Table of Contents

Location ........................................................................................................................................... 3
Conference Rooms .......................................................................................................................... 4
Foreword ......................................................................................................................................... 6
Preface ............................................................................................................................................ 8
Satellite Workshops ......................................................................................................................... 9
Keynote Speakers ........................................................................................................................... 9
Alife Pioneers Panel Discussion .................................................................................................... 10
Alife Art Exhibit and Performance ............................................................................................... 12
Program Committee ...................................................................................................................... 13
Support .......................................................................................................................................... 13
Organizing Committee ................................................................................................................... 14
Administrative and Onsite Staff ................................................................................................. 14
Week Overview ............................................................................................................................. 15
Day Overviews .............................................................................................................................. 16
Monday, August 8 .......................................................................................................................... 21
  Satellite workshops .................................................................................................................... 21
Tuesday, August 9 .......................................................................................................................... 23
  8:40-9:00 Introduction, Adenauer Auditorium ............................................................................. 23
  9:00-10:00 Keynote 1, Adenauer Auditorium .......................................................................... 23
  10:30-12:10 Track 1A, Adenauer Auditorium .......................................................................... 23
  10:30-12:10 Track 1B, CFB Auditorium .................................................................................... 24
  13:40-15:20 Track 2B, CFB Auditorium .................................................................................... 25
  15:50-16:20 Poster Pitch 1, Adenauer Auditorium .................................................................. 26
  16:20-17:20 Keynote 2, Adenauer Auditorium ........................................................................ 26
  17:30-18:00 Poster Pitch 2, Adenauer Auditorium .................................................................. 26
  18:00-20:00 Welcome Reception, Adenauer Halls .................................................................. 26
Wednesday, August 10 .................................................................................................................... 27
  9:00-10:00 Keynote 3, Adenauer Auditorium .......................................................................... 27
  10:30-12:10 Track 3A, Adenauer Auditorium .......................................................................... 27
  10:30-12:10 Track 3B, CFB Auditorium .................................................................................... 28
  13:40-15:20 Track 4A, Adenauer Auditorium .......................................................................... 29
  13:40-15:20 Track 4B, CFB Auditorium .................................................................................... 29
  15:50-17:30 Track 5A, Adenauer Auditorium .......................................................................... 30
  15:50-17:30 Track 5B, CFB Auditorium .................................................................................... 31
  18:00-20:00 Pioneers Panel Discussion, Adenauer Auditorium .............................................. 32
Thursday, August 11 ...................................................................................................................... 33
9:00-10:00 Keynote 4, Adenauer Auditorium ............................................................................. 33
10:30-12:10 Track 6A, Adenauer Auditorium ............................................................................. 33
10:30-12:10 Track 6B, CFB Auditorium...................................................................................... 34
13:40-15:20 Track 7A, Adenauer Auditorium ............................................................................. 34
13:40-15:20 Track 7B, CFB Auditorium ...................................................................................... 35
15:50-17:30 Track 8A, Adenauer Auditorium ............................................................................. 36
15:50-17:30 Track 8B, CFB Auditorium...................................................................................... 37
18:00-19:00 Keynote 5, Adenauer Auditorium ........................................................................... 38
19:00-20:00 Art Show, Adenauer Auditorium ............................................................................. 38
20:00-20:30 Pre-Banquet Concert, Adenauer Auditorium .......................................................... 38
20:30-23:30 Conference Banquet, Salon Honnorat ..................................................................... 38

Friday, August 12 ........................................................................................................................... 39
9:00-10:00 Keynote 6, Adenauer Auditorium ............................................................................. 39
10:30-12:10 Track 9A, Adenauer Auditorium ............................................................................. 39
10:30-12:10 Track 9B, CFB Auditorium...................................................................................... 40
12:10-12:40, Adenauer Auditorium ............................................................................................ 40
Satellite workshops .................................................................................................................... 41
Posters .......................................................................................................................................... 43

Complete Proceedings e-Book Available at:
http://mitpress.mit.edu/catalog/item/default.asp?type=2&tid=12760

Advances in Artificial Life, ECAL 2011: Proceedings of the
Eleventh European Conference on the Synthesis and Simulation of Living Systems,

Cover image: Vito Trianni and Manuele Brambilla (CA tower), Louis Bec (creatures), René Doursat (composition)
Program booklet: Regina Frei, Matthew Egbert and René Doursat
Art Exhibit: Louis Bec, François Mourre, Patrice Bersani, Vincent Monnier, Delphine Fabbri-Lawson
Location

The conference will be held at the Cité Internationale Universitaire de Paris (CIUP). The Cité Universitaire was created in the pacifist context of the 1920s to support exchanges among students of the whole world. It is located on a wooded park in the south of the French capital and represents the largest student housing and facilities in the Paris region (5,600 beds). The grounds of the Cité Universitaire accommodate 40 residences, doubling as an outdoor exhibit of architecture. The eclecticism of the buildings expresses the diversity of the countries that contributed to their construction. Residences evoke the architecture of their country of origin (e.g., English colleges), others originate from the international modern movement (decorative arts, Le Corbusier). Address: 17, boulevard Jourdan, 75014 Paris

