Editorial

I hope you had a good start in 2007. GECCO surely had. With 577 submissions, GECCO-2007 has beaten the 2005 record of 550 submissions by 4.4%. And there are still many events for which the submission is still open: the 16 workshops (the deadline is March 23rd), the late-breaking papers track (the deadline is April 28th), and the human competitive, the "Humies", awards (the deadline is May 28th). And what about the keynote event? To have Richard Dawkins, Lewis Wolpert and Steve Jones together is amazing. But to have the public debate in the Central Hall of the Natural History Museum, a place soaked in history and science, that's the cherry on the cake. Don't you have the impression that, as time goes by, GECCO becomes better and better?

And then there were four! This issue completes the first year of SIGEVOlution, a result that one year ago seemed a mirage to me. As the previous three issues, also this fourth issue delivers you as much content as we could get: three contributed papers by Zheng Yi Wu, Juan-Julián Merelo, Carlos Cotta, and William B. Langdon, several sections devoted to GECCO-2007, summaries of recently discussed PhD theses, the table of contents of the forthcoming issues of ECJ, and the calendar of EC events.

Many times a day we run tap water, for cooking, for drinking, for washing, etc. Tap water is something that most of us take for granted. Well, guess what? As Zheng Yi Wu explains to us in the first contributed paper, a genetic algorithm may have helped in bringing the water to our houses. Then, Juan-Julián Merelo and Carlos Cotta, in their continual exploration of our community (did you read their previous paper in SIGEVOlution?), take us inside the field of Metaheuristics. In the third contributed paper, William B. Langdon shows us how the GP bibliography, one of the most valuable resources of our community, is accessed online.

The cover is a detail taken from the metaheuristics coauthorship network provided by Juan-Julián Merelo and Carlos Cotta. The whole network is available on page 8.

And at the end, due thanks to the people who, with their invaluable help, made this issue possible: Dave Davis, Martin Pelikan, Pat Cattolico, Hod Lipson, Peter Bentley, Erik Goodman, Zheng Yi Wu, Carlos Cotta, Juan-Julián Merelo, Bill Langdon, Stewart W. Wilson, Leonora Bianchi, Toby O'Hara, and Vito Trianni.

Pier Luca
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Contents

Genetic Algorithm Plays a Role in Municipal Water Systems

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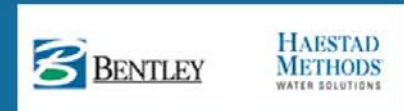
Tap water has been taken for granted as a daily resource for many people, but it may not be well known that genetic algorithm optimization has been playing an important role in managing and operating municipal drinking water systems by means of hydraulic and water quality models. Computer models have been built for analyzing water distribution systems since the mid-1960s. The models have become important tools for engineers to simulate various system scenarios. More recently, water quality models have been a critical means for conducting distribution system evaluation studies in order for water companies to comply with USA EPA's latest water quality regulations. However, before hydraulic and water quality models can be used for analysis and operational study of a real system, a model must be able to accurately predict what happens in a real system. The accuracy of modeling results is dependent on a set of model parameters that must be optimized for each water system. Parameter optimization is often referred to as model calibration, that is to minimize the difference between the simulated values and the field observed values. Model calibration is a vitally important process, but a time consuming task.

Over the last four decades, several approaches using optimization techniques have been proposed for model calibration. Although some of the methods can make the model agree with field observations to a certain degree, few are effective and efficient at achieving a good level of calibration in terms of determining robust model parameters. The previously developed methods appear to lack versatility for engineers and modelers to accurately specify the calibration task given real data for a real system.

Building accurate models has become even more challenging when all pipes are included in a model by using the data readily available and accessible from a geographic information system (GIS). Such a model often consists of tens or hundreds of thousands of pipes and is used for detailed water quality studies. Therefore, there is an imperative need for developing comprehensive innovative methodology and integrated user-friendly tools for practical engineers to build accurate and robust models.

Hydraulic Parameter Optimization

A hydraulic model of a water distribution system is defined as a connected network of pipes, nodes, pumps, valves, tanks and reservoirs. It is used to simulate the network hydraulic characteristics that are governed by the flow conservation law and by the energy conservation law. A large number of model parameters including pipe roughness coefficients, junction demands (how much water is consumed at a certain location) and valve/pump control settings (status of valve open or closed, flow or pressure settings, and pump speed factors etc.) needs to be identified to enable a model to accurately predict the flow and pressures throughout a system.

A comprehensive and flexible framework [8, 4, 1] has been developed for calibrating hydraulic network models. A model calibration is defined as an implicit nonlinear optimization problem, which is solved by employing a competent genetic algorithm [2, 3]. Calibration solutions are obtained by minimizing the discrepancy between the predictions of the model and the field observed values of junction pressures, tank levels,
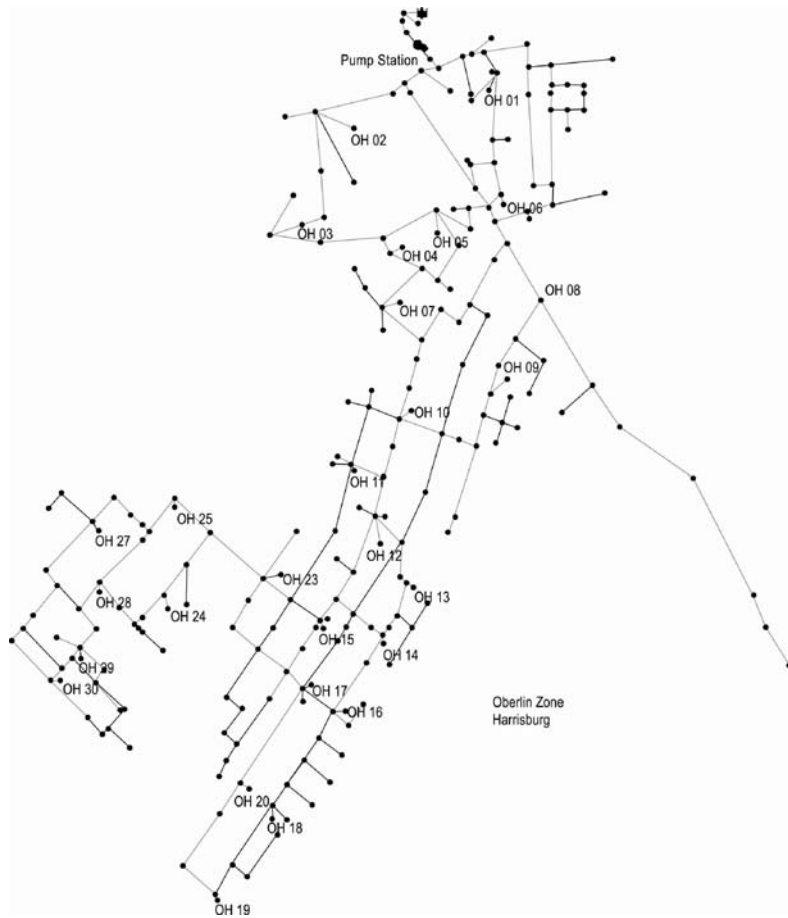
Figure 1: Oberlin supply zone of Harrisburg water distribution system.

Water Quality Parameter Optimization

A water quality model predicts chemical transport and destination throughout a water distribution system. The model is not only a promising alternative for analyzing disinfectant residuals in a cost-effective manner, but also a means of providing enormous engineering insights into the characteristics of water quality variation and constituent reactions. However, a water quality model is a reliable tool only if it predicts what occurs in a real system.

The GA-based hydraulic parameter optimization has been extended to perform water quality model optimization of the reaction mechanism that is characterized by the reaction within bulk water and the reaction in between the pipe wall and bulk water. The former is defined by the global water quality parameters of bulk water reaction order and concentration limit, and the latter is defined by the element-dependent pipe wall reaction order and coefficients as well as chemical reaction mechanisms in tank storage. All the global and element-dependent reaction parameters are considered as part of the integral formulation.

Coupled with a water quality analysis model, the extended parameter optimization approach permits engineers to construct a sound water quality model. The method is applied to the benchmark system as illustrated in Figure 1 [9]. The GA-based optimization method has been demonstrated to excel over previous results by optimizing a complete set of water quality model parameters to enable accurate modeling of chemical reaction mechanism of any constituent, instead of just simulating Chlorine decay in the previous study. The competent GA-based approach has improved the fit between the model simulated and the field observed Chlorine residuals over more than 30 hours (as shown in Figure 2) and retained multiple optimal solutions obtained in a single optimization run [5].

Benefit Municipality

This technology has benefited many municipalities. A typical example can be seen from the modeling practice adopted by the City of Sidney Ohio, which proved a successful application of intelligent optimization modeling technology.

pipe and pump flows. The optimization methodology has been implemented as an off-the-shelf modeling tool for engineers.

With the integrated optimization modeling tool, a modeler is fully assisted during the calibration process, and various calibration tasks can be specified for a water distribution system according to data availability and model application requirements. Some tests on realistic benchmark problems [7] shows that the tool enables engineers to improve their project productivity more than 400% over conventional paradigms, and also lays a solid basis for constructing water quality models.
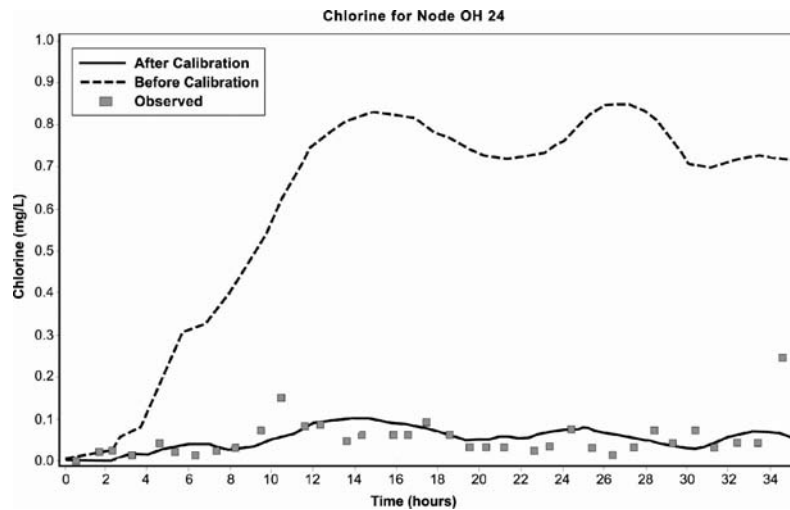
Figure 2: Comparison of water quality simulation results for the Oberlin supply zone of Harrisburg water system.

A hydraulic network model, constructed for the City of Sidney water distribution system, consists of 104 miles of water mains, some of which are well over a hundred years old and serve the original part of the system. The City intends to use the model for available fire flow analysis and a variety of many other applications. It is essential that the hydraulic model be able to accurately simulate the real system conditions. Model calibration is the critical step to achieve this goal.

To calibrate the model, Sidney's Public Utility Department collected the pressure data at twenty locations, along with the boundary conditions of the observed tank levels and pump operating status. The calibration proceeds by applying a well-integrated hydraulic simulation and genetic algorithm optimization tool in two phases including the systemic demand calibration to establish an extended period flow balance and hydraulic grade calibration under multiple loading conditions. The calibrated model assists the engineers to better understand the system hydraulics and conduct a wide range of system analysis tasks such as design of new City subdivision water supply systems, evaluation of new industrial users, and provision of flow capacity for firefighting to city engineers, architects and property developers.

Using the calibrated hydraulic model, the Fire Department is able to automatically predict the flow capacities for more than 1,400 hydrants in the city. This information is entered in a Fire House program and used to advise the firemen of the hydrant number as well as the physical location when a fire happens. Furthermore, the Fire Department categorized the hydrants according to the model predicted hydrant flows and color coded all the hydrants by following the guidelines of the National Fire Protection Association's (NFPA) Standards. The result is a Hydrant Tag System. As illustrated in Figure 3, not only does each hydrant have an identification number, but also each is color coded to its modeled fire flow. This is extremely beneficial to the Fire Department in that when a fire occurs, if the firemen see two hydrants available and one has a green band while the other has an orange band, they know that they can pull more water from the hydrant with the green band. This simple method has effectively increased their fire fighting ability. Finally, the hydrant bands are made of 3M Reflective Tape on aluminum bands. The material is made from the same material used in making "Stop" traffic signs. The hydrant bands are easily discernable at night. This conforms to the objective of the City in that all the fire hydrants will be re-modeled and re-tagged on a minimum of a 10 year cycle, which would account for any system changes.

Improve Utility Revenue

The GA-based parameter optimization not only facilitates the model calibration, but also assists engineers in detecting water losses. Identifying how much water is being lost from water networks and where the losses are occurring is of great importance to water utilities for operational and planning reasons. Water losses also impact their reputation. Water loss represents a major portion of non-revenue water (NRW) for a water system. According to the International Water Association (IWA)'s best practice recommendations for water balance studies, more than 65% of NRW arises from unauthorized water consumption, meter inaccuracies and leakages from the water mains source-to-taps infrastructure. Conventional water loss studies focus on the calculation of supply balances for water systems or their subsystems such as district meter areas.

Over the last decade, the concepts and methods developed for system wide water balance calculations have been based upon water assets' physical data and the statistics of pipe bursts, service connections and underground conditions.
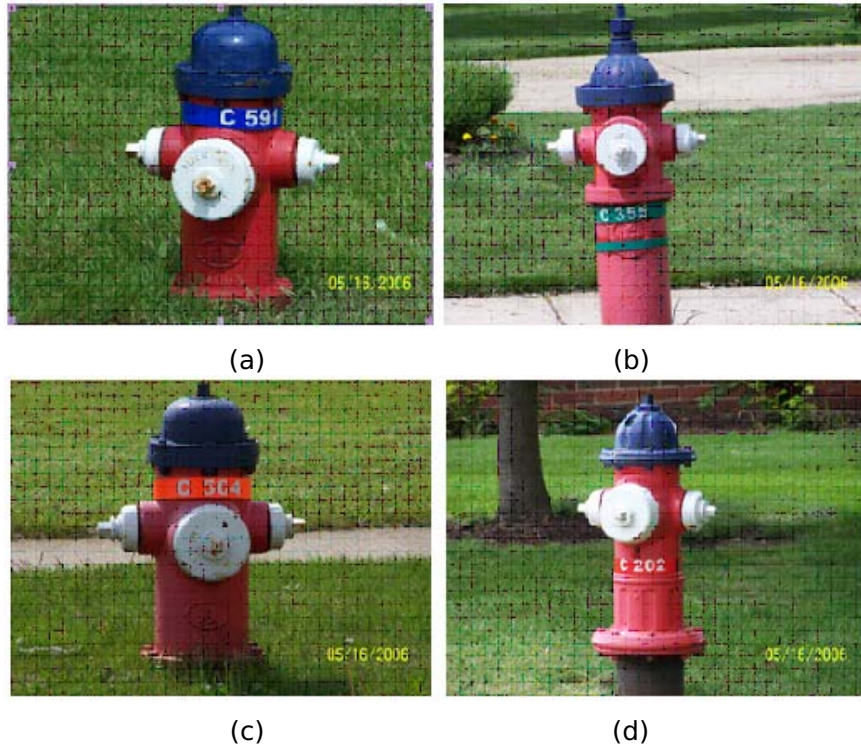
(a)   (b)

(c)   (d)

Figure 3: Hydrants color-coded for the supply capacity predicted by the GA-optimized model: (a) Blue hydrant >1500 gpm; (b) Green hydrant 1000 - 1500 gpm; (c) Orange hydrant 500 - 1,000gpm; (d) Red hydrant < 500 gpm.

