SIGEVOlution

newsletter of the ACM Special Interest Group on Genetic and Evolutionary Computation

September 2006
Volume 1 Issue 3

GECCO goes to London!

in this issue

Editorial

London! At last, GECCO, the admiral conference of SIGEVO, is sailing to Europe and will reach the shore of the United Kingdom next summer on July 7th. When I read Richard Dawkins's name on the GECCO website I was speechless. . . I actually reread the headline and mumbled "That Richard Dawkins???" I continued and I found the names of Lewis Wolpert and Steve Jones. At that point everything made sense and I remained speechless again. What an amazing keynote event!

After some delay, here is the third issue of SIGEVOlution. I hope that it is well worth the wait since this issue is fully loaded with content including a message from Erik Goodman, the chair of SIGEVO, detail of the upcoming GECCO-2007 keynote event from Hod Lipson and Peter Bentley, two contributed papers by Arthur Kordon and Xavier Llorà, a huge section devoted to highlights from GECCO-2006, summaries of two EC workshops, a letter about the synthesis of evolutionary algorithms and quantum computing, the table of contents of the forthcoming issues of ECJ and GPEM, and the calendar of EC events.

As always, I wish to thank all the people who helped me with the newsletter, the board members, Dave Davis and Martin Pelikan, Mike & Pat Cattolico from GECCO-2006, Hod Lipson & Peter Bentley from GECCO-2007, Erik Goodman from SIGEVO, the authors, Arthur Kordon and Xavier Llorà, and the people who organized the tracks and the workshops at GECCO-2006 who contributed to the GECCO-2006 highlights, James Foster, Sevan G. Ficici, Dirk Arnold, Martin Butz, Varun Aggarwal, Kumara Sastry, D.D. Johnson, Alexis L. Thompson, David E. Goldberg, Todd J. Martinez, Jeff Leiding, Jane Owens, Gustavo Olague, Edwin D. de Jong, Marc Toussaint, Tim Kovacs, Keiki Takadama, Stefano Cagnoni, Giuseppe Nicosia, and Leonardo Vanneschi.

This huge list of names clearly shows that the newsletter is mainly a product of the community and that the role of the editorial board is more or less just to help people bring their interesting information to a larger audience. Therefore, we are always open to contributions, suggestions, criticisms, and whatever might help us improve SIGEVOlution.

I almost forgot!

The cover is a photo of London's Tower Bridge by Kumara Sastry. More photos can be found here.

Pier Luca
October 27th, 2006

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Contributors to this Issue

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SIGEVO News

Wow! That's all I can say about the plans for GECCO-2007, in London, July 7-11, 2007. It's not only our first time taking GECCO across the Atlantic, but also the most exciting keynote event yet – with Richard Dawkins, Lewis Wolpert, and Steve Jones debating the emergence of complexity in evolution. My thanks go out to the organizers – it's been tough figuring out how to do GECCO in London – it needs to be a different model than our standard "take over a hotel" – that just won't work there. So Hod Lipson (GECCO-2007 general chair) and his co-organizers have had to deal with lots of difficult decisions that are usually "no-brainers." Most of you SIGEVOlutions readers now have an important assignment: get your papers for GECCO-2007 ready for submission by January 17, 2007!

It's an exciting time for SIGEVO – and not only for GECCO organizers. This excellent newsletter (thanks to Pier Luca Lanzi and his editorial board) is one of the clearest signs. The transition to becoming an ACM Special Interest Group is now complete – about the time you're reading this, I'll be participating for the first time as a voting member of the ACM SIG Governing Board, since SIGEVO went from a transitional SIG to a "regular" SIG in June of 2006. But there are still many things that we're doing for the first time through the ACM organization, including the upcoming FOGA (Jan. 7-11, Mexico City) and the first siting of GECCO (for 2007). So lots of people are still blazing ground for those who will follow. Pat Cattolico, has been doing a tremendous job getting up to speed with ACM procedures, and the ACM SIG Support staff, including Irene Frawley, Stephanie Smith, Elizabeth Grove, Adrienne Griscti, and Donna Cappo, have worked with us patiently and flexibly as we learn the new ways.

I feel like there's something different in the air, recently, when it comes to GEC. I've given several talks this year to lay audiences, including to people who have no background in computer science, engineering, or even the sciences. We now have good enough stories to tell that people get very excited about this "new" field. That really gets me energized! Things like the "Humies" competition (Human Competitive Results achieved by GEC, at GECCO each year) are proof of the power of what we're doing, and it's great finally to be able to communicate the power of these methods to the public! I encourage you all to do it as often as you get the chance. As entrepreneurs say, "Work on your elevator speech" – two minutes about what you do, in language that anyone can understand. Why not get people a little excited about the capabilities of GEC?

Erik Goodman, Chair
ACM SIGEVO

GECCO 2007 Keynote Event:

Public Debate on Complexity and Evolution with Profs Richard Dawkins, Steve Jones and Lewis Wolpert

We are pleased to announce that Prof Richard Dawkins, Prof Steve Jones and Prof Lewis Wolpert will take part in a public debate on the evening of 9 July, discussing the emergence of complexity in evolution. The debate will follow the format of the popular BBC television show “Question Time". Every member of the audience will be asked to write down their questions relating to evolution and complexity in advance. A selection of representative questions will then be chosen, and during the debate the authors of each one will be invited to stand up and put their question to the panel. The audience will also be given an opportunity to respond to the discussion to help stimulate an even more lively debate.

Each GECCO delegate will be able to provide their question using the on-line registration system (and they may modify it at any time later). We are hoping to explore some of the important and meaningful questions to do with evolution. The choice is up to you, but examples of interesting questions might be: “Are humans still evolving, and if so is the selection pressure caused more by cultural or monetary factors than disease or predation?", or “Do you believe horizontal gene transfer has affected the course of evolution as much as vertical gene transfer?" or, “Did the evolution of complex life require development, or did development require the evolution of complex life?" or, “Do you believe we will ever evolve something with a computer that could be called alive?" Everyone is encouraged to think carefully of their own question, which should be a single sentence, not a speech. We prefer not to have questions relating to religion.

Our three speakers are extremely well-known in their fields. Richard Dawkins is famous for his work in evolutionary biology and his best-selling books such as “The Selfish Gene", “The Blind Watchmaker" and “River Out of Eden". Steve Jones is well-known for his work in genetics, and his best-selling books which include, “Almost Like a Whale", “Y: the Descent of Man" and “The Language of the Genes". Lewis Wolpert is a pioneer in the field of developmental biology and known for his books “Six Impossible Things Before Breakfast: The Evolutionary Origins of Belief" and “Principles of Development."

This will be a once-in-a-lifetime opportunity to hear and interact with some of the most famous names in evolutionary biology.

Hod Lipson, GECCO-2007 General Chair
Peter J. Bentley, GECCO-2007 Local chair

Evolutionary Computation at Dow Chemical

Arthur Kordon, akordon@dow.com
The Dow Chemical Company

Dow Chemical is the largest US chemical company by sales ($46 billion in 2005). It is one of the most diversified global company in the business with more than 3000 products in the market, mostly plastics, polyurethanes, and different specialty chemicals. There are two key directions in introducing new emerging technologies, such as Evolutionary Computation (EC), in the company. The first direction is continuous improvement of manufacturing and supply-chain efficiency, which becomes critical in the current economic environment of skyrocketing energy prices. The second direction is faster invention of an attractive pipeline of new products, which is critical for the future competitiveness of the company. The more specific issues of the chemical industry in these two directions can be defined as:

- high-dimensionality of plant data (thousands of variables and control loops),
- scarcity of data in new product development,
- low speed of data analysis in High-Throughput Screening (which is at the basis of new product discoveries),
- increased requirements for model robustness toward process changes due to the cyclical nature of the industry,
- multiple optima,
- key process knowledge is in process operators and poorly documented,
- high uncertainty in new material market response,
- supply chain not as well developed as process modeling

There are tremendous opportunities for EC to satisfy these needs and contribute to process improvement and new product discovery. However, we need to take into account that as a result of the intensive modeling efforts in the last 20 years many manufacturing processes in the most profitable plants are already supplied by different types of models (steady-state, dynamic, model predictive control, etc.). This creates a culture of modeling "fatigue" and resistance to introduction of new solutions, especially based on unknown technologies. This makes the efforts of applying EC in the chemical industry especially challenging since demonstration of significant competitive advantages relative to the alternative modeling and hardware solutions is required.

Competitive Advantages of EC

EC has been applied in different businesses and technical areas in The Dow Chemical Company since the early 90s [1-2]. From our experience, one generic area where EC has demonstrated a clear competitive advantage is the development of simple empirical solutions in terms of models and rules. We have shown in several cases that the models generated by EC are a low-cost alternative to both high fidelity models [3] and expensive hardware analyzers [4]. The specific competitive advantages of EC related to the generic area of empirical modeling are defined as follows:

No *a priori* modeling assumptions

EC model development does not require limited assumption space by physical considerations (as is in case of first-principle modeling) or by

statistical considerations, such as variable independence, multivariate normal distribution and independent errors with zero mean and constant variance. This "assumption liberation" establishes a technical superiority of generating models from the data with minimal effort from the experts.[1] The cost savings are in the experts' reduced time for defining and especially for validating the model assumptions. In case of mechanistic models for chemical processes, which may require defining and validating the assumption space of hundreds of parameters by several experts, the savings could be significant. On the other hand, in estimating the total cost-of-ownership, we have to take into account the additional time from the experts to select and interpret the generated assumption-free models.

High Quality Empirical Models

The key EC approach for empirical model building is symbolic regression, generated by Genetic Programming (GP). A well-known issue of the conventional GP algorithm, however, is the high complexity of the generated expressions at the end of the simulated evolution. In most of the cases the high fitness is based on very inefficient structure due to the generation of useless sub-trees, called introns. The breakthrough method to resolve this issue is multi-objective simulated evolution where in addition to the performance as a first objective, the complexity of the generated symbolic regression expression is explicitly used as a second objective. In this case the optimal models fall on the curve of the nondominant solutions, called Pareto front, i.e., no other solution is better than the solutions on the Pareto front in both complexity and performance [5]. Using Pareto front GP allows the simulated evolution and model selection to be directed toward structures based on an optimal balance between accuracy and expression complexity. A current survey from several industrial applications in The Dow Chemical Company demonstrates that the selected final models have a very low level of complexity [2]. The derived symbolic regression models show improved robustness during process changes relative to conventional GP as well as neural network-based models.

Easy Integration in Existing Work Processes

In order to improve efficiency and reduce implementation cost, the procedures for development, implementation, and maintenance in industry are standardized by work processes and methodologies. For example, many companies use the Six Sigma and Design for Six Sigma methodologies to operate their processes and introduce new products more efficiently [6]. One of the positive effects of Six Sigma is the widespread use of statistical methods not only in empirical model building by the engineers but also in making statistically-based decisions by managers. Since the industry has already invested in developing and supporting the infrastructure of the existing work processes, the integration efforts of any new technology become a critical issue. From that perspective, EC in general and symbolic regression in particular, have a definite competitive advantage. The technology could be integrated within Six Sigma with minimal efforts as extension of the existing statistical modeling capabilities with additional nonlinear modeling capabilities in the form of explicit mathematical expressions. Another advantage of this type of solutions is that there is no need for a specialized software environment for their run-time implementation (as is the case of mechanistic and neural network models). This feature allows for a relatively easy software integration of this specific EC technology into most of the existing model deployment software environments.

Minimal Training of the Final User

The symbolic regression nature of the final solutions, generated by GP, is universally acceptable by any user with mathematical background at high school level. This is not the case, either with the first-principle models (where specific physical knowledge is required) or with the black-box models (where for example, some advanced knowledge on neural networks is a must). In addition, a very important factor in favor of symbolic regression is that process engineers prefer mathematical expressions and very often can find an appropriate physical interpretation. They usually don't hide their distaste toward black boxes.

[1] However, all necessary data preparation procedures, such as data cleaning, dealing with missing data, outlier removal, etc. are still valid.

Low Total Cost of Development, Deployment, and Maintenance

Development Cost. The development cost includes expenses from the internal research efforts, internal software development efforts, and the research-type of marketing efforts to sell the technology to industrial users. From our experience, the internal research efforts to evaluate the capabilities of EC are comparable with other similar approaches, such as neural networks. Since we estimated and demonstrated the potential value impact of EC in the early phase of the internal research efforts, we decided to allocate resources to develop our own software and to improve the technology. This obviously added significantly to the development cost, although it was a very good investment.

EC has a clear advantage in marketing the technology to potential users. The scientific principles are easy to explain to almost any audience. We also find that process engineers are much more open to take the risk to implement symbolic regression models in the manufacturing plant rather than the alternatives.

Deployment Cost. Most of the alternative approaches require high cost of deployment, especially in real-time process monitoring and control systems. The license fee of the available on-line versions of the software is at least an order of magnitude more expensive than the off-line development option. As was discussed earlier, symbolic regression models do not require special run-time versions of the software and can be directly implemented in any existing process monitoring and control system, i.e. the deployment cost is minimal.

Another deployment problem where EC can reduce the cost is in improving on the slow execution speed of some of the complex first-principle models. Very often, such models require at least 30-60 min calculation time for selected operating conditions and this prevents their use in real-time applications. One possible way to solve this problem and significantly speed up on-line execution time is by representing the complex mechanistic model with a set of empirical models, called emulators.

Maintenance Cost. Often maintenance and support cost of applied models is neglected in the initial total cost estimates. It turns out, that this may take the lion's share of the total cost-of-ownership. For example, first-principle models require specialized knowledge for their support. Model validation in continuously changing operating conditions becomes very time consuming and costly. Often the new operating conditions are outside the assumption space and the validity of the model becomes questionable. The changing operating conditions are even a bigger challenge for neural networks-based models and lead to frequent re-training and even completely new model re-design. As a result, gradually both complex mechanistic models and neural networks become a maintenance nightmare. The growing maintenance cost may also call into question the value of the model and lead to the decision of removing it from the process. In contrast, the simple symbolic regression models require minimal maintenance. From our experience the model re-design is very rare and most of the models perform with acceptable quality even in extrapolation mode within 20% outside their original model data range. There are symbolic regression models that have been in operation since 1997 [7].

Key EC Application Areas in Dow Chemical

Based on our recent experience from several applications on different real industrial processes in the Dow Chemical Company, we would recommend the following industrial problems as appropriate for EC:

Fast development of nonlinear empirical models

Symbolic-regression types of models are very well-fit for industrial applications and are often at the economic optimum of development and maintenance cost. One area with tremendous potential is inferential or soft sensors, i.e. empirical models that infer difficult-to-measure process parameters, such as NOx emissions, melt index, interface level, etc., from easy-to-measure process variables such as temperatures, pressures, flows, etc. [4]. The current solutions in the market, based on neural networks, require frequent re-training and specialized run-time software.

An example of an inferential sensor for a quality parameter in a distillation column prediction based on an ensemble of four different models is given in [8]. The models were developed from an initial large manufacturing data set of 23 potential input variables and 6900 data points. The size of the data set was reduced by variable selection to 7 significant inputs and the models were generated by five independent GP runs. As a result of the model selection, a list of 12 models on the Pareto front was proposed for further evaluation to process engineers. All selected models have high performance (R^2 of 0.97-0.98) and low complexity. After evaluating their extrapolation capabilities with "What-If" scenarios,

the diversity of model inputs, and by physical considerations, an ensemble of four models was selected for on-line implementation. Two of the models are shown below:

$$GP\_Model1 = A + B\left(\frac{Tray64\_T^4 \cdot Vapor^3}{Rflx\_flow^2}\right)$$

$$GP\_Model2 = C + D\left(\frac{Feed^3\sqrt{Tray46\_T - Tray56\_T}}{Vapor^2 \cdot Rflx\_flow^4}\right)$$

where A, B, C, and D are fitting parameters, and all model inputs in the equations are continuous process measurements.

The models are simple and interpretable by process engineers. The different inputs used in both models increases the robustness of the estimation scheme in case of possible input sensor failure. The inferential sensor is in operation since May 2004.