Access within Paris

- Suburban train (called “RER”, line B): “Cité Universitaire” station
- Metro (ligne 4): “Porte d’Orléans” station, then Tramway (line T3)
- Tramway (line T3): “Cité Universitaire” station
- Bus (line 21): “Cité Universitaire-Gazan” station
- Bus (line 88): “Jourdan-Montsouris” station
- Car: From the Paris beltway (called “Boulevard Périphérique”), take the “Porte d’Orléans” or “Porte de Gentilly” exits, then follow the signs to the nearby “Charlety” parking garage.

All Practical Information and Guidelines Available at:
http://ecal11.org/guides

for Attendees, CIUP Residents, Oral Presenters, Poster Presenters, Workshop Organizers, Track Chairs
Conference Rooms

Main Conference

- Aden Auditorium Adenauer
  - keynotes & pioneers
  - intro & poster pitch
  - art show & concert
  - all 'A' tracks

- Halls Galeries Adenauer
  - conference breaks & posters
  - art exhibit
  - welcome reception

- Lobby Mezzanine
  - registration
  - workshops breaks (Aug. 8 & 12 afternoon)

- CFB Auditorium CFB
  - all 'B' tracks

- Honn Salon Honorat
  - all 'C' tracks

Workshops

- Argl Salon de l’Argentine
  - Fondation Argentine, entrance floor
  - VIAMAT
  - INCUP

- Cam Salon du Cambodge
  - Maison du Cambodge, entrance floor
  - BioChemIT
  - BioMath

- Guli Salon Gulbenkian
  - Maison Internationale, level 1 west
  - AALE
  - MEV

- Weil Salon David-Weill
  - Maison Internationale, level 1 east
  - COSMOS
  - MAXIM

- Satl Salle Satsuma
  - Maison Internationale, level 1 east
  - ACCS
  - RUT8AC
  - DDLab / SynBioCC(2)

- Nath Salle Nathan
  - Maison Internationale, level -1 west
  - SynBioCC(1)
  - SIM-A
  - CS-Sports
Foreword

EC’11: Back to the Origins of Alife

to Francisco Varela (1946-2001),
Founder of ECAL

There is a long tradition of software simulations in theoretical biology to complement pure analytical mathematics, which are often limited in their ability to reproduce and understand self-organisation phenomena resulting from nonlinear and spatially grounded interactions of a huge number of various and evolving biological objects. Researchers in Artificial Life (Alife) bet that they can assist biologists in this domain, transcending their daily modelling and measuring practice by using software simulation in the first instance, and robotics, too, in order to abstract and elucidate the fundamental mechanisms common to living organisms. They hope to do so by discovering the most informative level of abstraction and resolutely neglecting a lot of physical and quantitative information deemed not indispensable. The computer is apparently the best microscope to achieve this. They want to focus on the rule-based mechanisms that make life possible, supposedly neutral with respect to their underlying material embodiment, and replicate them in a non-biochemical substrate. The hypothesis is that minimal life begins at the intersection of a series of processes that need to be isolated, differentiated and duplicated as such in computers, and that only software development and execution make possible to understand the way these processes are intimately interconnected in order for life to emerge at the crossroad.

The rejection of an authoritative definition of “life” is often compensated for by a list of functional properties that never finds unanimity amongst its authors. Some demand more properties, others require fewer of those properties that are often indicated in vague terms such as “self-maintenance”, “self-organisation”, “metabolism”, “autonomy”, “self-replication”, or “open-ended evolution”. A first determining role of Alife consists in writing and implementing software versions of these properties and the way they actually interact. The goal is to disambiguate them and make them algorithmically precise enough so that, in the end, the only remaining cause of disagreement on the definition of life would reside in the length or the composition of this list but not in its items.

Biologists obviously remain the most important partners; but what may they expect from this Alife business? What can they expect from these new “Merlin hackers”, whose ambitions seem, above all, disproportionally naïve. Computer platforms are useful and necessary in several ways. First of all, they open the door to a new style of teaching and advocating major biological ideas: in other words, computer software as a pedagogical tool. For example, Richard Dawkins is the best advocate of Darwinian ideas when running a computer simulation in which sophisticated creatures known as “biomorphs” evolve on a computer screen by means of a genetic algorithm. These same platforms and simulations can, insofar as they are sufficiently flexible, quantifiable and universal, be used more accurately by biologists, who will find in them a simplified way of simulating and validating a given biological system under study. Cellular automata, Boolean networks, genetic algorithms and algorithmic chemistry are excellent examples of softwares to download, parameterise and use to reproduce the required natural phenomenon. Their predictive power varies from very qualitative (where results apparently reproduce general trends of the real world) to very quantitative (where numbers produced by the computer may be precise enough to be compared with those measured in the real world).