Performance measures and indicators are used to support managerial approaches to minimize different components of water losses. Although leakage detection apparatus has been developed for detecting potential water loss or leakage from local water mains, it is time-consuming and costly for a leak detection crew to apply the current detection procedures to every main. Leaks are also becoming harder to find. One reason for this is pressure management. Not only is leakage being routinely suppressed by planned pressure reduction but the same reduction leads to less acoustic disturbance from those leaks. At the same time, sounding for leaks has become more difficult as ferrous water mains are replaced with less acoustically responsive plastic pipes.

By applying the parameter optimization approach, engineers are able to simultaneously quantify and locate water losses. Leakage detection is undertaken as a nonlinear optimization problem of identifying the correct demand of a hydraulic model such that the model accuracy is maximized by searching for the best-fit node demand. Water loss or leakage is the difference between the optimized demand and the recorded customer consumption. The study [6] has illustrated that the integrated optimization the tool successfully detects water loss for a district supply area in the UK. As shown in Figure 4, bigger the point, the greater the water loss is likely to occur. The results obtained show that the parameter optimization tool is effective at detecting water loss as compared with field observation. The application demonstrates the great potential of genetic algorithm optimization modeling for locating water loss hotspots, reducing the uncertainty of the water loss identification and thus improving operation revenues for water utilities.

Final Remarks

The genetic algorithm approach has been developed as robust, effective and efficient methods for constructing accurate network hydraulic and water quality models. These innovative methods have been implemented as a user-friendly off-the-shelf modeling tool. It proved to be powerful at optimizing model parameters, facilitating water loss or leakage detection, enhancing productivity and modeling accuracy so that computer models could be used for a variety of purposes with increased confidence, and thus benefit water companies, city public utilities and water engineering professionals around the world.

Bibliography

[1] Bentley Systems, Incorporated, 2006, "WaterCAD/WaterGEMS v8 Software Manual", Haestad Methods Solution Center, 27 Siemon Co Dr Suite200W, Watertown, CT06795, USA.

[2] Goldberg, D. E., Korb, B., & Deb, K., 1989, 'Messy genetic algorithms: Motivation, analysis, and first results', Complex Systems 3, 493-530.
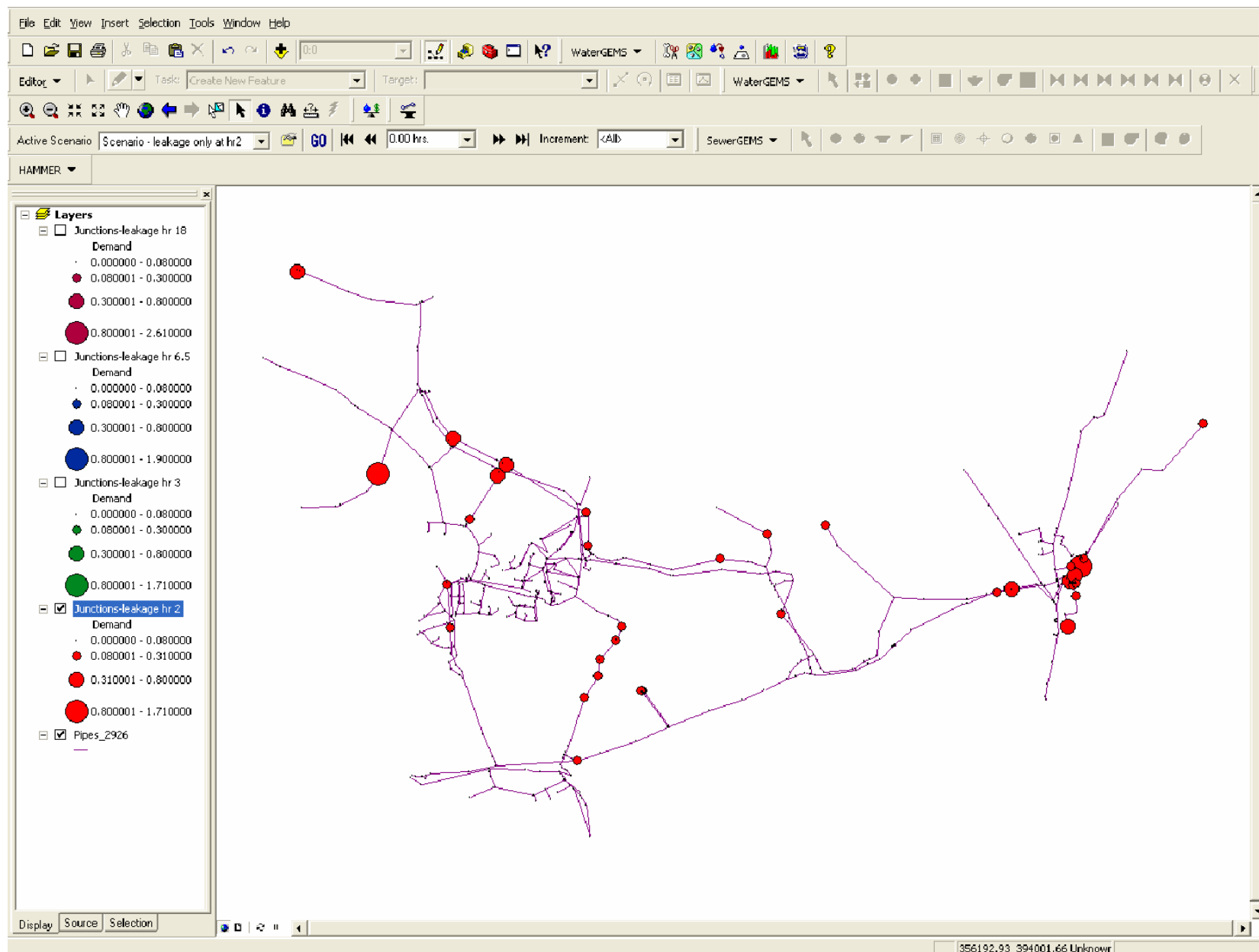
Figure 4: Leakage spots predicted by GA-optimized model for a water system in UK.

[3] Goldberg, D. E., Deb, K., Kargupta, H., & Harik G., 1993, 'Rapid, Accurate Optimization of Difficult Problems Using Fast Messy Genetic Algorithms', IlliGAL Report No. 93004, Illinois Genetic Algorithms Laboratory, University of Illinios at Urbana-Champaign, Urbana, IL 61801, USA.

[4] Haestad Methods, Inc. (2002) "WaterCAD v5 Software Manual", 34 Brookside Rd, Waterbury, CT06708, USA.

[5] Wu, Z. Y. (2006) "Optimal Calibration Method for Water Distribution Water Quality Model.", Journal of Environmental Science and Health Part A, Vol. 41, No.7, pp1363-1378.

[6] Wu, Z. Y. and Sage P. (2006) "Water Loss Detection via Genetic Algorithm Optimization-based Model Calibration" ASCE 8th Annual International Symposium on Water Distribution Systems Analysis, August 27-30, 2006, Cincinnati, Ohio, USA.

[7] Wu, Z. Y., Elio F. A. and Ernesto G. (2004) "Darwin Calibrator–Productivity and Model Quality for Large Water Systems", Journal of America Water Works Association, Vol. 96, No.10, pp27-34.

[8] Wu, Z. Y, Walski, T., Mankowski, R., Herrin G., Gurrieri R. and Tryby, M. (2002) "Calibrating Water Distribution Model Via Genetic Algorithms", in Proceedings of the AWWA IMTech Conference, April 16-19, Kansas City, MI.

[9] Vasconcelos, J.J.; Rossman, L.A.; Grayman, W.M.; Boulos, P.F.; Clark, R.M. (1997) "Kinetics of Chlorine Decay." Journal of America Water Works Association.

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Building bridges: the role of subfields in metaheuristics

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Very few fields in science are completely isolated; most disciplines have a fair amount of interdisciplinarity, even more so when the field is so settled that new results come only through interaction among one or several disciplines within a large field. This means that authors from initially separate fields end up converging, and creating new links in the coauthorship network. Besides, this implies a transfer of knowledge, so that authors initially focused in a single field (say, evolutionary computation) end up authoring papers in several other fields (such as, say, tabu search or scatter search) and thus extending their coauthorship ego-network and the coauthorship network in the field where both disciplines interact. This interaction also comes through horizontal applications (such as, for instance, scheduling), or broad problem areas, such as multiobjective optimization. Authors specialized on applications or on problem areas eventually coauthor papers in many different method areas, and thus build bridges that convey problem-solving (or, at least, paper-writing) expertise from a narrow field (such as evolutionary computation) to a broader one (such as metaheuristics).

Introduction

In this paper we will study the field of metaheuristics (MH) [6] as a whole, that is, we will consider Evolutionary Computation –EC– (whose coauthorship network we already studied in [3]), as well as other optimization strategies such as simulated annealing, swarm algorithms, and tabu search.

For the purposes of this study, we have grouped these techniques into three areas (shown in 1), namely, evolutionary methods (which include genetic algorithms and evolution strategies), non-evolutionary population-based methods –nECP– (such as scatter search and swarm algorithms), and local-search-based methods –LS– (tabu search, simulated annealing). It should be noted, however, that the boundaries between evolutionary and non-evolutionary population-based methods is not always clear; for example, it is typical for EC conferences and journals to accept papers about swarm algorithms, or scatter search. Thus, in our previous work [3, 2] we made the broader assumption that population-based methods are essentially 'evolutionary' for practical purposes. It is also true that some of these techniques –e.g., ant colony optimization– are usually more welcome than 'pure' evolutionary techniques in certain conferences. We have therefore found it reasonable to consider them as a subarea for the purposes of this work.

Thus, while these areas are in principle different, the NFL theorem [7] encourages us to test different search algorithms on a single problem. Furthermore, it is the case that areas such as memetic algorithms are largely built on hybridization principles. These facts along with those mentioned above, imply that there is a certain degree of overlap among all those areas, as is also shown in Figure 1, where circles are conventional and do not reflect the number of authors in each area.

In this paper we will study what the role of each field within the network is, and the importance and structure of the intersection among fields, as well as the macroscopic quantities that define the metaheuristics coauthorship network (hereafter SN, as in Social Network).
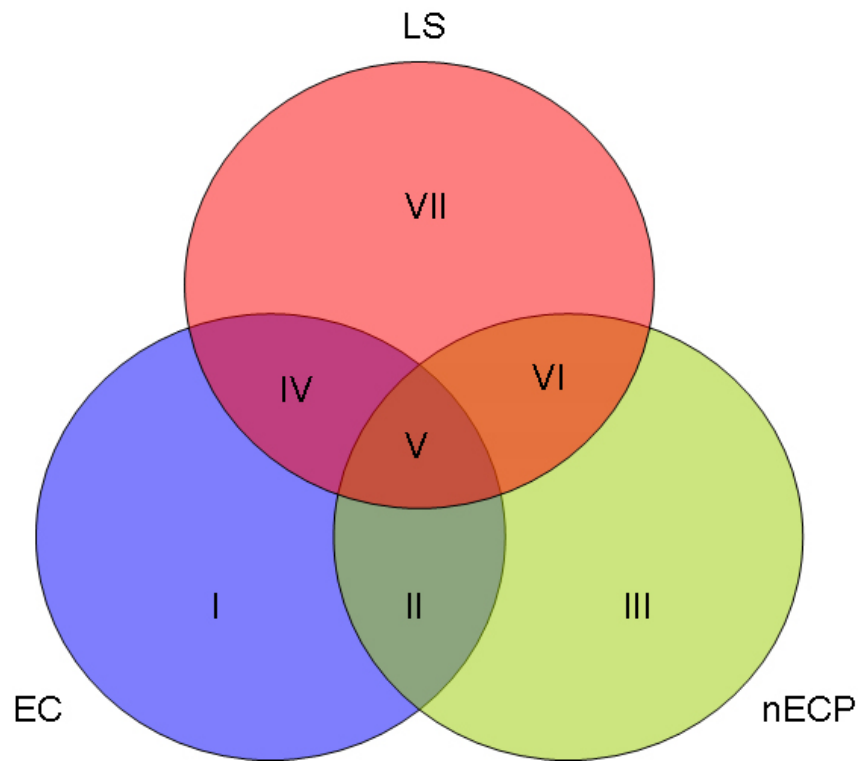
Figure 1: Scheme showing the three subfields that metaheuristics includes: evolutionary computation (EC), local search (LS) and swarm algorithms and scatter search (nECP). All fields have a certain amount of overlap, with the field labelled *V* being the intersection of all three

As we did in our previous work [3], we have used the DBLP –*Digital Bibliography & Library Project*– bibliography server, maintained by Michael Ley at the University of Trier. For each subarea, the initial search has been done using a set of appropriate keywords, and then expanded to include all authors of papers including those keywords. In all cases, a representative set of authors (kept constant in all cases) is used as the "seed" for starting the search[1]. Relevant conferences in the area were also included. Eventually, around 8000 authors were included in the graph[2].

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[1] For more details on this methodology please refer to [2]

[2] Versus 5,492 for the EC coauthorship network, which was, however, around 1.5 years prior

Macroscopic Network Properties

Macroscopic network properties are the first stab at analyzing any social network; they are easy to compute, and give an overall idea of its structure. Results for the metaheuristic SN are shown in table 1, alongside results for the EC* network (essentially comprising areas I to VI in Figure 1) presented in [3], and the NCSTRL (a computer science report repository) network, taken from [5]. In terms of discipline, it could be said that EC $\in$ MH $\in$ NCSTRL; a gradient of quantities should be, then, observed. In fact, some measures follow that trend. For example, we can see the increasing diameter from the smallest (EC) to the biggest (NCSTRL), and a decreasing clustering coefficient from EC (which, being a small field, should have a high degree of transitivity) to NCSTRL. The difference in this last quantity is, however, not very marked between EC and MH, due to the fact that EC –as defined in [3]– is the lion's share of the MH field. Notice nevertheless that there is a clear trend in the mean number of collaborators per author, and in the number of papers per author, approaching from above the mean of the Comp. Sci. field. Please note too that, even as EC is is the biggest component in the MH network, the diameter of MH is smaller that that of EC, which means that including authors from *outside* the EC field (resulting in the complete MH coauthorship graph) actually links authors within EC that were not previously linked. The clustering coefficient for MH is also smaller than for its three fields, taken separately, which also implies that their transitivity goes through the others.

