Список литературы

[1] Gualberto Asencio-Cortés, Jesús S. Aguilar-Ruiz, and Alfonso E. Márquez-Chamorro. A nearest neighbour-based approach for viral protein structure prediction. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 71–79, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: asenciocortes:2011:evobio

[2] Fabien Chhel, Adrien Goëffon, Frédéric Lardeux, Frédéric Saubion, Gilles Hunault, and Tristan Boureau. Experimental approach for bacterial strains characterization. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 139–144, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: chhel:2011:evobio

[3] Christian Darabos, Ferdinando Di Cunto, Marco Tomassini, Jason H. Moore, Paolo Provero, and Mario Giacobini. Validating a threshold-based boolean model of regulatory networks on a biological organism. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 61–70, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: darabos:2011:evobio

[4] Antonella Farinaccio, Leonardo Vanneschi, Paolo Provero, Giancarlo Mauri, and Mario Giacobini. A new evolutionary gene regulatory network reverse engineering tool. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 13–24, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: farinaccio:2011:evobio

[5] Luca Ferreri, Ezio Venturino, and Mario Giacobini. Do diseases spreading on bipartite networks have some evolutionary advantage? In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 145–150, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: ferreri:2011:evobio

[6] David L. González-Álvarez, Miguel A. Vega-Rodríguez, Juan A. Gómez-Pulido, and Juan M. Sánchez-Pérez. Finding motifs in DNA sequences applying a multiobjective artificial bee colony (MOABC) algorithm. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 92–103, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: gonzalez-alvarez:2011:evobio

[7] Georg Hinselmann, Andreas Jahn, Nikolas Fechner, Lars Rosenbaum, and Andreas Zell. Approximation of graph kernel similarities for chemical graphs by kernel principal component analysis. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 127–138, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: hinselmann:2011:evobio

[8] Emily R. Holzinger, Scott M. Dudek, Eric C. Torstenson, and Marylyn D. Ritchie. ATHENA optimization: The effect of initial parameter settings across different genetic models. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 49–60, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: holzinger:2011:evobio

[9] Sami Laroum, Béatrice Duval, Dominique Tessier, and Jin-Kao Hao. Multi-neighborhood search for discrimination of signal peptides and transmembrane segments. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 115–126, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: laroum:2011:evobio

[10] Filip Leonarski, Fabio Trovato, Valentina Tozzini, and Joanna Trylska. Genetic algorithm optimization of force field parameters. application to a coarse-grained model of RNA. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 151–156, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: leonarski:2011:evobio

[11] Alfonso E. Márquez-Chamorro, Federico Divina, Jesús S. Aguilar-Ruiz, and Gualberto Asencio-Cortés. An evolutionary approach for protein contact map prediction. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 104–114, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: marquezchamorro:2011:evobio

[12] Jianlong Qi, Tom Michoel, and Gregory Butler. Applying linear models to learn regulation programs in a transcription regulatory module network. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 37–48, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: qi:2011:evobio

[13] Saad Quader, Nathan Snyder, Kevin Su, Ericka Mochan, and Chun-Hsi Huang. ML-Consensus: a general consensus model for variable-length transcription factor binding sites. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 25–36, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: quader:2011:evobio

[14] Faisal Rezwan, Yi Sun, Neil Davey, Alisatir G. Rust, and Mark Robinson. Effect of using varying negative examples in transcription factor binding site predictions. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 1–12, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: rezwan:2011:evobio

[15] Eva Sciacca, Salvatore Spinella, Dino Ienco, and Paola Giannini. Annotated stochastic context free grammars for analysis and synthesis of proteins. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 80–91, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: sciacca:2011:evobio

[16] Sara Silva, Orlando Anunciao, and Marco Lotz. A comparison of machine learning methods for the prediction of breast cancer. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 163–174, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: silva:2011:evobio

[17] Cosme Ernesto Santiesteban Toca, Alfonso E. Márquez-Chamorro, Gualberto Asencio-Cortés, and Jesús S. Aguilar-Ruiz. A decision tree-based method for protein contact map prediction. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 157–162, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: santiesteban-toca:2011:evobio

[18] Daniele Toti, Paolo Atzeni, and Fabio Polticelli. An automatic identification and resolution system for protein-related abbreviations in scientific papers. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 175–180, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: toti:2011:evobio

[19] Yunku Yeu, Jaegyoon Ahn, Youngmi Yoon, and Sanghyun Park. Protein complex discovery from protein interaction network with high false-positive rate. In Clara Pizzuti, Marylyn D. Ritchie, and Mario Giacobini, editors, 9th European Conference Evolutionary Computation on Machine Learning and Data Mining in Bioinformatics: EvoBIO 2011, volume 6623 of LNCS, pages 181–186, Turin, Italy, 27-29 April 2011. Springer Verlag.

Key: veu:2011:evobio