Pierre Collet
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Artificial Evolution

5th International Conference, Evolution Artificielle, EA 2001
Le Creusot, France, October 2001
Selected Papers

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Foreword

The Evolution Artificielle cycle of conferences was originally initiated as a forum for the French-speaking evolutionary computation community. Previous EA meetings were held in Toulouse (EA'94), Brest (EA'95, LNCS 1063), Nîmes (EA'97, LNCS 1363), Dunkerque (EA'99, LNCS 1829), and finally, EA 2001 was hosted by the Université de Bourgogne in the small town of Le Creusot, in an area of France renowned for its excellent wines.

However, the EA conferences have been receiving more and more papers from the international community: this conference can be considered fully international, with 39 submissions from non-francophonic countries on all five continents, out of a total of 68.

Out of these 68 papers, only 28 were presented orally (41%) due to the formula of the conference (single session with presentations of 30 minutes) that all participants seem to appreciate a lot.

The Organizing Committee wishes to thank the members of the International Program Committee for their hard work (mainly due to the large number of submissions) and for the service they rendered to the community by ensuring the high scientific content of the papers presented.

Actually, the overall quality of the papers presented was very high and all 28 presentations are included in this volume, grouped in 8 sections which more or less reflect the organization of the oral session:

1. **Invited Paper:** P. BENTLEY gave a great talk on his classification of interdisciplinary collaborations, and showed us some of his work with musicians and biologists.
2. **Theoretical Issues:** Current theoretical issues concern measurement, adaptation, and control of diversity, even though connections with other disciplines are still very fruitful. MORRISON and DE JONG introduce a unified measurement of population diversity with some interesting issues on the computation complexity of diversity measures. SIDANER *et al.* also propose a diversity measurement, which they use to analyse the way Walksat explores its search space. BIENVENUE *et al.* investigate the adaptation of EA niching strategies to Monte Carlo Filtering Algorithms. CERRUTI *et al.* show how an EA can be usefully exploited to tackle a hard mathematical problem related to the measure of randomness of a binary measure. BERNY investigates the extension of a PBIL-like algorithm (more exactly a selection learning algorithm) for d-ary strings. BROWN *et al.* present a very original Markov Random Field modeling of GAs, where they build an explicit probabilistic model of any fitness function. This work also seems to have some interesting connections with epistasis analysis approaches.
3. **Algorithmic Issues:** Devising new algorithmic issues and understanding the behavior of genetic operators and mechanisms is an important research topic in evolutionary computation. JOHNSON and SHAPIRO explain the importance of selection mechanism in the case of distribution estimation

algorithms. In order to accelerate the convergence of EAs, ABBOUD and SCHOENAUER propose building and evaluating a surrogate model and introduce a surrogate mutation. To avoid stagnation in evolutionary search, LA TENDRESSE *et al.* propose re-initializing parts of the population at given time intervals. Dealing with noisy functions is an important topic in evolutionary computation, LEBLANC *et al.* propose exploiting historical information to devise new search strategies.

4. **Applications:** This section demonstrates the successful applicability of EAs to a broad range of problems. OUDEYER presents an evolutionary model of the origins of syllable systems. Optimizing portfolio is a challenging task. KORCZAK *et al.* use artificial trading experts discovered by GA to optimize portfolio. HAMIEZ and HAO propose a scatter search approach to solve the graph coloring problem. By introducing an appropriate indirect representation, BOUSONVILLE allows the application of evolutionary methods for solving the two stage continuous parallel flow shop problem. BÉLAIDOUNI and HAO present an analysis of the search space of the famous SAT problem based on a measure called "density of states", and ROUDENKO *et al.* use a multi-objective evolutionary algorithm to find optimal structures for car front end design.
5. **Implementation Issues:** Until very recently, researchers in evolutionary computing used to design their own programs. This section concerns the use of tools to alleviate researchers of the task of programming. LUTTON *et al.* present the EASEA (EAsy Specification of Evolutionary Algorithms) language and extensive tests on some famous functions. KEIJZER *et al.* present the EO (evolving objects) library, an object-oriented framework aimed at building evolutionary applications.
6. **Genetic Programming:** Genetic Programming emerged in the 1990s as a very promising paradigm for automatic generation of programs. ROBILLIARD and FONLUPT propose a way to overcome overfitting in a remote sensing application. RATLE and SEBAG introduce a grammar-based GP approach, which uses an approach *a la* PBIL during evolution, and a technique called boosting is presented by PARIS *et al.* to improve genetic programming.
7. **Constraints Handling:** This section collects studies reflecting ways to handle constraints in evolutionary computation. LE RICHE and GUYON provide a new insight on function penalization for constraints handling, and SMITH proposes to deal with constraints using the augmented Lagrangian penalty functions.
8. **Coevolution and Agent Systems:** Alternative evolutionary paradigms are introduced in this section. CASILLAS *et al.* use the coevolutionary paradigm for the learning of fuzzy-rule based systems. SRIVASTAVA and KALDATE present a multi-agent simulation modeling two competing groups in the sphere of social and ecological resources while EDMONDS simulates a foraging agent in environments with varying ecological structures. DELEPOULLE *et al.* give some insights on the ability of learning. SEREDYŃSKI and ZOMAYA report results on developing parallel algorithms for multiprocessor scheduling with use of cellular automata.