The right hand side of Table 1 also shows the coarse-grain structure of the MH network. As anticipated before, "pure" EC (corresponding to regions I+II+IV+V in Figure 1) encompasses most of the network; nECP and LS are an order of magnitude smaller. Upon inspecting these quantities, the question of whether this is due to some bias in the database pops out immediately. It is true that a major metaheuristics conference (MIC) does not seem to be included in the DBLP. However, this is also the case for a very important EC conference, namely CEC, and a huge network still arises. It can be argued that there are many other EC conferences providing additional coverage of the EC network, and that this may not be the case for other subareas. Then again, this would tell us something important about the vitality and/or the publication practices of different subareas. We nevertheless believe that the size of the nECP and LS subnetworks is large enough to assume that they are a significant sample of the community.

	EC*	MH	NCSTRL	EC	nECP	LS
total authors	5492	7549	11994	6433	625	934
mean papers per author (PA)	2.9	2.75	2.6	2.73	1.83	1.88
mean authors per paper (AP)	2.56	2.62	2.22	2.58	2.84	2.68
collaborators per author (CA)	4.2	3.93	3.6	3.85	3.32	3.02
size of the giant component	3686	4415	6396	3674	82	134
as a percentage	67.1%	58%	57.2%	57%	13%	14%
2nd largest component	36	112	42	71	14	64
clustering coefficient (CC)	0.808	0.809	0.496	0.814	0.877	0.846
mean distance	6.1	9.80	9.7	8.41	2.70	4.05
diameter (maximum distance)	18	21	31	23	8	10

Table 1: Summary of results of the analysis of the subareas in the MH field. Two computer science collaboration networks: NCSTRL (taken from [5] and EC* [3]) are included for comparison purposes.

Taking a look at the other macroscopic properties of these subnetworks, we firstly observe that EC (in the more strict definition considered in this work) still amounts to most of the MH network. As such, many of the global properties have very similar values to those of the EC network. nECP and LS have however distinctive values, for example, a lower number of collaborators per author (CA). Differences in CA values among the three subareas can be shown to be significant using a Wilcoxson ranksum test [4]. Although some of the variation could be attributed here to lower coverage of a certain subarea in the database, notice that the CA value for nECP is notably higher than the CA value of LS, despite the fact that it seems to be a smaller network (hence more sensitive to under-coverage in the database).

In general, the higher value for CA in EC contributes to the existence of a clearly defined giant component. By contrast, the nECP and LS communities seem to be much more fragmented, with a relatively small largest component. Notice also that the nECP community seems to be much more compact, as the higher clustering coefficient and the smaller mean distance between authors indicate.

Let us look at the structure of these subgroups and their relations in the next section.

Subgroup relations within the MH coauthorship network

After having inspected the macroscopic properties of the networks, we turn our attention to their mesostructure and microstructure. This fine grain information can provide some hints on how the field is structured. First of all, the overlapping among different subareas that we mentioned before may have some impact in the way actors interact. Let us focus in the LS and nECP subareas (that is, everything but zone I in Figure 1), and more precisely in their largest components, depicted in Figure 2. If we consider the union of these two networks (something reasonable, since they naturally fit together in some conferences) and compute the resulting components, we observe a major change. First of all, the largest component of this combined network is essentially the same as in the LS network (it grows merely from 134 to 151 actors). The second largest component of this network comprises the largest component of the nECP network, enriched with many more actors: it grows from 82 to 141 actors.
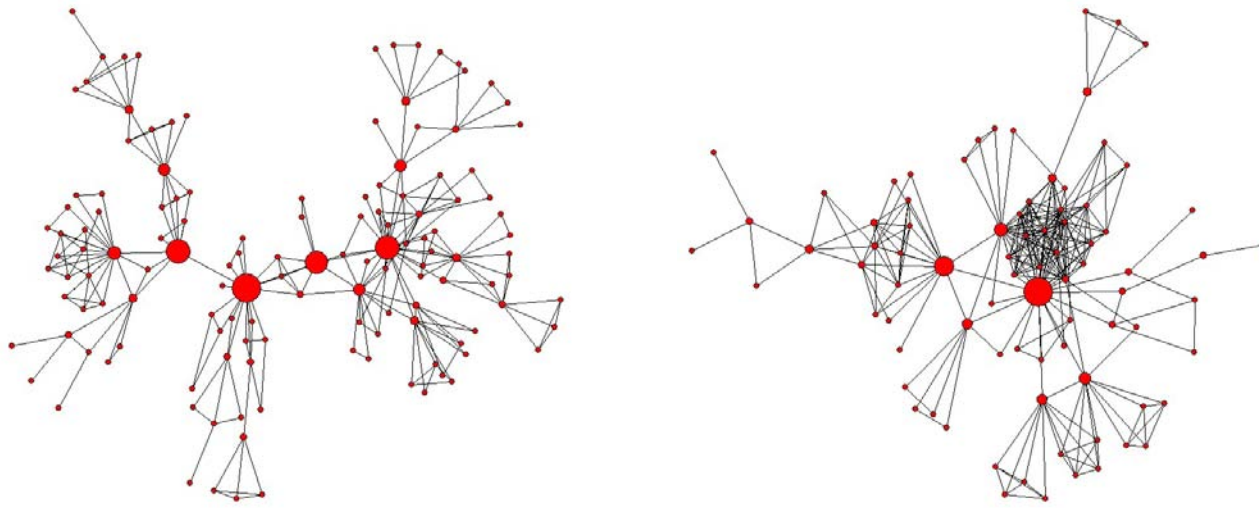
Figure 2: The largest components of the LS network (left) and the nECP network. Node sizes are proportional to betweenness centrality. The most central actors (those represented by the biggest circles) in each network are Fred Glover, and Marco Dorigo respectively.
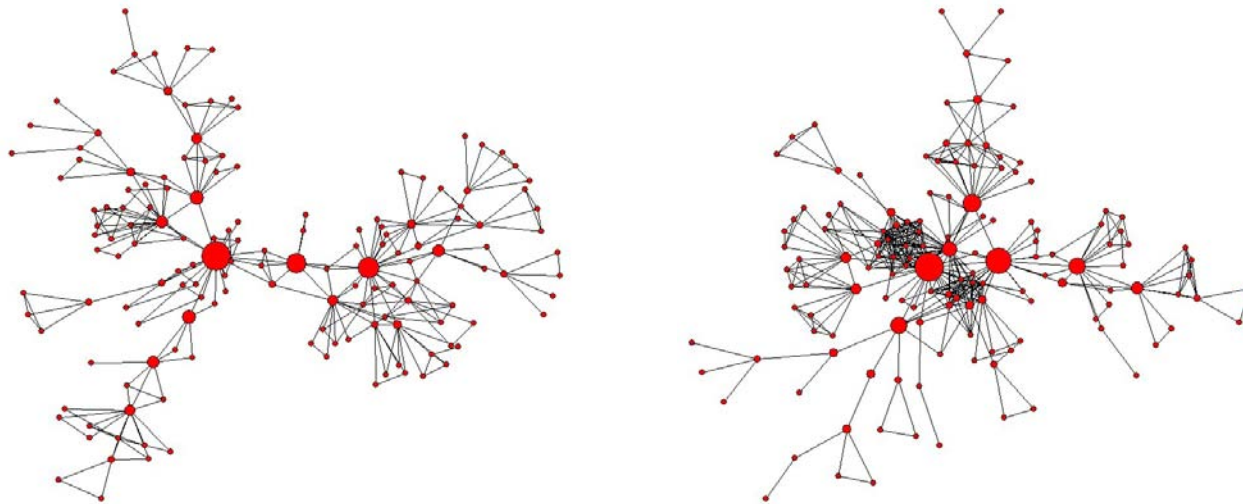

Figure 3: The two largest components in the combined LS/nECP network. Again, node sizes are proportional to betweenness centrality. The left component comprises people working on non-biologically motivated techniques, whereas the right component includes researchers working on ant colony optimization, and particle swarms.

Largest component		Second largest component		Global LS+EC+nECP network	
Fred Glover	7788	Marco Dorigo	4311	Marco Dorigo	444471
Michel Gendreau	5126	Thomas Stützle	3661	Thomas Stützle	293345
Michel Toulouse	4905	Martin Middendorf	2337	Oscar Cordón	247473
Erwin Pesch	2777	Holger H. Hoos	2063	Martin Middendorf	246075
Manuel Laguna	2377	Christian Blum	1962	Erwin Pesch	233502
Jacek Blazewicz	2315	Luca Maria Gambardella	1651	Michel Gendreau	214349
Rafael Martí	2040	Ian P. Gent	1193	Luca Maria Gambardella	214056
Philippe Galinier	1829	Guy Theraulaz	863	Fred Glover	122235
Teodor Gabriel Crainic	1622	Eric Bonabeau	777	Jacek Blazewicz	98859
Oscar Cordón	1558	Andrea Roli	679	Christian Blum	79352

Table 2: Ten most central actors in the two largest components of the combined LS/nECP network (right and middle). The rightmost group indicate the top ten among the previous two groups when the complete network is considered. The numerical values indicate each actor's betweenness in the corresponding component.

These two components are depicted in Figure 2, and the ten most central (according to betweenness) actors in each of them are shown in Table 2. It is interesting to see that the first component is mostly composed of people working on techniques without biological motivation (such as tabu search, variable neighborhood search or scatter search) whereas the second component mostly comprises people working on ant colony optimization, and particle swarms, together with people involved in local search strategies, and hybrids thereof. This latter aspects adds much connectivity to the components, and is responsible for its growth. The fact that these two groups stand as separate components (i.e., that there are apparently no direct links between them, at least within the subset of considered authors) is also somewhat interesting. It must be noted that these two groups are indeed linked in the giant component of the MH network, via EC authors, which accounts for the *bridge* that gives the title to this paper. Drilling down on this fact reveals an interesting mesostructure in the field. In principle, the nexus of all fields might be composed by the people whose work encompasses them all (zone V in Figure 1 above). This zone comprises around 100 authors, around 2% of the whole network, and unsurprisingly, is not completely connected: the biggest connected component in this zone, shown in Figure , includes 25 authors, among which we find six of the most central actors in the second largest component of the LS+nECP network, in Table 2 (right).

This last subnetwork is mostly composed by people working in ant optimization algorithms, including some of the most popular figures in the field: Dorigo, Middendorf, Gambardella, Stützle et al. (see also in Table 2 that the centrality of ACO-oriented people is much increased when the whole network is considered). But it also reveals the structure of the *bridge*; this small subnetwork, in fact, is the nexus to all the different fields that compose MH. Through Carlos Coello, for instance, this subgraph is linked to a whole lot of authors working in Mexico and Latin America, as well as figures in multiobjective optimization. Riccardo Poli links to a large groups of authors working on theoretical aspects. The branch leading to Ben Paechter links it to people working in scheduling applications, and the branch to Stützle links to many people working on stochastic local search and combinatorial optimization. A similar analysis can be done for most members of this component.
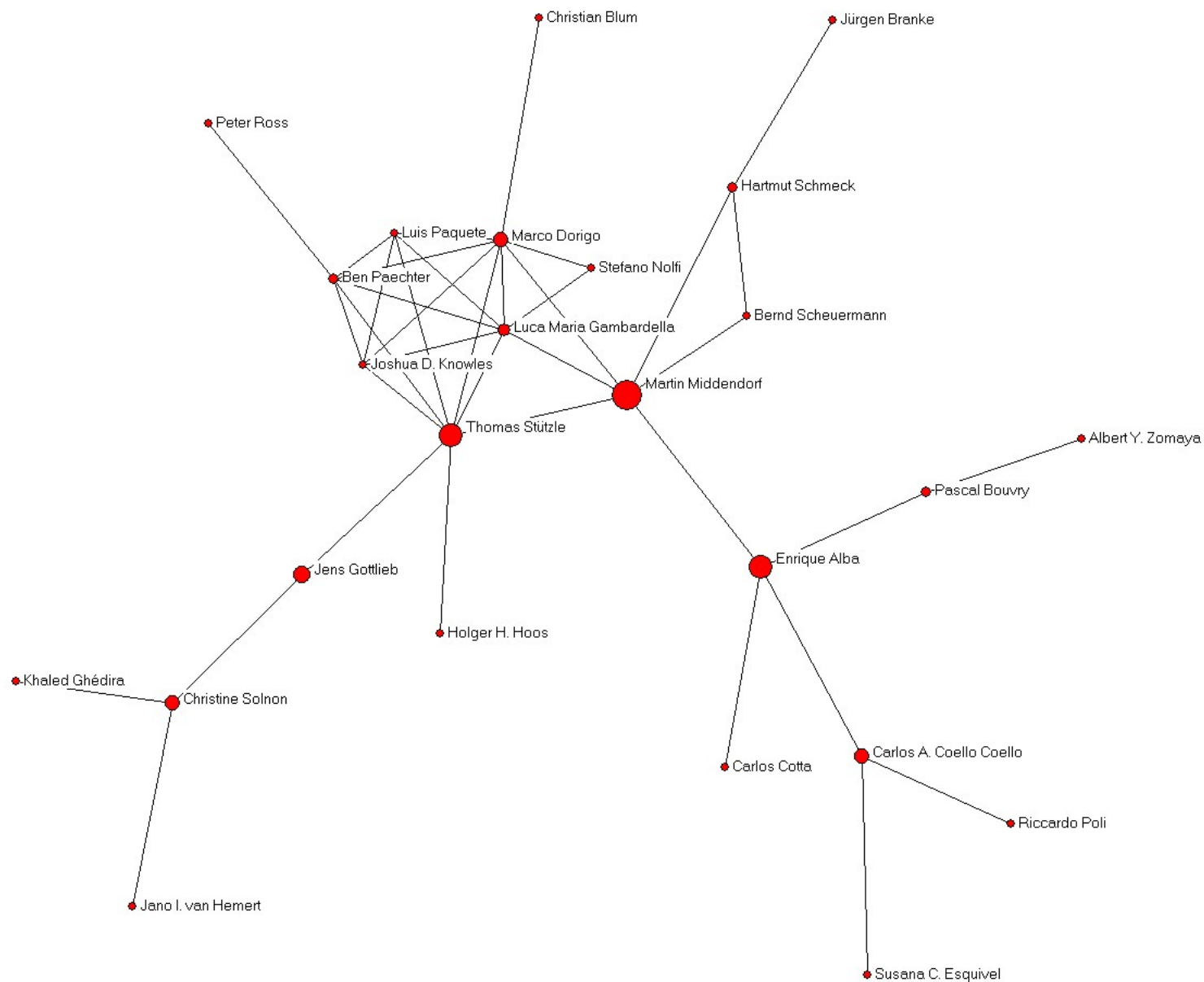
Figure 4: Biggest connected component in zone V (intersection of all MH subfields), which includes 25, or around $\frac{1}{4}$ actors in that zone. Node size corresponds to betweenness centrality (within that subnetwork). Note that Carlos Cotta is one of the authors of this paper.

