

## Список литературы

- [Giacobini et al.(2012)Giacobini, Vanneschi, and Bush] 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.
- [Manning and Walsh(2012)] 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.
- [Manzoni et al.(2012)Manzoni, Castelli, and Vanneschi] 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.
- [Rosenbaum et al.(2012)Rosenbaum, Jahn, and Zell] 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.
- [Darabos et al.(2012)Darabos, Giacobini, Hu, and Moore] 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.
- [Marini and Conversi(2012)] 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.
- [Franken et al.(2012)Franken, Seitz, Lehmann, Häring, Stefan, and Zell] 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.
- [Nobile et al.(2012)Nobile, Besozzi, Cazzaniga, Mauri, and Pescini] 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.
- [Pinheiro et al.(2012)Pinheiro, Santos, and Pacheco] 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.
- [Vanneschi et al.(2012)Vanneschi, Mondini, Bertoni, Ronchi, and Stefano] 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.

- [González-Álvarez et al.(2012)González-Álvarez, Vega-Rodríguez, Gómez-Pulido, and Sánchez-Pérez] 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.
- [Pan et al.(2012)Pan, Darabos, and Moore] 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.
- [hol(2012)] “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.
- [Santander-Jiménez et al.(2012)Santander-Jiménez, Vega-Rodríguez, Gómez-Pulido, and Sánchez-Pérez] 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.
- [Asencio-Cortés et al.(2012)Asencio-Cortés, Aguilar-Ruiz, Márquez-Chamorro, Ruiz, and Santiesteban-Toca] 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.
- [Kancherla and Mukkala(2012)] K. Kancherla 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.
- [Spirov et al.(2012)Spirov, Golyandina, Holloway, Alexandrov, Spirova, and Lopes] 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.
- [Granizo-Mackenzie and Moore(2012)] 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.
- [Buchanan et al.(2012)Buchanan, Wallace, Frase, Torstenson, Pendergrass, and Ritchie] 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.

[Pizzuti et al.(2012)Pizzuti, Rombo, and Marchiori] 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.

[Santesteban-Toca et al.(2012)Santesteban-Toca, Márquez-Chamorro, Asencio-Cortés, and Aguilar-Ruiz] C. E. Santesteban-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.

[Márquez-Chamorro et al.(2012)Márquez-Chamorro, Divina, Aguilar-Ruiz, Bacardit, Asencio-Cortés, and Santesteban-Toca] A. E. Márquez-Chamorro, F. Divina, J. S. Aguilar-Ruiz, J. Bacardit, G. Asencio-Cortés, and C. E. Santesteban-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.

[Langdon and Arno(2012)] 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.

[Cerutti et al.(2012)Cerutti, Bertolotti, Goldberg, and Giacobini] 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.