At this point, we would like to thank all sponsoring institutions who generously helped the Evolution Artificielle conference: the Conseil Régional de Bourgogne, the Université de Bourgogne, the Centre Universitaire Condorcet, the Communauté Urbaine Le Creusot – Montceau, the DGA (Délégation Générale pour l'Armement), the INRIA (Institut National de Recherche en Informatique et Automatique), the AFIA (Association Française pour l'Intelligence Artificielle, and the CMAPX (Centre de Mathématiques Appliquées de l'Ecole Polytechnique).

We would also like to mention all the people who donated time and energy and who therefore contributed to the success of EA 2001, namely (in alphabetical order) Valérie COLLET (to whom we owe much of the local and financial organization as well as many of the photos), Chantal LABEILLE (secretary of the Centre Condorcet), Jean-Philippe RENNARD (for the great web site), Nathalie GAUDECHOUX (secretary of the Fractales research group at INRIA), as well as Amine BOUMAZA, Benoît LEBLANC, Hélène SYNOWIECKI, and Josy LIARDET (for their kind help during the conference), and last but not least Alain BLAIR, who generously double-registered to the conference.

January 2002

Pierre COLLET
Evelyne LUTTON
Marc SCHOENAUER
Cyril FONLUPT
and Jin-Kao HAO

Evolution Artificielle 2001 – EA 2001

October 29-31, 2001

Université de Bourgogne, Le Creusot, France

5th International Conference on Artificial Evolution

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Invited Talk

Why Biologists and Computer Scientists Should Work Together
P. Bentley (University College London)

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Invited Paper

Why Biologists and Computer Scientists Should Work Together

Peter J. Bentley

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Abstract. This is a time of increasing interdisciplinary research. Computer science is learning more from biology every day, enabling a plethora of new software techniques to flourish. And biology is now beginning to see the returns, with new models, analyses and explanations being provided by computers. The merging of computer science and biology is a hard thing to achieve. It takes a lot of effort. You have to overcome much resistance on both sides. But it's worth it.

In this paper, which accompanies the keynote presentation for Evolution Artificielle 2001, Peter J. Bentley discusses a new breed of scientist called the Digital Biologist, and why they are so important. Examples of research that benefit both fields will be provided, including swarming systems, computational development, artificial immune systems and models of ecologies. Only by working together will biology learn how nature works, and computer science develop techniques that have some of the awesome power of nature.

1 Introduction

"What do you get when you cross a computer scientist with a biologist?"

No, it's not the first line of a joke, although many computer scientists and biologists might laugh at the idea of working together. The biologists might find the idea that computers could have any relevance to biology very amusing. The computer scientists might find the idea that the natural world was related to their work quite funny too. But this is not a joke. It's a way of performing research.

So what do you get when they cross? Or to be more precise, what do you get when they collaborate? In truth, you get misunderstandings: headaches of new terminology or different meanings for existing terms, and sometimes even a complete inability to understand the words of your collaborator. You also get confusing ideas, strange motivations, different ways of performing experiments, alternative ways of interpreting the results and unlikely-sounding theories. Should you pluck up the courage to attend (or even present a paper) at the conference in your collaborator's field, you get overwhelmed with all of the above multiplied by several hundred.

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As difficult as all this sounds – and it is difficult – it's worth it. After a few weeks of learning each other's vocabulary you are able to communicate. The chances are you'll also find some fascinating new concepts along the way. The new ideas you hear will spark off exciting ideas of your own, the different motivations might suggest new applications to you. The alternative ways of performing experiments and analysing the results could suggest new ways for you to test your own work. The unlikely-sounding theories might explain something in your own field. And although you may feel a little lost in the alien territory of your collaborator's conference, you can guarantee there'll be at least one or two papers that will have your heart beating faster with excitement at the possibilities for your own work.

Many of the problems will never go away: you will probably always have different ways of thinking, different vocabularies and different motivations. But these are good things. Once you understand how your collaborator works, the differences produce far more significant and original research than you could have produced alone.

And sometimes, after computer scientists and biologists have worked together long enough, they change a little. They realise the value of using computers to model biological processes. They see the new understandings of nature and the new computational techniques that such interdisciplinary research can bring. They become *digital biologists*.

In this paper I argue that collaborations between biologists and computer scientists are providing the next crucial steps on the road to understanding biology and exploiting biological processes in computation. I discuss the problems of beginning collaborations and how to make them succeed. Examples of such collaborations at University College London (UCL) are provided.

2 Starting Collaborations

Scientists can be very territorial creatures who loathe venturing far from their familiar surroundings. Computer scientists are perhaps more adventurous than biologists in this respect: because computers are a means to an end, these scientists have to find something for the computers to *do*. This normally means finding applications or problems to solve. While computer scientists can be talented at making up theoretical problems, these are often unsatisfying and even insufficient to test their ideas. Instead they need a real application, and this is provided by industry or academics in different fields. So, many computer scientists are quite used to working with people from outside of their field. Biologists, on the other hand, tend to be more insular. They train, research and present their results only within their communities (and sometimes to the outside world via press releases). Now and again, some may get together from different fields and grudgingly compare notes, but this is less common. Perhaps more than any other field of science, biology is subdivided and segregated into a huge number of separate disciplines.

The nature of the fields means that should a computer scientist wish to learn about techniques inspired from biology or even about modelling biology, most will still only

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