Although being at first very qualitative, precise and clear coding is already the guarantee of an advanced understanding accepted by all. Algorithmic writing is an essential stage in formalising the elements of the model and making them objective. The linguistic and qualitative style of many biological papers could benefit in clarity by attempting a software instantiation of their contents. The more the model allows to integrate what we know about the reality being reproduced, the detailed structure of the objects and the relationships between them, the more the predictions will move from qualitative to precise, and the more easily the model will be validated according to Karl Popper’s “falsification” process of good scientific practice.

Ideally, through systematic software experiments, these platforms can lead to the discovery of new natural laws, whose impact will be all the greater as the simulated abstractions will be present in many biological realms. In the 1950’s, when Alan Turing discovered that a simple diffusion phenomenon, propagating itself at different speeds, depending on whether it is subject to a negative or positive influence, produces zebra or alternating motifs, it had a considerable effect on a whole section of biology studying the genesis of forms. This was Alife at its best. The same happened with John von Neumann’s self-replicating automata. Because of these seminal works, Turing and von Neumann remain the two spiritual fathers of the field. When scientists discovered that the number of attractors in a Boolean network (Kauffman) or a neural network (Hopfield) exhibited a given dependency on the number of units in these networks, these results could equally well apply to the number of cell types expressed as dynamic attractors in a genetic network or the quantity of information capable of being memorised in a neural network. Entire chapters of biology dedicated to networks (neural, genetic, protein, immune, hormonal) had to be re-written in the light of these discoveries. When other scientists recently observed non-uniform connectivity in many networks, whether social, technological or biological, showing a small number of hubs with a large number of connections and a greater number
of nodes with far fewer, and when, in addition, they explained the way in which these networks are built in time by preferential attachment (Barabási), again biology was clearly affected.

Alife is of course at its best when it reveals new biological facts, destabilizing biologists’ presuppositions or generating new knowledge, rather than simply illustrating or refining the old. Roughly said, we could construe Alife as being to theoretical biology what mathematics is to physics, that is, a more neutral scientific endeavour to provide open-minded biologists with new tools and new formal terms to describe and conceptualize the objects of their study. At the moment, the fact that this discourse is still young and shows relative immaturity in comparison with mainstream biology might explain why some observers remain skeptical in front of the current discrepancy between promises and reality. In our opinion, however, they tend to underestimate the importance of the results already obtained, as they are too riveted to their microscope. They should show less reluctance, indifference or even arrogance – and more curiosity and conviviality – towards these new computer explorers who have set out on the conquest of life, just like them but in front of their computer screens.

This is how we saw Alife when Francisco Varèla, Paul Bourgine and myself decided to organize the first European Conference on Artificial Life (ECAL) in Paris twenty years ago. We were very impressed by the Sante Fe workshops, which Chris Langton had started, and decided to initiate a European counterpart. We were aware of this very long tradition of theoretical biology in Europe, nevertheless a tradition still largely unaffected by the new opportunities offered by software simulations. We also realized that an opportunity existed to expand Alife “toward a practise of autonomous systems” with their “embodied cognition”, including not only all forms of life but also autonomous robots and collective intelligence. We emphasised the importance of developing artificial life toward new trends in theoretical biology, based on such practise of autonomous systems and not only on purely literary descriptions or purely mathematical formulations.

This opportunity exists more than ever for the future and we wanted to provoke discussions at ECAL about all major forms of autonomous systems, characterized by self-organized architectures, morphogenesis and adaptation, from minimal forms of life to the ecosphere, from minimal forms of cognition to human social intelligence, mediated through internet and the web. Besides, we did not want artificial life to become a sub-branch of engineering only weakly inspired by biology. In fact, other conferences already existed for that. ECAL ought to be different and unique, genuinely centred on theoretical biology and the physics of complex autonomous systems.

Today, although we are proud of this series of very successful and exciting ECAL conferences, we feel that the domain of Alife should look back to these origins and take even more inspiration from the new high-throughput developments at the intersection between computer science and theoretical biology. Closing a loop, this year’s ECAL will mark the 20th anniversary of the first ECAL and will be framed as a tribute to the late Francisco Varela. It was summer 1990, the three of us, with Paul Bourgine, were sitting in a café in Paris, drinking an excellent wine, when Francisco proposed to make our own version of an Alife conference. Thanks Francisco, we miss you.

Welcome to ECAL 2011!

Hugues Bersini
Brussels
August 2011
Preface

ECAL, the European Conference on Artificial Life, is a biennial event that alternates with the US-based Alife conference series. In the early 1990’s, the first two ECAL conferences in Paris and Brussels were mainly centered on theoretical biology and the physics of complex systems. After 20 years and 10 editions of this event, we felt that the domain should look back on these origins and our wish was to refocus the ECAL conference on complex biological systems.

