Список литературы

- [hol(2012)] (2012). Comparison of methods for meta-dimensional data analysis using in silico and biological data sets. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 132–143.
- [Asencio-Cortés et al.(2012)Asencio-Cortés, Aguilar-Ruiz, Márquez-Chamorro, Ruiz, & Santiesteban-Toca] Asencio-Cortés, G., Aguilar-Ruiz, J. S., Márquez-Chamorro, A. E., Ruiz, R., & Santiesteban-Toca, C. E. (2012). Prediction of mitochondrial matrix protein structures based on feature selection and fragment assembly. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 156–167.
- [Buchanan et al.(2012)Buchanan, Wallace, Frase, Torstenson, Pendergrass, & Ritchie] Buchanan, C., Wallace, J., Frase, A., Torstenson, E., Pendergrass, S., & Ritchie, M. (2012). A biologically informed method for detecting associations with rare variants. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 204–215.
- [Cerutti et al.(2012)Cerutti, Bertolotti, Goldberg, & Giacobini] Cerutti, F., Bertolotti, L., Goldberg, T. L., & Giacobini, M. (2012). Improving phylogenetic tree interpretability by means of evolutionary algorithms. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 253–256.
- [Darabos et al.(2012)Darabos, Giacobini, Hu, & Moore] Darabos, C., Giacobini, M., Hu, T., & Moore, J. H. (2012). Lévy-flight GP: towards a new mutation paradigm. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 37–48.
- [Franken et al.(2012)Franken, Seitz, Lehmann, Häring, Stefan, & Zell] Franken, H., Seitz, A., Lehmann, R., Häring, H.-U., Stefan, N., & Zell, A. (2012). Inferring disease-related metabolite dependencies with a bayesian optimization algorithm. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 61–72.
- [Giacobini et al.(2012)Giacobini, Vanneschi, & Bush] Giacobini, M., Vanneschi, L., & Bush, W. S. (Eds.) (2012). 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, vol. 7246 of LNCS. Malaga, Spain: Springer Verlag.
- [González-Álvarez et al.(2012)González-Álvarez, Vega-Rodríguez, Gómez-Pulido, & Sánchez-Pérez] González-Álvarez, D. L., Vega-Rodríguez, M. A., Gómez-Pulido, J. A., & Sánchez-Pérez, J. M. (2012). Finding motifs in DNA sequences applying a multiobjective artificial bee colony (MOABC) algorithm. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 108–119.
- [Granizo-Mackenzie & Moore(2012)] Granizo-Mackenzie, D. & Moore, J. H. (2012). Artificial immune systems perform valuable work when detecting epistasis in human genetic datasets. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 192–203.
- [Kancherla & Mukkala(2012)] Kancherla, K. & Mukkala, S. (2012). Feature selection for lung cancer detection using SVM based recursive feature elimination method. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning

- and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 168–179.
- [Langdon & Arno(2012)] Langdon, W. B. & Arno, J. (2012). In silico infection of the human genome. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 249–252.
- [Manning & Walsh(2012)] Manning, T. & Walsh, P. (2012). Automatic task decomposition for the neuroevolution of augmenting topologies (NEAT) algorithm. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 1–12.
- [Manzoni et al.(2012)Manzoni, Castelli, & Vanneschi] Manzoni, L., Castelli, M., & Vanneschi, L. (2012). Evolutionary reaction systems. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 13–24.
- [Marini & Conversi(2012)] Marini, S. & Conversi, A. (2012). Understanding zooplankton long term variability through genetic programming. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 49–60.
- [Márquez-Chamorro et al.(2012)Márquez-Chamorro, Divina, Aguilar-Ruiz, Bacardit, Asencio-Cortés, & Santiesteban-Too Márquez-Chamorro, A. E., Divina, F., Aguilar-Ruiz, J. S., Bacardit, J., Asencio-Cortés, G., & Santiesteban-Toca, C. E. (2012). A NSGA-II algorithm for the residue-residue contact prediction. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 238–248.
- [Nobile et al.(2012)Nobile, Besozzi, Cazzaniga, Mauri, & Pescini] Nobile, M., Besozzi, D., Cazzaniga, P., Mauri, G., & Pescini, D. (2012). A GPU-based multi-swarm PSO method for parameter estimation in stochastic biological systems exploiting discrete-time target series. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 73–84.
- [Pan et al.(2012)Pan, Darabos, & Moore] Pan, Q., Darabos, C., & Moore, J. H. (2012). The role of mutations in whole genome duplication. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 120–131.
- [Pinheiro et al.(2012)Pinheiro, Santos, & Pacheco] Pinheiro, F., Santos, F., & Pacheco, J. (2012). Tracking the evolution of cooperation in complex networked populations. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 85–95.
- [Pizzuti et al.(2012)Pizzuti, Rombo, & Marchiori] Pizzuti, C., Rombo, S. E., & Marchiori, E. (2012). Complex detection in protein-protein interaction networks: a compact overview for researchers and practitioners. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 216–227.
- [Rosenbaum et al.(2012)Rosenbaum, Jahn, & Zell] Rosenbaum, L., Jahn, A., & Zell, A. (2012). Optimizing the edge weights in optimal assignment methods for virtual screening with particle swarm optimization. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 25–36.

- [Santander-Jiménez et al.(2012)Santander-Jiménez, Vega-Rodríguez, Gómez-Pulido, & Sánchez-Pérez] Santander-Jiménez, S., Vega-Rodríguez, M. A., Gómez-Pulido, J. A., & Sánchez-Pérez, J. M. (2012). Inferring phylogenetic trees using a multiobjective artificial bee colony algorithm. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 144–155.
- [Santiesteban-Toca et al.(2012)Santiesteban-Toca, Márquez-Chamorro, Asencio-Cortés, & Aguilar-Ruiz] Santiesteban-Toca, C. E., Márquez-Chamorro, A. E., Asencio-Cortés, G., & Aguilar-Ruiz, J. S. (2012). Short-range interactions and decision tree-based protein contact map predictor. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 228–237.
- [Spirov et al.(2012)Spirov, Golyandina, Holloway, Alexandrov, Spirova, & Lopes] Spirov, A., Golyandina, N., Holloway, D., Alexandrov, T., Spirova, E., & Lopes, F. (2012). 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 M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 180–191.
- [Vanneschi et al. (2012) Vanneschi, Mondini, Bertoni, Ronchi, & Stefano] Vanneschi, L., Mondini, M., Bertoni, M., Ronchi, A., & Stefano, M. (2012). GeNet: A graph-based genetic programming framework for the reverse engineering of gene regulatory networks. In M. Giacobini, L. Vanneschi, & W. S. Bush (Eds.), 10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012. Malaga, Spain: Springer Verlag, vol. 7246 of LNCS, 96–107.