Emulation of complex first-principle models

Symbolic regression models can substitute parts of fundamental models for on-line monitoring and optimization. The execution speed of the majority of the complex first-principle models is too slow for real time operation. One effective solution is to emulate a portion of the fundamental model, by a symbolic regression model, called an emulator, built only with selected variables, related to process optimization. The data for the emulator are generated by design of experiments from the first-principle model. One interesting benefit of emulators is that they can be used as fundamental model validation indicators as well. Complex model validation during continuous process changes requires tremendous efforts in data collection and numerous model parameter fittings. It is much easier to validate the simple emulators and to infer the state of the complex model on the basis of the high correlation between them. An example of such an application for optimal handling of by-products is given in [3]. The mechanistic model is very complex and includes over 1500 chemical reactions with more than 200 species. Ten input variables and 12 output variables that need to be predicted and used in process optimization were selected from the experts. A data set, based on four-level design of experiments, was generated and used for model development and validation. For 7 of the outputs, a linear emulator gave acceptable performance. For the remaining 5 emulators, a nonlinear model was derived by GP. An example of a nonlinear emulator, selected by the experts is given below:

$$Y_5 = \frac{6x_3 + x_4 + x_5 + 2x_6 + x_2x_9 - \frac{x_2 - 3x_3\sqrt{x_6}}{(x_2^2 + x_7x_1^3)}}{\ln(\sqrt{x_9x_{10}^2})}$$

where Y is the predicted output, used for process optimization, and the x variables are measured process parameters. The emulators are used for by-product optimization between two chemical plants in The Dow Chemical Company since March 2003.

Accelerated first-principle model building

The key creative process in fundamental model building is hypothesis search. Unfortunately, the effectiveness of hypothesis search depends very strongly on creativity, experience, and imagination of the model developers. The broader the assumption space (i.e., the higher the complexity and dimensionality of the problem), the larger the differences in modelers' performance and the higher the probability for ineffective fundamental model building.

In order to improve the efficiency of hypothesis search and to make the fundamental model discovery process more consistent, a new "accelerated" fundamental model building sequence is proposed. The key idea is to reduce the fundamental hypothesis search space by using symbolic regression, generated by GP. The main steps in the proposed methodology are shown in Fig. 1.

The key difference from the classical modeling sequence is in running simulated evolution before beginning the fundamental model building. As a result of the GP-generated symbolic regression, the modeler can identify the key variables and assess the physical meaning of their presence/absence. Another significant side effect from the simulated evolution is the analysis of the key transforms with high fitness that persist during the GP run. Very often some of the transforms have direct physical interpretation that can lead to better process understanding at the very early phases of fundamental model development. The key result from the GP-run, however, is the list of potential nonlinear empirical models in the form of symbolic regression. The expert may select and interpret several empirical solutions or repeat the GP-generated symbolic regression until an acceptable model is found. The fundamental model building step 5 is based either on a direct use of empirical models or on independently derived first principles models induced by the results from the symbolic regression. In both cases, the effectiveness of the whole modeling sequence could be significantly improved.

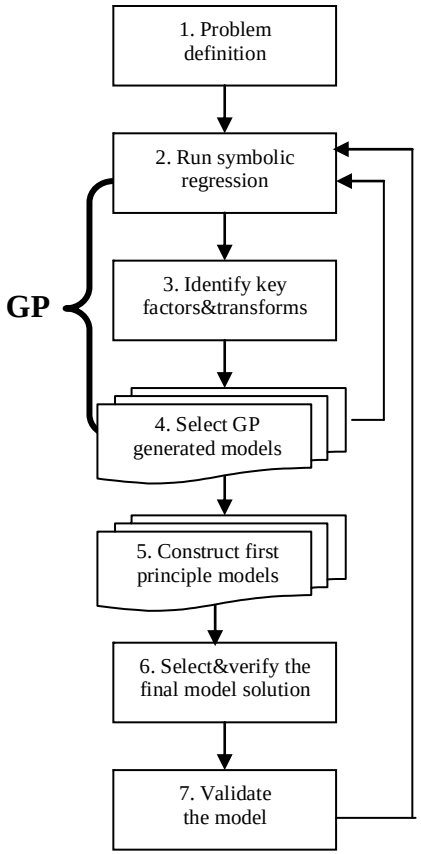

Figure 1: Accelerated new product development by using Genetic Programming.

The large potential of genetic programming (GP)-based symbolic regression for accelerated fundamental model building was demonstrated in a case study for structure-property relationships [10]. The generated symbolic solution was similar to the fundamental model and was delivered with significantly less human effort (10 hours vs. 3 months). By optimizing the capabilities for obtaining fast and reliable GP-generated functional solutions in combination with the fundamental modeling process, a real breakthrough in the speed of new product development can be achieved.

Linearized transforms for Design Of Experiments

GP-generated transforms of the input variables can eliminate significant lack of fit in linear regression models without the need to add expensive experiments to the original design, which can be time-consuming, costly, or maybe technically infeasible because of extreme experimental conditions. An example of such type of application for a chemical process is given in [9].

Complex Process Optimization

Process optimization is an area where EC technologies can make almost immediate economic impact and demonstrate value. Since the early 90s various evolutionary computation methods, mostly genetic algorithms, have been successfully applied in industry, including in The Dow Chemical Company. Recently, a new approach, Particle Swarm Optimization (PSO) is found to be very attractive for industrial applications. The main attractiveness of PSO is that it is fast, it can handle complex high-dimensional problems, it needs a small population size, and it is simple to implement and use. Different types of PSO have been explored in The Dow Chemical Company. A hybrid PSO and Levenberg-Marquardt method was used for quick screening of complicated kinetic models [11]. The PSO successfully identified the promising regions of parameter space that are then optimized locally. A different, multi-objective PSO was investigated in [12] and applied for real-time optimization of a color spectrum of plastics based on 15 parameters.

Conclusion

EC created significant value in The Dow Chemical Company by improving manufacturing processes and accelerating product discovery. The key competitive advantages of EC, based on industrial applications in the company are defined as: no *a priori* modeling assumptions, high quality empirical models, easy integration in existing industrial work processes, minimal training of the final user, and low total cost of development, deployment, and maintenance. Examples of successful application areas are: inferential sensors, empirical emulators of mechanistic models, accelerated new product development, complex process optimization, and effective industrial design of experiments.

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Arthur K. Kordon received the M.S. in Electrical Engineering from the Technical University in Varna, Bulgaria in 1974 and his Ph.D. degree from the Technical University in Sofia, Bulgaria in 1990. Since 1996 he is a Research & Development Leader in Engineering & Process Sciences Department of Core R&D, The Dow Chemical Company in Freeport, TX. In the company he had applied evolutionary computation in different areas in manufacturing and new product design, such as: inferential sensors, empirical emulators of mechanistic models, accelerated new product development, and effective industrial design of experiments. His research interests include application issues of computational intelligence, robust empirical modeling, intelligent process monitoring and control, and data mining. He has published more than 60 papers and 7 book chapters in the area of applied computational intelligence and advanced control.

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E2K: Evolution to Knowledge

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Simulink [8] has become a reference framework to accurately design, simulate, implement, and test control, signal processing, communications, and other time-varying systems. A key element of its success is a simple visual programming approach. It allows users to create targeted designs by reusing basic building-block functionalities and graphically creating a flow of execution among them. Users just need to focus on the target problem, not being disturbed by implementation details. Few attempts have been conducted in the evolutionary computation community to provide such a framework that allows beginners and researchers to share a common ground that allow them to deploy and quickly reuse the basic components of evolutionary algorithms. Evolvica [1] was a first effort to push toward this endeavor. Developed at Technical University of Ilmenau, it provided a first attempt to create a visual programming oriented framework. The last Evolvica release dates back to July 2004. Other tools such as ECJ [7] and Open BEAGLE [2] have been more oriented to cover researchers' needs than to create such an integration framework.

E2K (*evolution to knowledge*) targets the creation of a common shared framework for the evolutionary computation community. E2K allows users to reuse evolutionary components and, using a visual programming paradigm, connect them to create applications that fulfill the targeted needs. E2K is a project built around the D2K (*data to knowledge*) framework developed by the *Automated Learning Group* at the National Center for Supercomputing Applications. D2K dataflow architecture provides users with a simple workbench where they can rapidly create applications visually by just dragging and connecting components (modules) together. E2K modules provide simple computation activities—such as evaluation, selection, and recombination mechanisms—that when combined together create complex evolutionary computation algorithms. Due to the module standardization in D2K, it can act as integrator of evolutionary techniques and library—for instance wrapping ECJ or Open BEAGLE components—and also take advantage of the data mining techniques provided with the D2K framework.

Data to knowledge (D2K)

D2K (Data to Knowledge) [9] is a rapid, flexible data mining and machine learning system that integrates analytical data mining methods for prediction, discovery, and deviation detection, with data and information visualization tools. It offers a visual programming environment that allows users to connect programming components together to build data mining applications and supplies a core set of modules, application templates, and a standard API for software component development.

An architecture for data flow processes

The main characteristic of D2K applications is the data-driven nature of its applications. The programming components (D2K modules) are connected in a data flow graph (D2K itinerary) to form an application. The basic architecture of D2K is shown in Figure 1. D2K infrastructure is in charge of providing the basic dataflow environment. D2K modules provide the basic computation *building blocks*, that are hooked together by D2K itineraries. The basic computational task that D2K can run is the D2K itineraries. D2K applications are a composition of D2K itineraries.

Figure 1: The basic architecture of D2K.

Besides the basic infrastructure and task oriented applications (composed by D2K itineraries), D2K also provide a workbench for rapid creation of applications, the D2K Toolkit, distributed computing facilities via D2K servers and D2K proximities, and finally standardized D2K web services provide a general purpose interface to manage and run D2K itineraries remotely. A complete description of all D2K facilities is beyond the scope of this paper and can be found elsewhere [9].

The toolkit

The D2K toolkit is a workbench designed to provide access to the main functionalities provided by D2K. Figure 2 presents a screenshot of the D2K toolkit. The toolkit allows the quick creation of itineraries to perform a specific computational task. The available modules (*marked as 1 in the figure*) can be dragged & dropped into the itinerary manipulation area (*marked as 9*). The dropped modules can then be connected to create the workflow describing the task to perform. The itineraries can be saved and reused later as *nested* itineraries, creating increasingly more complex compound itineraries, by just dragging and dropping them from the itineraries area (*marked as 3*). Besides processed data, the execution of any D2K itinerary (*the controls are marked as 8*) may potentially generate two elements as a result of the analytic tasks: models and visualizations. For instance, a model may be a decision tree learned out of a data set, whereas the visualization is a graphic visualization of such a tree to allow the user to explore it. The generated models and visualization of a run are temporally stored in dedicated areas (*marked as 5 and 6*). These components can be persistently stored and reused—for instance the decision tree can be use to classify new unseen data—using the same drag & drop approach (*areas 2 and 4*).

Data-mining in D2K's basic modules

The D2K release contains a set of modules and itineraries that allow the user to run data mining tasks. Some basic D2K capabilities include discovery capabilities—based on several clustering and rule associations techniques—and predictive modeling—including several decision tree, instance-based, naïve Bayes, neural networks, and support vector machines techniques to mention a few. A complete description of all D2K facilities can be found elsewhere [9]. Figure 3 presents an example of an itinerary that given a data set induces a decision tree using the C4.5 algorithm. The figure also shows the tree and performance visualization capabilities associated with this itinerary.

Evolution to knowledge (E2K)

Evolution to knowledge (E2K) is a set of D2K modules and itineraries that perform genetic algorithms (GA) and genetics-based machine learning (GBML) related tasks. The goal of E2K is to fold: simplify the process of building GA/GBML related tasks, and provide a simple exploratory workbench to help users to interact with evolutionary processes. It can help to create complex tasks or help the newcomer to get familiarized and trained with the evolutionary methods and techniques provided. Moreover, due to its integration into D2K, the creation of combined data mining and evolutionary task can be effortlessly done via the visual programming paradigm provided by the workflow environment and also wrap other evolutionary computation software.

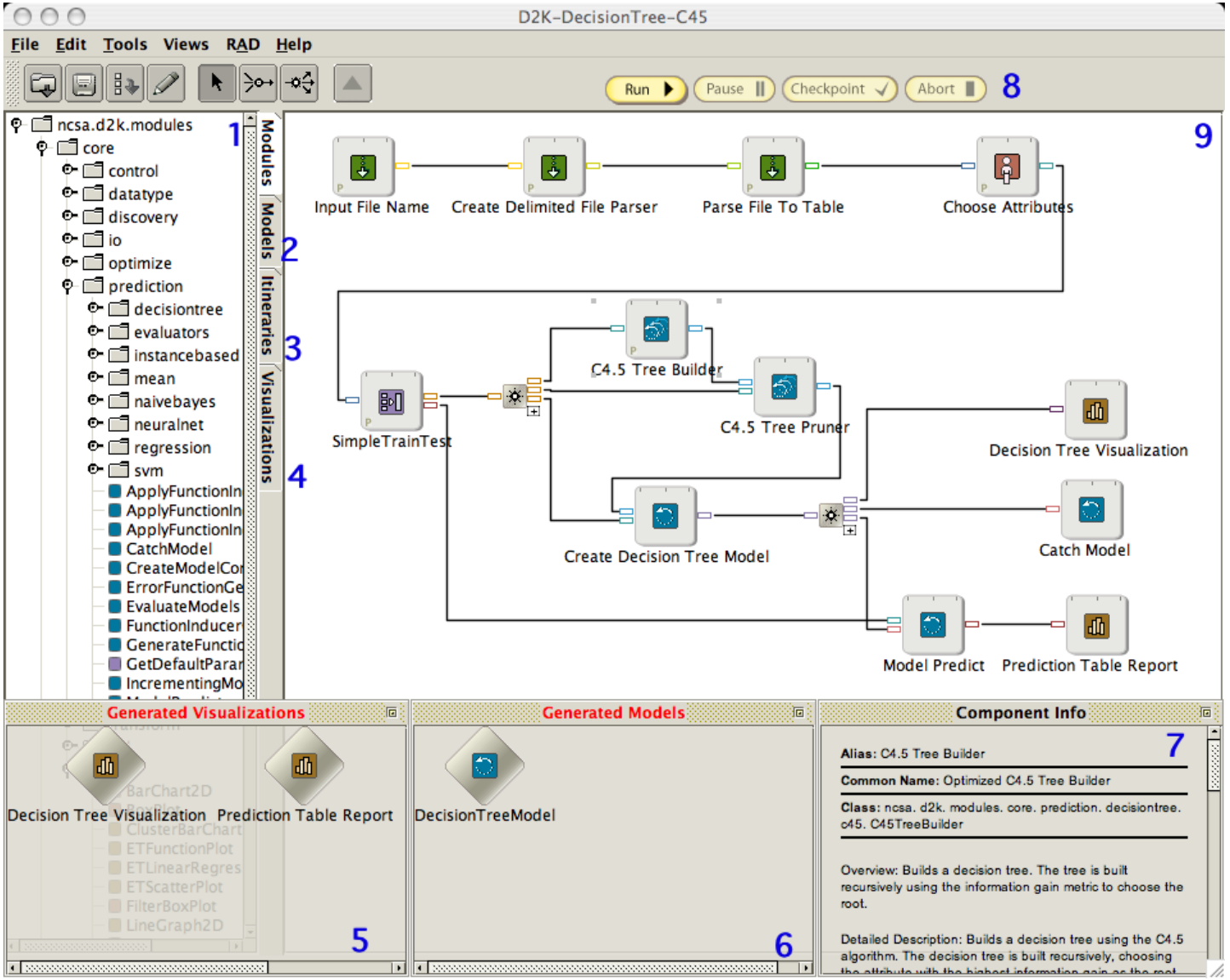
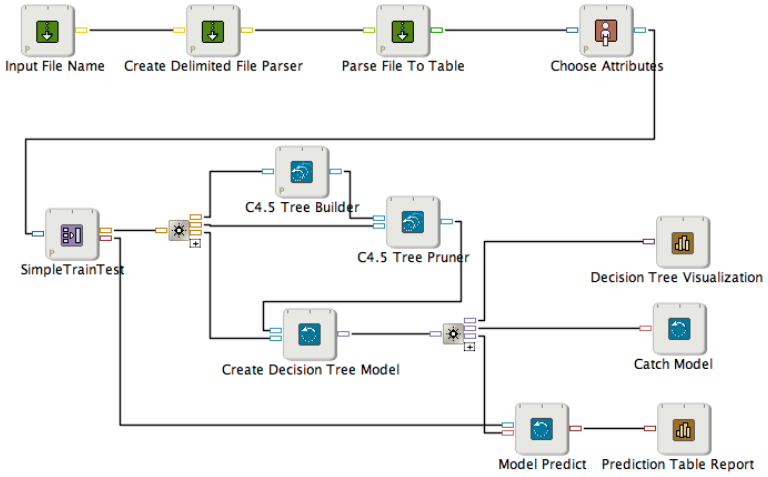
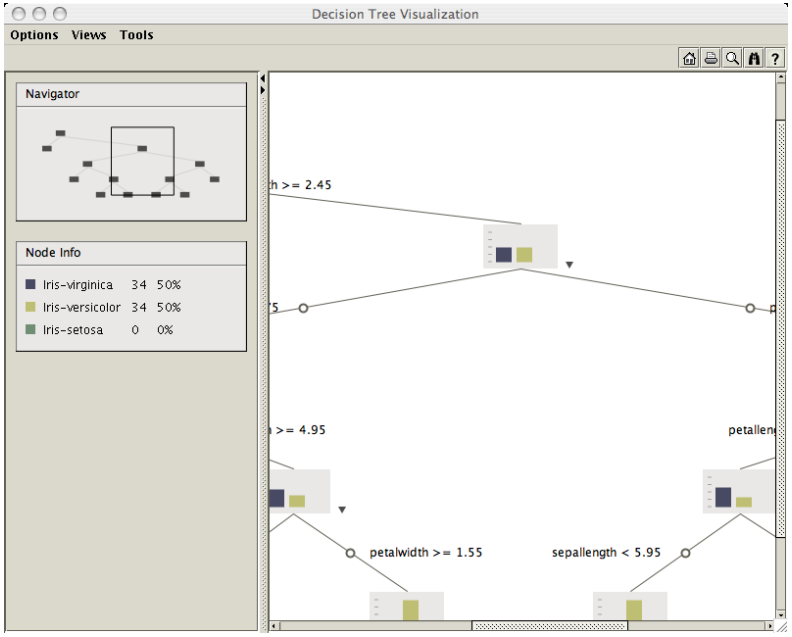


