## Список литературы

- [hol(2012)] (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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 132–143. (Malaga, Spain: Springer Verlag).
- [Asencio-Cortés et al.(2012)Asencio-Cortés, Aguilar-Ruiz, Márquez-Chamorro, Ruiz, & Santiesteban-Toca] Asencio-Cortés, G., Aguilar-Ruiz, J. S., Márquez-Chamorro, A. E., Ruiz, R., & Santiesteban-Toca, C. E. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 156–167. (Malaga, Spain: Springer Verlag).
- [Buchanan et al.(2012)Buchanan, Wallace, Frase, Torstenson, Pendergrass, & Ritchie] Buchanan, C., Wallace, J., Frase, A., Torstenson, E., Pendergrass, S., & Ritchie, M. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 204–215. (Malaga, Spain: Springer Verlag).
- [Cerutti et al.(2012)Cerutti, Bertolotti, Goldberg, & Giacobini] Cerutti, F., Bertolotti, L., Goldberg, T. L., & Giacobini, M. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 253–256. (Malaga, Spain: Springer Verlag).
- [Darabos et al.(2012)Darabos, Giacobini, Hu, & Moore] Darabos, C., Giacobini, M., Hu, T., & Moore, J. H. (2012). Lévy-flight GP: towards a new mutation paradigm. In 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 37–48. (Malaga, Spain: Springer Verlag).
- [Franken et al.(2012)Franken, Seitz, Lehmann, Häring, Stefan, & Zell] Franken, H., Seitz, A., Lehmann, R., Häring, H.-U., Stefan, N., & Zell, A. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 61–72. (Malaga, Spain: Springer Verlag).
- [Giacobini et al.(2012)Giacobini, Vanneschi, & Bush] Giacobini, M., Vanneschi, L., & Bush, W. S. eds. (2012). 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, vol. 7246 of *LNCS*, Malaga, Spain. Springer Verlag.
- [González-Álvarez et al.(2012)González-Álvarez, Vega-Rodríguez, Gómez-Pulido, & Sánchez-Pérez] González-Álvarez, D. L., Vega-Rodríguez, M. A., Gómez-Pulido, J. A., & Sánchez-Pérez, J. M. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 108–119. (Malaga, Spain: Springer Verlag).
- [Granizo-Mackenzie & Moore(2012)] Granizo-Mackenzie, D. & Moore, J. H. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 192–203. (Malaga, Spain: Springer Verlag).
- [Kancherla & Mukkala(2012)] Kancherla, K. & Mukkala, S. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 168–179. (Malaga, Spain: Springer Verlag).
- [Langdon & Arno(2012)] Langdon, W. B. & Arno, J. (2012). In silico infection of the human genome. In 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 249–252. (Malaga, Spain: Springer Verlag).
- [Manning & Walsh(2012)] Manning, T. & Walsh, P. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 1–12. (Malaga, Spain: Springer Verlag).
- [Manzoni et al.(2012)Manzoni, Castelli, & Vanneschi] Manzoni, L., Castelli, M., & Vanneschi, L. (2012). Evolutionary reaction systems. In 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 13–24. (Malaga, Spain: Springer Verlag).
- [Marini & Conversi(2012)] Marini, S. & Conversi, A. (2012). Understanding zooplankton long term variability through genetic programming. In 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 49–60. (Malaga, Spain: Springer Verlag).
- [Márquez-Chamorro et al.(2012)Márquez-Chamorro, Divina, Aguilar-Ruiz, Bacardit, Asencio-Cortés, & Santiesteban-Too Márquez-Chamorro, A. E., Divina, F., Aguilar-Ruiz, J. S., Bacardit, J., Asencio-Cortés, G., & Santiesteban-Toca, C. E. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 238–248. (Malaga, Spain: Springer Verlag).
- [Nobile et al.(2012)Nobile, Besozzi, Cazzaniga, Mauri, & Pescini] Nobile, M., Besozzi, D., Cazzaniga, P., Mauri, G., & Pescini, D. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 73–84. (Malaga, Spain: Springer Verlag).
- [Pan et al.(2012)Pan, Darabos, & Moore] Pan, Q., Darabos, C., & Moore, J. H. (2012). The role of mutations in whole genome duplication. In 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 120–131. (Malaga, Spain: Springer Verlag).
- [Pinheiro et al.(2012)Pinheiro, Santos, & Pacheco] Pinheiro, F., Santos, F., & Pacheco, J. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 85–95. (Malaga, Spain: Springer Verlag).
- [Pizzuti et al.(2012)Pizzuti, Rombo, & Marchiori] Pizzuti, C., Rombo, S. E., & Marchiori, E. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 216–227. (Malaga, Spain: Springer Verlag).
- [Rosenbaum et al.(2012)Rosenbaum, Jahn, & Zell] Rosenbaum, L., Jahn, A., & Zell, A. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 25–36. (Malaga, Spain: Springer Verlag).

- [Santander-Jiménez et al.(2012)Santander-Jiménez, Vega-Rodríguez, Gómez-Pulido, & Sánchez-Pérez] Santander-Jiménez, S., Vega-Rodríguez, M. A., Gómez-Pulido, J. A., & Sánchez-Pérez, J. M. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 144–155. (Malaga, Spain: Springer Verlag).
- [Santiesteban-Toca et al.(2012)Santiesteban-Toca, Márquez-Chamorro, Asencio-Cortés, & Aguilar-Ruiz] Santiesteban-Toca, C. E., Márquez-Chamorro, A. E., Asencio-Cortés, G., & Aguilar-Ruiz, J. S. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 228–237. (Malaga, Spain: Springer Verlag).
- [Spirov et al.(2012)Spirov, Golyandina, Holloway, Alexandrov, Spirova, & Lopes] Spirov, A., Golyandina, N., Holloway, D., Alexandrov, T., Spirova, E., & Lopes, F. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of *LNCS*, pp. 180–191. (Malaga, Spain: Springer Verlag).
- [Vanneschi et al.(2012) Vanneschi, Mondini, Bertoni, Ronchi, & Stefano] Vanneschi, L., Mondini, M., Bertoni, M., Ronchi, A., & Stefano, M. (2012). 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, M. Giacobini, L. Vanneschi, & W. S. Bush, eds., vol. 7246 of LNCS, pp. 96–107. (Malaga, Spain: Springer Verlag).