Over the past two decades, biological knowledge has grown at an unprecedented rate, giving rise to new disciplines such as systems biology, testimony of the striking progress of modeling and quantitative methods across the field. During the same period, highly speculative ideas have matured, and entire conferences and journals are now devoted to them. Synthesizing artificial cells, simulating large-scale biological networks, storing and making intelligent use of an exponentially growing amount of data (e.g., microarrays), exploiting biological substrates for computation and control, and deploying bio-inspired engineering are all cutting-edge topics today.

ECAL’11 leveraged this remarkable development of biological modeling and extended the topics of Artificial Life to the fundamental properties of living organisms: their multiscale pattern-forming morphodynamics, their autopoiesis, robustness, capacity to self-repair, cognitive capacities, and co-adaptation at all levels, including ecological ones. Bringing together a large interdisciplinary community of biologists, computer scientists, physicists, and mathematicians, the conference gave them a moment to reflect on how traditional boundaries between disciplines have become blurred, and to revisit in depth what constitutes “life”.

In order to make the event attractive to researchers from a wide range of disciplines, we decided to open the possibility to submit 2-page abstracts discussing work previously published by the authors in a journal. In addition to 148 full-length (8-page) articles reporting on new, unpublished work, we received 29 overview abstracts, for a total of 177 submissions.

Although intrinsically interdisciplinary, these submissions referred in particular to the main conference topics, as described by the histogram below. All submissions were subject to peer review. The work of our excellent Program Committee (see list of members below) allowed us to select 128 papers, subdivided into 72 oral presentations (for a 40.7% acceptance rate) and 56 posters (31.6%), with no distinction being made between the two submission options, full paper or abstract. Two accepted papers were later withdrawn by their authors, reducing the total number to 126 (72 + 54).

All papers were presented during the four days of the plenary conference, which was held at the Cité Internationale Universitaire de Paris, France from August 9 to 12, 2011. Oral and poster sessions alternated with six world-class keynote speakers, whose invited contributions (abstracts or full papers) are also published in the front section of these proceedings: Jacques Demongeot, David Harel, James D. Murray, Jordan Pollack, Ricard Solé, and Eric Wieschaus (see their biosketches below). We thank them for taking the time and effort to participate in the conference.
Satellite Workshops

In addition to the plenary conference, we were also pleased to give Alife researchers the opportunity to organize satellite workshops and tutorials in two “bookend” sessions, on the first day (August 8) and last afternoon (August 12). These special sessions were dedicated to the same general topics as the main conference, while allowing for more focused interactions among participants. They were independently managed by their organizers and could comprise any combination of peer-reviewed papers, posters, invited talks, panel discussions, etc. Workshop contributions were not included in these proceedings. We received 15 proposals, of which 14 effectively took place, testimony of the liveliness of the field:

- **AAALE: Alife Approaches to Artificial Language Evolution**
  Luc Steels and Tony Belpaeme

- **ACCS: Artificial Chemical Computing Systems**
  Hideaki Suzuki and Hiroki Sayama

- **BioChemIT: 1st COBRA Workshop on Biological and Chemical Information Technologies**
  Peter Dittrich, Zarka Khan and Martyn Amos

- **CoSMoS: 4th Workshop on Complex Systems Modelling and Simulation**
  Paul Andrews, Susan Stepney, Peter Welch and Carl Ritson

- **CS-Sports: Complex Systems in Sports**
  Juan Julián Merelo Guervós, Antonio Mora García and Carlos Cotta Porras

- **DDLab: Exploring Discrete Dynamics: From Cellular Automata to Random Networks**
  Andy Wuensche, Andy Adamatzky and Genaro Juárez Martínez

- **iBioMath: First International Workshop on Integral Biomathics**
  Plamen Simeonov, Andrée Ehresmann and Leslie Smith

- **INCUP: Information Coding in Unconventional Computing Substrates**
  Jerzy Gorecki and Andy Adamatzky

- **MASmms: Workshop on Multi-Agent Systems in Biology at meso or macroscopic scales**
  Pascal Ballet, Marie Beurton-Aimar, Guillaume Hutzler and Bertrand Laforge

- **MEW: 3rd Morphogenetic Engineering Workshop**
  René Doursat and Hiroki Sayama

- **RUTSAC: Research Using The Stringmol Artificial Chemistry**
  Simon Hickinbotham, Ed Clark and Adam Nellis

- **SIM-A: System Immunology Models of Autopoiesis**
  Uri Hershberg and Sol Efroni

- **SynBioCCC: Workshop on the Design, Simulation, Construction and Testing of Synthetic Gene Regulatory Networks for Computation, Control and Communications**
  Nawwaf Kharma and Taras Kowaliw

- **WAAT: Workshop on Artificial Autonomy: 20 years of practice of autonomous systems**
  Tom Froese, Matthew Egbert and Xabier Barandiaran

