## Список литературы

- [1] M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, editors, 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, volume 7246 of LNCS, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 1–12, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 13–24, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 25–36, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 37–48, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 49–60, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 61–72, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 73–84, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 85–95, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. Bush, volume 7246 of LNCS, pp. 96–107, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 108–119, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 120–131, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 132–143, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 144–155, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 156–167, Malaga, Spain, 2012, Springer Verlag.
- [16] 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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 168–179, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 180–191, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 192–203, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 204–215, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. Giacobini, L. Vanneschi, and W. S. Bush, volume 7246 of LNCS, pp. 216–227, Malaga, Spain, 2012, Springer Verlag.

- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 228–237, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. Bush, volume 7246 of LNCS, pp. 238–248, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 249–252, Malaga, Spain, 2012, Springer Verlag.
- [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, edited by M. GIACOBINI, L. VANNESCHI, and W. S. BUSH, volume 7246 of LNCS, pp. 253–256, Malaga, Spain, 2012, Springer Verlag.