Discussion and Conclusions

In this paper we have followed an admittedly quite ad-hoc methodology for researching how different subfields within a field integrate to form the main component of its coauthorship network, and we have found out that the nexus lies within people whose work comprises several subfields within the field, but not necessarily within the subfield that could be considered the most central, or even the most widely represented, within the field-at-large (which, in this case, would be evolutionary computation).

By examining each field separately, some of them together, and finally, the intersection of all subfields, we have shown that ant optimization algorithms, which are population-based algorithms, but, at the same time, tap the knowledge gleaned from diverse metaheuristic methods, lie at the *center* (coauthorship-graph-wise speaking) of metaheuristics. Some EC authors included in that area also serve as link to the EC field at large. From our point of view, this shows how interdisciplinary research not only produces new results within a mature field, but also helps to transfer knowledge from separate fields, spawning links, that is, collaborations, that ultimately benefit the whole field.

Acknowledgments

Bibliography

[1] Borgatti, S., Everett, M., and Freeman, L. (2002). *Ucinet for Windows: Software for Social Network Analysis*. Analytic Technologies, Harvard, MA.

[2] Cotta, C. and Merelo, J. (2005). The complex network of evolutionary computation authors: An initial study. Preprint available at `http://arxiv.org/abs/physics/0507196`.

[3] Cotta, C. and Merelo, J. (2006). The complex network of EC authors. *SIGEvolution*, 1(2):2–9.

[4] Lehmann, E. and D'Abrera, H. (1998). *Nonparametrics: Statistical Methods Based on Ranks*. Prentice-Hall, Englewood Cliffs, NJ.

[5] Newman, M. (2001). Scientific collaboration networks. I. Network construction and fundamental results. *Physical Review E*, 64(1):016131.

[6] Wikipedia (2006). Metaheuristic — wikipedia, the free encyclopedia. [Online; accessed 15-December-2006].

[7] Wolpert, D. H. and Macready, W. G. (1997). No free lunch theorems for optimization. *IEEE Transactions on Evolutionary Computation*, 1(1):67–82.

About the authors

Juan-Julián Merelo Guervós got a degree in theoretical physics from the University of Granada in 1988 and a PhD in Physics in 1994. He got interested in evolutionary algorithms more or less at the same time, having published papers on evolutionary optimization of neural networks and an evolutionary algorithm that plays MasterMind. He is currently an Associate Professor at the Computer Architecture Department of the University of Granada. (Photo: Elena Merelo Molina).

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Web Usage of the GP Bibliography

William B. Langdon, Mathematical and Biological Sciences, University of Essex, UK, wlangdon@essex.ac.uk

A recent upgrade to the Genetic Programming bibliography enables monitoring of its www usage. Downloads are dominated by automated software robotic agents (web bots), particularly Yahoo and other search engine spiders. These are very variable and cast doubt that some world wide web hits statistics relate to people. Some 62% of GP papers are on line. PDF is twice as common as postscript. On average papers in the cache can be downloaded in two seconds.

Introduction

Until recently, the genetic programming bibliography has been exclusively a description of GP papers, albeit in many cases it also contains links to those papers [4, 2]. While [6] and [3] looked at social links within the evolutionary computing community implied by co-authorship links, we take links to refer to URL world wide web links, principally URLs between the bibliography and ftp sites holding copies of GP papers. Some 62% of entries have links to the papers. More than half of the links can be freely accessed. However at present it is in the nature of the world wide web that links rapidly become "stale". I.e. no longer lead directly to the referenced paper. The bibliography does not have an automatic way of recognising broken links, instead the original URL is left *in situ* since 1) it indicates the paper did at some time appear on the web in electronic form and 2) it gives a hint where to start looking for it.

Prof. Banzhaf of Memorial University proposed that the bibliography be extended to cover papers as well as pointers to them. In October 2006 a disk cache of actively downloaded papers was added. Because of shortage of disk space at the current site and with the support of Memorial, the cache has been located at Memorial University of Newfoundland. This gives a three site, two time zones operation.

Major Components of the GP Bibliography

The major public interfaces are shown in Figure 1. References to new GP papers, articles, technical reports, PhD theses etc. are entered either by hand or via WBT.cgi (top). These are validated and then added to the central store (middle). Author WWW home pages (right) are used to disambiguate multiple spellings and word order of author names.

Every so often a new version of the bibliography is released. This includes traditional bibliography formats which can be downloaded for use in LATEXdocuments (BibTEX) and microsoft word (via Refer and EndNote or plain text) etc. At regular intervals the BibTEXversion is uploaded by the collection of computer science bibliographies, ensuring the GP literature is widely available. The collection also includes sophisticated search tools and RSS feeds.

This year we added graphs which show the connections between GP co-authors and co-editors.
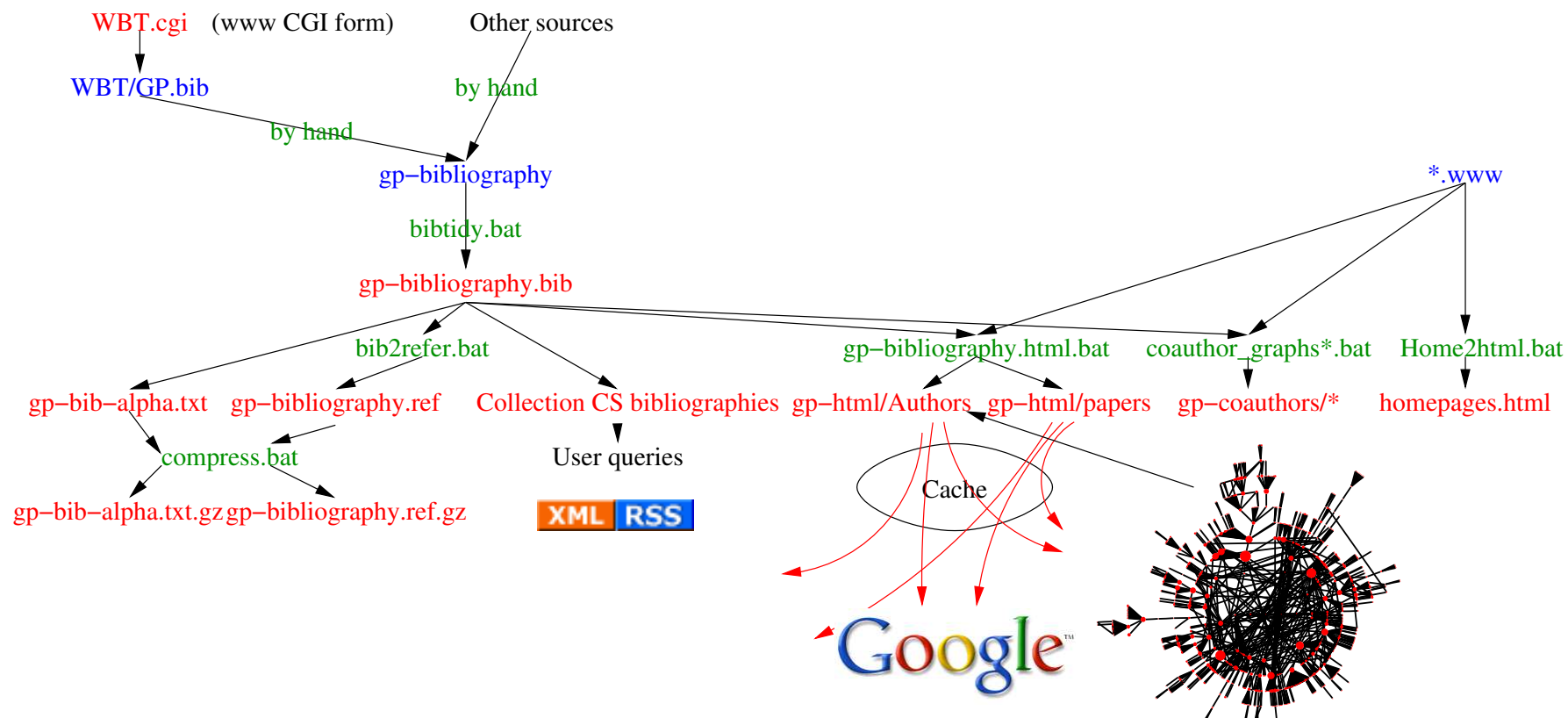
Figure 1: Major components of the GP bibliography. Internal files in blue. Conversion routines in green. B<small>IB</small>T<small>E</small>X can be submitted via http://www.cs.ucl.ac.uk/cgi-bin/external/W.Langdon/WBT.cgi or by email. Other public interfaces are available via both ftp and http and so can be Googled. The coauthor graphs can be searched by author name and link to their papers via gp-html. The collection of CS bibliographies includes sophisticated search and RSS feeds. The paper cache is inserted between gp-html and the Internet.
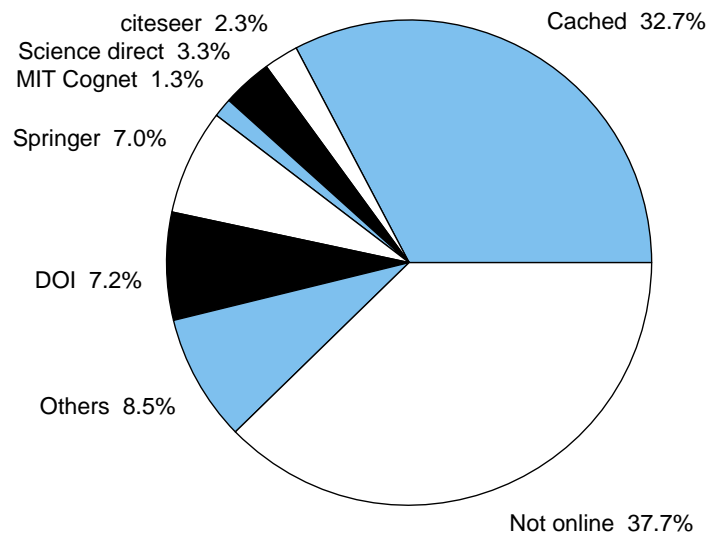
Figure 2: Locations of GP papers. DOI typically link to a publisher. Where there are multiple copies of a paper the clockwise segment takes precedence. I.e. a paper both in the cache and in citeseer is shown as cached.

From the world wide web the most visible components are the HTML files which contain references of all the GP papers produced by individual authors. There are 3269 such files, one per author. The same directory also contains one HTML file per paper (4546).

More than half of GP papers are available via the Internet. See Figure 2. Note that in some cases a payment may be required.

Addition of Cache

Where one or more URLs or a DOI (Digital Object Identifier) are known for the paper, this information is used to form a hyperlink between both types of HTML and the paper. (Cf. red curved arrows in Figure 1.) Previously, as far was possible, these linked directly to the paper. Now they pass via the cache at Memorial University. If the paper is in the cache, the paper is retrieved from it, otherwise the user's web browser attempts to obtain the paper from its original source. An offline process is used to refresh the cache.
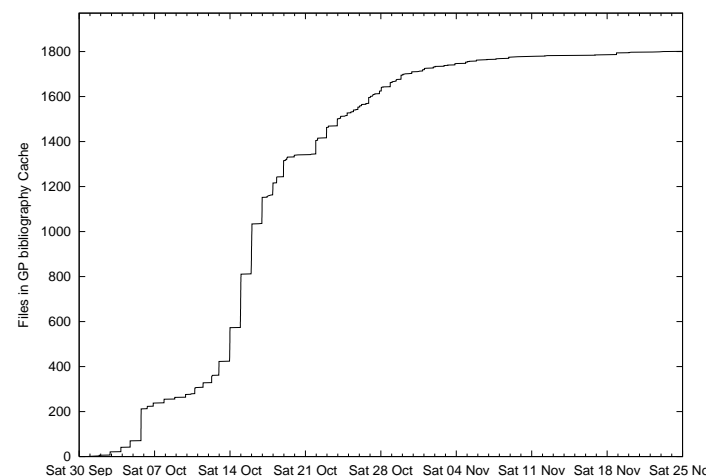
Figure 3: Number of papers in the GP bibliography cache

Performance of Cache

The cache has been operating since the end of September 2006. (see Figure 3). In principle it can store papers in any format, however only PDF and postscript are fully supported (see Figure 4).

The additional latency introduced by checking the cache first is small. It is within the normal variability of the www and so does not appear to be a particular problem. There is considerable variation in the available bandwidth. The median is 81 kbytes/S, giving a median load time of 2 seconds (for an average, 203 kbytes, paper). There is also considerable variation in paper size (min 1275 bytes, quartiles 106–439kb, max $>$ 10Mb).

From 1st October to 24 November (1307 hours) the system was used in all but 16 hours. Except for one case, all inactive periods were in the middle of the night. The longest break (6 hours) is known to be due to a network failure near Memorial. Others may be either due to Internet problems or low loading at night. The average (median) loading was 24 hits per hour but the peak load was 286 per hour.

Figure 4: PDF and Postscript files using a variety of compression types can be automatically saved in the cache.

Figure 5: Rate of paper downloads from GP-bibliography cache. Note increase after 1st November corresponds to increase in number of papers in cache (cf. Figure 3) and increase in requests (cf. Figure 7).

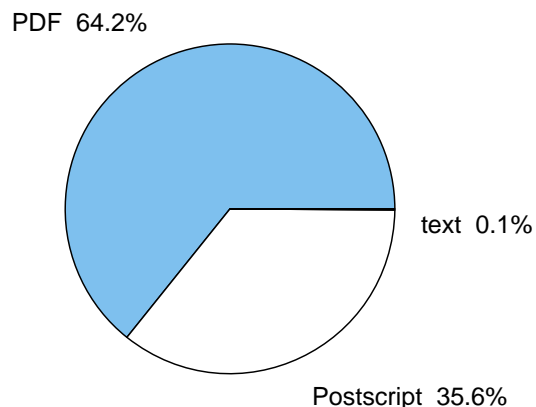Figure 5 plots downloads of GP papers from the cache. Note firstly cache hits are, like the total, highly variable. Secondly cache usage increases after 1st November. I.e. about the time the cache started to saturate (cf. Figure 3). From 4th November the median (21, quartiles 17 and 28, max 88) hit rate for the cache is about half that of the total over the same period (49 (37–74) max 264).

Web Bots

From Figure 6 it is clear that most traffic via the cache is automatically generated by computers interrogating other computers. Much of the chatter appears to be due to poor coding and often includes multiple attempts to read the same files. Figure 7 shows some robots have very different patterns of usage. Yahoo scans the bibliography more or less continuously, whilst others concentrate their activity. Some bursts of activity appear to be concentrated at weekend nights to avoid inconveniencing other users.

While the cache works well with standard user browsers, many of the 23 identified web crawlers generate bad requests. Between 20% and 100% of the requests generated by six spiders[1] are invalid.