Keynote Speakers

**James D. Murray** - **Universities of Princeton, Oxford and Washington**

Tuesday 9 August, 9:00

James D. Murray, FRS, Foreign Member of the French Academy, is Professor Emeritus of Mathematical Biology at the University of Oxford, Professor Emeritus of Applied Mathematics at the University of Washington, and Senior Scholar at Princeton University. His research is characterized by its great scope and depth: an early example is his fundamental contributions to understanding the biomechanics of the human body when launched from an aircraft in an ejection seat. He has made contributions to many other areas, ranging from understanding and preventing severe scarring, to fingerprint formation, sex determination, modeling of animal coat patterns, territory formation in wolf-deer interacting populations, growth and control of brain tumors, quantifying patient treatments prior to use, and modeling marital interaction and divorce prediction with 94% accuracy in a 12-year longitudinal study. He is best known for his authoritative and extensive work entitled *Mathematical Biology*, whose 3rd edition in two volumes came out in 2004.
Ricard Solé - Universitat Pompeu Fabra, Barcelona  
Tuesday 9 August, 16:20

Ricard Solé heads the Complex Systems Lab at Universitat Pompeu Fabra, and is an External Professor at the Santa Fe Institute. One of his main research interests is understanding the possible presence of universal patterns of organization in complex systems, from prebiotic replicators to evolved artificial objects. Key questions are how robust structures develop, how information is incorporated into these structures and how computation emerges. He is also interested in how to determine what are the contributions of selection, chance and self-organization to the evolution of complexity. One of his main goals is searching for the principles of organization responsible for the emergence of fundamental components of complexity, including the origins of self-reproduction, development, life cycles, computational processes and multicellularity. His work has been featured in newspapers as well as several popular and technical books.

David Harel - Weizmann Institute of Science  
Wednesday 10 August, 9:00

David Harel is a professor of computer science at the Weizmann Institute of Science in Israel. Harel is best known for his work on dynamic logic, computability and software engineering. In the 1980s he invented the graphical language of Statecharts, which has been adopted as part of the UML standard. He has also published expository accounts of computer science, such as his award winning 1987 book “Algorithmics: The Spirit of Computing” and has made appearances on Israeli radio and television. He currently works on many diverse topics, including visual languages, graph layout, systems biology and the communication of odours. He is now working on a computer model of a nematode, ‘Caenorhabditis elegans’, which was the first multicellular organism to have its genome completely sequenced. The eventual completeness of such a model depends on his updated version of the test developed by Alan Turing to identify whether computers could reason well enough that a human communicating with them could not tell whether a human or a machine was at the other end of the communication.

Eric Wieschaus - Princeton University, 1995 Nobel Prize in Physiology  
Thursday 11 August, 9:00

Eric Wieschaus is the Squibb Professor in Molecular Biology at Princeton. His research work has focused on embryogenesis in the fruit fly Drosophila melanogaster, specifically in the patterning that occurs in the early Drosophila embryo. Most of the gene products used by the embryo at these stages are already present in the unfertilized egg and were produced by maternal transcription during oogenesis. A small number of gene products, however, are supplied by transcription in the embryo itself. He has focused on these “zygotically” active genes because he believes the temporal and spatial pattern of their transcription may provide the triggers controlling the normal sequence of embryonic development. In 1995, he was awarded the Nobel Prize in Physiology or Medicine with Edward B. Lewis and Christiane Nüsslein-Volhard as co-recipients, for their work revealing the genetic control of embryonic development.

Jordan Pollack - Brandeis University  
Thursday 11 August, 18:00

Jordan Pollack is professor of computer science and complex systems professor at Brandeis University, where he is also chairman of the computer science department and director of the Dynamical and Evolutionary Machine Organization (DEMO) lab. The laboratory’s work on AI, Artificial Life, Neural Networks, Evolution, Dynamical Systems, Genomes, Self-designed Robotics, Machine Learning, and Educational Technology has been reported on by the New York Times, Time, Science, NPR, Slashdot.org and many other media sources worldwide.

Jacques Demongeot - Université Joseph Fourier, Grenoble  
Friday 12 August, 9:00

Jacques Demongeot is presently director of the TIMC-IMAG Laboratory, “Techniques of Medical Engineering & Complexity” (CNRS 5525) and is also head of the Institute of Bioengineering (IFRT 130 IpV) at the University Joseph Fourier, Grenoble, France. He has an MD and a PhD in mathematics and has been appointed Chairman of Biomathematics at the Institut Universitaire de France in 1994. Jacques Demongeot is also in charge of the Department of Medical Information at the University Hospital of Grenoble (CHUG) and is the founder of the doctoral school of bioengineering “Health, Cognition & Environment”. He is currently creating a new laboratory AGIM, in Archamps near Geneva, devoted to studies of development and ageing.