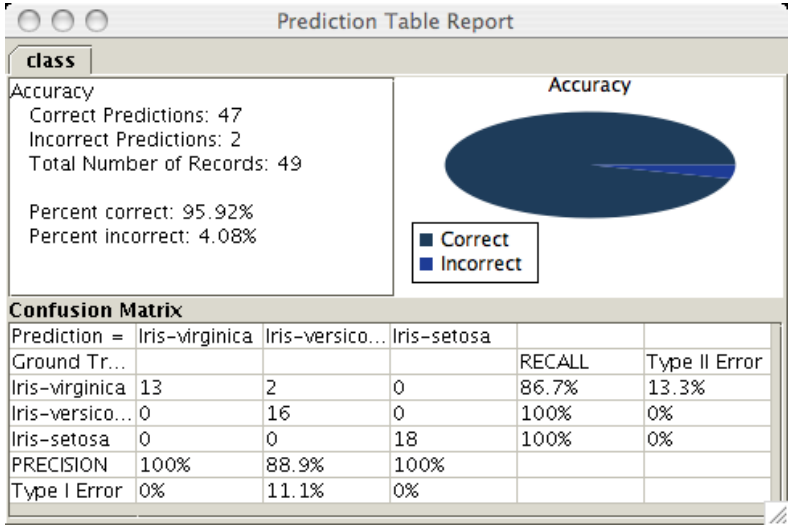
Figure 2: The D2K Toolkit. The toolkit groups the main D2K components: (1) modules available, (2) saved models, (3) stored itineraries, (4) saved visualizations, (5) generated visualizations, (6) generated models, (7) component information, (8) execution controls, and (9) the current loaded itinerary.



D2K's C4.5 itinerary



Visualization of the C4.5 tree.



Visualization of the tree performance.

Figure 3: D2K provides a basic collection of data mining tools. This figure illustrates a simple data mining task based on the induction of a decision tree using the C4.5 algorithm. The figure also shows the visualization of the induced tree and its performance.

Breaking it down

Several modules and itineraries compose E2K. Once deployed in D2K, these modules and itineraries are accessible in the same manner any other D2K component is manipulated. The basic E2K design guidelines broke down evolutionary processes into a set of minimal functionality components that take the form of a D2K module. For instance, some modules may perform simple evaluation tasks, others perform specialized selection schemes and so forth. Hence, creating a simple genetic algorithm can be achieved by connecting the inputs and outputs of the proper modules to create the appropriate D2K itinerary. Such an approach also empowers the user to quickly change the behavior of a simple task by replacing the appropriate E2K module.

Module and itinerary organization

The E2K modules breakdown can be summarized as follows.

Initialization: These modules create initial populations for different representation encodings. It also provides some modules that facilitate the initialization of random number generator engines.

Finalization: These modules implements several finalization criteria for a given evolutionary process. For instance, the criteria for finalizing a run can be measured by population convergence criteria or epochs elapsed—to mention some examples.

Evaluation: The evaluation modules allow serial (sequential) and reentrant (parallel using multiprocessors or distributed D2K proximities) evaluation of populations. It also contains basic evaluation functions and relaxation schemes.

Selection: Selection modules implement several selection schemes.

Mutation: Implement various mutation schemes for the different representations available.

Recombination: Implement various recombination schemes for the different representations available. Besides the traditional techniques, there are modules that provide model-based recombination schemes.

Replacement: These E2K modules provide several techniques for population replacement.

Population models: These modules are dedicated to model-building schemes. Some of the provided functionalities allow building models that describe the provided population and also allow sampling the learned models.

Statistics: Provide the basic functionalities to accumulate population statistic during the execution of an E2K itinerary.

Input/Output: Modules to provide access to the D2K input/output facilities including files, relational databases, or metadata stores.

Transformations: These modules allow data transformation that allow to interface the E2K specific data structures with the D2K. Thus, data mining and E2K itineraries can be effortlessly integrated.

Visualizations: The visualization modules allow to generate and display information and statistics collected during and E2K itinerary execution.

E2K also provide a few examples of itineraries that implement: the simple genetic algorithm (SGA) [3], the univariate marginal distribution algorithm for continuous problem (UMDAc) [4], the extended compact genetic algorithm (ecGA) [5], and the χ-ary extended compact classifier system (χeCCS) [6]—to mention a few. A detailed list of the modules and itineraries provided by E2K can be found in the release documentation and the E2K website [WWW].

A simple example: The simple GA

To illustrate how E2K works, this subsection shows how an E2K implements the simple GA [3]. The simple GA requires, at least, the following components: an evaluation module that computes the fitness of the individuals, a module that selects a new population using roulette-wheel selection, a module that recombines the individuals using one-point crossover, a module that mutates the individuals, and finally a module that decides when to stop. Figure 4 presents these modules. To complete an itinerary that implements the simple GA we also require two more modules; a module that creates and initial population and a module that provides that fitness function to use, and finally connect these modules to implement the workflow that will evolve the initial population pushed by the population initialization module—since D2K relies on a data-driven paradigm. Figure 6 present the complete simple GA itinerary.

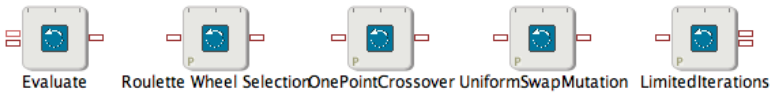


Figure 4: The E2K modules that form the simple GA itinerary.

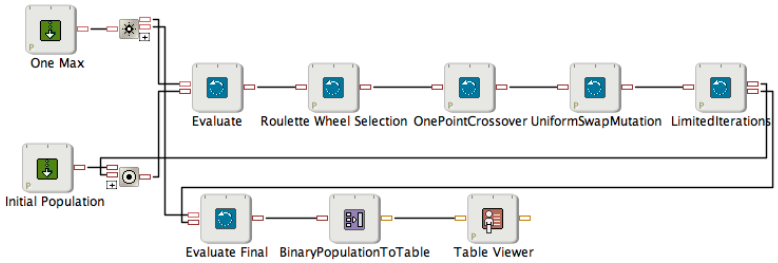


Figure 5: The simple GA itinerary implemented using E2K.

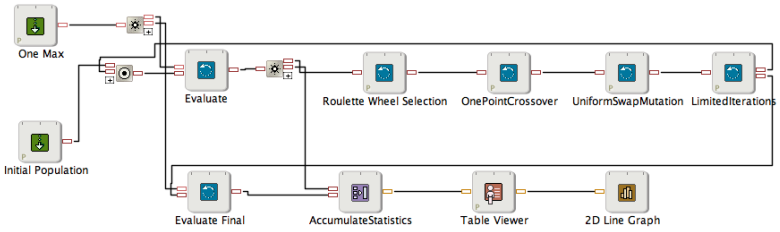


Figure 6: Statistics can be easily collected using the provided E2K statistic modules.

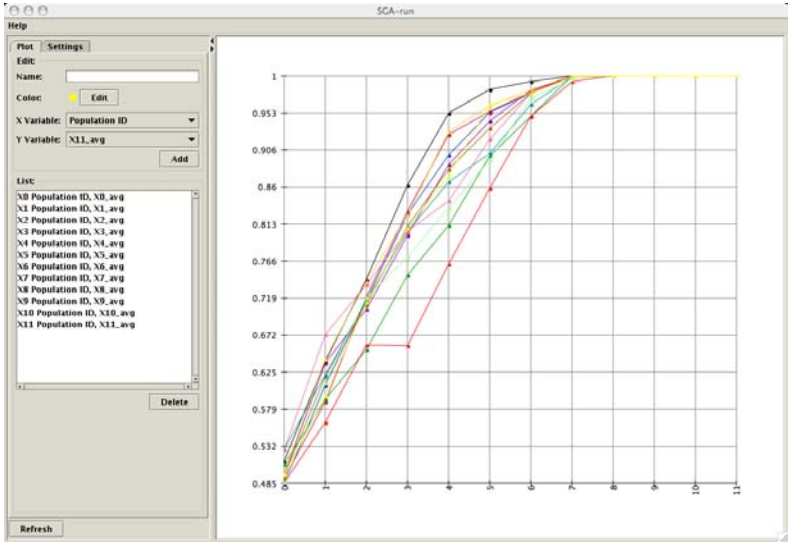


Figure 7: One of the D2K's available visualizations of the simple GA run statistics. This visualization presents the gene convergence to during the run.

Collecting data during a run

E2K also provides modules for data gathering during the run of an itinerary. A module designed to accumulate statistics inspects the evaluated population accumulating several statistics related to the individuals and their fitness. Figure 6 presents the modifications introduce to the simple GA itinerary in order to achieve such a goal. These statistics can be piped into a D2K module that creates and stores visualizations, which the user can retrieve later allowing the exploration and interaction with the result of the run. Figure 7 shows the gene convergence achieved during the run. Other visualizations provided by E2K include the graphical inspection of the models evolved by model-building GA such as ecGA [5]. Figure 8 presents the succession of models evolve by ecGA during on run on an $m - k$ trap.

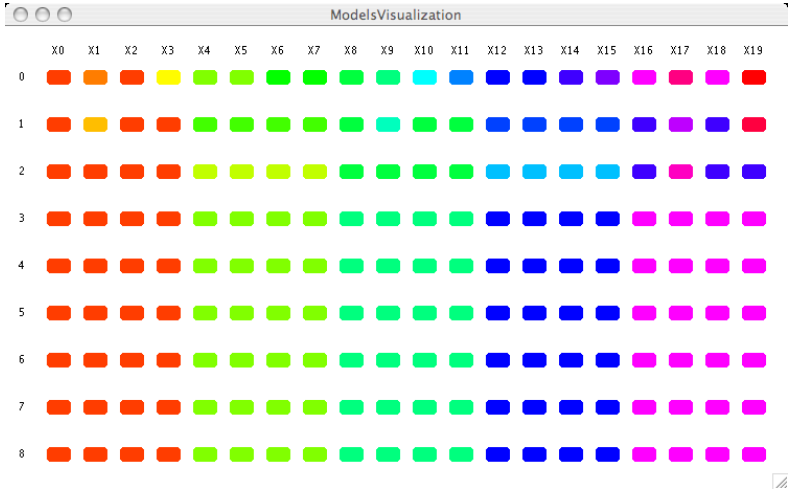


Figure 8: A visualization of the evolution of the MPM models used during an ecGA run. Colors represent the different building blocks identified by ecGA for a $m-k$ trap ($m=5$, $k=4$).

Modules available

E2K is an ongoing project. The initial release includes the necessary modules to be able to assemble the simple genetic algorithm (SGA) [3], the univariate marginal distribution algorithm for continuous problem (UMDAc) [4], the extended compact genetic algorithm (ecGA) [5], and the χ-ary extended compact classifier system (χeCCS) [6]. A detailed list of the modules and itineraries provided by E2K can be found in the release documentation and the E2K website [WWW].

The E2K release also includes the source code of the modules under an open-source license and the genetic algorithms core library used. Users can quickly create new fitness functions and modules suited to their needs and deploy them into the D2K framework to create custom made itineraries combining them with the provided E2K modules and the D2K analytic capabilities.

Summary and future work

E2K is a set of modules and itineraries that perform basic evolutionary computation tasks. E2K simplifies the process of defining and executing evolutionary computation tasks by relying on an exploratory workbench that allows users to directly interact with evolutionary processes. Due to its integration into the D2K framework, the creation of combined data mining and evolutionary task can be effortlessly done via the visual programming paradigm provided by D2K. Moreover, the standardization provided by D2K modules allow E2K to became a repository of components for the evolutionary computation community.

E2K is an open source effort hosted at the National Center for Supercomputing Applications. Future work will keep focusing on expanding the set of E2K modules provided to further develop its facet as an integration framework. To achieve such a goal, E2K efforts will also focus on creating the proper wrapper to integrate methods and techniques and evolutionary computation paradigms provided by other packages—for instance ECJ [7].

Acknowledgments

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About the author

Xavier Llorà's 2002 PhD dissertation challenged traditional data-mining techniques by showing the effectiveness of GBML approaches. Llorà, awarded with a young research fellowship by the Catalan Government, started his academic career at the Ramon Llull University (Barcelona, Spain) where he earned his PhD degree with honors. In 2003 he moved to the University of Illinois at Urbana-Champaign where he joined the Illinois Genetic Algorithms Laboratory and collaborated with the National Center for Supercomputing Applications to develop collaborative tools to support human-innovation and creativity. In summer 2005, Llorà was named research assistant professor at the University of Illinois at Urbana-Champaign.

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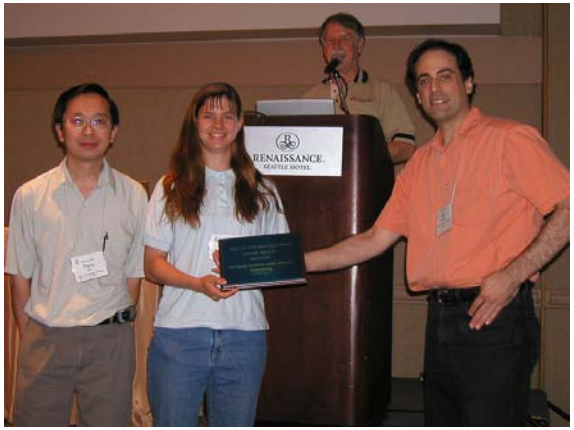
RENAISSANCE
GEGEO
2006

GECCO-2006 Highlights

The Best Papers

Ant Colony Optimization and Swarm Intelligence



An Ant-Based Algorithm for Finding Degree-Constrained Minimum Spanning Tree
Thang N. Bui, Catherine M. Zrncic

Artificial Immune Systems

Applicability Issues of the Real-Valued Negative Selection Algorithms Zhou Ji, Dipankar Dasgupta

Artificial Life, Evolutionary Robotics, Adaptive Behavior

A Method for Parameter Calibration and Relevance Estimation in Evolutionary Algorithms
Volker Nannen, A.E. Eiben

Estimation of Distribution Algorithms

Probabilistic Modeling for Continuous EDA with Boltzmann Selection and Kullback-Leibeler Divergence
Yunpeng Cai, Xiaomin Sun, Peifa Jia

Biological Applications

Genetic Programming for Human Oral Bioavailability of Drugs
Francesco Archetti, Stefano Lanzeni, Enza Messina, Leonardo Vanneschi

Evolution Strategies, Evolutionary Programming

On the Local Performance of Simulated Annealing and the (1+1) Evolutionary Algorithm
Thomas Jansen, Ingo Wegener

Coevolution

The Effects of Interaction Frequency on the Optimization Performance of Cooperative Coevolution
Elena Popovici, Kenneth De Jong

Evolutionary Combinatorial Optimization

A New Hybrid Evolutionary Algorithm for the k-cardinality Tree Problem
Christian Blum

Evolutionary Multiobjective Optimization

On The Effect of Populations in Evolutionary Multi-objective Optimization
Oliver Giel, Per Kristian Lehre

Genetic Programming

Alternative Evolutionary Algorithms for Evolving Programs
Darrell Whitley, Ross Beveridge,
Marc Richards, Andre Barreto

Genetic Algorithms

Comparing Evolutionary and Temporal Difference Methods in a Reinforcement Learning Domain
Matthew E. Taylor, Shimon Whiteson, Peter Stone

LCS and other GBML

Classifier Prediction based on Tile Coding
Pier Luca Lanzi, Daniele Loiacono,
Stewart W Wilson, David E. Goldberg

Real-World Applications

Multiobjective Genetic Algorithms for Multiscaling Excited State Direct Dynamics in Photochemistry
K. Sastry, D.D. Johnson, A.L. Thompson, D.E. Goldberg, T.J. Martinez, J. Leiding, J. Owens

Search-Based Software Engineering

Search-based Determination of Refactorings for Improving the Class Structure of Object-Oriented Systems
Olaf Seng, Johannes Stammel, David Burkhart

Biological Applications

James A. Foster, foster@uidaho.edu, (WWW)
Jason H. Moore, Jason.H.Moore@Dartmouth.EDU, (WWW)

We had another successful Biological Applications (BA) track at GECCO this year, the third year that the track has been part of GECCO. For the first two years, this track was a Biological Applications workshop at GECCO. so it has been meeting for five years altogether. The goal of BA is to bring evolutionary computation to bear on problems of biological interest.