Many cache misses appear to be due to web bots remembering for weeks broken links and re-testing them later, even when the problem is corrected in a new release of the bibliography. Overall 21% of requests appear invalid. However such requests should be dealt with efficiently and so impose no great overhead.

Initially two PHP scripts were provided to indicate the popular papers. I.e. those downloaded most frequently. However it became apparent that downloads by real people were totally dwarfed by robot activity and the PHP figures could not be relied upon and so have been removed.

Possible Hardware Upgrades

Shortly there should be sufficient disk space to hold the cache with the rest of the bibliography (which has a fast Internet connection). It is also hoped to increase the speed of the connection between the current location of the cache and the Internet.

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[1] IU_CSCI, Krichel, goo.ne.jp, unknown, hmdevlab and WGet
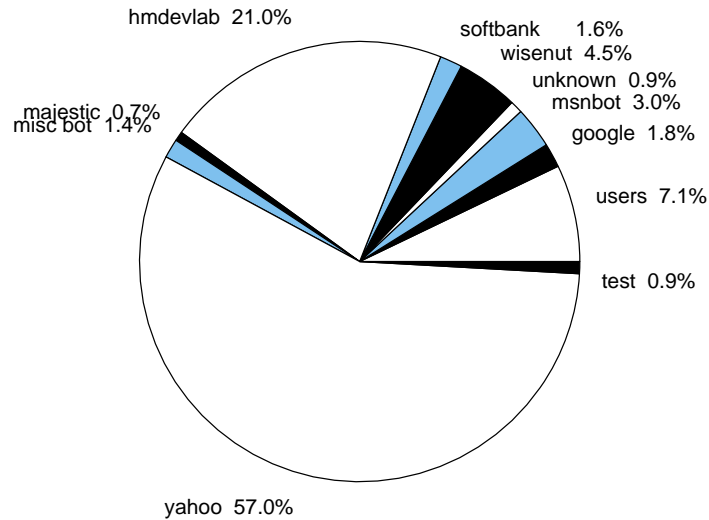
Figure 6: Usage of GP bibliography out links broken down by robot type. Note the small residual fraction (users) which may be due to people.
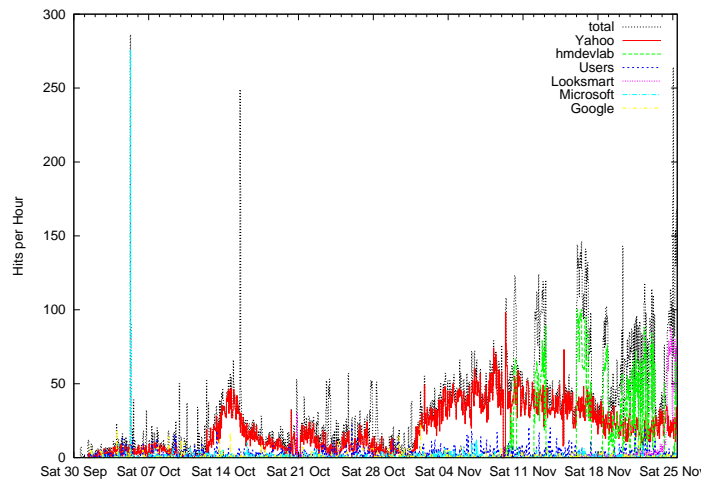
Figure 7: Usage of the GP bibliography links to papers (black) and broken down by major web bots and users (colour).

Maintenance of the GP bibliography

The bibliography relies on volunteers. It is built from a central BibTeX source which links to the Collection of Computer Science Bibliographies (Karlsruhe University) and other bibliographies. BibTeX is also converted to plain text, refer, thousands of web pages and online coauthorship graphs. This takes some time and so the GP bibliography proceeds in a series of incremental releases. (The BibTeX file itself has been through over 1200 revisions). Thus there may be a delay of several weeks between a new reference becoming available and it being fully integrated across all forms world wide.

Conclusions

To sum up. It seems obvious that for individual papers to have an impact they must be available and that now a days this means available via the Internet [5]. Yet some 40% of our papers are not (as far as is known) on line.

The world wide web is a very dynamic environment with many URLs having a short shelf life. While search tools such as Google are a great boon, tracking papers with broken URLs is time consuming and error prone. Hence, in practise, electronic versions of GP papers have been lost.

The GP bibliography tries to act as a central information store about all things GP. The cache, if long term support and maintenance is available, will extend its usefulness.

Acknowledgements

The GP Bibliography was started in 1995 from data supplied by John Koza and published in [1, Appendix F]. The bibliography has been greatly extended with the help of Steve Gustafson and many other GPers. The bibliography website [WWW] uses WebBibTeX which was written by Erol Sahin.

Bibliography

[1] John R. Koza. *Genetic Programming II: Automatic Discovery of Reusable Programs*. MIT Press, Cambridge Massachusetts, 1994.

[2] W. B. Langdon and S. Gustafson. Genetic programming and evolvable machines: Five years of reviews. *Genetic Programming and Evolvable Machines*, 6(2):221–228, June 2005.

[3] W. B. Langdon, R. Poli, and W. Banzhaf. An eigen analysis of the GP community. *Submitted*.

[4] William B. Langdon. A bibliography for genetic programming. In Peter J. Angeline and K. E. Kinnear, Jr., editors, *Advances in Genetic Programming 2*, appendix B, pages 507–532. MIT Press, 1996.

[5] Steve Lawrence. Free online availability substantially increases a paper's impact. *Nature*, 411(6837):521, 31 May 2001.

[6] Marco Tomassini, L. Luthi, M. Giacobini, and W. B. Langdon. The structure of the genetic programming collaboration network. *Genetic Programming and Evolvable Machines*, 2007. Online first.

About the author

Dr. W. B. Langdon is a research officer in Biological Sciences at Essex University. After he gained a PhD in genetic programming and data structures he worked at the University of Birmingham, the CWI, UCL and, most recently, in Essex University.

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GECCO-2007 Sets Submissions Record

A record number of submissions: 577. Previously 578 submissions were reported, however, a student withdrew a paper before the review process started, due to lack of funding to attend the conference.

GECCO-2007 involves 496 Program Committee Members, 21 Track Chairs, 14 Tracks (2 new).

Paper Submissions per Track

Ant Colony Optimization, Swarm Intelligence, and Artificial Immune Systems	59
Artificial Life, Evolutionary Robotics, Adaptive Behavior, Evolvable Hardware	25
Biological Applications	25
Coevolution	14
Estimation of Distribution Algorithms	34
Evolution Strategies, Evolutionary Programming	21
Evolutionary Multiobjective Optimization	44
Formal Theory	11
Generative and Developmental Systems	24
Genetic Algorithms	109
Genetic Programming	54
Genetics-Based Machine Learning and Learning Classifier Systems	28
Real World Applications	99
Search-Based Software Engineering	18

Distribution of Submissions per Track
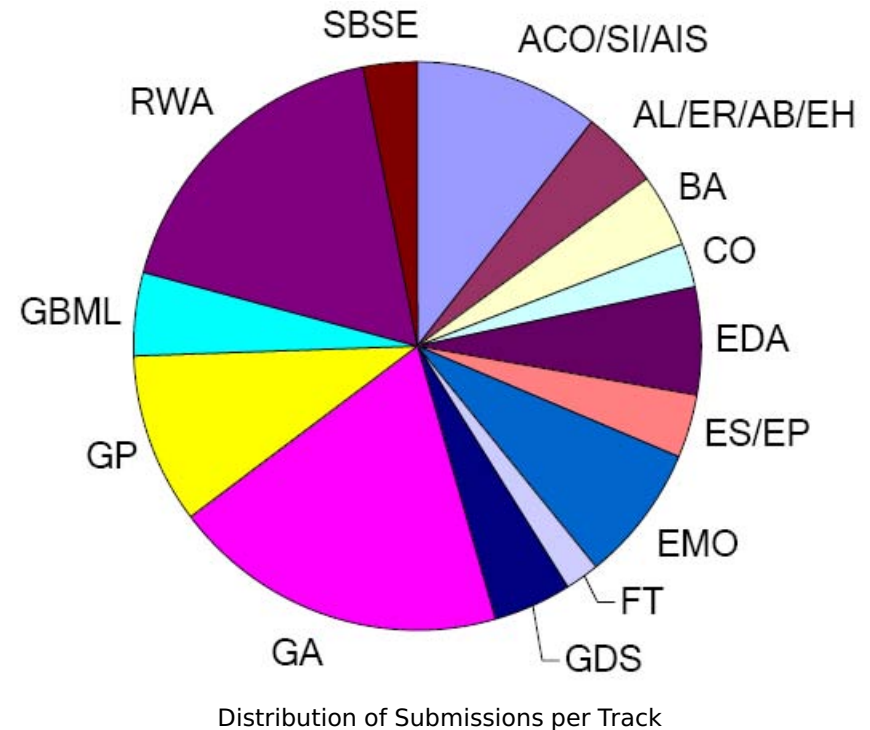
Submissions Still Open!

Workshops and Late Breaking Papers, and the Evolutionary Computation in Practice sessions are still accepting papers. Late Breaking Papers submissions close April 20. Check with workshop chairs for workshop paper deadlines.

Registration is Now Open

Registration is open at www.regonline.com/gecco2007 – When you register, be sure to enter your question to be considered for the Keynote Debate. Early registration rates ends on April 20.

Natural History Museum

The interior of the Natural History Museum.
The debate will take place here.

Keynote Debate

The Keynote Debate (Monday, 9 July) will be held in the Central Hall of the Natural History Museum.

We are grateful to the Science Department of the Natural History Museum (www.nhm.ac.uk) for their generous support of the Debate, and to Peter J. Bentley for his time and effort in securing this very special venue.
By all accounts, the Central Hall is **the** premiere special event venue in London. For more information about the debate please visit the GECCO-2007 keynotes page.

GECCO sessions will end early on Monday to allow people time to enjoy the Museum before it closes, have dinner, and return for the Debate.

Debate Format

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).

The GECCO-2007 workshops will be held on Saturday, July 7 and Sunday, July 8, 2007. The deadline for submissions is March 23, 2007. The proceedings will be published on CD-ROM, and distributed at the conference.

Particle Swarms: The Second Decade

Organized by Riccardo Poli, Jim Kennedy, Tim Blackwell, and Alex Freitas

Duration: Half Day

[summary | details]

Open-Source Software for Applied Genetic and Evolutionary Computation (SoftGEC)

Organized by Jason H. Moore

Duration: 2-hours

[summary | details]

Optimization by Building and Using Probabilistic Models

Organized by Kumara Sastry and Martin Pelikan.

Duration:Half Day

[summary | details]

Graduate Student Workshop

Organized by Anikó Ekárt

Duration:Full Day

[summary]

Undergraduate Student Workshop

Organized by Laurence Merkle, Clare Bates Congdon and Frank Moore.

Duration: Half Day

[summary]

Evolutionary Algorithms for Dynamic Optimization Problems

Organized by Peter A.N. Bosman and Jürgen Branke

Duration: Half Day

[summary | details]

Parallel Bioinspired Algorithms

Organized by Francisco Fernández and Erick Cantú-Paz

Duration: Half Day

[summary | details]

Learning Classifier Systems

Organized by Jaume Bacardit, Ester Bernadó-Mansilla, Martin V. Butz

Duration: Full Day

[summary | details]

Evolutionary Computation & Multi-Agent Systems and Simulation (ECoMASS)

Organized by Bill Rand, Sevan G. Ficici

Duration: Half Day

[summary | details]

Petroleum Applications of Evolutionary Computation

Organized by Alexandre Castellini, Charles Guthrie, David Wilkinson, Burak Yeten, Tina Yu

Duration: Half Day

[summary | details]

Defense Applications of Computational Intelligence

Organized by Frank Moore, Laurence D. Merkle, Stephen C. Upton

Duration: Full Day

[summary | details]

**The Evolution of Natural and Artificial Systems
Metaphors and Analogies in Single and Multi-Objective Problems**

Organized by Ami Moshaiov, Steven Hecht Orzack, Joshua Knowles

Duration: Half Day

Medical Applications of Genetic and Evolutionary Computation

Organized by Stephen L. Smith, Stefano Cagnoni

Duration: Half-day

[summary | details]

**FX-SBSE - Foundations and cross cutting issues in Search Based
Software Engineering**

Organized by Mark Harman, John Clark, Xin Yao, Joachim Wegener,
Christine McCulloch, Tanja Vos

Duration: Half-day

User-centric Evolutionary Computation

Organized by Iam Parmee

Duration: Half-day

[summary | details]

FD-ET: Future Directions in Evolutionary Testing

Organized by Mark Harman, John Clark, Xin Yao, Joachim Wegener,
Christine McCulloch, Tanja Vos

Duration: Half-day

$10,000 in Awards
The 2007 "Humies" for Human-Competitive Results

Homepage: www.human-competitive.org

Deadline May 28, 2007

Techniques of genetic and evolutionary computation are being increasingly applied to difficult real-world problems - often yielding results that are not merely interesting, but competitive with the work of creative and inventive humans. At the Genetic and Evolutionary Computation Conference (GECCO) in 2004, $5,000 in 2004 awards for human-competitive results were awarded for human-competitive results that had been produced by some form of genetic and evolutionary computation in the previous year. Similarly, at GECCO-2005 and GECCO-2006, $10,000 in awards were made for human-competitive results.

Entries are now being solicited for awards totaling $10,000 for 2007 awards for human-competitive results that have been produced by any form of genetic and evolutionary computation (including, but not limited to genetic algorithms, genetic programming, evolution strategies, evolutionary programming, learning classifier systems, grammatical evolution, gene expression programming, differential evolution, etc.) and that have been published in the open literature between May 29, 2006 (the deadline for the previous competition) and the deadline for 2007 entries. The competition will be held as part of the 2007 Genetic and Evolutionary Computation conference (GECCO) . This prize competition is based on published results. The publication may be a paper at the GECCO-2007 conference (i.e., regular paper, poster paper, or late-breaking paper), a paper published anywhere else in the open literature (e.g., another conference, journal, technical report, thesis, book, book chapter), or a paper in unchangeable final form that has been unconditionally accepted by a publication and is "in press" (that is, the entry must be identical to something that will be published imminently in precisely the form submitted for this competition, and not an intermediate or draft version that may be changed).

The publication must meet the usual standards of a scientific publication. In particular, the publication must clearly describe a problem, the methods used, and the results obtained and must contain sufficient information to enable the work described to be replicated by an independent person.

An automatically created result is considered "human-competitive" if it satisfies at least one of the eight criteria below.

(A) The result was patented as an invention in the past, is an improvement over a patented invention, or would qualify today as a patentable new invention.

(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.

(C) The result is equal to or better than a result that was placed into a database or archive of results maintained by an internationally recognized panel of scientific experts.

(D) The result is publishable in its own right as a new scientific result - independent of the fact that the result was mechanically created.