Alife Pioneers Panel Discussion  
Wednesday 10 August, 18:00

Moderator: Hugues Bersini - IRIDIA, Université Libre de Bruxelles

Mark Bedau - Reed College, Portland and Initiative for Science, Society and Policy, Denmark

Mark Bedau pioneered the field of quantifying and comparing the evolutionary activity in artificial and natural systems, and is an international leader in the evolutionary design of complex biochemical systems using statistical models and prediction algorithms. Because he combines training in analytical philosophy with over a decade of experience in artificial life, he is recognized as a uniquely qualified expert in the philosophical foundations of complex adaptive systems. Mark Bedau is Editor-in-Chief of the international journal Artificial Life (published by MIT Press), he co-organized five international conference on artificial life, co-founded a startup company, ProtoLife SRL, and co-founded the European Center for Living Technology, a research institute in Venice, Italy, that investigates theoretical and practical issues associated with living systems.
Takashi Ikegami - University of Tokyo

Takashi Ikegami is a professor at the Department of General Systems Sciences of the Graduate School of Arts and Sciences, University of Tokyo, where he specializes in complex systems and artificial life. Takashi takes a computational/philosophical approach to designing artificial life, exploring issues at the margins of his discipline. He is also an arts collaborator with Keichiro Shibuya (ATAK) on making three-dimensional sound installations. Keywords: chemical computing, smart chemical agents, chemotaxis, living technology, artificial life, first cell.

Barry McMullin - Rince Research Institute, Dublin City University (DCU)

Barry McMullin’s primary research activity is in the domain of Artificial Life. He serves on the organizing committees of both ECAL and Alife conferences, and as a member of the Editorial board of the Artificial Life journal. He has a secondary research interest in the area of Web Accessibility, engineering web sites and services to best meet the requirements of all users, specifically including those with disabilities. Between 1999 and 2004, Barry McMullin was the first DCU Dean of Teaching and Learning. In this role he was responsible for the development of a wide series of initiatives to significantly enhance the quality of the student learning experience at DCU. Barry McMullin was appointed to the rank of Associate professor at DCU in September 2010, and became Director of RINCE, a national research institute specializing in Engineering technology innovation, in February 2010.

Norman Packard - European Center for Living Technology, Venice

Norman Packard has worked in the areas of chaos, learning algorithms, predictive modeling of complex time series, statistical analysis of evolution, artificial life, and complex adaptive systems. He was co-founder of Prediction Company in 1991 and served as its CEO (1997-2003) and chairman until 2005. Norman Packard is currently working in a new scientific and business direction based on development of evolutionary chemistry in programmable microfluidic technology. Long-range applications of this technology include the fabrication of artificial cells from non-living material, and their programming for useful functionality. In 2004, Norman Packard was co-founder of ProtoLife S.r.l. (Venice, Italy), which applies machine learning techniques to the design of experiments (DoE) for high throughput experiments in biotechnology. As part of the PACE project (Programmable Artificial Cell Evolution, 2004-2008), he also participated in the founding of ECLT, the European Center for Living Technology.

Steen Rasmussen - University of Southern Denmark, Odense

Steen Rasmussen is currently the Head of the Center for Fundamental Living Technology (FLinT), a Research Director at the Department for Physics and Chemistry at University of Southern Denmark, and External Research Professor at the Santa Fe Institute. He has pioneered approaches, methods, and applications for self-organizing processes in natural and artificial systems: abstract self-programmable matter, molecular dynamics (MD) lattice gas simulations for molecular self-assembly, rational and evolutionary protocell design, disaster mitigation and decision support systems based on collective intelligence, as well as novel simulations for large-scale sociotechnical systems. Steen Rasmussen was heading the Protocell Assembly (LDRD-DR) project and the Astrobiology program (origins of life) at Los Alamos, developing experimental and computational protocells and cell-like entities. He also co-directed the European PACE project (Programmable Artificial Cell Evolution) project.

Luc Steels - Free University of Brussels and Sony Computer Science Lab, Paris

Luc Steels is professor of Computer Science (at the moment part-time) at the Free University of Brussels (VUB), founder and director (since 1983) of the VUB Artificial Intelligence Laboratory and co-founder and chairman (1990-1995) of the VUB Computer Science Department. He has also been the director of Sony CSL in Paris since its creation in 1996. His scientific research interests cover the whole field of artificial intelligence, including natural language, vision, robot behavior, learning, cognitive architecture, and knowledge representation. At the moment his focus is on dialogs for humanoid robots and fundamental research into the origins of language and meaning. Current work focuses on developing the foundations of semiotic dynamics and on fluid construction grammars.

