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 and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Asencio-Cortés et al.(2012)Asencio-Cortés, Aguilar-Ruiz, Márquez-Chamorro, Ruiz and Santiesteban-Toca] **Asencio-Cortés, G., Aguilar-Ruiz, J. S., Márquez-Chamorro, A. E., Ruiz, R. and Santiesteban-Toca, C. E.** (2012). Prediction of mitochondrial matrix protein structures based on feature selection and fragment assembly. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Buchanan et al.(2012)Buchanan, Wallace, Frase, Torstenson, Pendergrass and Ritchie] **Buchanan, C., Wallace, J., Frase, A., Torstenson, E., Pendergrass, S. and Ritchie, M.** (2012). A biologically informed method for detecting associations with rare variants. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Cerutti et al.(2012)Cerutti, Bertolotti, Goldberg and Giacobini] **Cerutti, F., Bertolotti, L., Goldberg, T. L. and Giacobini, M.** (2012). Improving phylogenetic tree interpretability by means of evolutionary algorithms. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Darabos et al.(2012)Darabos, Giacobini, Hu and Moore] **Darabos, C., Giacobini, M., Hu, T. and Moore, J. H.** (2012). Lévy-flight GP: towards a new mutation paradigm. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Franken et al.(2012)Franken, Seitz, Lehmann, Häring, Stefan and Zell] **Franken, H., Seitz, A., Lehmann, R., Häring, H.-U., Stefan, N. and Zell, A.** (2012). Inferring disease-related metabolite dependencies with a bayesian optimization algorithm. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Giacobini et al.(2012)Giacobini, Vanneschi and Bush] **Giacobini, M., Vanneschi, L. and Bush, W. S.**, eds. (2012). *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[González-Álvarez et al.(2012)González-Álvarez, Vega-Rodríguez, Gómez-Pulido and Sánchez-Pérez] **González-Álvarez, D. L., Vega-Rodríguez, M. A., Gómez-Pulido, J. A. and Sánchez-Pérez, J. M.** (2012). Finding motifs in DNA sequences applying a multiobjective artificial bee colony (MOABC) algorithm. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Granizo-Mackenzie and Moore(2012)] **Granizo-Mackenzie, D. and Moore, J. H.** (2012). Artificial immune systems perform valuable work when detecting epistasis in human genetic datasets. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Kancherla and Mukkala(2012)] **Kancherla, K. and Mukkala, S.** (2012). Feature selection for lung cancer detection using SVM based recursive feature elimination method. In M. Giacobini,

L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Langdon and Arno(2012)] **Langdon, W. B. and Arno, J.** (2012). In silico infection of the human genome. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Manning and Walsh(2012)] **Manning, T. and Walsh, P.** (2012). Automatic task decomposition for the neuroevolution of augmenting topologies (NEAT) algorithm. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Manzoni et al.(2012)Manzoni, Castelli and Vanneschi] **Manzoni, L., Castelli, M. and Vanneschi, L.** (2012). Evolutionary reaction systems. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Marini and Conversi(2012)] **Marini, S. and Conversi, A.** (2012). Understanding zooplankton long term variability through genetic programming. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Márquez-Chamorro et al.(2012)Márquez-Chamorro, Divina, Aguilar-Ruiz, Bacardit, Asencio-Cortés and Santiesteban-To **Márquez-Chamorro, A. E., Divina, F., Aguilar-Ruiz, J. S., Bacardit, J., Asencio-Cortés, G. and Santiesteban-Toca, C. E.** (2012). A NSGA-II algorithm for the residue-residue contact prediction. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Nobile et al.(2012)Nobile, Besozzi, Cazzaniga, Mauri and Pescini] **Nobile, M., Besozzi, D., Cazzaniga, P., Mauri, G. and 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 and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Pan et al.(2012)Pan, Darabos and Moore] **Pan, Q., Darabos, C. and Moore, J. H.** (2012). The role of mutations in whole genome duplication. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Pinheiro et al.(2012)Pinheiro, Santos and Pacheco] **Pinheiro, F., Santos, F. and Pacheco, J.** (2012). Tracking the evolution of cooperation in complex networked populations. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Pizzuti et al.(2012)Pizzuti, Rombo and Marchiori] **Pizzuti, C., Rombo, S. E. and Marchiori, E.** (2012). Complex detection in protein-protein interaction networks: a compact overview for researchers and practitioners. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Rosenbaum et al.(2012)Rosenbaum, Jahn and Zell] **Rosenbaum, L., Jahn, A. and Zell, A.** (2012). Optimizing the edge weights in optimal assignment methods for virtual screening with particle swarm optimization. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European*

Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Santander-Jiménez et al.(2012)Santander-Jiménez, Vega-Rodríguez, Gómez-Pulido and Sánchez-Pérez] **Santander-Jiménez, S., Vega-Rodríguez, M. A., Gómez-Pulido, J. A. and Sánchez-Pérez, J. M.** (2012). Inferring phylogenetic trees using a multiobjective artificial bee colony algorithm. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Santiesteban-Toca et al.(2012)Santiesteban-Toca, Márquez-Chamorro, Asencio-Cortés and Aguilar-Ruiz] **Santiesteban-Toca, C. E., Márquez-Chamorro, A. E., Asencio-Cortés, G. and Aguilar-Ruiz, J. S.** (2012). Short-range interactions and decision tree-based protein contact map predictor. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Spirov et al.(2012)Spirov, Golyandina, Holloway, Alexandrov, Spirova and Lopes] **Spirov, A., Golyandina, N., Holloway, D., Alexandrov, T., Spirova, E. and 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 and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.

[Vanneschi et al.(2012)Vanneschi, Mondini, Bertoni, Ronchi and Stefano] **Vanneschi, L., Mondini, M., Bertoni, M., Ronchi, A. and Stefano, M.** (2012). GeNet: A graph-based genetic programming framework for the reverse engineering of gene regulatory networks. In M. Giacobini, L. Vanneschi and W. S. Bush, eds., *10th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2012*, volume 7246 of *LNCS*. Malaga, Spain: Springer Verlag.