Since the BA workshop/track was introduced, evolutionary computation papers have begun to appear regularly in other tracks, especially the Real World Applications track. GECCO has also hosted several new related workshops and tutorials, such as this year's workshop on biomedical applications and tutorials on systems biology and bioinformatics. Meanwhile, the BA track itself continues to have strong submissions and participation.

This year, several papers and submissions dealt with questions of medical treatment and diagnosis. This is a shift in emphasis from "traditional" bioinformatics, which was present this year but dominated in past years. Also, this year the strength of GP as a useful classifier for biological data was very clearly demonstrated.

This year's BA track was hosted by James A. Foster, University of Idaho, and Jason Moore, Dartmouth. We are pleased to announce that the BA track will again be part of GECCO next year, with Jason Moore chairing the track.

Coevolution

Sevan G. Ficici, sevan@eecs.harvard.edu, (WWW)

As with previous editions of the Coevolution Track at GECCO, the 2006 conference showed vibrant interest in coevolutionary algorithm research. In addition to the coevolution conference track, two tutorials on coevolutionary algorithms (one introductory, another advanced) were presented at GECCO for the first time and were also well attended. The papers presented at this year's coevolution track include not only many aspects of algorithm theory, but also expand into applications and algorithm testing. A coevolutionary algorithm can evaluate an individual only by having it *interact* with other individuals. This property is fundamentally game-theoretic in nature; the outcome for an individual depends upon whom it interacts with—a notorious complication. More recently, the centrality of *solution concepts* has also received attention; what properties do we seek in a solution, and how do we build an algorithm to implement the desired solution concept? Both issues—interactivity and solution concepts—are intrinsic to coevolution research, as this year's papers show.

E. Popovici and K. De Jong (best-paper award winners) looked at a cooperative coevolutionary algorithm in which, alternately, one population is subjected to evolution while the other remains frozen. The evolving population becomes increasingly adapted to the other, but how many generations of evolution ("epoch length") should be applied to one population before it is frozen, allowing the other population to adapt, in turn? They show how the ideal epoch length follows from measurable game-theoretic, *best-response* properties of the game being played.

R. Wiegand and M. Potter argued that conventional cooperative coevolutionary algorithms optimize robustness; that is, the quality of an overall solution discovered by cooperative coevolution will tend not to decline precipitously when a component of that solution is modified. Their paper provides a formal framework for defining the solution concept of robustness and then provides empirical results that illustrate the type of robustness they define.

L. Panait, S. Luke, and J. Harrison introduced an archive-based cooperative coevolutionary algorithm designed around a different solution concept; the intent here is to find the overall solution that best solves the problem at hand (regardless of that solution's robustness). Their algorithm attempts to identify, for each individual in one population, the best individuals in the other population to interact with. The archive improves the assessment of adaptiveness and reduces the number of interactions required for evaluation.

E. de Jong and A. Bucci described how to apply a novel coordinate system to phenotype (or "strategy") space that decomposes the space into some relatively small number of "behavioral" dimensions; individual phenotypes can then be ordered along these different behavioral dimensions according to their competences in these dimensions. Such an ordering can be used to facilitate more effective evaluation by indicating appropriate individuals for interaction.

S. Ficici presented results concerning the dynamics of various selection methods when applied to symmetric variable-sum two-player games in two-population coevolutionary algorithms. The examined alternatives to fitness-proportional selection are found to create dynamics that maintain the Nash-equilibrium attractors of proportional selection; nevertheless, these alternatives also introduce new non-Nash point attractors and cyclic dynamics.

For purposes of exposition, many coevolutionary techniques are introduced in the context of simple abstract domains. Two papers this year provided investigations of some previously published techniques in more recognizable and complex game domains. G. Monroy, K. Stanley, and R. Miikkulainen used the game of Pong to examine the effectiveness of E. de Jong's Layered Pareto Coevolution Archive when combined with Stanley and Miikkulainen's NeuroEvolution of Augmenting Topologies representation. Their preliminary results show that the combination of the two methods can achieve good Pong players. F. Oliehoek, E. de Jong, and N. Vlassis extended Ficici's Nash-memory mechanism to asymmetric zero-sum games and applied it to simplified games of poker. The Nash memory is a phenotype archive that organizes the results of search according to the Nash-equilibrium solution concept. The authors solve partially observable Markov decision processes to discover new poker strategies that are best responses to the Nash-memory's current approximation of the solution; the Nash memory then integrates these best responses to further improve the Nash approximation.

Another paper that contained a real-world application is that of L. Vanneschi, G. Mauri, A. Valsecchi, and S. Cagnoni. They investigated variations of cooperative coevolution, including heuristics to determine when a population should be evolved or frozen. Their methods are applied to symbolic regression; one population evolves genetic programs that represent regression expressions, while the other population evolves bitstrings that represent expression constants. Their approach is tested on a biotechnology application and found to give promising results.

More information on current research is found at the Coevolution Wiki: demo.cs.brandeis.edu/coec-wiki.html

Evolution Strategies, Evolutionary Programming

Dirk Arnold, dirk@cs.dal.ca, (WWW)

Both authors and reviewers helped ensure that the Evolution Strategies and Evolutionary Programming (ES/EP) track of GECCO'06 enjoyed especially strong contributions. Presentations of the eight accepted papers and one poster were well attended, and lively discussions ensued. Thematically, two trends that had been observable at previous GECCOs became even more prevalent: first, a push toward more rigour (more than half of the papers state their results rigorously and contain proofs), and second, an increased focus on adaptation.

Rigorous run time analyses on discrete objective functions are the subject of two papers. In a contribution that received the best paper award, T. Jansen and I. Wegener compare the ability to overcome obstacles of simulated annealing and a $(1+1)$-EA. D. Sudholt compares the performance of a simple memetic algorithm with that of a $(1+1)$-EA and with randomised local search.

Interesting in that it presents a rigorous analysis of an adaptive algorithm is the contribution by J. Jägersküpper that considers $(1 \stackrel{+}{,} \lambda)$-ES using the 1/5th success rule on the sphere model. In a second paper considering the sphere model, A. Auger and N. Hansen show that the commonly employed definition of progress can be inadequate in low-dimensional search spaces, and they provide an alternative definition.

More than a decade after the introduction of hierarchically organised evolution strategies, D. V. Arnold and A. MacLeod present a first analysis of their behaviour on parabolic ridge functions. Ridges are also the focus of the contribution by A. Soltoggio.

In an innovative paper, C. Igel et al. introduce a modification of the covariance matrix adaptation algorithm that eliminates the need for (computationally expensive) eigen decompositions, and they propose to use it in connection with the $(1+1)$-ES. Covariance matrix adaptation is also employed in the contribution by M. Lunacek and D. Whitley that introduces a dispersion metric for classifying multimodal optimisation problems. Finally, several variants of differential evolution are compared empirically in the paper by E. Mezura-Montes et al.

Altogether, the high quality of the contributions was enjoyed by all participants who attended the presentations, and it makes the ES/EP track at GECCO'07 an event to look forward to.

LCS and other GBML

Martin V. Butz, mbutz@psychologie.uni-wuerzburg.de, (WWW)

The GECCO 2006 conference once again showed a growing interest in learning classifier system and other genetics-based machine learning (LCSaoGBML) research. After the explicit opening of the track to other combinations of evolutionary computation (EC) and ML techniques in 2005, the LCS GBML track became the fifth largest track at this year s GECCO conference with 36 submissions—only one submission less than the Evolutionary Multi-optimization track. The distribution of submitted papers reflects this progress. As every year, a base-rate of high-quality, state-of-the art advancements of learning classifier system techniques were received. But also other GBML techniques gained further impact, including evolutionary clustering techniques, the evolution of ensemble classifiers, evolutionary learning with Kernels, and evolutionary approaches to reinforcement learning. This progress indicates that while LCS approaches remain solidly represented in the track, the competition with other related techniques increases leading to the desired exchange of ideas, knowledge, and approaches to foster the advancement of LCSaoGBML systems in general.

Most LCS-based publications successfully integrated state-of-the art ML techniques in the base LCS architecture. Novel representations were integrated such as Gaussian kernels, convex hulls, vector-instruction-based matching, and the best-paper award winning tile-coding approach. Approximation techniques were improved investigating optimal gradient-based approximations including recursive least squares and Kalman-filtering, averaging reinforcement learning, and Bayesian-based rule quality approximations. Finally, the evolutionary side of the spectrum was enhanced with improved recombinatory operators as well as targeted mutation operators. Similarly, ML-based publications explored considerations that have been under discussion in the LCS literature such as multi-objective feature selection in semi-supervised and unsupervised learning scenarios, the maintenance of classifier diversity, or the usage of EC techniques to evolve Kernel structures. Besides the successful combinations of EC techniques with ML, performance was evaluated on the same problems. One LCS-based and one neural network (NN)-based approach were both tested on the Mountain Car problem, which is well-known in the RL literature. The one algorithm uses the XCS architecture to learn an optimal Q-value function approximation evolving a tile-coding representation in conjunction with an iterative gradient-based optimization technique (modified delta rule). The other algorithm uses the NeuroEvolution with Augmenting Topologies (NEAT) approach integrating reinforcement learning knowledge on balancing exploration and exploitation to evolve NN-based control structures. Similarly, LCS-based and other algorithms were tested on the same datasets taken from the UCI repository. While the one approach enhanced recombination efficiency of their LCS-based algorithm, the other approach showed advantages of utilizing EC techniques for the evolution of Kernel structures.

Lots of work remains to be done and lots of options to be explored when working on the combination of ML approaches with EC techniques. The papers at GECCO 2006 confirm that there is lots of room for research advancements on both sides of the spectrum. EC techniques can be improved to make the evolutionary process more efficient with respect to the evolved ML technique as well as the, potentially ML-derived, involved knowledge representation. Similarly, the integration of advanced ML techniques into an evolutionary learning framework offers lots of room for future advancements. EC techniques especially enable superior performance in problem domains in which plain ML techniques are hard to be applied successfully to, such as hard non-linear control problems, or cannot guarantee to yield optimal performance due to problems such as premature convergence or overfitting. GECCO 2006 showed that effective combinations of EC and ML techniques can lead to successful, competitive, and superior learning systems in problems as diverse as datamining, model learning, function approximation, reinforcement learning, or control. Thus, it will not come as a big surprise when the next couple of years yield novel system combinations that significantly outperform currently available systems on challenging, real-world problems.

GECCO-2006 Highlights

Human Competitive Awards – The “Humies"

Gold

Varun Aggarwal, Selçuk KILINÇ,
Varun Jain, and Uğur ÇAM (WWW)

Silver

K. Sastry, D.D. Johnson, A.L. Thompson, D.E. Goldberg,
T.J. Martinez, J.Leiding, and J. Owens (WWW)

Bronze

Jie Yao, Nawwaf Kharma, and Peter Grogono (WWW)

Bronze

Gustavo Olague and Leonardo Trujillo (WWW)

Practically-usable analog design using evolutionary algorithms

Varun Aggarwal, varun_ag@mit.edu, CSAIL, MIT, USA

My work (with co-authors) presented at HUMIES 2006 showcased four sine-wave oscillator designs which were better than the state-of-art in oscillator design and fifteen oscillators which served as alternatives to the state-of-art. Sine-wave oscillators are a fundamental building block for analog circuits and extensively used in communication (modulation/demodulation), signal processing and measurement systems (e.g., oscilloscope). All these oscillators were automatically invented by a genetic algorithm!

There has been considerable success in automatic evolutionary design. However, in many cases the evolved designs are incomprehensible, idiosyncratic and practically unusable. Evolution finds a way to bluff the fitness function or the evolved designs work only on simulation, aren't robust or are too complex to be understood, re-used or implemented practically. A way to resolve this is to restrict the solution space intelligently. In tradeoff, as the restriction on the space is increased, evolution looses the ability to innovate. The problem of circuit design poses similar challenges. To address this, we chose a nice trade-off between practical usability and design innovation. We not only evolved practically-usable oscillators, but evolution also invented new re-usable design principles.

To restrict our design space rationally, we let evolution work at the level of linear active and passive components. We used first-order models for active components. This relieves the design process of the idiosyncrasy of transistor non-linearity and non-ideality. It is similar to using registers, adders, summers, etc. in the design vocabulary for evolving a CPU rather than using transistors or digital gates. The choice of the right abstraction level (components and models) ensured sensible designs, while it left enough room for innovation. The fitness function was inspired by the human design process. Human designers don't use the SPICE simulator to innovate, instead they analyze the circuit! To mimic this, I used symbolic analysis for fitness evaluation. This leads to decomposition of the design process decoupling circuit topology search and circuit component values search. It is in fact this decoupling which makes the problem tractable for the human mind and the same benefit carries over to automated design. The component values are constrained adequately given the structure of the symbolic equations and can be solved for deterministically. This design decomposition brings down the computational cost of automatic design of oscillators to that achievable on a desktop PC today.

Inspired by a network synthesis class and encouraged by Prof. Senani, I designed the algorithm for oscillator synthesis when I was a senior in my undergraduate school. I presented my first paper about this work at The 2003 NASA/DoD Conference on Evolvable Hardware. Subsequently, I collaborated with Dr. U. Cam, Selcuk Kilinc and Varun Jain. We published more than 19 oscillators complete with simulation results in the last 4 years and discovered many new design principles.

One of our most recent paper notes, "...the second topology changes the notion of minimum-components required for realization of a variable frequency oscillator using a single active element, which should now be considered four instead of five." In yet another paper, we show that the designed oscillator requires one terminal less of the active element in comparison to previous designs, thus saving power and area. All these principles were invented automatically and there is more to come...
All related papers, video and HUMMIES presentation present at [WWW].

Fast and Accurate Photochemistry via Genetic Algorithms

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Photochemical reactions are fundamental in many settings such as biological (e.g., photosynthesis and vision) and technological (e.g., solar cells and LEDs), and the associated dynamics are energetically subtle, requiring highly accurate descriptions of the molecular forces. Reliable quantum chemistry predictions are costly even for small molecular reactions, but rapidly approach the impossible in complex environments, such as in solvents, in solid cages of zeolites, or with protein ion channels. Hence, having substantially faster semiempirical potentials that accurately reproduce high-level quantum chemistry results would make it possible to address critical biological processes and technologically chemical reactions, or dramatically reduce searches for potentially technological useful light-activated reactions.

Semi-empirical methods, known by acronyms such as MNDO, AM1, and PM3 with well-established parameter databases and software such as MOPAC, MOLCAS, and MOLPRO, have had the critical parameters hand-designed and optimized to predict ground-state energies —not excited-state energies. In ethylene, for example, AM1 or PM3 parameter sets obtain (incorrectly) a *pyramidalized* structure as the lowest-energy excited-state. Thus, these carefully established parameter sets yield inaccurate potential energy surfaces and unphysical reaction dynamics. Additionally, attempts at optimizing parameters to yield globally-accurate, excited-state, potential energy surfaces have been of limited success.

We reoptimize the parameter sets for different classes of molecules via multiobjective genetic algorithms (MOGA) to yield globally accurate potential energy surfaces and excited-states based upon very limited learning data from *ab initio* and/or experimental data. Notably, the reoptimization is massively multimodal and involves conflicting and competing objectives, such as minimizing the difference between calculated and predicted energies, gradients of energies, and stationary-point geometries, which is why MOGA methods have been developed.

In our initial tests on ethylene and benzene (C_6H_6), we obtain parameter sets that are 230% lower error in energy and 87% lower error in energy gradient over the current best results. Moreover, unlike previous results, our MOGA results yield globally accurate potential energy surfaces, and near-ideal energies for critical, excited-state geometries that were not contained in the learning sets. For ethylene the MOGA-based semiempirical potential predicts the correct *twisted* geometry as the lowest excited-state, and, for benzene, it predicts a *100 fs* excited-state lifetime, in agreement with experiment.