(E) The result is equal to or better than the most recent human-created solution to a long-standing problem for which there has been a succession of increasingly better human-created solutions.

(F) The result is equal to or better than a result that was considered an achievement in its field at the time it was first discovered.

(G) The result solves a problem of indisputable difficulty in its field.

(H) The result holds its own or wins a regulated competition involving human contestants (in the form of either live human players or human-written computer programs).

Contestants should note that a pervasive thread in most of the above eight criteria is the notion that the result meet an "arms length" standard - not a yardstick based on the opinion of the author, the opinion of people in the author's own institution, or the author's close associates or collaborators. "Arms length" may be established in numerous ways. For example, if the result is a solution to "a long-standing problem for which there has been a succession of increasingly better human-created solutions," it is clear that the scientific community (not the author, the author's own institution, or the author's close associates) has vetted the significance of the problem. Similarly, a problem's significance may be established if the result replicates or improves upon a scientific result published in a peer-reviewed scientific journal, replicates or improves upon a patented invention, or replicates or improves a result that was considered an achievement in its field at the time it was first discovered. Similarly, a problem's significance may be established if the result holds its own or wins a regulated competition involving live human players or human-written computer programs. In the absence of a clear "arms length" standards, contestants relying only on criterion G ("The result solves a problem of indisputable difficulty in its field") must make a clear and convincing case that the "difficulty" is "indisputable."

Presentations of entries will be made at the Genetic and Evolutionary Computation Conference (GECCO-2007). The awards and prizes will be announced and presented during the GECCO conference. The judging committee is in formation, but will include

- ■ Wolfgang Banzhaf
- ■ Erik Goodman
- ■ Riccardo Poli
- ■ John R. Koza
- ■ Darrell Whitley

Cash prizes of $5,000 (gold), $3,000 (silver), and bronze (either one prize of $2,000 or two prizes of $1,000) will be awarded for the best entries that satisfy the criteria for human-competitiveness. The awards will be divided equally among co-authors unless the authors specify a different division at the time of submission.

Instructions for Entering the 2007 "Humies" Awards

The deadline for entries is Monday May 28, 2007.

All entries are to be sent electronically to koza@stanford.edu.

An entry consists of one TEXT file and one or more PDF files.

The TEXT file must contain the following nine items. Please be very careful to include all required information. Contestants are alerted to the fact that items 6 and 9 are especially important and will be the main basis by which entries will be judged.

(1) the complete title of one (or more) paper(s) published in the open literature describing the work that the author claims describes a human-competitive result,

(2) the name, complete physical mailing address, e-mail address, and phone number of EACH author of EACH paper,

(3) the name of the corresponding author (i.e., the author to whom notices will be sent concerning the competition),

(4) the abstract of the paper(s),

(5) a list containing one or more of the eight letters (A, B, C, D, E, F, G, or H) that correspond to the criteria (see above) that the author claims that the work satisfies,

(6) a statement stating why the result satisfies the criteria that the contestant claims (see the examples below as a guide to aid in constructing this part of the submission),

(7) a full citation of the paper (that is, author names; publication date; name of journal, conference, technical report, thesis, book, or book chapter; name of editors, if applicable, of the journal or edited book; publisher name; publisher city; page numbers, if applicable);

(8) a statement either that "any prize money, if any, is to be divided equally among the co-authors" OR a specific percentage breakdown as to how the prize money, if any, is to be divided among the co-authors; and

(9) a statement stating why the judges should consider the entry as "best" in comparison to other entries that may also be "human-competitive."

The PDF file(s) are to contain the paper(s). The preferred method is that you send a separate PDF file for each of your paper(s) relating to your entry. Both the text file and the PDF file(s) for each entry will be permanently posted on a web page shortly after the deadline date for entries (for use by the judges and anyone interested) and will remain posted on the web as a permanent record of the competition. If your paper is available on your publisher's web site and your publisher specifically requires that your published paper may only appear only on your own personal page, the second non-preferred choice is that you send link(s) to a SEPARATE web page on your personal web site containing link(s) to the PDF file(s) of the paper(s) that constitute your entry. This separate web page is to contain nothing else, so the interested parties may quickly locate your paper(s). If you use this second-choice non-preferred option, you must also supply a link to a permanent web site maintained by your publisher where your specific paper may be viewed or purchased (that is, not a link merely to the publisher's main home page, but a link to the specific web page on the publisher's site containing your paper).

The judging committee will review all entries and identify a short list of approximately 8-10 finalists for presentation at the Genetic and Evolutionary Computation (GECCO) conference. Finalists will be notified by Monday June 25, 2007 by an e-mail to the corresponding author. Finalists must then make a 10-minute presentation to the judging committee at the GECCO conference. The presentations are currently scheduled for Monday July 9, 2007.

At the conference, there will be 10-minute oral presentations by the finalists before the judging committee. The presentations will be open to all conference attendees at a special session (2 hours). The oral presentation should primarily focus on why the result qualifies as being human-competitive and why the judges should consider the entry as "best" in comparison to other entries that may also be "human-competitive", since these are the two main standards by which entries will be judged by the judges. In this short presentation to the judges, a description of the details of the work itself should be decidedly secondary. In other words, the focus is on why the work being presented should win a prize – not an explanation or presentation of the work itself. The presenting author for each entry must register for the GECCO conference. After the oral presentations, the award committee will meet and consider the presentations. The awards are will announced at the Wednesday July 11, 2007, morning plenary session at the GECCO conference.

Finalists must submit a presentation in the form of a PowerPoint file or a PDF file by Wednesday July 4, 2007 by e-mail to koza@stanford.edu. These presentations will be added to the web page for the competition so that the judging committee (and anyone else interested) may preview the presentations.

Authors generally enter their own work; however, a person may make an entry on behalf of someone else; however, the entry must be complete in every respect and the entry must be made with the consent of the actual authors (one of whom must be willing to make a presentation of their work).

No prize may be awarded to anyone associated with any member of the judging committee (e.g., academic advisor, collaborator, co-author of the work involved) or the company donating the prize funds (i.e., Third Millennium On-Line Products Inc.).

Important Dates

May 28, 2007 (Monday) – Entries (consisting of one TEXT file and one or more PDF files) are due by e-mail.

June 25, 2007 (Monday) – Finalists will be notified by e-mail

July 4, 2007 (Wednesday) – Finalists must submit their presentation to (e.g., PowerPoint, PDF) for posting on competition web site.

July 9, 2007 (Monday) – Date for presentations before judging committee at public session at GECCO conference

July 11, 2007 (Wednesday) – Announcement of awards at morning plenary session of GECCO conference.

Example of a "statement" using criteria A & F

This is an illustrative example of a "statement" as to which an entry in the competition should be considered to be "human-competitive."

Harry Jones of The Brown Instrument Company of Philadelphia patented the PID-D2 controller topology in 1942. The PID topology was a significant invention in the field of control engineering and is in industrial use today. The PID-D2 controller was an improvement over the PID controller patented in 1939 by Callender and Stevenson. Because the genetically evolved controller has proportional, integrative, derivative, and second derivative blocks, it infringes the 1942 Jones patent.

Referring to the eight criteria for establishing that an automatically created result is competitive with a human-produced result, the rediscovery by genetic programming of the PID-D2 controller satisfies the following two of the eight criteria:

(A) The result was patented as an invention in the past, is an improvement over a patented invention, or would qualify today as a patentable new invention.

(F) The result is equal to or better than a result that was considered an achievement in its field at the time it was first discovered.

The rediscovery by genetic programming of the PID-D2 controller came about six decades after Jones received a patent for his invention. Nonetheless, the fact that the original human-designed version satisfied the Patent Office's criteria for patent-worthiness means that the genetically evolved duplicate would also have satisfied the Patent Office's criteria for patent-worthiness (if only it had arrived earlier than Jones' patent application).

Additional Example of a "Statement" Using Criteria B, D, E, F & G

This is another illustrative example of a "statement" as to which an entry in the competition should be considered to be "human-competitive."

The 1942 Ziegler-Nichols tuning rules for PID controllers were a significant development in the field of control engineering. These rules have been in widespread use since they were invented. The 1995 strm-Hgglund tuning rules were another significant development. They outperform the 1942 Ziegler-Nichols tuning rules on the industrially representative plants used by strm and Hgglund. strm and Hgglund developed their improved tuning rules by applying mathematical analysis, shrewdly chosen approximations, and considerable creative flair. The genetically evolved PID tuning rules are an improvement over the 1995 strm-Hgglund tuning rules. Referring to the eight criteria for establishing that an automatically created result is competitive with a human-produced result, the creation by genetic programming of improved tuning rules for PID controllers satisfies the following five of the eight criteria:

(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.

(E) The result is equal to or better than the most recent human-created solution to a long-standing problem for which there has been a succession of increasingly better human-created solutions.

(F) The result is equal to or better than a result that was considered an achievement in its field at the time it was first discovered.

(G) The result solves a problem of indisputable difficulty in its field.

Example of Something that May Be "Difficult," but not "Human-Competitive"

Although the solution produced by genetic and evolutionary computation for this problem is, in fact, better than a human-produced solution, that fact alone does not qualify the result as "human-competitive" under the eight criteria for human-competitiveness. For example, the fact that a problem appears in a college textbook is not alone sufficient to establish the problem's difficulty or importance or "human-competitiveness." A result is "human-competitive" if it satisfies one or more of the 8 criteria listed above. A textbook problem might, or might not, satisfy one or more of the eight criteria.

Introductory Tutorials

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, Martin V. Butz

Probabilistic Model-Building GAs, Martin Pelikan

Grammatical evolution, Conor Ryan

Coevolution, E. de Jong, K. Stanley, & P. Wiegand

Particle Swarm Optimization, A. Engelbrecht & X. Li

Beowulf Clusters for EC, A. Khoshla, P.K. Singh, & D.G. Chowdhary

Advanced Tutorials

GA Theory, Jonathan Rowe

GP Theory, R. Poli, B. Langdon

Representations for Evolutionary Algorithms, Franz Rothlauf

No Free Lunch, Darrell Whitley

Bioinformatics, Jason Moore

Human Competitive Results, John Koza

Evolutionary Multiobjective Optimization, E. Zitzler & K. Deb

Industrial Evolutionary Computation, A. Kordon, G. Smits, & Mark Kotanchek

Constraint Handling Techniques Used with EAs, Carlos Coello Coello

Statistics for EC, Mark Wineberg

Coevolution, S. Ficici, A. Bucci

Evolutionary Practical Optimisation, Kalyanmoy Deb

Computational Complexity and EC, T. Jansen, F. Neumann

Complex networks and EC, J.J. Merelo, Carlos Cotta

Particle Swarm Optimization for Fuzzy Models, Arun Khosla

Fitness Landscapes and Problem Hardness in EC, L. Vanneschi, S. Verel

An Information Perspective on EC, Yossi Borenstein

Specialized Techniques and Applications

Experimental Research in EC, M. Preuss, T.B. Beielstein

Symbolic Regression in GP, Maarten Keijzer

Evolutionary Neural Networks, Risto Miikkulainen

Quantum Computing, Lee Spector

Evolvable Hardware, Lukas Sekanina

Artificial Development, P. Haddow, G. Tufte

Evolutionary Games, Marco Tomassini

Evolutionary Design, Ian Parmee

Evolutionary Multiobjective Combinatorial Optimization, Rajeev Kumar

Evolving Neural Network Ensembles, Xin Yao

Evolutionary Computer Vision, Gustavo Olague

Bio-inspired Telecommunications, Muddassar Farooq

Distributed EC for Fun and Profit, J.J. Merelo, J.L.J. Laredo

Ant Colony Optimization and Local Search for the Probabilistic Traveling Salesman Problem

Doctoral Thesis by Leonora Bianchi

In this thesis we focus on Stochastic Combinatorial Optimization Problems (SCOPs), a wide class of combinatorial optimization problems under uncertainty, where part of the information about the problem data is unknown at the planning stage, but some knowledge about its probability distribution is assumed.

Optimization problems under uncertainty are complex and difficult, and often classical algorithmic approaches based on mathematical and dynamic programming are able to solve only very small problem instances. For this reason, in recent years metaheuristic algorithms such as Ant Colony Optimization, Evolutionary Computation, Simulated Annealing, Tabu Search and others, are emerging as successful alternatives to classical approaches.

In this thesis, metaheuristics that have been applied so far to SCOPs are introduced and the related literature is thoroughly reviewed. In particular, two properties of metaheuristics emerge from the survey: they are a valid alternative to exact classical methods for addressing real-sized SCOPs, and they are flexible, since they can be quite easily adapted to solve different SCOPs formulations, both static and dynamic. On the base of the current literature, we identify the following as the key open issues in solving SCOPs via metaheuristics: (1) the design and integration of ad hoc, fast and effective objective function approximations inside the optimization algorithm; (2) the estimation of the objective function by sampling when no closed-form expression for the objective function is available, and the study of methods to reduce the time complexity and noise inherent to this type of estimation; (3) the characterization of the efficiency of metaheuristic variants with respect to different levels of stochasticity in the problem instances.

We investigate the above issues by focusing in particular on a SCOP belonging to the class of vehicle routing problems: the Probabilistic Traveling Salesman Problem (PTSP). For the PTSP, we consider the Ant Colony Optimization metaheuristic and we design efficient local search algorithms that can enhance its performance. We obtain state-of-the-art algorithms, but we show that they are effective only for instances above a certain level of stochasticity, otherwise it is more convenient to solve the problem as if it were deterministic. The algorithmic variants based on an estimation of the objective function by sampling obtain worse results, but qualitatively have the same behavior of the algorithms based on the exact objective function, with respect to the level of stochasticity. Moreover, we show that the performance of algorithmic variants based on ad hoc approximations is strongly correlated with the absolute error of the approximation, and that the effect on local search of ad hoc approximations can be very degrading.

Finally, we briefly address another SCOP belonging to the class of vehicle routing problems: the Vehicle Routing Problem with Stochastic Demands (VRPSD). For this problem, we have implemented and tested several metaheuristics, and we have studied the impact of integrating in them different ad hoc approximations.

Leonora Bianchi received the M.Sc. degree in theoretical physics from the Università dell'Insubria, Como, Italy, in 1999 and the Ph.D. in applied sciences from the Universié Libre de Bruxelles, Brussels, Belgium, in 2006. She is currently Postdoctoral Researcher at the Dalle Molle Institute for Artificial Intelligence (IDSIA), Manno, Switzerland. Her research interests include combinatorial optimization, optimization under uncertainty, and metaheuristics.

