Список литературы

- [1] Giacobini, M., Vanneschi, L., and Bush, W. S., 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] Manning, T. and Walsh, P., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 1–12, Malaga, Spain, 2012, Springer Verlag.
- [3] Manzoni, L., Castelli, M., and Vanneschi, L., Evolutionary reaction systems, in 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, edited by Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 13–24, Malaga, Spain, 2012, Springer Verlag.
- [4] Rosenbaum, L., Jahn, A., and Zell, A., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 25–36, Malaga, Spain, 2012, Springer Verlag.
- [5] Darabos, C., Giacobini, M., Hu, T., and Moore, J. H., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 37–48, Malaga, Spain, 2012, Springer Verlag.
- [6] Marini, S. and Conversi, A., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 49–60, Malaga, Spain, 2012, Springer Verlag.
- [7] Franken, H. et al., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 61–72, Malaga, Spain, 2012, Springer Verlag.
- [8] Nobile, M., Besozzi, D., Cazzaniga, P., Mauri, G., and Pescini, D., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 73–84, Malaga, Spain, 2012, Springer Verlag.
- [9] Pinheiro, F., Santos, F., and Pacheco, J., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 85–95, Malaga, Spain, 2012, Springer Verlag.
- [10] Vanneschi, L., Mondini, M., Bertoni, M., Ronchi, A., and Stefano, M., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 96–107, Malaga, Spain, 2012, Springer Verlag.
- [11] González-Álvarez, D. L., Vega-Rodríguez, M. A., Gómez-Pulido, J. A., and Sánchez-Pérez, J. M., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 108–119, Malaga, Spain, 2012, Springer Verlag.

- [12] Pan, Q., Darabos, C., and Moore, J. H., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 132–143, Malaga, Spain, 2012, Springer Verlag.
- [14] Santander-Jiménez, S., Vega-Rodríguez, M. A., Gómez-Pulido, J. A., and Sánchez-Pérez, J. M., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 144–155, Malaga, Spain, 2012, Springer Verlag.
- [15] Asencio-Cortés, G., Aguilar-Ruiz, J. S., Márquez-Chamorro, A. E., Ruiz, R., and Santiesteban-Toca, C. E., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 156–167, Malaga, Spain, 2012, Springer Verlag.
- [16] Kancherla, K. and Mukkala, S., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 168–179, Malaga, Spain, 2012, Springer Verlag.
- [17] Spirov, A. et al., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 180–191, Malaga, Spain, 2012, Springer Verlag.
- [18] Granizo-Mackenzie, D. and Moore, J. H., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 192–203, Malaga, Spain, 2012, Springer Verlag.
- [19] Buchanan, C. et al., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 204–215, Malaga, Spain, 2012, Springer Verlag.
- [20] Pizzuti, C., Rombo, S. E., and Marchiori, E., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 216–227, Malaga, Spain, 2012, Springer Verlag.
- [21] Santiesteban-Toca, C. E., Márquez-Chamorro, A. E., Asencio-Cortés, G., and Aguilar-Ruiz, J. S., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 228–237, Malaga, Spain, 2012, Springer Verlag.
- [22] Márquez-Chamorro, A. E. et al., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 238–248, Malaga, Spain, 2012, Springer Verlag.

- [23] Langdon, W. B. and Arno, J., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 249–252, Malaga, Spain, 2012, Springer Verlag.
- [24] Cerutti, F., Bertolotti, L., Goldberg, T. L., and Giacobini, M., 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 Giacobini, M., Vanneschi, L., and Bush, W. S., volume 7246 of LNCS, pages 253–256, Malaga, Spain, 2012, Springer Verlag.