## Список литературы

- [Ahmed et al.(2013)Ahmed, Zhang, & Peng] Ahmed, S., Zhang, M., & Peng, L. (2013). Feature selection and classification of high dimensional mass spectrometry data: A genetic programming approach. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 43–54. (Vienna, Austria: Springer Verlag).
- [Castaldi et al.(2013)Castaldi, Maccagnola, Mari, & Archetti] Castaldi, D., Maccagnola, D., Mari, D., & Archetti, F. (2013). Mining for variability in the coagulation pathway: A systems biology approach. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 151–162. (Vienna, Austria: Springer Verlag).
- [Darabos et al.(2013)Darabos, Desai, Cowper-Sallari, Giacobini, Graham, Lupien, & Moore] Darabos, C., Desai, K., Cowper-Sallari, R., Giacobini, M., Graham, B. E., Lupien, M., & Moore, J. H. (2013). Inferring human phenotype networks from genome-wide genetic associations. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 23–34. (Vienna, Austria: Springer Verlag).
- [Fisher et al.(2013)Fisher, Andrews, Kiralis, Sinnott-Armstrong, & Moore] Fisher, J. M., Andrews, P., Kiralis, J., Sinnott-Armstrong, N. A., & Moore, J. H. (2013). Alternative cell-based metrics improve the detection of multifactor dimensionality reduction. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 198–209. (Vienna, Austria: Springer Verlag).
- [Gaudesi et al.(2013)Gaudesi, Marion, Musner, Squillero, & Tonda] Gaudesi, M., Marion, A., Musner, T., Squillero, G., & Tonda, A. (2013). An evolutionary approach to wetlands design. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 175–185. (Vienna, Austria: Springer Verlag).
- [Gonzalez-Alvarez & Vega-Rodriguez(2013)] Gonzalez-Alvarez, D. L. & Vega-Rodriguez, M. A. (2013). Hybrid multiobjective artificial bee colony with differential evolution applied to motif finding. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 67–78. (Vienna, Austria: Springer Verlag).
- [Granizo-Mackenzie & Moore(2013)] Granizo-Mackenzie, D. & Moore, J. H. (2013). Multiple threshold spatially uniform ReliefF for the genetic analysis of complex human diseases. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 1–10. (Vienna, Austria: Springer Verlag).
- [Manning & Walsh(2013)] Manning, T. & Walsh, P. (2013). Improving the performance of CGPANN for breast cancer diagnosis using crossover and radial basis functions. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 163–174. (Vienna, Austria: Springer Verlag).
- [Orsenigo & Vercellis(2013)] Orsenigo, C. & Vercellis, C. (2013). Dimensionality reduction via isomap with lock-step and elastic measures for time series gene expression classification. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 91–102. (Vienna, Austria: Springer Verlag).
- [Pan et al.(2013)Pan, Hu, Malley, Andrew, Karagas, & Moore] Pan, Q., Hu, T., Malley, J. D., Andrew, A. S., Karagas, M. R., & Moore, J. H. (2013). Supervising random forest using

- attribute interaction networks. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 103–114. (Vienna, Austria: Springer Verlag).
- [Rosenthal et al.(2013)Rosenthal, El-Sourani, & Borschbach] Rosenthal, S., El-Sourani, N., & Borschbach, M. (2013). Impact of different recombination methods in a mutation-specific MOEA for a biochemical application. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 186–197. (Vienna, Austria: Springer Verlag).
- [Salama & Freitas(2013)] Salama, K. & Freitas, A. (2013). Dimensionality reduction via isomap with lock-step and elastic measures for time series gene expression classification. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of LNCS, pp. 79–90. (Vienna, Austria: Springer Verlag).
- [Santander-Jimenez & Vega-Rodriguez(2013)] Santander-Jimenez, S. & Vega-Rodriguez, M. A. (2013). A multiobjective proposal based on the firefly algorithm for inferring phylogenies. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 139–150. (Vienna, Austria: Springer Verlag).
- [Sharma & Gedeon(2013)] Sharma, N. & Gedeon, T. (2013). Hybrid genetic algorithms for stress recognition in reading. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 115–126. (Vienna, Austria: Springer Verlag).
- [Sivley et al.(2013)Sivley, Fish, & Bush] Sivley, R. M., Fish, A. E., & Bush, W. S. (2013). Knowledge-constrained k-medoids clustering of regulatory rare alleles for burden tests. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of LNCS, pp. 35–42. (Vienna, Austria: Springer Verlag).
- [Sulovari et al.(2013)Sulovari, Kiralis, & Moore] Sulovari, A., Kiralis, J., & Moore, J. H. (2013). Optimal use of biological expert knowledge from literature mining in ant colony optimization for analysis of epistasis in human disease. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 127–138. (Vienna, Austria: Springer Verlag).
- [Tan et al.(2013)Tan, Grant, Whitfield, & Greene] Tan, J., Grant, G., Whitfield, M., & Greene, C. (2013). Time-point specific weighting improves coexpression networks from time-course experiments. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of LNCS, pp. 11–22. (Vienna, Austria: Springer Verlag).
- [Vanneschi et al.(2013)Vanneschi, Bush, & Giacobini] Vanneschi, L., Bush, W. S., & Giacobini, M. eds. (2013). 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, vol. 7833 of LNCS, Vienna, Austria. Springer Verlag.
- [Whigham et al.(2013)Whigham, Dick, Wright, & Spencer] Whigham, P. A., Dick, G., Wright, A., & Spencer, H. G. (2013). Structured populations and the maintenance of sex. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of *LNCS*, pp. 55–66. (Vienna, Austria: Springer Verlag).
- [Zagorski(2013)] Zagorski, M. (2013). Emergence of motifs in model gene regulatory networks. In 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, L. Vanneschi, W. S. Bush, & M. Giacobini, eds., vol. 7833 of LNCS, pp. 210–213. (Vienna, Austria: Springer Verlag).