



Message from the BIO 2013 Workshop Chairs



This year, the International Workshop on Evolutionary Computation in Bioinformatics (BIO 2013) will be held as part of GECCO'13, the largest international conference in the field of genetic and evolutionary computation (with proceedings published by ACM Digital Library).

Numerous problems encountered in Bioinformatics can be formulated as optimization problems, and thus lend themselves to the application of very diverse Evolutionary Computation techniques. In fact, Bioinformatics is one of the most exciting research areas in which Evolutionary Computation finds application. In this sense, BIO 2013 offers a set of original, high-quality research works, clearly focused on the application of Evolutionary Computation to different Bioinformatics problems.

It is worth mentioning that the workshop received 12 high-quality submissions from different countries (USA, Australia, Japan, Italy, Spain, Turkey, United Arab Emirates, Viet Nam, and Jordan). All these twelve papers were reviewed by at least two expert reviewers. Eight papers of high quality in emerging research areas were accepted for inclusion in the workshop proceedings and presentation at the conference (acceptance rate = $8/12 = 66\%$). In conclusion, we think these papers bring us an international sampling of significant work.

As we will see, the papers in BIO 2013 cover important bioinformatics problems as: protein folding, NMR structure based assignment, prediction of protein inter-domain linkers, patterns search in breast cancer databases, transcription factor binding sites (TFBSs) detection, motif discovery, phylogenetic inference, DNA computing, etc. In the same way, very diverse evolutionary computation techniques are proposed to solve these bioinformatics problems, some examples are: cellular automata implemented with artificial neural networks optimized with differential evolution, ant colony optimization, simulated annealing, genetic programming, hybrid multiobjective artificial bee colony, multiobjective firefly algorithm, non-dominated sorting genetic algorithm II (NSGA-II), strength pareto evolutionary algorithm 2 (SPEA2), etc.

We sincerely hope that BIO 2013 workshop stimulates your interest in the many issues surrounding Bioinformatics and Evolutionary Computation. The topics covered in the papers are timely and important, and the authors have done an excellent job of presenting the material. In fact, this workshop would not have been possible without the assistance of both the authors and the reviewers, to whom we give many thanks. We also express our gratitude to the presenters as well as the participants for making this workshop a success.

Finally it is important to highlight that BIO 2013 will be held in the modern and lovely city of Amsterdam (The Netherlands), we hope you enjoy your stay.

Miguel A. Vega-Rodríguez

BIO 2013 Chair

University of Extremadura, Spain

Jose M. Chaves-González

BIO 2013 Chair

University of Extremadura, Spain

David L. González-Álvarez

BIO 2013 Chair

University of Extremadura, Spain

Sergio Santander-Jiménez

BIO 2013 Chair

University of Extremadura, Spain

BIO 2013 Organization

General Chairs: Miguel A. Vega-Rodríguez (*University of Extremadura, Spain*)
Jose M. Chaves-González (*University of Extremadura, Spain*)
David L. González-Álvarez (*University of Extremadura, Spain*)
Sergio Santander-Jiménez (*University of Extremadura, Spain*)