In essence, we use a multiobjective genetic algorithm to bridge high-level quantum chemistry and semiempirical methods to provide accurate representation of complex molecular excited-state and ground-state behavior, well beyond previous attempts, or expectation of human experts, and a dramatic reduction (from 100 to 1000x) in computational cost. Even more surprising and potentially groundbreaking, our MOGA results produce *transferable* potentials—i.e., parameters from one molecular system can be used for similar systems. *Transferability* to chemists is analogous to building blocks to a GA researchers. Optimized semiempirical paramters of a small number of relatively simple molecules can be used to predict accurately the behavior of large complex molecules. More work needs to be done, but transferability of ethylene parameters to accurately simulate benzene and vice versa is strongly suggestive that GAs will enable the fast, accurate simulation of complex molecules from a standard GA-tuned database. If this pans out it will transform the way chemicals are modeled and designed radically.

The GA-discovered potentials *inherit* the accuracy of the *ab initio* data, permit simulations to orders of magnitude larger time scales (multi-picoseconds) than currently possible by *ab initio* methods, even for simple molecules, and exhibit transferability in initial tests—the "Holy Grail" for materials and chemistry simulations. This multiobjective optimization approach is an enabling technology to simulate successfully, and within reasonable time frame and with sufficient accuracy, complex, multiscale biological, chemical and materials problems that are ubiquitous in science and engineering and thus impacting our ability to address critical biophysical simulations of, for example, vision and photosynthesis, and for automated design of pharmaceuticals and functional materials.

For more details, the interested reader is referred elsewhere [1] and the references therein.

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Synthesis of Interest Point Detectors Through Genetic Programming

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The design of low-level feature detectors in computer vision is nowdays a main research theme in the scientific communities devoted to solve the problem of endowing a machine with visual capacities. Interest point detectors are commonly used to approach such low-level tasks as part of the pre-attentive stage that localize distintive parts of the image that will be used in the attentive stage, in which relationships between these features and grouping takes place. The contribution achieved with this work is on the idea of applying genetic programming to synthesize a low-level detector that was able to discover an improved version of the DET operator [1], which shows a surprisingly high-level of performance. Moreover, our genetic programming based approach was able to propose a detector with an extremely simple structure, which is known as the difference of

Gaussian. However, this is not used in the literature as an interest point detector [2]. The work presented in GECCO and later at ICPR could be considered as an example of how genetic programming could be applied to achieve results that are equal or better than human created solutions in the domain of computer vision. This work is based on domain knowledge expertise formulated through a well-known benchmark metric used in the computer vision literature, which is known as the repeatability rate [3]. Considering the new approach, the fitness function was completed after considering the entropy related to the point distribution across the image. In this way, both measures promote geometric stability and global separability under several types of image transformations. The range of application of the methodology is very promissing. We can imagine a whole avenue of applications devoted to synthesize operators for tasks such as: image indexing, image web browsing, face recognition, tracking, object classification to mention but a few.

The original idea was based on the discussion on how to determine which detector is the "best" in some sense [4,5]. Those works attempts to compare several human-designed detectors through analythical and experimental methodologies. We decided to extend the experimental approach with the genetic programming paradigm to try to synthesize with the computer an interest point detector. At the beggining we believe that the task will be very hard for the machine because we did not fully understand the search space. Surprisingly, the computer showed us that the best or optimal solution, is yet to be discovered. By possing this classical computer vision problem in optimization terms we were able to show that the problem of interest point detection could be efficiently and robustly solved with genetic programming. Moreover, the contribution could be considered as a new step towards what is becoming to be known in the Evolutionary Computation Community as a new field called "Evolutionary Computer Vision".

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Workshop on Adaptive Representations

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The Workshop on Adaptive Representations focuses on the question of how an evolutionary algorithm may adapt its own representation. The representation of an evolutionary algorithm is known to have a strong influence on the performance that may be expected, and hand-picking an appropriate representation can be an effective way to obtain satisfactory results in practical applications. However, since this is typically a time-consuming process that may introduce harmful biases into the search process, and because choosing a representation requests a significant time investment from the practitioner, automatic methods for finding appropriate representations for a given problem form a worthwhile goal. Moreover, in long-term, open-ended evolutionary scenarios, the optimal choice of representation may not always be clear in advance, and may change over time. The workshop on adaptive representations aims to encourage work that investigates how evolutionary algorithms may adapt their own representation, and thereby find an appropriate representation for the problem at hand.

The 2006 edition of the workshop featured five talks on the topic of representations. The workshop started off with a presentation by Keki Burjorjee from Jordan Pollack's DEMO Lab at Brandeis University. Keki introduced a recursive visualization scheme that displays the distribution of the population of a GA over carefully selected schemata. Using this visualization scheme, it was shown that on a specified class of fitness landscapes a simple fitness-proportional GA with uniform recombination performs adaptation not by recombining 'good' genetic material – i.e. building blocks, but rather by an alternate process named Progessive Pivotal Sequestration.

Greg Hornby, currently at the University of California Santa Cruz, presented work that investigates the structural organization of computer-automated designs. Three metrics of structural organization are proposed: modularity, regularity, and hierarchy. Extensive experiments with table designs showed that the combination of all three ingredients produced the best designs, and that all three metrics correlate positively with the fitness of evolved designs.

Next, two talks on work by Rolv Seehuus, Alberto Moraglio, and Riccardo Poli focused on the use of geometric crossover. The main idea of geometric crossover is that the offspring of two parents should lie geometrically between the two parents. The first talk discussed theoretical aspects of geometric crossover, and demonstrated its connection with sequence homology. In the second talk, geometric crossover was applied to the problem of supervised motif discovery. In this bioinformatics task, the challenge is to identify frequent patterns in bio-molecular sequences (protein sequences here) that have biological relevance. The use of the geometric crossover operator was found to produce favorable results for this problem.

The final talk of the workshop was given by Joseph Reisinger of Miikkulainen's Neural Networks Research Group at the University of Texas, Austin. Joseph's talk discussed the question of how an algorithm that adapts its own representation may enhance evolvability. As an example, the task of evolving tables was used; rather than optimizing a table design by performing many small-scale adaptations, an algorithm that adapts its own representation might first learn aspects of the structure of tables. For example, partial encodings that represent flat surfaces may be identified as part of the search, which can subsequently be combined into large flat surfaces that form the table top. Employing such learned information, a representation adapting algorithm can lead to more complex, high fitness designs in the long run.

The last talk was introduced as a speculative talk that was intended to generate discussion, and succeeded in doing so. A question from the audience challenged the claim that adapting the representation would lead to improved results; given that a substantial part of the search effort will be spent on changing the representation, this may well lead to an increase in the number of fitness evaluations without any corresponding fitness benefit. After an engaging discussion, it became clear that the value of adaptive representations is to be expected most in long-term evolutionary scenarios, or in problems where multiple problems may be addressed by an evolutionary method over time. By extracting information from a sequence of related problems, or from an environment posing multiple related tasks, the algorithm may apply the structural information learned early in the search to establish better performance in later phases of the run. Related work on multi-task learning for instance demonstrates that learning multiple problems, and gathering information about the structure of problems while doing so, can pay for itself by leading to better performance on individual problems.

For more details, see the workshop homepage:
http://homepages.inf.ed.ac.uk/mtoussai/gecco06/

The 9th International Workshop on Learning Classifier Systems (IWLCS 2006)

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Since Learning Classifier Systems (LCSs) were introduced by Holland as a way of applying evolutionary computation to machine learning problems the LCS paradigm has broadened greatly into a framework encompassing many representations, rule discovery mechanisms, and credit assignment schemes. Classifier systems are a very active area of research and, in addition to theoretical studies, applications range from data mining to automated innovation to on-line control. LCS are also benefiting from advances in the field of reinforcement learning and there is a trend toward developing connections between the two areas.

IWLCS is the only event to bring together most of the core researchers in classifier systems and is thus the key yearly LCS event. The 2006 workshop featured 11 presentations from a mix of veteran and new IWLCS participants and concluded with an open discussion. The workshop was logically divided into several sessions, although overlap with the World Cup resulted in some last-minute alterations to the schedule.

The Pittsburgh session was concerned with Pittsburgh-style LCS, in which chromosomes code entire solutions. This contrasts with the more widely used Michigan approach in which each chromosome is only one part of the solution. Jaume Bacardit presented work with Natalio Krasnogor on applying ideas from ensembles to GAssist, a Pittsburgh LCS. They evaluated a method in which they ran GAssist N times, each with a different random seed. For each run they extracted the single best solution. For test set classification the majority class of these N rules was used. This is very similar to Bagging in which N (possibly overlapping) subsets of the training data are formed by sampling with replacement and a learning method trained on each subset. The difference is that whereas Bagging relies on stochastic sampling to produce the diverse classifiers needed for an ensemble, the GAssist approach relies on the stochastic nature of evolutionary search to produce diverse classifiers. This method was found to significantly improve performance on several domains. They also evaluated a hierarchical ensemble for use in ordinal classification and found it reduced the importance of misclassifications, which is of particular concern in ordinal domains.

The other Pittsburgh talk was by Xavier Llorà, who presented work with Kumara Sastry and David E. Goldberg on a *competent* Pittsburgh LCS that automatically *mines* important substructures of the underlying problems and takes problems that were *intractable* with first-generation Pittsburgh LCS and renders them *tractable*. The proposed χ-ary extended compact classifier system uses (1) a competent genetic algorithm, and (2) a niching method in the form of restricted tournament replacement, to evolve a set of maximally accurate and maximally general rules. The results show that linkage exists in the multiplexer problem, which needs to be accurately discovered and efficiently processed in order to solve the problem in *tractable* time.

The method and analysis session consisted of four talks. Pier Luca Lanzi presented work with Matteo Zanini on a version of XCS with computed prediction (XCSF) in which classifiers could either select their prediction functions through evolution or select the most adequate prediction functions through a voting process.

The next presentation was by Daniele Loiacono, presenting work with Jan Drugowitsch, Alwyn Barry and Pier Luca Lanzi. This presentation highlighted potential pitfalls of the classifier error estimate used in XCS with computed prediction (XCSF). A new classifier error definition was introduced along with two more accurate estimation techniques. Results showed that the proposed classifier error estimate allows for a more effective generalization pressure, preventing the evolution of overgeneral classifiers, especially when subsumption is used.

The third presentation in this session was by Atsushi Wada, presenting work with Keiki Takadama and Katsunori Shimohara. This presentation focused on the serious performance decrease of XCS, the mainstream accuracy-based LCS introduced by Stewart Wilson, which occurs by introducing a standard gradient-descent-based update to its reinforcement process. They introduced a new LCS called DCS (Dual-structured Classifier System) which successfully merges the advantages of both a standard gradient-descent reinforcement process and the XCS discovery process. DCS also benefits from consistency with popular reinforcement learning methods with rigorous proofs. Empirically, DCS was competitive with XCS on common benchmarks for LCSs.

The final presentation in this session was by Albert Orriols-Puig, who presented work with Ester Bernado-Mansilla on their relatively recent UCS system. UCS is related to XCS but while XCS is a reinforcement learner UCS is supervised and thus more appropriate for many data mining tasks. This work added fitness sharing to UCS and found improved performance on the decoder problem. Even more significant was that UCS was unable to solve the more extreme versions of the class-imbalanced 11-multiplexer problem without fitness sharing, but was able to do so with it. Analysis of populations suggested fitness sharing inhibited overgeneral rules on the majority class and allowed accurate rules to emerge and replace them.

The third session was on distributed and multiagent systems. The first talk was by Ivette Martinez on work with David Ojeda and Ezequiel Zamora applying XCS to the RoboCup Rescue Simulation League competition, a multi-agent problem. They used XCS as a decision-making component within a larger system and obtained performance competitive with previously published approaches. XCS was also able to learn rules which generalised successfully from one map to another, although they noted a problem in which the size of action sets became one and evolution consequently stalled. The second presentation was by Yutaka Suematsu on work with Keiki Takadama, Katsunori Shimohara and Osamu Katai, who presented COPXCS, a novel learning mechanism for multi-agent systems. COPXCS was developed based on the concept of Community of Practice (CoP) from organizational theory and implemented with XCS. COPXCS consists of grouping the agents in communities, specifically to exchange only experience, and performing learning in three levels: (1) the individual level, where every agent learns by itself with XCS; (2) the group level, where agents within communities exchange their most valuable knowledge; and (3) the collective level, where common knowledge within the community is collected and shared to every agent. A variation of the maze problem was employed to evaluate COPXCS, showing better performance than using only level 1 (only XCS) or level 1 and level 2 (XCS + knowledge exchange between all agents). The final talk in the session was by Setsuya Kurahashi on work with Takao Terano. They proposed a method to extract plant operation knowledge from time series data using LCS. The method consists of the following phases: (1) Collect continuous process data and event data in a target plant; (2) Get the delay time, which maximizes the correlation between two given time series data; (3) Develop a process response model to describe the relations; (4) Discover control rules and workflows from the process data. The main contribution of the research is to establish a method to mine a set of meaningful control rules and workflows using LCS with the Minimum Description Length criterion and Tabu search. The method has been applied to an actual process of a biochemical plant and has shown its validity and effectiveness.

The final session was on advanced architectures. Julian Bishop presented ongoing work developing a new real-valued endogenous-fitness LCS named ALCSR. The current version handles noise-free single-step reinforcement learning problems but in future it should handle noise and multi-step problems. This work re-examined many core issues for LCS including credit assignment, generalisation, covering of the input space, and control of evolutionary processes from novel perspectives, drawing inspiration from Artificial Life. Like XCS, ALCSR learns a complete map of the reward function. Other interesting features include emergent GA timing and population sizing, an Alife-inspired breeding scheme and covering which continues throughout training. Experiments on Wilson's real-valued multiplexer problem indicated ALCSR learns much more slowly than Wilson's XCSR but eventually achieves somewhat better performance. Analysis of populations found good rules for each niche but also many over-specific rules around decision surfaces.

The final talk of the day was by Dave Toney on preliminary work with Johanna Moore and Oliver Lemon on developing conversational interfaces, which allow humans to interact with machines using spoken natural language. XCS was used to learn conversational policies, which map between anticipated user inputs and appropriate responses. This sequential decision problem is a new and very challenging domain for LCS, featuring very large state spaces and partial observability, which have caused difficulties for other reinforcement learning approaches. This work investigated the use of reward functions with different magnitudes and found that this affected whether XCS found the optimal policy or not. Other experiments in which the reward function was decomposed to give rewards for completing some but not all objectives had mixed results.

Following the talks a considerable discussion on various issues occurred. As in the past extended versions of IWLCS papers will be considered for a post-proceedings volume to be published by Springer. We look forward to IWLCS-2007 and wish its organisers well.

(EC)^{2}AI & GSICE2/WIVA3

Stefano Cagnoni, Giuseppe Nicosia, and Leonardo Vanneschi

Between the end of August and mid-September, Italy has hosted successfully two workshops on Evolutionary Computation: (i) (EC)^{2}AI, the ECAI Workshop on Evolutionary Computation, held in Riva del Garda (Trento), as part of ECAI, the world-renowned European Conference on Artificial Intelligence, and (ii) GSICE2, the second edition of the Italian Workshop on Evolutionary Computation, which was held in Siena jointly with WIVA3, the third edition of the Italian Workshop on Artificial Life (a well-established event focused on evolutionary robotics, simulation in social sciences, computational economics, synthetic biology, neurosciences, and computational psychology). A common feature of both workshops was the aim of laying a bridge between the Evolutionary Computation community and related communities, namely the Artificial Intelligence community at large, and the Artificial Life community, as well as attracting PhD students and perspective ones, who could benefit of strongly reduced registration fees which also allowed them to participate in the main Conference at (EC)^{2}AI, and of free registration at GSICE2/WIVA3. In the end, about 50% of participants in both events were students. Both events were successfully attended, with (EC)^{2}AI being one of the over 30 workshops held at ECAI with the richest program, with 13 contributions, and GSICE2 largely exceeding the attendance of the first edition with 12 presentations and 40 participants, who were joined by the over 60 participants in WIVA3 in a crowded and successful joint session consisting of 5 presentations and a plenary talk. The two events clearly testify once more about the fruitful and promising research and organizational activity of the Italian community in Evolutionary Computation.