Homepage: www.idsia.ch/ leo/

Learning Classifier Systems with Neural Network Representation

Doctoral Thesis by Tobias Anthony O'Hara

The effective combination of evolutionary computing and neural computing is a goal of machine learning. This thesis explores the use of a hybrid of an LCS (XCS) and neural computing (multilayer perceptron, MLP) called X-NCS. This version of XCS, where one or more MLPs are embedded in a rule, is more complex than standard XCS, and does not provide transparent rules, which is one of the key strengths of any LCS. Additionally, more rules are needed to solve a problem, which again causes longer run times than XCS. Set against this, is the ease which the embedded neural network can accept all types of input, i.e. binary, integer, real or ordinal in any combination, and that unlike in the traditional use of neural networks, where the neural network has to cover the whole of the problem space, like XCS, the rule itself determines what part of the problem space, or niche, it will cover without reference to external domain expertise. It then evolves simple neural networks to describe those niches. X-NCS also allows 'multiple action' rules to emerge such that rules are evolved which represent generalizations (in the LCS sense) over both the input and action space, whereas in standard XCS generalizations occur only in the input space.

The hybrid uses an MLP which allows local search by backpropagation (BP) [2] to complement the global exploration of the GA. This proved very successful despite the complexity of this hybrid. The local search is restricted to those rules that are active within the niches, so the overall computing effort spent on local search is comparatively small, and the local search process itself much simpler. In addition, local search provides solutions having better performance than standard X-NCS.

A variant on X-NCS was explored with each rule containing two networks [3]. In the first case the networks worked together, one providing the action and the other calculating the prediction of the rule. X-NCS contains MLPs, so using genetic operators, particularly crossover, is theoretically problematic because of the "competing conventions" problem and epistasis.

These considerations did not seem to affect the performance of single network rules, but with two close coupled networks per rule the results were disappointing. This was both because rules did not emerge with multiple prediction values, and also performance was unreliable. However in a continuous output problem, where the two networks worked in a quasi-independent way, using the dual network was successful.

In the other case of a dual network rule, the task of the second network was to anticipate the next state of the rule [1], so the two networks were working independently. This proved very successful. This methodology also caused the generality of the rule to decrease compared to rules without the second network, and performance to improve with harder problems. The effect of the second network seems to have an additional pressure against over-general rules. Interestingly using local search in combination with the second lookahead network rule worked well in spite of the extra complexity and the fact that the local learning was altering both networks.

Other work with the single network X-NCS, included function approximation tasks. A variant included a version of X-NCS using radial basis function networks (RBF) for the networks contained in each rule. For these tasks X-NCS with MLPs achieved better performance when one neural network emerged to cover the whole problem space, rather than through co-operative neural networks. With the RBF rules, by contrast, solutions contained composite networks. The performance of both types of network was similar. Again local learning was beneficial.

With X-NCS using MLPs the solution lies within all the connections of the network, rather than through explicit patterns, and this should mean that X-NCS is more robust and should perform well in those areas where the problem space is unknown and sparse. This to some extent offsets the lack of comprehension in the rules.

It should also perform well for those tasks where transparency is not required like in control situations where speed and accuracy are paramount. To a human interpreter, lack of transparency over a hundred rules is a serious barrier to using a system, however in a control system, especially using neural networks with fast computation time, a thousand rules or more is a trivial overhead, more so as the network logic can be readily embedded into chips.

Bibliography

[1] O'Hara, T. and Bull, L. (2005) Building Anticipations in an Accuracy-based Learning Classifier System by use of an Artificial Neural Network. In Proceedings of the IEEE Congress on Evolutionary Computation. IEEE Press, pp. 2046-2052.

[2] O'Hara, T. and Bull, L. (2006) Backpropagation in Accuracy-based Neural Learning Classifier Systems. In T. Kovacs, X. Llora and K. Takadama (eds) Advances in Learning Classifier Systems: Proceedings of the Fifth, Sixth and Seventh International Workshops on Learning Classifier Systems. Springer.

[3] O'Hara, T. and Bull, L. (2004) Prediction Calculation in Accuracy-based Neural Learning Classifier Systems. UWE Learning Classifier Systems Group Technical Report UWELCSG04-004. Available from http://www.cems.uwe.ac.uk/lcsg.

Toby O'Hara is a Visiting Lecturer at the University of the West of England Bristol. His research interests include using mathematical objects like neural networks in LCS specifically accuracy based ones like XCS.
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On the Evolution of Self-Organising Behaviours in a Swarm of Autonomous Robots

Doctoral Thesis by Vito Trianni

According to Hölldobler and Wilson, ants are the "dominatrices of the insect fauna", thanks to the fundamental role they play in the different ecosystems in which they live [8]. Moreover, ants feature a very complex colony organisation, which contrasts with the limited cognitive abilities that characterise the single individual. Not surprisingly, the principles that lay behind the organisation of an ant colony have been so far exploited by scientists and engineers in multiple domains, resulting in the development of robust optimisation algorithms (see, for example, [5]), and giving birth to the *swarm intelligence* research domain [1, 2]. Also robotics could benefit from this biologically-inspired approach, as demonstrated by the continuously growing interest for *swarm robotics* [4]. The subject of this thesis concerns exactly a swarm robotic system, that is, a system composed of a number of autonomous robots, which need to interact and to cooperate to achieve a common goal. In such a context, it is useful to allow for *self-organisation* while designing the different parts of the robotic system. Self-organisation can be defined as the emergence of order in a system as the result of interactions among the system components. It is often observed in biology, and in particular in animal societies, not limited to social insects like ants, bees or termites (see [3] for a review). From an engineering perspective, there are multiple advantages in designing a self-organising robotic system. Among these, it is worth mentioning that such a system is inherently robust to individual failures, as it is normally redundant in its constituent parts. It can adapt to varying environmental conditions and it can maintain its organisation notwithstanding certain external perturbations.

However, designing a self-organising behaviour for a group of simulated and/or real robots is not a trivial task. The classic approach to this design problem consists in two decomposition phases: (i) the behaviour of the system should be described as the result of interactions among individual behaviours, and (ii) the individual behaviours must be encoded into controllers. Both phases are complex because they attempt to decompose a process (the global behaviour or the individual one) that is a result of dynamical interactions among its sub-components (interactions among individuals or between individual actions and the environment).

These dynamic aspects are in general difficult to be predicted by the observer. In such a context, we believe that *Evolutionary Robotics* (ER) should be the methodology to be exploited [7, 10, 6]. ER bypasses the problem of decomposition at both the levels of finding the mechanisms that lead to the emergent global behaviour, and of implementing those mechanisms into a suitable controller. In fact, ER relies on the evaluation of the system as a whole, that is, on the emergence of the desired global behaviour starting from the definition of the individual controllers. Moreover, ER can exploit the richness of possible solutions offered by the dynamic robot-environment interactions, which may not be *a priori* evident to the experimenter [10].

In this thesis, we propose the use of ER techniques for the design of self-organising group behaviours, for both simulated and real robots. In this respect, the contribution brought forth in this thesis is twofold. From an engineering perspective, we propose an automatic methodology for synthesising complex behaviours in a robotic system. We believe that ER techniques should be used in order to obtain robust and efficient group behaviours based on self-organisation. The use of evolutionary techniques for the synthesis of group behaviours has been relatively modest up to now. Moreover, the synthesis of self-organising group behaviours through artificial evolution has been limited to simulated scenarios, and the few examples of collective evolutionary robotics research tested in reality rarely exploit self-organisation (see, for example, [11, 12, 9]). To the best of our knowledge, the experiments presented in this thesis constitute the first examples of self-organising behaviours synthesised through artificial evolution and successfully tested on real robots.

From a more theoretical point of view, the second important contribution brought forth by our experiments concerns the understanding of the basic principles underlying self-organising behaviours and collective intelligence. In our experimental work, the evolved behaviours are analysed in order to uncover the mechanisms that have led to a certain organisation. For example, we observed that an extremely simple rule at the individual level, which can be summarised as "do what the others are doing", is at the basis of a cooperative behaviour that proved to be very flexible and efficient.

Similarly, in other experiments we observed the evolution of simple communication forms that lead to an improved performance of the system, if compared to experimental setups that either ignore or handcraft the communication paradigm. Analysing the obtained results, we show that performance improvements are based on simple mechanisms, such as inhibition of signalling, that are counter-intuitive if decontextualised. Another experiment studies a collective decision-making process that emerges from complex robot-robot and robot-environment interactions. In this case, we show that there is no single robot that takes the lead and drives the decision-making process. Instead, the decision emerges as a result of a self-organising process.

In summary, the work presented in this thesis tries to mediate between two apparently opposed perspectives: engineering and cognitive science. The experiments presented and the results obtained contribute to the assessment of ER not only as a design tool, but also as a methodology for modelling and understanding intelligent adaptive behaviours.

Bibliography

[1] Beni, G. and Wang, J. 1989. Swarm intelligence. In *Proceedings of the Seventh Annual Meeting of the Robotics Society of Japan*. RSJ Press, Tokio, Japan, 425–428.

[2] Bonabeau, E., Dorigo, M., and Theraulaz, G. 1999. *Swarm Intelligence: From Natural to Artificial Systems*. Oxford University Press, New York, NY.

[3] Camazine, S., Deneubourg, J.-L., Franks, N., Sneyd, J., Theraulaz, G., and Bonabeau, E. 2001. *Self-Organization in Biological Systems*. Princeton University Press, Princeton, NJ.

[4] Dorigo, M. and Şahin, E. 2004. Swarm robotics — special issue editorial. *Autonomous Robots 17,* 2–3, 111–113.

[5] Dorigo, M. and Stützle, T. 2004. *Ant Colony Optimization*. MIT Press/Bradford Books, Cambridge, MA.

[6] Harvey, I., Di Paolo, E. A., Wood, R., Quinn, M., and Tuci, E. 2005. Evolutionary robotics: A new scientific tool for studying cognition. *Artificial Life 11,* 1–2, 79–98.

[7] Harvey, I., Husbands, P., and Cliff, D. 1993. Issues in evolutionary robotics. In *From Animals to Animats 2. Proceedings of the Second*

International Conference on Simulation of Adaptive Behavior (SAB 92), J.-A. Meyer, H. Roitblat, and S. W. Wilson, Eds. MIT Press, Cambridge, MA, 364–373.

[8] Hölldobler, B. and Wilson, E. O. 1990. *The Ants*. Belknap Press, Harvard University Press, Cambridge, MA.

[9] Nelson, A. L., Grant, E., and Henderson, T. C. 2004. Evolution of neural controllers for competitive game playing with teams of mobile robots. *Robotics and Autonomous Systems 46*, 135–150.

[10] Nolfi, S. and Floreano, D. 2000. *Evolutionary Robotics: The Biology, Intelligence, and Technology of Self-Organizing Machines*. MIT Press/Bradford Books, Cambridge, MA.

[11] Quinn, M., Smith, L., Mayley, G., and Husbands, P. 2003. Evolving controllers for a homogeneous system of physical robots: Structured cooperation with minimal sensors. *Philosophical Transactions of the Royal Society of London, Series A: Mathematical, Physical and Engineering Sciences 361*, 2321–2344.

[12] Watson, R. A., Ficici, S. G., and Pollack, J. B. 1999. Embodied evolution: embodying an evolutionary algorithm in a population of robots. In *Proceedings of the 1999 Congress on Evolutionary Computation (CEC 99)*, P. J. Angeline, Z. Michalewicz, M. Schoenauer, X. Yao, and A. Zalzala, Eds. IEEE Press, Piscataway, NJ, 335–342.

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Forthcoming Papers

Evolutionary Computation 15(1)

- **Covariance Matrix Adaptation for Multi-objective Optimization**, Christian Igel, Nikolaus Hansen, and Stefan Roth, pp 1–30

- **On Replacement Strategies in Steady State Evolutionary Algorithms**, Jim Smith, pp 31–62

- **A Monotonic Archive for Pareto-Coevolution**, Edwin D. de Jong, pp 63–96

- **Understanding the Biases of Generalised Recombination: Part II**, Riccardo Poli and Christopher R. Stephens, pp 67–133

Genetic Programming and Evolvable Machines 8(1)

- **Evolutionary morphogenesis for multi-cellular systems**, D. Roggen, D. Federici and D. Floreano

- **The structure of the genetic programming collaboration network**, M. Tomassini, L. Luthi, M. Giacobini and W.B. Langdon

- **Problem solution sustenance in XCS: Markov chain analysis of niche support distributions and the impact on computational complexity**, M.V. Butz, D.E. Goldberg, P.L. Lanzi and K. Sastry

- **Genetic programming incorporating biased mutation for evolution and adaptation of Snakebot**, I. Tanev

- **Review of Engelbrecht's Fundamentals of Computational Swarm Intelligence**, J. Kennedy

- **Review of Cellular Automaton Modeling of Biological Pattern Formation: Characterization, Applications, and Analysis**, T. Lundh

Calls and Calendar

April 2007

IEEE Symposium Series on Computational Intelligence 2007

April 1-5, 2007, Honolulu, Hawaii.

Homepage: WWW

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)

EuroGP 2007
Tenth European conference on Genetic Programming

April 11-13, 2007, Valencia, Spain.

Homepage: WWW

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.

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

April 11-13, 2007, Valencia, Spain.

Homepage: WWW

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, Evo-COP 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

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.

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

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

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.

GECCO-2007 Late Breaking Papers

Held as a part of GECCO-2007 July 7-11, 2007, London, England.

Homepage: WWW

Deadline April 20, 2007

Papers describing late-breaking developments in the field of genetic and evolutionary computation are being solicited for presentation at the 2007 Genetic and Evolutionary Computation Conference (GECCO-2007) to be held 7-11 July 2007 (Saturday-Wednesday), at University College London, Gower Street in London, UK, and inclusion in a special CD-ROM to be distributed to all attendees of the conference.

Submissions must be in camera-ready format, no longer than eight (8) pages in length.

Selection Process

Late-breaking papers will be briefly examined for relevance and minimum standards of acceptability, but will not be peer reviewed in detail. Paper acceptance decisions will be made as soon as possible after receipt of the submission, until the 20 April 2007 deadline.

Note that at least one author of each accepted Late Breaking Paper must register for the conference by 20 April 2007, must attend the conference and present the paper at the scheduled time. Papers with no authors registered by the deadline will not appear in the Late-Breaking Papers section of the CD-ROM.

Authors will individually retain copyright (and all other rights) to their late-breaking papers and should feel free to submit them (either before or after the above deadline) for publication by other conferences or journals. However, authors must submit an ACM permission to publish form.

Submission Procedure

Because the late-breaking papers are published on a very tight time schedule, please be very attentive in carrying out the requirements for submission by 20 April 2007.

1. Upload your camera-ready electronic file (PDF) formatted to comply with ACM format requirements, and no longer than EIGHT (8) pages in length, to the submissions website by 20 April 2007. No paper-based submissions can be accepted. The URL for the Submission Site is: https://ssl.linklings.net/conferences/gecco/

   Late-Breaking Papers must comply with ACM format requirements, must use ACM Templates for native files (Microsoft Word, LaTex, or Adobe Framemaker) and must use ACM PDF Settings. ACM templates: www.acm.org/sigs/pubs/proceed/template.html

2. Agree to the "permission to publish" agreement on the submission website. Authors will individually retain copyright (and all other rights) to their late-breaking papers.