Susan Stepney - York Centre for Complex Systems Analysis, University of York

Susan Stepney leads the Non-Standard Computation research group, and is one of the instigators of the new interdisciplinary York Centre for Complex Systems Analysis. Originally a theoretical astrophysicist, she has spent the bulk of her professional career in industrial R&D (GEC-Marconi and Logica), mostly in mathematical and computational modelling, researching aspects of novel computation. She is a moderator of the UKCRC Grand Challenge 7 in Non-Classical Computation and is helping to build a conceptual meta-framework for bio-inspired computation. Current research interests also include theories of emergence and self-organising systems, and nature-inspired computational metaphors. She is the PI of the Complex Systems Modelling and Simulation project and was PI of the EIVIS novel computation cluster, rated “outstanding”. She also teaches complex biosystems simulation and is responsible for designing the new Masters course in Natural Computation at York.
Alife Art Exhibit and Performance

Inspiration, imagination and aesthetics are an integral part of science — and they are of particular importance in the Alife community, which fuels some of the most creative and provocative research at the edge (of chaos) between biology and technology. Accordingly, ECAL 2011 has the great pleasure to welcome prominent visual artists and musicians (some of them scientists, too), who will showcase their exciting work in the exhibit rooms and the auditorium. Be ready for a unique stimulation of your mind, your various sensory modalities, and your sense of humor!

Louis Bec - Institut Scientifique de Recherche Paranaturaliste

Louis Bec, born in Algeria and living in France, is a biologist and zoosystemician who extends his scientific field with a fabulatory epistemology based on Artificial Life and Technozoosemiotics. In 1972, Bec founded the Institut Scientifique de Recherche Paranaturaliste, where he studies the incapability of living beings to understand their own existence. Bec is both artist and scientist in the field of artificial life and 3D technologies. He is as much a biologist, artist, curator and educator, and has been a ministry officer for new technologies in arts. Bec is Director of CYPRES (Centre Interculturel de Pratiques et Echanges Transdisciplinaires) in Marseille. He has presented his ideas in many exhibitions, such as Alife II (invited by Chris Langton) and From Animals to Animats, and articles.

Upokrinomenes: a fabulated epistemology – Zoosystemician Louis Bec forces us to question the validity of each claim by reformulating and staging scientific discourse. His reasoning possesses all the marks of scientific assertiveness, combining scientific jargon with scholarly neologisms. Questioning life and our inability to understand it through traditional investigative methods, he founded the field of Upokrinomenology. It is a theory of life using models based on computer science, robotics, video and other interactive devices, where irony holds a significant place. By putting scientific discourse into perspective, he challenges us to investigate, unravel and interpret the propositions that he makes. In this research, scientific discourse becomes poetic and Louis Bec becomes a storyteller. Founder of the Scientific Institute of Paranaturalistic Research, he invites us to discover a life we did not know existed, one that looms at the border between shapes, language and behavior [after C. Beaugrand & A. Charre, Reinventing the museum]. (Art exhibit at ECAL'11 designed and installed with François Mourre, Patrice Bersani, Vincent Monnier and Delphine Fabbri-Lawson.) His presentation will be followed by 7p., cuis., s. de b., ... à saisir (6BR, kitch., bath., ... selling now), a short film by Agnès Varda featuring Louis Bec.

François Pachet - Sony Labs, Paris

François Pachet is a Civil Engineer (Ecole des Ponts and Chaussées) and was an Assistant Professor in Artificial Intelligence and Computer Science, University of Paris 6, until 1997. He then set up the music research team at the Sony Computer Science Laboratories, Paris, and developed the vision that metadata can greatly enhance the musical experience in all its dimensions, from listening to performance. His team conducts research in interactive music listening and performance and musical metadata and developed several innovative technologies and award winning systems (MusicSpace, constraint-based spatialization, PathBuilder, intelligent music scheduling using metadata, The Continuator for Interactive Music Improvisation). He is the author of over 80 scientific publications in the fields of musical metadata and interactive instruments.

The Continuator Project: playing with virtual musicians – François Pachet (guitar player) and Jeff Suzda (professional sax player) will perform a short Jazz concert with their band “Quintet of Two”. They comprise the two human musicians in the group, performing alongside three “software” musicians. The goal of this project is to play “standard” jazz using virtual instruments intimately controlled by the human players. The technologies employed, developed at Sony CSL, involve Markov chains, constraint programming, signal processing, and a great degree of musical tuning. The performance is still exploratory, but we hope to convey a sense of the direction we are heading to: enhance musical expressivity through controllable machines.
Program Committee

An event like ECAL’11 would not have been possible without the following dedicated members of the Program Committee and additional reviewers. Our gratitude goes to all of them.

Hussein Abbass
Andy Adomatzyk
Chris Adami
Andreas Albrecht
Fernando Almeida e Costa
Lee Altenberg
Paul Andrews
Takaya Arita
Wolfgang Banzhaf
Xabier E. Barandiaran
Andrea Baranchelli
Jacob Beal
Mark Bedau
Randall Beer
Tony Belpaeme
Peter Bentley
Hugues Bersini
Luc Berthouze
Luigi Bertolotti
Mauro Birattari
Joris Bleys
Josh Bongard
Paul Bourgine
Seth Bullock
Stefano Cagnoni
Alexandre Campo
Philippe Capdepy
Ciro Cattuto
Anders Christensen
Dominique Chu
Netta Cohen
Luis Correia
Ernesto Costa
Tamás Czárán
Christian Darabos