(EC)^{2}AI,
ECAI Workshop on Evolutionary Computation
Riva del Garda, 28 August 2006

The papers presented at (EC)^{2}AI (whose proceedings are downloadable at [WWW]) dealt with application and theory of several different Evolutionary Computation and Collective Intelligence paradigms. Of particular interest were the presentations about Learning Classifier Systems by Daniele Loiacono ("*Evolving Neural Networks for Classifiers Prediction with XCSF*") and by Jan Drugowitsch ("*Towards Convergence of Learning Classifier Systems Value Iteration*"), as well as those dealing with Collective Intelligence by Alessandro Passaro ("*Clustering Particles for Multimodal Function Optimization*") and Olfa Sammoud ("*Ant Colony Optimization for Multivalent Graph Matching Problems*"). Alberto Moraglio reported on the most recent results obtained during his PhD studies about crossover in Genetic Programming with an excellent presentation about "*Inbreeding Properties of Geometric Crossover and Non-geometric Recombinations*". Combinatorial optimization was the topic of the presentation by José Luis Montana ("*An Evolutionary Approximation Scheme for the Multidimensional 0/1 Knapsack Problem*"). The rich and multifaceted session on Pattern Recognition included the presentations by Laura Dioşan ("*Evolving Kernel Function for Support Vector Machines*"), Jakub Řiçný ("*Genetic Segmentation of High-resolution Satellite Images*") and by José María Martínez-Otzeta ("*Genetically Searched Classifier Hierarchies for Surface Identification*"). Finally, a very original contribution was given by Amaury Hazan, who presented an interesting application of Evolutionary Computation to art ("*Measuring Expressive Performance Using Consistent Evolutionary Regression Trees*").

GSICE2/WIVA3,
Italian Workshops on Evolutionary Computation and Artificial Life,
Siena, 12-15 September 2006

The four-day event was structured as a tutorial day and a three-day conference. The tutorial day comprised tutorials as well as demo sessions. Tutorials were aimed at providing background, common language, theoretical and experimental methodology to non-specialists in computational social sciences, simulation of cognitive processes, complexity in cellular automata and evolutionary robotics. The joint workshops focused onto the following areas: evolutionary robotics, simulation in social sciences, nature-inspired computing, computational economics, synthetic biology, neurosciences, computational psychology, and evolutionary computation. The over 100 participants comprised delegates from both academia and industry, graduate and undergraduate students, as well as key invited experts in artificial life and evolutionary computation. This year the plenary lectures were given by:

- Stefano Cagnoni, University of Parma,"*Evolution and Artificial Life: cooperation and integration*".
- Carl Chiarella, University of Technology, Sidney, "*Dynamic and Heterogeneous Beliefs in Capital Asset Pricing Model*".
- Vittorio Gallese, University of Parma, "*Intentional attunement: from mirror neurons to social cognition*".
- Pier Luigi Luisi, University of Roma Tre and ETH, Zurich, "*Approaches to the experimental implementation of minimal cellular life*".
- Stefano Nolfi, CNR Institute of Cognitive Sciences and Technologies, Rome, "*Behavior as a Complex Adaptive System*".

Within the joint event, GSICE2 was held on the last day as a one-day workshop, consisting of (i) a poster session with six contributions, (ii) a joint session with WIVA featuring five contributions, the plenary talk by Stefano Cagnoni and a round table, and (iii) a further oral session including six presentations. The presentations regarded (references to the most interesting ones are reported in parentheses): modeling of complex metabolic networks and other complex systems like small-world automata networks ("*A New Fault-Tolerance Measure for Evolved Small-World Automata Networks*" presented by Mario Giacobini), boolean networks with scale-free topology or other forms of graphs or networks, complex cooperative/interactive systems based on evolutionary algorithms ("*A Genetic Approach to Solve Interactive Production Problems*" presented by Alfredo Milani), some interesting applications to image processing ("*Genetic Programming for Prediction of Fat Content in Meat Images*" presented by Lucia Ballerini), recognition of malicious software or intruders by means of evolutionary computation or a hybrid fuzzy-genetic approach, reverse handwriting ("*Reverse handwriting: from electronic ink to generation model parameter estimation. A Comparative study*" presented by Antonio della Cioppa), artificial immune systems and multi-objective optimization ("*Evolutionary Optimization of Dynamic Multi-objective Test Functions*" presented by Thomas Wagner). The workshops also included a joint round table, in which the present and future of Evolutionary Algorithms and Artificial Life studies in Italy was discussed. The most important result achieved by GSICE in the last two years has been the birth of a new coordination action which joins all Italian researchers in Evolutionary Computation. Furthermore, the liaison with the Artificial Life community has been made stronger by this year's edition, which is testified by the fact that GSICE will join WIVA again next year for a common event in the wonderful location of Catania.

The Synthesis of Evolutionary Algorithms and Quantum Computing

Jack Lenahan, Staff Scientist, Imagine-One Corporation

The purpose of this letter is to describe the beneficial relationship between evolutionary and quantum computational models. Evolutionary computation has proved successful in achieving human competitive results [1] in varied disciplines including the evolution of quantum algorithms. Similarly, applying quantum computing models to evolutionary computation has also been shown to exceed the capabilities of traditional evolutionary algorithms in selected cases. The emerging fusion of evolutionary computation with quantum computing models is simply elegant.

Quantum Algorithm

This type of algorithm specifically targets the peculiar features of quantum mechanics such as superposition, interference, and entanglement to achieve computational results not possible with the use of classical computers. At the risk of sounding tautological, quantum algorithms are algorithms which are executed on a quantum computer in order to exploit the dramatic promise of quantum computing.

The motivation for pursuing quantum computers is very simple, they are incredibly fast. Quantum computing will provide truly awesome computational power. For example, citing and applying Kuk-Hyun Han's PhD thesis [2] regarding Shor's algorithm, in order to factor a 5000 digit number, the best known classical algorithm using a classical computer requires an amount of time equal to $2^{n1/3\log(n)2/3}$, thus for n = 5000 one would need over 80 billion years to finish the calculation (assuming 1 execution step per nanosecond on the classical machine); but a quantum computer can perform the factoring in less than two seconds or in a time proportional to $n^2\log(n)\log(\log n)$. Another example of the computational power of quantum computers is available for the case of database searches. This example [3] known as Grover's algorithm, has demonstrated how a quantum computer could find an item in an unsorted list of n items in $O(\sqrt{n})$ steps, while classical algorithms require $O(n)$ steps. As Spector points out [4], this is accomplished because the database is queried by "address qubits in a superposition of all possible addresses". An improvement of a factor of the square root of n while not as impressive as Shor's factorization algorithm is still a major achievement.

Quantum Inspired Evolutionary Algorithms

The exploitation of quantum computational models to the benefit of evolutionary computation techniques has become known in the literature as Quantum-Inspired Evolutionary Algorithms or QEA [5]. A QEA executes on a classical computer. A QEA is not a quantum algorithm; it does not need a quantum computer to execute. QEA chromosomal structures exploit qubits rather than rely upon the traditional classical bit. The classical bit is the well known single bit which may have values of one or zero. The qubit may be in a zero state or a one state or in any superposition of the two. The Dirac notational representation of the state of a qubit is described in the following equation $|\Psi>=\alpha|0>+\beta|1>$, where α is the probability that the qubit will be in state 0 after measurement and β is the probability that the qubit will be found in state 1 after measurement. If a given system contains n qubits, then the system can simultaneously represent 2^n states. The application of these and other quantum concepts to chromosomal structures are the primary reasons for the performance improvement of QEA based approaches over conventional evolutionary algorithm approaches. Note: for a detailed analysis of the QEA please refer to the PhD Thesis of Kuk-Hyun Han as cited in the recommended reading section of this paper.

Selected criteria for determining successful human competitive results

In order to properly assess the value of the results of genetic programming in respect to the bold claim of matching or exceeding a human's similar discoveries, one needs a clear set of criteria. The criteria [6] for assessing human competitive results for our purposes are of the following types:

- B: The result is equal to or better than a result that was accepted as a new scientific result at the time when it was published in a peer-reviewed scientific journal.
- D: The result is publishable in its own right as a new scientific result independent of the fact that the result was mechanically created.

Integrating Quantum Computing Theory with Evolutionary Computing Theory

There are at least three intriguing integrations of evolutionary computation techniques and quantum computing techniques. They are:

1. The creation of novel chromosomal structures using quantum theory to improve evolutionary algorithm performance.
2. The evolution of existing quantum algorithms.
3. The evolution of new quantum algorithms.

The creation of novel chromosomal structures using quantum theory to improve evolutionary algorithm performance

QEAs exploit key features of quantum theory in order to improve search space traversal time. But again, a QEA is not a quantum algorithm but rather a very clever adaptation of evolutionary algorithms. Kuk-Hyun Han has provided a rich foundation for applying quantum constructs to evolutionary structures. To quote Kuk-Hyun Han's PhD Thesis [7]: QEA can "explore the search space with a smaller number of individuals and exploit the search space for a global solution within a short span of time." And again quoting Kuk-Hyun Han: "The Qubit individual has the advantage that it can represent a linear superposition of states and also has a better characteristic of generating diversity in population than any other representation." Qubits permit more sophisticated chromosomal structures to be devised than structures containing only singular values. The results for QEA are very promising. QEA has been shown to exceed the capabilities of traditional evolutionary algorithms. In the work of Kuk-Hyun Han, the knapsack problem [8] was solved with better performance than solutions using classical evolutionary algorithms. For the N-Queens [9] problem, Draa, Talbi, and Batouche have demonstrated significant improvements using a variation of the QEA. This N-Queens problem research exceeded not only classical genetic algorithms but also performed better than Hopfield Neural Networks (HNN). Citing their results, this approach "offers a faster convergence with a very limited number of chromosomes". The authors also show that the application of quantum structures to classical genetic algorithms provides an optimal solution to the N-Queens problem in a limited number of iterations as compared to the HNN. These encouraging experimental results seem to demonstrate that quantum theory properly applied will improve evolutionary algorithm theory and practice.

The evolution of existing quantum algorithms

The 1-bit OR, 2-bit AND/OR, 2 bit Grover database search and 1 bit Deutsch-Jozsa problems are well known and analyzed samples of quantum algorithms. These quantum algorithms were discovered or invented by human beings. The question then arises as to whether or not quantum algorithms can be automatically discovered. The answer is yes. Evolutionary computation techniques immediately lend themselves to discovering known quantum algorithms and discovering original quantum algorithms. Several researchers, particularly Lee Spector, have used genetic programming as their evolutionary model. In Spector's work [10], he demonstrates that it is possible to evolve human competitive results for the following solved quantum challenges:

1. 1 bit Deutsch-Jozsa (XOR) – Type B Evidence: Original results (by Deutch, Jozsa, and others) were published as new and significant results.
2. 2 bit Grover database search - Type B Evidence: Original results (by Grover) were published as new and significant results.

The evolution of new quantum algorithms

Continuing the analysis presented by Spector, we find that indeed new quantum approaches have been discovered by genetic programming prior to their discovery by humans for the following quantum problems:

1. 1-bit OR result – Types B and D Evidence, The first quantum program solving this problem.
2. 2-bit AND/OR – Types B and D Evidence, The first quantum program solving this problem.

Thus, Spector's efforts clearly demonstrate that the application of genetic programming to problems in quantum computing is a useful endeavor. I cannot overstate the significance of this work. The interested researcher is encouraged to purchase the book, "Automatic Quantum Computer Programming: A Genetic Programming Approach", which lays out the process of discovery.

Summary

This letter has attempted to elucidate the point that quantum theory properly applied will improve evolutionary algorithm performance and genetic programming properly applied can rediscover existing quantum algorithm solutions and make first time discoveries of new quantum algorithms. The proof offered to demonstrate the successful improvements of evolutionary algorithms is the PhD thesis of Kuk-Hyun Han which demonstrates impressive results using the knapsack problem as a test case and the N-Queens paper offered by Draa, Talbi, and Batouche. The proof offered to demonstrate that evolutionary computation can make human competitive discoveries in the field of quantum algorithms is the work of Lee Spector in solving the 1-bit OR, 2-bit AND/OR, 2 bit Grover database search , and 1 bit Deutsch-Jozsa problems. I consider the emerging fusion of evolutionary and quantum computing theories as exemplified by the material cited in this letter to be of extreme importance in the advancement of computer science.

Acknowledgements

I would like to thank Springer Science and Business Media and Lee Spector for their kind permission to cite "Automatic Quantum Computer Programming: A Genetic Programming Approach", Kuk-Hyun Han for his kind permission to cite his PhD thesis, Lee Spector for permission to use his presentation and other materials, and Amer Draa for his kind permission to use the material regarding the N-Queens Problem in preparation for this paper.

Recommended Reading

I would like to strongly encourage the interested scholar or serious researcher to acquire and study the following material:

- Lee Spector, "Automatic Quantum Computer Programming: A Genetic Programming Approach", Springer Science and Business Media, Original Publisher Kluwer Academic Publishers. ISBN 1-4020-7894-3, Boston, 2004.
- Kuk-Hyun Han's PhD Thesis "Quantum-inspired Evolutionary Algorithm" available at: http://www.khhan.com/profile1.htm, also related work appearing in "Quantum-Inspired Evolutionary Algorithms, With a New Termination Criterion, He Gate, and Two-Phase Scheme", Kuk-Hyun Han, Associate Member, IEEE, and Jong-Hwan Kim, Senior Member, IEEE, IEEE Transactions on Evolutionary Computation, Vol. 8, No. 2, April 2004
- Draa, Talbi, and Batouche, "A Quantum-Inspired Genetic Algorithm for Solving the N-Queens Problem", by 1Amer DRAA, 2Hichem TALBI, 3Mohamed BATOUCHE, Vision & Computer Graphics Team, LIRE Laboratory, Computer Science Department, Engineering Faculty, Mentouri University, Constantine, Algeria, 1draa_amer@yahoo.fr, 2 hichem_talbi@hotmail.com, 3 batouche@wissal.dz

Bibliography

[1] Lee Spector, Presentation Slides, "*Human-Competitive Results first Appearing in Automatic Quantum Computer Programming: A Genetic Programming Approach*", slides by Lee Spector, available at lspector@hampshire.edu, [WWW], cited with permission of the author.

[2] Kuk-Hyun Han, "*Quantum-inspired Evolutionary Algorithm, Doctoral Thesis*", Korea Advanced Institute of Science and Technology, Department of Electrical Engineering and Computer Science, Division of Electrical Engineering, 2003, page 2, cited with permission of the author. Available at [WWW]

[3] Ibid. page 14

[4] Lee Spector, "*Automatic Quantum Computer Programming: a Genetic Programming Approach*", Springer Science and Business Media. Original Publisher and copyright: Kluwer Academic Publishers. ISBN 1-4020-7894-3, 2004. Cited with kind permission from Springer Science and Business Media who controls the copyright, Springer grants "Permission free of charge on this occasion does not prejudice any rights we might have to charge for reproduction of our copyrighted material in the future." Also cited with permission of the author, Lee Spector. Page 31

[5] Kuk-Hyun Han, "*Quantum-inspired Evolutionary Algorithm, Doctoral Thesis*", abstract page iv., Korea Advanced Institute of Science and Technology, Department of Electrical Engineering and Computer Science, Division of Electrical Engineering, 2003, page 2, cited with permission of the author. Available at: [WWW],

[6] Lee Spector, "*Automatic Quantum Computer Programming: a Genetic Programming Approach*", Springer Science and Business Media. Original Publisher and copyright: Kluwer Academic Publishers. ISBN 1-4020-7894-3, 2004. Cited with kind permission from Springer Science and Business Media who controls the copyright, Springer grants "Permission free of charge on this occasion does not prejudice any rights we might have to charge for reproduction of our copyrighted material in the future." Also cited with permission of the author, Lee Spector. Pages 118 and 119.

[7] Kuk-Hyun Han, "*Quantum-inspired Evolutionary Algorithm, Doctoral Thesis*", pages 2 and 4, Korea Advanced Institute of Science and Technology, Department of Electrical Engineering and Computer Science, Division of Electrical Engineering, 2003, cited with permission of the author. Available at [WWW]

[8] ibid page 3.

[9] Draa, Talbi, and Batouche, 7th ISPS' Algiers May 2005 –"*Quantum-Inspired Genetic Algorithm for Solving the N-Queens Problem*", 1Amer DRAA, 2Hichem TALBI, 3Mohamed BATOUCHE, Vision & Computer Graphics Team, LIRE Laboratory, Computer Science Department, Engineering Faculty, Mentouri University, Constantine, Algeria 1draa_amer@yahoo.fr, 2hichem_talbi@hotmail.com, 3batouche@wissal.dz, cited with permission of Amer Draa, cited with permission of the author. Available at [WWW]

[10] Lee Spector, Presentation Slides, "*Human-Competitive Results first Appearing in Automatic Quantum Computer Programming: A Genetic Programming Approach*", slide 16 (claims), by Lee Spector, available from lspector@hampshire.edu, at [WWW], cited with permission of the author.