3. If your paper is accepted, fill out and fax by the 20 April 2007 deadline, the appropriate ACM permission to publish forms.

4. Register at least one author of the Late-Breaking Paper for the conference by the deadline for camera-ready papers (20 April 2007). At least one author must register for and attend the conference, and present the paper at the scheduled time. See the registration page for more information.

Deadline Extensions

Please be very careful about formatting your paper (and testing it, by printing it out) because of the very tight time schedule. No paper-based submissions can be accepted. No deadline extensions will be granted. Since there will be no opportunity for revisions, authors should be especially careful that their original submission is fully compliant with all requirements above.

Producing a PDF Version of Your Manuscript

PDF documents can be produced either by using commercial software available from Adobe or by using free conversion tools for Windows or the ps2pdf and pdflatex utilities under Unix/Linux. In addition, recent versions of MS Word may be able to save directly in PDF format. Please, preview your PDF file with acrobat reader to check that all the fonts and figures are properly reproduced before submitting the manuscript.

For more information, contact Late Breaking Papers Chair Peter A.N. Bosman.

Defense Applications of Computational Intelligence Workshop

Held as a part of GECCO-2007 July 7-11, 2007, London, England.

Homepage: WWW

Deadline March 23, 2007

Organizers

Stephen C. Upton (Referentia Systems, Inc.)

Laurence D. Merkle (Rose-Hulman Institute of Technology)

Frank W. Moore (University of Alaska Anchorage)

Within the last decade, the use of computational intelligence techniques for solving challenging defense related problems has achieved widespread acceptance. The genesis of this interest lies in the fact that repeated attempts of using more traditional techniques have left many important problems unsolved, and in some cases, not addressed. Additionally, new problems have emerged that are difficult to tackle with conventional methods, since social, cultural, and human behavioral factors tend to be at the heart of these new types of problems (e.g., within the broad areas of the global war on terrorism, homeland security, and force protection).

The purpose of this full-day workshop is to introduce and discuss current and ongoing efforts in using computational intelligence techniques in attacking and solving defense-related problems, with a focus on genetic and evolutionary computation techniques. These include, but are not limited to, the following:

- Genetic and evolutionary techniques in the design of military systems and sub-systems.

- Genetic and evolutionary techniques for logistics and scheduling of military operations.

- Genetic and evolutionary algorithms (GEAs) in strategic planning and tactical decision making.

- Multi-objective GEAs for examining tradeoffs in military, security, and counter-terrorism procedures.

- Automated discovery of tactics and procedures for site security, force protection, and consequence management.

- Genetics-based knowledge discovery and data mining of large databases used to recognize patterns of individual behavior.

- Co-evolution for simultaneous red-blue team strategic-tactical simulation and gaming.

- Other computational intelligence techniques for applications in the areas listed above.

The workshop invites completed or ongoing work in using computational intelligence techniques for addressing these or any other applications to defense related problems. It is intended to encourage communication between active researchers and practitioners to better understand the current scope of efforts within this domain. The ultimate goal is to understand, discuss, and help set future directions for computational intelligence in defense problems.

For additional information, please visit the workshop web site.

Evolutionary Algorithms for Dynamic Optimization Problems (EvoDOP-2007)
Held as a part of GECCO-2007 July 7-11, 2007, London, England.
Homepage: WWW
Deadline March 10, 2007
Many real-world optimization problems are dynamic. New jobs are to be added to a schedule, the quality of the raw material may be changing, new orders have to be included into the routing of a fleet of vehicles, etc. In such cases, when the problem changes over the course of the optimization, the purpose of the optimization algorithm changes from finding an optimal solution to being able to continuously track the movement of the optimum through time. Since in a sense natural evolution is a process of continuous adaptation, it seems straightforward to consider evolutionary algorithms as appropriate candidates for dynamic optimization problems.

The goal of this workshop is to foster interest in the important subject of evolutionary algorithms for dynamic optimization problems, get together the researchers working on this topic, and to discuss recent trends in the area.

Submission Guidelines

To submit your contribution, send your ACM-formatted paper in Postscript or PDF by e-mail to Peter A.N. Bosman at Peter.Bosman@cwi.nl. Papers should not exceed the limit of 8 pages and must meet with deadline of the workshop (see important dates for details). In case you can not submit your paper electronically, please contact one of the workshop chairs.

Please note that all contributions must abide ACM formatting rules because all contributions will be on the conference CD as well as in the ACM digital library. Failing to comply with the ACM formatting rules will result in exclusion from the proceedings. For formatting details, visit http://www.sigevo.org/gecco-2007/papers.html.

Workshop on Medical Applications of Genetic and Evolutionary Computation (MEDGEC)
Held as a part of GECCO-2007 July 7-11, 2007, London, England.
Homepage: WWW
Deadline 1 March 2007
We are pleased to invite you to submit a paper to MedGEC 2007, the GECCO Workshop on Medical Applications of Genetic and Evolutionary Computation.
Full details can be found at the MedGEC Web site at [WWW]
Subjects will include (but are not limited to) applications of GEC to:

- Medical imaging

- Medical signal processing

- Clinical diagnosis and therapy

- Data mining medical data and records

- Clinical expert systems

- Modeling and simulation of medical processes

The Workshop has two main aims: (i) to provide delegates with examples of the current state of the art of applications of GEC to medicine; (ii) to provide a forum in which researchers can discuss and exchange ideas, support and advise each other in theory and practice.

2nd Workshop on Parallel Bioinspired Algorithms

Held as a part of GECCO-2007 July 7-11, 2007, London, England.

Homepage: WWW

Deadline March 23, 2007

The application of Bioinspired Algorithm to solving difficult problems has shown that they need high computation power and communications technology. During the last few years researchers have tried to embody parallelism into this kind of algorithms, so that a very interesting research area has emerged and matured. The combination of Bioinspired algorithms and Parallel systems has allowed researchers to develop new algorithms, and also solve hard problems. Nevertheless any effort for increasing the performances in this kind of meta heuristics would be very welcome by the community. Grid and P2P technologies could thus be of great interest for improving performances obtained when using Bioinspired Algorithms. The topics of interest include (but are not limited to):

- Parallel Evolutionary Algorithms (PEAs), including but not limited to Genetic Algorithms, Genetic Programming, Evolutionary Programming, and Evolution Strategies.

- Other biologically inspired parallel algorithms: Ant Colonies, Immune Systems, Artificial Life, Cultural Algorithms.

- P2P and Grid implementation of PEAs.

- Fault tolerant implementations of PEAs.

- Analytical modeling of PEAs.

- Performance evaluation of PEAs.

- Improvement in system performance through optimization and tuning.

- Case studies showing the role of PEAs when solving hard real-life problems.

Submission Guidelines

Manuscripts should be prepared according to the standard format of regular papers specified in GECCO 2007 and be restricted to a maximum of 8 pages.

2007 Conference on Unconventional Computing

July 12-14 2007, Bristol, United Kingdom.

Homepage: WWW

Deadline May 5, 2007

Unconventional computing is the quest for groundbreaking new algorithms and physical implementations of novel and ultimately — compared to classical approaches – more powerful computing paradigms and machines. This event will bring together work that focuses on non-traditional theoretical constructions, experimental prototypes, and genuine implementations of non-classical computing devices. A further goal is to revisit existing approaches in unconventional computing, to provide scientists and engineers with blueprints of realisable computing devices, and to take a critical glance at the design of novel and emergent computing systems to point out failures and shortcomings of both theoretical and experimental approaches.

We aim to encourage interdisciplinary interactions in emergent computing paradigms and architectures; develop an interface between computer science, biology, mathematics, chemistry, electronic engineering and physics; create new research communities of collaboration in non-classical computation; promote the transfer of knowledge and encourage new collaborative research activity in unconventional computation.

The conference will result in the formation of a new interdisciplinary research community; the identification of new interdisciplinary research topics; reciprocal knowledge transfer between the field of unconventional computing and computer science, mathematics, and electronic engineering; attraction of experimental scientists from physics, chemistry and biology laboratories; educating them in principles of unconventional computing and inspiring them to develop working laboratory prototypes of non-classical computing devices.

We welcome submissions from computer scientists, physicists, mathematicians, chemists, engineers, biologists and everyone who is inspired by the topic of the conference and by natural phenomena in non-standard computing schemes.

September 2007

Ninth European Conference on Artificial Life

September 10-14, 2007, Lisbon, Portugal.

Homepage: WWW

The conference will take place in a splendidly situated, historic location of Lisbon [take a tour around the Venue and the City!] and will comprise a one-track main session, several workshops, tutorials and associated events.

Artificial Life aims at the study of all phenomena characteristic of natural living systems, through methodologies of synthesis implemented in computational, robotic or other artificial architectures. Its wide scope ranges from the investigation of how life or life-like properties develop from inorganic components to how cognitive processes emerge in natural or artificial systems.

The "European" in European Conference on Artificial Life - ECAL, merely refers to the conference location, but participation is worldwide. In this ECAL we envisage maintaining and enlarging this worldwide scope and want to emphatically encourage novelty and daring ideas, particularly amongst young researchers. Both technical and conceptual work is welcome.

We want the conference to be of importance not only to the participating researchers but also to the general public with an interest in science. Hence a diversity of parallel open events will be promoted in venues throughout the city of Lisbon, aimed at communicating A-Life ideas, and the scientific practice and consequences, to a broader audience.

A further focus will be the involvement of industry. Relevant space and time will be allocated to the presentation of demos. This will constitute an opportunity to involve people from industry, inviting them to be present and sponsoring a prize to award particularly relevant work.

ECAL 2007 Workshop on Machine Epigenesis

September 10, 2007, Lisbon, Portugal.

Homepage: WWW

Creating a machine that exhibits life-like behavior has been the very core motivation of Artificial Life since its onset. Self-replication has remained the prime study since von Neumann, however, biological systems show a far wider range of generative hehavior, including differentiation and morphogenesis of multicellular structures from a single zygote, and adaptive de-differentiation and regeneration of parts in case of system failure. These characters remain largely missing in manmade, engineered systems, as well indicated by the late John Maynard-Smith in his writing:

"One reason why we find it so hard to understand the development of form may be that we do not make machines that develop: often we understand biological phenomena only when we have invented machines with similar properties... [and] we do not make 'embryo' machines ..." - John Maynard-Smith, The Problems of Biology (1986)

The Workshop on Machine Epigenesis aims to address this issue – the means, methods and models of machine epigenesis. It is expected to establish a field of research on any constructional and epigenetic processes of machines and to initiate a collective effort of formalization of models of such epigenetic machines. Here a "machine" is broadly construed to include abstract automata, electro-mechanical devices, molecular structures, and any other physical or informational instantiation. Topics to be covered in the workshop include (but are not limited to):

- Formal theories and abstract models of machine epigenesis
- Theories of universal and non-universal constructors
- Physical implementation of epigenetic machines
- Self-replicating and self-repairing machines
- Self-organization in modular and swarm robots
- Biological analogs relevant to the realization of machine epigenesis
- Philosophical and ethical issues in creating epigenetic machines
- Extending the mechanist model of living systems - philosophy

Readers are invited to submit a paper on original research or discussion on any aspect of machine epigenesis. Papers should be formatted following the guidelines for the ECAL 2007 proceedings (http://www.ecal2007.org/submissions.htm). Papers should not exceed 10 pages in length and must be made in PDF format.

Papers should be submitted electronically by email addressed to both the program chairs. Submitted papers will be reviewed and judged by the Programme Committee members based on their relevance to the workshop and conference, originality, clarity of the presentation, and overall quality.

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.

The 7th International Conference on Evolvable Systems: From Biology to Hardware
September 21-23, 2007, Wuhan, China
Homepage: WWW
Deadline March 31, 2007
The 7th International Conference on Evolvable Systems: From Biology to Hardware (ICES 2007) will be held on September 21-23, 2007 at Wuhan, China.

ICES 2007 will address the theme "From Laboratory to Real World", explaining how to shorten the gap between evolvable hardware research and design for real-world applications. Cross-fertilization of evolvable hardware, intelligent computation and newly emerging technologies is strongly encouraged. It will feature world-renowned plenary speakers, state-of-the-art special sessions, regular technical sessions, poster interactions, and entertaining social activities.

All papers in PDF format should be submitted electronically through the conference website. The conference proceedings will be published by Springer in the series of Lecture Notes in Computer Science (LNCS) in both hard copy and electronic form. The manuscripts should be written in English and follow the LNCS format provided by Springer. Full papers are limited to maximum 12 pages.

International Symposium on Intelligence Computation and Applications (ISICA 2007)
September 21-23, 2007, Wuhan, PRC,
Homepage: WWW
Deadline March 31, 2007
The 2nd International Symposium on Intelligence Computation and Applications (ISICA 2007) will be held on September 21-23, 2007 in Wuhan , China, at the same time as the 7th International Conference on Evolvable Systems: From Biology To Hardware (ICES 2007).

In order to cover both high-level and most up-to-date results, the ISICA Program Committee plan to publish two separate proceedings. Papers from the oral presentations will be published in the Lecture Notes by the Springer. These papers will emphasise the development of theories and methodologies in the field of computational intelligence.

Papers from the poster sessions will be collected in a separate proceedings which will be published by the China University of Geosciences Press. The ISICA 2005 proceedings were also published by the China University of Geosciences Press, and have been accepted into the Index To Scientific & Technical Proceedings (ISTP). Papers in the poster sessions will focus on innovative applications of computational intelligence.

All papers in PDF format should be submitted electronically through the conference website. The manuscripts should be written in English and follow the LNCS format provided by Springer). Full papers are limited to maximum 8 pages.

October 2007

7th International Conference on Intelligent Systems Design and Applications (ISDA'07)

October 22-24, 2007, Rio de Janeiro, Brazil

Homepage: WWW

Deadline March 16th, 2007

Intelligent Systems Design and Applications (ISDA'07) is the 7th International conference that brings together international soft computing, artificial intelligence, computational intelligence researchers, developers, practitioners and users. The aim of ISDA'07 is to serve as a forum to present current and future work as well as to exchange research ideas in this field.

ISDA'07 will focus on the following topics:

- Intelligent Systems Architectures and Applications
- Intelligent Image and Signal Processing
- Intelligent Internet Modeling
- Intelligent Data mining
- Intelligent Business Systems
- Intelligent Control and Automation
- Intelligent Agents
- Intelligent Knowledge Management

Prospective authors are invited to submit a full paper of 8 pages (PDF), for oral presentation. Authors must use the double columns IEEE format.

The submission of a paper implies that the paper is original and has not been submitted under review or copyright protected by the author if accepted. Besides papers in regular sessions, papers in special sessions are also invited to provide forums for focused discussions on new topics and innovative applications of established approaches. A special session consists of at least four related papers.

All papers should be submitted electronically via Online Paper Submission System (electronic link available). The format of the initial submissions can be PDF. The file of the final accepted papers should be in either Word or Latex.

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.

All the issues of SIGEVOlution are also available online at www.sigevolution.org.

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