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EvoBIO Best Paper

2 mensajes

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Dear EvoStar friends

this is to let you know that your paper "**Hybrid Multiobjective Artificial Bee Colony with Differential Evolution Applied to Motif Finding**" has been nominated as a EvoBIO best paper at this year's EvoStar conferences taking place in Vienna on 3-5 April. The winning paper will be announced at the closing ceremony on the last day (5 April).

congratulations and best of luck!

jennifer

Jennifer Willies

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www.evostar.org : EvoStar Coordinator for Europe's premier co-located events on evolutionary computing

www.focas.eu : Project Manager for FoCAS, the FET Coordination Action on Fundamentals of Collective Adaptive Systems

www.aware-project.eu : Project Manager for AWARE, the FET Coordination Action for Self-Awareness in Autonomic Systems

www.perada.eu : Project Manager for PerAda, the FET Coordination Action for Pervasive Adaptation

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EvoIASP
EvoINDUSTRY
EvoNUM
EvoPAR
EvoRISK
EvoROBOT
EvoSTOC

Important Dates

Submission deadline
~~1 November 2012~~
11 November 2012

Camera Ready Deadline
15 January 2013

Author Instructions

Registrations Open
7 January 2013
Early Registration Deadline
1 March 2013
Bursary Deadline
25 February 2013
Registration Close
25 March 2013
EvoStar Conference Dates
3-5 April 2013

Programme

Overview Programme (TBA)
Invited Speakers (TBA)
Abstracts (TBA)

Local Information


Venue
Transport
Accommodation
Poster, WIFI, Equipment

Registration

Registration
Letters of Invitation
Student Bursaries

Organisers and Contacts

Previous Events

Malaga 2012 
Torino 2011
Istanbul 2010
Tübingen 2009

EvoBIO

The European Conference on Evolutionary Computation, Machine Learning and Data Mining in Computational Biology

[EvoBio 2013 Accepted Papers](#)

EvoBIO is a multidisciplinary conference that brings together researchers working in Bioinformatics and Computational Biology that apply advanced techniques coming from Evolutionary Computation, Machine Learning, and Data Mining to address important problems in biology, from the molecular and genomic dimension, to the individual and population level. The primary focus of the conference is to present the latest advances of these approaches for Bioinformatics and Computational Biology, and to provide a forum for the discussion of new research directions.

The 11th edition of EvoBIO will take place in the wonderful location of Wien, Austria. The conference will be held in conjunction with the EuroGP (16th European Conference on Genetic Programming), EvoCOP 2010 (13th European Conference on Evolutionary Computation in Combinatorial Optimisation), EvoMUSART (11th European Conference on Evolutionary and Biologically Inspired Music, Sound, Art and Design), and EvoApplications 2013, the specialist conference on a range of evolutionary computation topics and applications.

For more information, visit our web page at <http://www.evostar.org>, or follow us on Twitter @EVOBio2013, join our evobio2013 group on LinkedIn and our EvoBIO group on Facebook, or email to [evobio.conference\(at\)gmail.com](mailto:evobio.conference(at)gmail.com).

Areas of Interest and Contributions

The conference invites contributions on the application of techniques typical of the Evolutionary Computation, Machine Learning, and Data Mining domains to address problems in Bioinformatics and Computational Biology.

Topics include but are not limited to:

- biomarker discovery
- cell simulation and modelling
- ecological modelling
- fluxomics
- biological networks analysis
- high-throughput biotechnology
- metabolomics
- microarray analysis
- phylogeny
- protein interaction
- proteomics
- sequence analysis and alignment
- biological networks modelling
- systems biology

Publication Details

Each accepted paper will be presented orally or as a poster at the conference and will be printed in the proceedings published by Springer Verlag in the LNCS series. The accepted papers of the previous editions of EvoBIO were published in the Springer Verlag LNCS. The first 4 editions (2003–2006) were published in the LNCS 2611, 3005, 3449, 3907, together with the remaining EvoWorkshops. Since 2007 evobio became a EVO* conference and its proceedings were published in Springer Verlag LNCS 4447, 4973, 5483, 6023, 6622, and 7246 respectively.

Post-conference Journal Publication

The authors of papers which receive the best reviews will be nominated for the Best Paper Award. Papers nominated for the best paper award will also be invited to expand their article for post-conference publication in the BioMed Central journal BioData

Naples 2008
Valencia 2007
Budapest 2006
Lausanne 2005
Coimbra 2004
Essex 2003
Kinsale 2002
Lake Como 2001
Edinburgh 2000
Göteborg 1999
Paris 1998

Mining, with a 25% discount on the publication fees. Moreover, the winner of the Best Paper Award will have a full waiver of the publication fees for the authors.

Special joint session with EuroGP

Following the success of last year's joint session, we especially encourage submissions applying genetic programming to problems in computational biology and new biology-inspired extensions of the genetic programming framework for a special joint session of EvoBIO with EuroGP. These papers can be submitted either to EvoBIO or EuroGP.

