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 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, pp. 1–12, Malaga, Spain, 2012, Springer Verlag.
- [3] MANZONI, L., CASTELLI, M., and VANNESCHI, L., Evolutionary reaction systems, in 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, pp. 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 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, pp. 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 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, pp. 37–48, Malaga, Spain, 2012, Springer Verlag.
- [6] MARINI, S. and CONVERSI, A., Understanding zooplankton long term variability through genetic programming, in 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, pp. 49–60, Malaga, Spain, 2012, Springer Verlag.
- [7] FRANKEN, H., SEITZ, A., LEHMANN, R., et al., Inferring disease-related metabolite dependencies with a bayesian optimization algorithm, in 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, pp. 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 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, pp. 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 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, pp. 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 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, pp. 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 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, pp. 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 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, 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 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, pp. 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 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, pp. 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 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, pp. 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 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, pp. 168–179, Malaga, Spain, 2012, Springer Verlag.
- [17] SPIROV, A., GOLYANDINA, N., HOLLOWAY, D., 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 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, pp. 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 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, pp. 192–203, Malaga, Spain, 2012, Springer Verlag.
- [19] BUCHANAN, C., WALLACE, J., FRASE, A., et al., A biologically informed method for detecting associations with rare variants, in 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, pp. 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 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, pp. 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 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, pp. 228–237, Malaga, Spain, 2012, Springer Verlag.
- [22] MÁRQUEZ-CHAMORRO, A. E., DIVINA, F., AGUILAR-RUIZ, J. S., et al., A NSGA-II algorithm for the residue-residue contact prediction, in 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, pp. 238–248, Malaga, Spain, 2012, Springer Verlag.
- [23] LANGDON, W. B. and ARNO, J., In silico infection of the human genome, in 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, pp. 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 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, pp. 253–256, Malaga, Spain, 2012, Springer Verlag.