Forthcoming Papers

Evolutionary Computation 14(4)

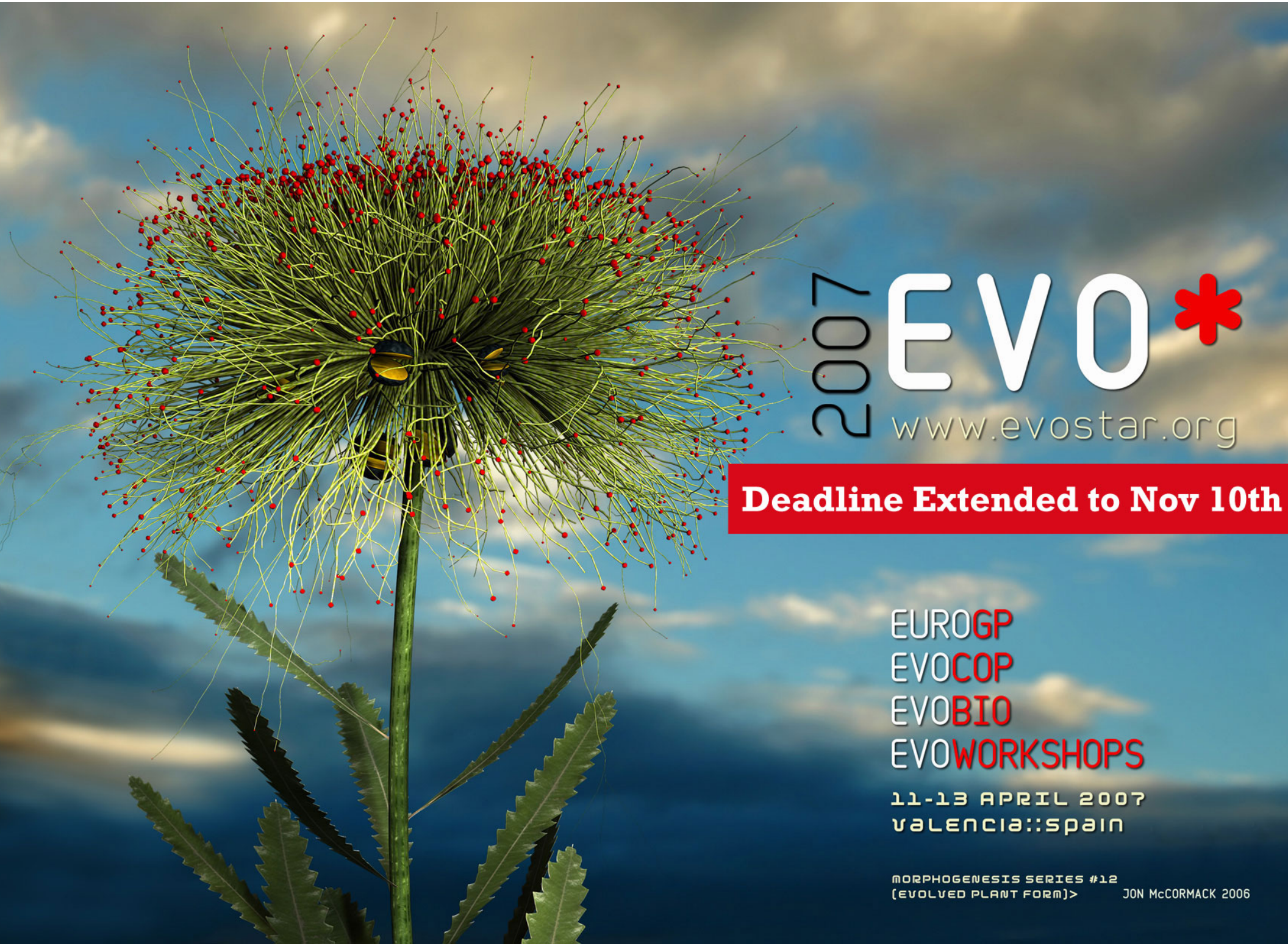
- **Linkage Identification by Fitness Difference Clustering**, Miwako Tsuji, Masaharu Munetomo, and Kiyoshi Akama, pp 383–410
- **Understanding the Biases of Generalised Recombination: Part I**, Riccardo Poli and Christopher R. Stephens, pp 411–432
- **Evolving Combinatorial Problem Instances that are Difficult to Solve**, Jano I. van Hemert, pp 433–462
- **Introducing Robustness in Multi-Objective Optimization**, Kalyanmoy Deb and Himanshu Gupta, pp 463–494

Genetic Programming and Evolvable Machines 7(3)

- **Multi-objective evolutionary design and knowledge discovery of logic circuits based on an adaptive genetic algorithm**, Shuguang Zhao and Licheng Jiao, pp 195–210 [DOI 10.1007/s10710-006-9005-7]
- **GP-Sumo: Using genetic programming to evolve sumobots**, Shai Sharabi and Moshe Sipper, pp 211–230 [DOI 10.1007/s10710-006-9006-6]
- **Shortcomings with using edge encodings to represent graph structures**, Gregory S. Hornby, pp 231–252 [DOI 10.1007/s10710-006-9007-5]
- **Unbounded evolutionary dynamics in a system of agents that actively process and transform their environment**, Alastair Channon, pp 253–281 [DOI 10.1007/s10710-006-9009-3]
- **Book Review by Steven J. Barrett:** Intelligent Bioinformatics: The Application of Artificial Intelligence Techniques to Bioinformatics Problems John Wiley & Sons Ltd., Chichester, UK, Keedwell, Edward and Narayanan, Ajit, 2005, 280 p., Hardcover, ISBN 0-470-02175-6, pp 283–284 [DOI 10.1007/s10710-006-7003-4]
- **Book Review by Mak Kaboudan:** Biologically Inspired Algorithms for Financial Modelling Published by: Springer, A. Brabazon and M. O'Neill, 2006, ISBN 3-540-26252-0, $85, pp 285–286 [DOI 10.1007/s10710-006-9010-x]
- **Book Review by Nataša Jonoska:** Theoretical and Experimental DNA Computation Published by: Springer-Verlag, Martyn Amos 172 pages, 78 figures, 2005, ISBN-10 3-540-65773-8, pp 287–29 [DOI 10.1007/s10710-006-9011-9]

Genetic Programming and Evolvable Machines 7(4) Special Issue on EC in Dynamic Environments

- **Editorial to special issue on evolutionary computation in dynamic and uncertain environments**, Shengxiang Yang, Yew-Soon Ong and Yaochu Jin [DOI 10.1007/s10710-006-9016-4]
- **Self-adaptation of evolution strategies under noisy fitness evaluations**, Hans-Georg Beyer and Silja Meyer-Nieberg [DOI 10.1007/s10710-006-9017-3]
- **A hierarchical Particle Swarm Optimizer for Noisy and Dynamic Environments**, Stefan Janson and Martin Middendorf
- **Estimation of Evolvability GA and Dynamic Environments**, Yao Wang and Mark Wineberg
- **Inverse multi-objective robust evolutionary design**, Dudy Lim, Yew-Soon Ong, Yaochu Jin, Bernhard Sendhoff and Bu Sung Lee [DOI 10.1007/s10710-006-9013-7]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Calls and Calendar

November

Genetic Programming and Evolvable Machines
Special Issue on “Medical Applications"

www.springer.com/10710

Submission Deadline November 15, 2006
Authors Notification: February 28, 2007
Camera-ready Submission: April 30, 2007

Although the application of evolutionary computation (EC) to medicine is not new, the reporting of new work tends to be distributed among various technical and clinical publications in a somewhat disparate manner. A special issue of Genetic Programming and Evolvable Machines satisfies the need for a much needed focus for medical related applications of EC, not only providing a clear definition of the state of the art, but also support to practitioners for whom EC might not be their main area of expertise or experience.

Traditionally, medical applications have used straightforward implementations of evolutionary algorithms, such as genetic algorithms, to optimize traditional data analysis in a wide range of medical applications including signal and image processing, expert systems, data mining, etc. More recently, however, exploitation of advanced evolutionary computation paradigms such as genetic programming and artificial immune systems have been applied directly to challenging applications such as diagnosis and monitoring.

The aim of this Special Issue is to provide the reader with a snapshot of the current practice and an indication of future trends in this exciting and demanding application area.

Subjects will include (but are not limited to) applications of Genetic and Evolutionary Computation to: Medical imaging, Medical signal processing, Clinical diagnosis and therapy, Data mining of medical data and records, Clinical expert systems, and Modeling and simulation of medical processes.

All electronic submissions must be sent to Steve Smith.

Manuscripts should conform to the standard format of the Genetic Programming and Evolvable Machine journal as indicated in the Information for Authors available at the Journal website (WWW).

All submissions will be peer reviewed subject to the standards of the journal. Manuscripts based on previously published conference papers must be extended substantially. Electronic submissions in postscript or PDF are strongly preferred. Please send all submissions to one of the guest editors.

All enquiries on this special issue should be sent to Steve Smith.

Prospective authors are also invited to send an email to Steve Smith indicating their interest in submitting a paper and the specific topics addressed.

Guest editors:

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Scalable Computing: Practice and Experience, Journal Special Issue on "Parallel Evolutionary Algorithms"

http://www.scpe.org

Submission Deadline November 15, 2006

Authors Notification: December 15, 2006

Camera-ready Submission: January 15, 2007

Evolutionary Algorithms (EA) are computer-based solving systems, which use evolutionary computational models as a key element in their design and implementation. They have a conceptual base of simulating the evolution of individual structures via the Darwinian natural selection process. EA's has been widely accepted for solving several important practical applications in engineering, business, commerce etc. As we all know, the problems of the future will be more complicated in terms of complexity and data volume. Generally, evolutionary computation requires a massive computational effort to yield efficient and competitive solution to real-size engineering problems.

This special issue is focussed on all theoretical and practical aspects related to the parallelisation of evolutionary computation. The topics of interest include, but are not limited to: parallel genetic operators, parallel fitness evaluation, evolutionary multi-objective optimization in a parallel environment, multipopulation and coevolutionary approaches, synchronous and asynchronous parallel distributed evolutionary algorithms, distributed/parallel genetic programming, distributed and cellular evolutionary algorithms, hybrid distributed/parallel algorithms (evolutionary algorithms hybridized with other meta-heuristics), parallel evolutionary algorithms implementations, applications, including real world applications, and the others connected.

All papers will be peer reviewed by three independent referees. The time schedule for this publication is as follows:

For further details, please do not hesitate to contact the editors:

- Ajith Abraham (ajith.abraham@ieee.org),
- Pawel B. Myszkowski (pmyszkowski@wsiz.wroc.pl), and
- Shahram Rahimi (rahimi@cs.siu.edu).

10th Asia-Pacific Workshop on Intelligent and Evolutionary Systems

November 25-26, 2006, Seoul, Korea

http://sc.snu.ac.kr/SCLAB/Conference/ies2006/

To encourage in-depth technical discussions, the number of participants of the workshop is limited to 40 or less. The workshop will allocate ample time for discussions in addition to paper presentations. It covers two major areas:

Intelligent and Adaptive Systems: Designing and developing intelligent and adaptive systems using machine learning and/or evolutionary computation techniques; other artificial intelligence techniques will also be considered. Examples of topics include, but are not limited to, evolutionary learning, neural network learning, autonomous agents/robots, artificial life, evolutionary games, hybrid learning systems, other machine learning systems.

Optimisation with Intelligent Systems: Both numerical and combinatorial optimisation will be considered. Examples of the topics include, but are not limited to, analysis of algorithms (e.g., convergence and complexity), intelligent optimisation algorithms, hybrid algorithms, and applications (e.g., resource allocation, planning, scheduling, facility layout, optimal design, etc.).

December

ICARA 2006: Special Session on Artificial Life and Living Robots

December 12-14, 2006, Palmerston North, New Zealand

http://icara.massey.ac.nz/

Organised by Peter J. Bentley, University College, London

The study of living systems has never been more relevant to robotics. Artificial life now informs us of how organisms can reproduce, build and repair themselves. Bio-inspired algorithms give our technology the ability to adapt, evolve and learn. Bio-mimetics teaches us how novel materials may be exploited to achieve new capabilities. This special session focuses on such exciting new areas, and aims to produce an in-depth discussion about how biology should be used to improve our technology. Papers should be submitted to Peter Bentley p.bentley@cs.ucl.ac.uk following the ICARA conference guidelines.

BIONETICS 2006

December 11-13, 2006, Madonna di Campiglio, Italy.

http://www.bionetics.org/

Deadline July 31, 2006

The BIONETICS conference aims at bringing together researchers and scientists from several disciplines in computer science and engineering where bio-inspired methods are investigated. We are soliciting high-quality original papers in the following five areas including but not limited to the following topics: a) Bio-inspired mathematical models, methods and tools; b) Bio-inspired software; c) Bio-inspired security mechanisms; d) Bio-inspired networks and communication systems; e) Bio-inspired and bio-based nano-scale communication and information systems. Submission instructions at [WWW].

January 2007

Foundations of Genetic Algorithms

7-11 January 2007, Mexico City, Mexico

http://www.sigevo.org/foga-2007/

We invite submissions of extended abstracts for the ninth biennial workshop on the Foundations of Genetic Algorithms. The workshop covers the theoretical foundations of all forms of evolutionary computation. FOGA will be held 7-11 January, 2007 in Mexico City. Attendance at the workshop will be limited; the goal is to create a small interdisciplinary forum with close interaction among participants from different fields - evolutionary computation, population genetics, animal behaviour, physics and biochemistry, among others. Individuals submitting papers will be given priority for attendance, and some slots will be reserved for students. Anyone wishing to attend must indicate this by either submitting a paper or requesting attendance in advance (see deadline).

Extended abstracts must be received by 20th September, 2006. Submissions should address theoretical issues in evolutionary computation. Papers that consider foundational issues and/or are of a multidisciplinary nature are especially encouraged. This does not preclude the acceptance of papers that use an experimental approach, but such work should be directed towards validation of suitable hypotheses concerning foundational matters.

Extended abstracts should be between 10-12 pages (single column). To submit an extended abstract, please email a compressed postscript or a pdf file to stephens@nucleares.unam.mx and mtoussai@inf.ed.ac.uk no later than 20th September 2006. In their submission message authors should provide the title of the paper, and the name, address and affiliation of the author(s). Authors should submit papers in single column format with standard spacing and margins, and 11pt or 12pt font for the main text. Authors using LaTeX should either use the standard article style file or the FOGA style file which can be found at the conference web-site.

April 2007

EuroGP 2007

Tenth European conference on Genetic Programming

April 11-13, 2007, Valencia, Spain.

Homepage: WWW

Deadline November 10, 2006

EuroGP is the premier conference in Europe devoted entirely to genetic programming. We invite submissions on all aspects of evolutionary generation of computer programs featuring new original research. The standard for submissions is high. Reviewing is double-blind. The conference will feature a mixture of oral presentations and poster sessions. Accepted papers will be published as papers in a volume of the Springer Lecture Notes in Computer Science.

EuroGP2007 will be held in Valencia, Spain, in conjunction with EvoBIO (5th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics), EvoCOP2007 (7th European Conference on Evolutionary Computation in Combinatorial Optimization) and EvoWorkshops. High quality papers are sought on topics strongly related to the evolution of computer programs, ranging from theoretical work to innovative applications.

IEEE Symposium Series on Computational Intelligence 2007

April 1-5, 2007, Honolulu, Hawaii.

Homepage: WWW

Deadline October 31, 2006

Honolulu, Hawaii, hosts the first IEEE Symposium Series on Computational Intelligence (IEEE SSCI 2007). This international event brings together at one location 12 symposia running concurrently, each highlighting various aspects of computational intelligence.

The symposium series will be held at the Hilton Hawaiian Village Beach Resort & Spa in famous Waikiki. Sponsored by the IEEE Computational Intelligence Society, this event will bring together top researchers, practitioners, and students from around the world on April 1-5, 2007 to discuss the latest advances in the field of computational intelligence. Your registration gains you entry to every session of every symposium, as well as the complete set of proceedings for all the meetings, the reception, and the banquet. The participating symposia are:

- IEEE Symposium on Computational Intelligence in Image and Signal Processing (CIISP 2007)
- IEEE Symposium on Approximate Dynamic Programming and Reinforcement Learning (ADPRL 2007)
- IEEE Symposium on Computational Intelligence and Data Mining
- IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2007)
- IEEE Symposium on Computational Intelligence and Games
- IEEE Symposium on Computational Intelligence in Scheduling (CI-Sched 2007)
- IEEE Symposium on Foundations of Computational Intelligence (FOCI'07)
- IEEE Symposium on Computational Intelligence in Multicriteria Decision Making (MCDM '07)
- IEEE Symposium on Artificial Life (CI-ALife'07)
- IEEE Swarm Intelligence Symposium (SIS2007)
- IEEE Symposium on Computational Intelligence in Security and Defense Applications (CISDA 2007)
- IEEE Workshop on Evolvable and Adaptive Hardware (WEAH2007)

EvoCOP 2007 - Seventh European Conference on Evolutionary Computation in Combinatorial Optimisation

April 11-13, 2007, Valencia, Spain.

