167.
  - [16] K. Kancharla and S. Mukkala, “Feature selection for lung cancer detection using SVM based recursive feature elimination method,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 168–179.
  - [17] A. Spirov, N. Golyandina, D. Holloway, T. Alexandrov, E. Spirova, and F. Lopes, “Measuring gene expression noise in early drosophila embryos: the highly dynamic compartmentalized micro-environment of the blastoderm is one of the main sources of noise,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 180–191.
  - [18] D. Granizo-Mackenzie and J. H. Moore, “Artificial immune systems perform valuable work when detecting epistasis in human genetic datasets,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 192–203.
  - [19] C. Buchanan, J. Wallace, A. Frase, E. Torstenson, S. Pendergrass, and M. Ritchie, “A biologically informed method for detecting associations with rare variants,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 204–215.
  - [20] C. Pizzuti, S. E. Rombo, and E. Marchiori, “Complex detection in protein-protein interaction networks: a compact overview for researchers and practitioners,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 216–227.
  - [21] C. E. Santiesteban-Toca, A. E. Márquez-Chamorro, G. Asencio-Cortés, and J. S. Aguilar-Ruiz, “Short-range interactions and decision tree-based protein contact map predictor,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics,*

- EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 228–237.
- [22] A. E. Márquez-Chamorro, F. Divina, J. S. Aguilar-Ruiz, J. Bacardit, G. Asencio-Cortés, and C. E. Santiesteban-Toca, “A NSGA-II algorithm for the residue-residue contact prediction,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 238–248.
  - [23] W. B. Langdon and J. Arno, “In silico infection of the human genome,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 249–252.
  - [24] F. Cerutti, L. Bertolotti, T. L. Goldberg, and M. Giacobini, “Improving phylogenetic tree interpretability by means of evolutionary algorithms,” in *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, ser. LNCS, M. Giacobini, L. Vanneschi, and W. S. Bush, Eds., vol. 7246. Malaga, Spain: Springer Verlag, 11-13 April 2012, pp. 253–256.