

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.