Homepage: WWW

Deadline November 10, 2006

The EvoCOP series, started in 2001 and held annually since then, was the first event specifically dedicated to the application of evolutionary computation and related methods to combinatorial optimization problems. Following the general trend of hybrid metaheuristics and diminishing boundaries between the different classes of metaheuristics, EvoCOP has broadened its scope and now explicitly invites submissions on any kind of metaheuristic for combinatorial optimization. Each accepted paper will be presented orally at the conference and printed in the proceedings published by Springer in the LNCS series (see LNCS volumes 2037, 2279, 2611, 3004, 3448, and 3906 for the previous proceedings).

The conference will be held in conjunction with the 10th European Conference on Genetic Programming (EuroGP 2007), the Fifth European Conference on Evolutionary Computation (EvoBIO 2007) and EvoWorkshops 2007, a collection of application-oriented workshops in the field of evolutionary computation.

EvoBIO 2007 - Fifth European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics

April 11-13, 2007, Valencia, Spain.

Homepage: WWW

Deadline November 10, 2006

EvoBIO covers research in all aspects of Evolutionary Computation, Machine Learning and Data Mining in bioinformatics.

The goal of the conference is to not only present recent research results and to identify and explore directions of future research, but also stimulatesynergy and cross fertilization among Evolutionary Computation, Machine Learning and Data Mining for Bioinformatics.

The emphasis is on novel advanced techniques addressing important problems in molecular biology, proteomics, genomics and genetics, that have been implemented and tested in simulations and on real-life datasets, in particular microarray analysis, phylogeny, biomarker discovery, proteomics, high-throughput biotechnology, sequence analysis and alignment, ecological modelling, cell simulation and modelling, protein interaction. The conference will be held in conjunction with EuroGP2007, EvoCOP2007, and EvoWorkshops.

EvoWorkshops 2007

April 11-13, 2007, Valencia, Spain.

Deadline November 10, 2006

EvoWorkshops 2007 is a joint event of eight different workshops on Applications of Evolutionary Computation. Since 1998, EvoWorkshops has represented a unique opportunity for a broad and continuously increasing number of researchers to meet and present their advances in various application areas of evolutionary computation techniques. As a result, over the last seven years, EvoWorkshops has become one of the major events focusing solely on applicational aspects of EC, constituting an important link between EC research and the application of EC in a a wide range of domains. The standard of submissions is high, and the reviewing process is double-blind. Accepted papers are published in a volume of Springer Lecture Notes in Computer Science.

EvoWorkshops 2007 will be held in conjunction with the Tenth European Conference on Genetic Programming, the Seventh European Conference on Evolutionary Computation in Combinatorial Optimisation, and the Fifth European Conference on Evolutionary Computation on Evolutionary Bioinformatics. Next year's EvoWorkshops will comprise of the following individual workshops:

- EvoCOMNET: Communications, networks, and connected systems
- EvoIASP: Image analysis and signal processing
- EvoHOT: Evolutionary algorithms for hardware optimization techniques
- EvoInteraction: Interactive evolution and humanized computational intelligence
- EvoMUSART: Evolutionary music, art, and creative systems
- EvoPhD: Graduate student workshop on evolutionary computation
- EvoSTOC: Stochastic and dynamic environments
- EvoTransLog: Transportation and logistics

IEEE Symposium Series on Computational Intelligence and Scheduling

April 1-5, 2007, Hilton Hawaii Village Resort, Honolulu, HI, USA

Deadline October 31 2006

http://www.cs.nott.ac.uk/~rxq/cis/CIS2007.htm

CISched 2007 aims to bring together leading researchers and practitioners in computational intelligence and scheduling. Scheduling problems are often not amenable to be being tackled by exact approaches due to the huge search spaces that have to be explored. Therefore we often resort to techniques which fall under the term of Computational Intelligence. These can include Evolutionary Computation, Neural Networks, Fuzzy Logic etc. This symposium aims to explore recent advances in this area.

July 2007

Genetic and Evolutionary Computation Conference (GECCO-2007)

July 7-11, 2007, University College London, London, UK

http://www.sigevo.org/gecco-2007

Deadline January 17, 2007

The Genetic and Evolutionary Computation Conference (GECCO-2007) will present the latest high-quality results in the growing field of genetic and evolutionary computation. Topics include: genetic algorithms, genetic programming, evolution strategies, evolutionary programming, real-world applications, learning classifier systems and other genetics-based machine learning, evolvable hardware, artificial life, adaptive behavior, ant colony optimization, swarm intelligence, biological applications, evolutionary robotics, coevolution, artificial immune systems, and more.

Keynote Event

On Monday evening, 9 July 2007, Professors Richard Dawkins, Lewis Wolpert, and Steve Jones will take part in a public debate, discussing the emergence of complexity in evolution. This will be a once-in-a-lifetime opportunity to hear and interact with some of the most famous names in evolutionary biology.

Program Tracks

Three days of presentations in 15 separate and independent program tracks specializing in various aspects of genetic and evolutionary computation. Proceedings will be published and distributed to all registered attendees.

Free Tutorials and Workshops

Two days of free tutorials and workshops (included with conference registration) presented by some of the world's foremost experts in topics of interest to genetic and evolutionary computation researchers and practitioners.

Review Process

Each paper submitted to GECCO will be rigorously reviewed, in a blind review process, meaning that reviewers should not be able to infer the identities of the authors of the papers under review, and, of course, that authors will not know the identities of their reviewers. One of at least 15 separate and independent program committees specializing in various aspects of genetic and evolutionary computation review submitted papers. These committees make their own final decisions on submitted papers for their areas, subject only to conference-wide space limitations and procedures. Review criteria includes significance of the work, novelty, clarity, writing quality, and sufficiency of information to permit replication, if applicable. GECCO notifies the first-named author (or other corresponding author designated by the authors at submission) of acceptance or rejection on March 14, 2007.

How to Submit a Paper

Meet the Submission Deadline: The deadline for ARRIVAL of submissions is Wednesday, January 17, 2007.

Submit substantially new work: The material in a paper must represent substantially new work that has not been previously published by conferences, journals, or edited books in the genetic and evolutionary computation field. GECCO allows submissions of material that is substantially similar to a paper being submitted contemporaneously for review in another conference. However, if the submitted paper is accepted by GECCO, the authors agree that substantially the same material will not be published by another conference in the evolutionary computation field. Material may be later revised and submitted to a journal, if permitted by the journal.

Visit www.sigevo.org/gecco-2007 for detailed instructions, including categories, keywords, and formatting requirements. Be sure to check the web page for changes that may appear as the paper submission deadline approaches.

Accept author agreement

By submitting a paper, the author(s) agree that, if their paper is accepted, they will:

- Submit a final, revised, camera-ready version by the deadline for camera-ready papers: Wednesday, April 11, 2007
- Register at least one author to attend the conference By the deadline for camera-ready papers,
- Attend the conference (at least one author)
- Present the accepted paper at the conference

September 2007

IEEE Congress on Evolutionary Computation

September 25-28, 2007, Singapore.

Deadline March 15, 2007

www.cec2007.org

CEC 2007 will feature a world-class conference that aims to bring together researchers and practitioners in the field of evolutionary computation and computational intelligence from all around the globe. Technical exchanges within the research community will encompass keynote speeches, special sessions, tutorial workshops, panel discussions as well as poster presentations. On top of this, participants will be treated to a series of social functions, receptions and networking sessions, which will serve as a vital channel to establish new connections and foster everlasting friendship among fellow counterparts.

About the Newsletter

SIGEVOlution is the newsletter of SIGEVO, the ACM Special Interest Group on Genetic and Evolutionary Computation.

To join SIGEVO, please follow this link [WWW]

Contributing to SIGEVOlution

We solicite contributions in the following categories:

Art: Are you working with Evolutionary Art? We are always looking for nice evolutionary art for the cover page of the newsletter.

Short surveys and position papers: We invite short surveys and position papers in EC and EC related areas. We are also interested in applications of EC technologies that have solved interesting and important problems.

Software: Are you are a developer of an EC software and you wish to tell us about it? Then, send us a short summary or a short tutorial of your software.

Lost Gems: Did you read an interesting EC paper that, in your opinion, did not receive enough attention or should be rediscovered? Then send us a page about it.

Dissertations: We invite short summaries, around a page, of theses in EC-related areas that have been recently discussed and are available online.

Meetings Reports: Did you participate to an interesting EC-related event? Would you be willing to tell us about it? Then, send us a short summary, around half a page, about the event.

Forthcoming Events: If you have an EC event you wish to announce, this is the place.

News and Announcements: Is there anything you wish to announce? This is the place.

Letters: If you want to ask or to say something to SIGEVO members, please write us a letter!

Suggestions: If you have a suggestion about how to improve the newsletter, please send us an email.

Contributions will be reviewed by members of the newsletter board.

We accept contributions in LaTeX, MS Word, and plain text.

Enquiries about submissions and contributions can be emailed to editor@sigevolution.org.

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Call for Papers

2007 Genetic and Evolutionary Computation Conference

July 7-11, 2007 (Saturday-Wednesday), University College London, London UK (pending ACM approval)
Largest Conference in the Field of Genetic and Evolutionary Computation
A recombination of
the 16th International Conference on Genetic Algorithms (ICGA)
and the 12th Annual Genetic Programming Conference (GP)
www.sigevo.org/gecco-2007

One Conference – Many Mini-Conferences

The Genetic and Evolutionary Computation Conference (GECCO-2007) will present the latest high-quality results in the growing field of genetic and evolutionary computation. Topics include: genetic algorithms, genetic programming, evolution strategies, evolutionary programming, real-world applications, learning classifier systems and other genetics-based machine learning, evolvable hardware, artificial life, adaptive behavior, ant colony optimization, swarm intelligence, biological applications, evolutionary robotics, coevolution, artificial immune systems, and more.

Program Tracks: Three days of presentations in 14 separate and independent program tracks specializing in various aspects of genetic and evolutionary computation. Proceedings will be published and distributed to all registered attendees.

Free Tutorials and Workshops: Two days of free tutorials and workshops (included with conference registration) presented by some of the world's foremost experts in topics of interest to genetic and evolutionary computation researchers and practitioners.

Review Process

Each paper submitted to GECCO will be rigorously reviewed, in a double-blind review process, meaning that reviewers should not be able to infer the identities of the authors of the papers under review, and, of course, that authors will not know the identities of their reviewers. One of at least 14 separate and independent program committees specializing in various aspects of genetic and evolutionary computation review submitted papers. These committees make their own final decisions on submitted papers for their areas, subject only to conference-wide space limitations and procedures. Review criteria includes significance of the work, novelty, clarity, writing quality, and sufficiency of information to permit replication, if applicable.

GECCO notifies the first-named author (or other corresponding author designated by the authors at submission) of acceptance or rejection on March 14, 2007.

How to Submit a Paper

Meet the Submission Deadline: The deadline for **ARRIVAL** of submissions is Wednesday, January 17, 2007.

Submit substantially new work: The material in a paper must represent substantially new work that has not been previously published by conferences, journals, or edited books in the genetic and evolutionary computation field. GECCO allows submissions of material that is substantially similar to a paper being submitted contemporaneously for review in another conference. However, if the submitted paper is accepted by GECCO, the authors agree that substantially the same material will not be published by another conference in the evolutionary computation field. Material may be later revised and submitted to a journal, if permitted by the journal.

Visit **www.sigevo.org/gecco-2007** for detailed instructions, including categories, keywords, and formatting requirements. Be sure to check the web page for changes that may appear as the paper submission deadline approaches.

Accept author agreement: By submitting a paper, the author(s) agree that, if their paper is accepted, they will:

- Submit a final, revised, camera-ready version by the deadline for camera-ready papers: Wednesday, April 11, 2007
- Register at least one author to attend the conference By the deadline for camera-ready papers,
- Attend the conference (at least one author)
- Present the accepted paper at the conference

About University College London: UCL was the first university to be established in England after Oxford and Cambridge, providing a progressive alternative to those institutions' social exclusivity, religious restrictions and academic constraints. Today UCL is one of the intellectual powerhouses of British higher education. Located at Gower Street, London WC1E 6BT, UK. Website: www.ucl.ac.uk

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Keynote 9 July: Professors Richard Dawkins, Lewis Wolpert, and Steve Jones

Richard Dawkins, Lewis Wolpert and Steve Jones will take part in a public debate on the evening of 9 July, discussing the emergence of complexity in evolution. This will be a once-in-a-lifetime opportunity to hear and interact with some of the most famous names in evolutionary biology.

GECCO Organizers

Conference Chair: Hod Lipson
Editor-in-Chief: Dirk Thierens
Business Committee: David E. Goldberg, Erik Goodman, John R. Koza, Hod Lipson, Mike Cattolico
Workshops Chair: Tina Yu
Tutorials Chair: Anikó Ekárt
Competitions Chair: Stefano Cagnoni
Graduate Student Workshop Chair: Anikó Ekárt
Late Breaking Papers Chair: Peter A.N. Bosman
Evolutionary Computation in Practice Chairs: David Davis and Rajkumar Roy
Local Arrangements and Publicity Chair: Peter Bentley

Program Tracks and Chairs:

Genetic Algorithms: Jürgen Branke, Kumara Sastry
Genetic Programming: Riccardo Poli
Evolution Strategies, Evolutionary Programming: Hans-Georg Beyer
Real-World Applications: Dave Cliff
Genetics-Based Machine Learning and Learning Classifier Systems: Tim Kovacs
Biological Applications: Jason H. Moore, Clare Congdon
Artificial Life, Evolutionary Robotics, Adaptive Behavior, Evolvable Hardware: Josh Bongard
Ant Colony Optimization, Swarm Intelligence, and Artificial Immune Systems: Thomas Stützle, Mauro Birattari
Evolutionary Multiobjective Optimization: Kalyanmoy Deb
Coevolution: Richard Watson
Estimation of Distribution Algorithms: Martin Pelikan
Search-Based Software Engineering: John Clark
Formal Theory: Frank Neumann, Ingo Wegener, Benjamin Doerr

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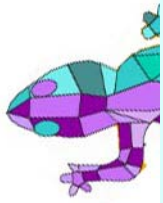

Planned Free Tutorials

Introductory

Genetic Algorithms	Erik Goodman
Genetic Programming	John Koza
Evolution Strategies	Thomas Bäck
A Unified Approach to EC	Kenneth De Jong
Ant Colony Optimization	Christian Blum
Learning Classifier Systems	Tim Kovacs
Probabilistic Model-Building GAs	Martin Pelikan
Grammatical Evolution	Conor Ryan
Coevolution	Edwin de Jong, Kenneth Stanley, Paul Wiegand

Advanced

GA Theory	Jonathan Rowe
GP Theory	Riccardo Poli, Bill Langdon
Representations	Franz Rothlauf
No Free Lunch	Darrell Whitley
Bioinformatics	Jason Moore
Human Competitive Results	John Koza
Evolutionary Multiobjective Optimization	Eckart Zitzler, Kalyanmoy Deb
Industrial Evolutionary Computing	Arthur Kordon, Guido Smits, Mark Kotanchek Constraint Handling Techniques
Used with EAs	Carlos Coello Coello
Statistics for EC	Mark Wineberg
Coevolution	Sevan Ficici, Anthony Bucci
Evolutionary Practical Optimization	Kalyanmoy Deb

Specialized Techniques and Applications

Experimental Research in EC	Mike Preuss, Thomas Bartz-Beielstein
Symbolic Regression in GP	Maarten Keijzer
Evolving Neural Networks	Risto Miikulainen
Quantum Computing	Lee Spector

To Propose a Tutorial or Workshop

To propose a tutorial, contact Anikó Ekárt at **ekarta@aston.ac.uk**. To propose a workshop, contact Tina Yu at **tinayu@cs.mun.ca**. Please include "GECCO" in your subject line.

More Information

Visit **www.sigevo.org/gecco-2007** for about electronic submission procedures, formatting details, student travel grants,, the latest list of tutorials and workshop, late-breaking papers, and more.

For technical matters contact Conference Chair Hod Lipson at **Hod.Lipson@cornell.edu**. For conference administration matters contact Primary Support Staff at **gecco-admin@tigerscience.com**.

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