Submission Details

Submissions must be original and not published elsewhere. The submissions will be peer reviewed by at least three members of the program committee. The authors of accepted papers will have to improve their paper on the basis of the reviewers' comments and will be asked to send a camera ready version of their manuscripts. At least one author of each accepted work has to register for the conference and attend the conference and present the work.

The reviewing process will be double-blind, please omit information about the authors in the submitted paper. Submit your manuscript in [Springer LNCS format](#) at <http://myreview.csregistry.org/evobio13/>. EvoBIO is interested in papers in three major areas:

1. Full research articles (maximum 12 pages) describing new methodologies, approaches, and/or applications (oral or poster presentation).
2. Short reports (maximum 8 pages, poster presentation) describing new methodologies, approaches, and/or applications and System Demonstrations (maximum 8 pages) outlining the nature of the system and describe why the demonstration is likely to be of interest for the conference. Demonstrations of interest include systems under development or in active use in research or practice domains. Selected demo submissions may be asked to give an oral presentation in the conference sessions.
3. Abstracts (maximum 4 pages) discussing work previously published in a journal: it is therefore essential that a reference to the previous article is clearly cited in the abstract (oral or poster presentation).

Submission deadline: ~~4 November 2012~~ Extended to 11 November 2012

EvoBIO programme chairs

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EVOBIO 2013 - ACCEPTED PAPERS

EVOBIO ORAL PRESENTATIONS

Feature Selection and Classification of High Dimensional Mass Spectrometry Data: A Genetic Programming Approach

Soha Ahmed, Mengjie Zhang, Lifeng Peng

Biomarker discovery using mass spectrometry (MS) data is very useful in disease detection and drug discovery. The process of biomarker discovery in MS data must start with feature selection as the number of features in MS data is extremely large (e.g. thousands) while the number of samples is comparatively small. In this study, we propose the use of genetic programming (GP) for automatic feature selection and classification of MS data. This GP based approach works by using the features selected by two feature selection metrics, namely information gain (IG) and relief-f (REFS-F) in the terminal set. The feature selection performance of the proposed approach is examined and compared with IG and REFS-F alone on five MS data sets with different numbers of features and instances. Naive Bayes (NB), support vector machines (SVMs) and J48 decision trees (J48) are used in the experiments to evaluate the classification accuracy of the selected features. Meanwhile, GP is also used as a classification method in the experiments and its performance is compared with that of NB, SVMs and J48. The results show that GP as a feature selection method can select a smaller number of features with better classification performance than IG and REFS-F using NB, SVMs and J48. In addition, GP as a classification method also outperforms NB and J48 and achieves comparable or slightly better performance than SVMs on these data sets.

Hybrid Multiobjective Artificial Bee Colony with Differential Evolution Applied to Motif Finding (EvoBIO Best Paper Candidate)

David L. González-Álvarez, Miguel A. Vega-Rodríguez, Juan A. Gómez-Pulido, Juan M. Sánchez-Pérez

The Multiobjective Artificial Bee Colony with Differential Evolution (MO-ABC/DE) is a new hybrid multiobjective evolutionary algorithm proposed for solving optimization problems. One important optimization problem in Bioinformatics is the Motif Discovery Problem (MDP), applied to the specific task of discovering DNA patterns (motifs) with biological significance, such as DNA-protein binding sites, replication origins or transcriptional DNA sequences. In this work, we apply the MO-ABC/DE algorithm for solving the MDP using as benchmark genomic data belonging to four organisms: *drosophila melanogaster*, *homo sapiens*, *mus musculus*, and *saccharomyces cerevisiae*. To demonstrate the good performance of our algorithm we have compared its results with those obtained by four multiobjective evolutionary algorithms, and their predictions with those made by thirteen well-known biological tools. As we will see, the proposed algorithm achieves good results from both computer science and biology point of views.

Multiple Threshold Spatially Uniform ReliefF for the Genetic Analysis of Complex Human Diseases

Delaney Granizo-Mackenzie, Jason H. Moore

Detecting genetic interactions without running an exhaustive search is a difficult problem. We present a new heuristic, multiSURF*, which can detect these interactions with high accuracy and in time linear in the number of genes. Our algorithm is an improvement over the SURF* algorithm, which detects genetic signals by comparing individuals close to, and far from, one another and noticing whether differences correlate with different disease statuses. Our improvement consistently outperforms SURF* while providing a large runtime decrease by examining only individuals very near and very far from one another. Additionally we perform an analysis on real data and show that our method provides new information. We conclude that multiSURF* is a better alternative to SURF* in both power and runtime.

Supervising Random Forest Using Attribute Interaction Networks

*Qinxin Pan, Ting Hu, James D. Malley, Angeline S. Andrew, Margaret R. Karagas
Jason H. Moore*