Joachim De Beule
Bart De Boer
Ralf Der
Gianni Di Caro
Cecilia Di Chio
Peter Dittrich
Mauricio Dorigo
Alan Dorin
René Doursat
Marc Ebner
Arantzaz Etxeberria
Nazim Fates
Christoph Flamm
Luca Gambardella
Carlos Gershenson
Mario Giacobini
Roderich Gross
Thilo Gross
Pauline C Haddow
Emma Hart
Inman Harvey
Paulien Hogeweg
Phil Husbands
Fumiya Iida
Yaochu Jin
Colin Johnson
Istvan Karsai
Joze Klemen
Serge Kernbach
Daeun Kim
Taras Kowalik
Kalevi Kull
Renaud Lambiotte
Doron Lancet

Pedro U. Lima
Daniel Lobo
Fernando Lobo
Robert Lowe
Penousal Machado
Steven Maere
Chris McEwan
Barry McMullin
Jose Mendes
Olivier Michel
Martin Middendorf
Luis Moniz Pereira
Sara Montagna
Jason Moore
Federico Moran
Christoph L. Nehaniv
Jason Noble
Stefano Nolfi
Ann Nowe
Charles Ofria
Joshua Payne
Andrew Philippides
Raphaël Plasson
Daniel Polani
Paolo Provera
Charles Richter
Luis M. Rocha
Miguel Rocha
Pierre Rouze
Kepa Ruiz Mirazo
Erol Sahin
Francisco C. Santos
Hiroki Sayama

Matthias Scheutz
Thomas Schmickl
Marc Schoenauer
Luis Seabra Lopes
Roberto Serra
Cosma Shalizi
Ricard Sole
Antoine Spicher
Peter Stadler
Susan Stepney
Charles Taylor
Tim Taylor
Gianluca Tempesti
Christof Teuscher
Jon Timmis
Peter Todd
Marco Tomassini
Arne Traulsen
Vito Trianni
Elio Tuci
Gunnar Tuft
Ali Emre Turgut
Karl Tuyls
Jon Umezura
Patricia A. Vargas
Mirko Viroli
Paul Vogt
Richard Watson
Alan Winfield
Rachel Wood
Andrew Wensche
Larry Yaeger
Tom Ziemke

Additional Reviewers

Philipp Altrock
Joshua Auerbach
Julian Garcia
Heather Goldsby
Laura Grabowski
Nanda Maheshwari
Pedro Mariano
Hugi Marques
Bjørn Østman
Danilo Pianini

Gabriel Piedrafita
Flavio Pinheiro
Stuart Rossiter
Pedro Santana
Porfirio Silva

Nikolaos Vlassopoulos
Liyu Wang
Nicole-Radu Zabet

Support

We are also very grateful to the following institutions for their financial support:

- Complex Systems Institute, Paris Ile-de-France, itself sponsored by the Région Ile-de-France
- CREA, Ecole Polytechnique & CNRS, Paris
- IRIDIA, Université Libre de Bruxelles
- Fondation Jean-Marie Delwart, Bruxelles
Organizing Committee

- René Doursat (General Chair)  
  Complex Systems Institute, Paris Ile-de-France, CNRS – CREA, Ecole Polytechnique & CNRS, Paris
- Hugues Bersini (Co-Founder)  
  IRIDIA, Université Libre de Bruxelles
- Paul Bourgine (Co-Founder)  
  Complex Systems Institute, Paris Ile-de-France, CNRS – CREA, Ecole Polytechnique & CNRS, Paris
- Tom Lenaerts (Program Chair)  
  MLG, Université Libre de Bruxelles – AI-lab, Vrije Universiteit Brussel
- Mario Giacobini (Program Chair)  
  Dept. of Animal Productions, Epidemiology and Ecology – Molecular Biotechnology Center, University of Torino
- Marco Dorigo (Co-Organizer)  
  IRIDIA, Université Libre de Bruxelles

Administrative and Onsite Staff

Finally, we want to thank for their invaluable help all those who were involved in the preparation of the event, in particular

- Marcel Skrobek (office head)
- Geneviève Tual (office manager)
- Stéphanie Bayou-Zaba (admin assistant)
- Razvan Dordea (MSc student)  
  Complex Systems Institute, Paris Ile-de-France, CNRS – CREA, Ecole Polytechnique & CNRS, Paris
- Muriel Decreton (office manager)
- Manuele Brambilla (PhD student)
- Eliseo Ferrante (PhD student)
- Alessandro Stranieri (PhD student)
- Vito Trianni (postdoc)  
  IRIDIA, Université Libre de Bruxelles
- Matthew Egbert (research fellow)  
  University of Sussex
- Luca Ferreri (PhD student)  
  University of Torino
- Regina Frei (postdoc)  
  Imperial College London
- Carlos Quintana (PhD student)  
  University of Malaga
- Gabriel Varela (student)  
  Bowdoin College, Brunswick, Maine

Art Exhibit: Graphic & Electronic Engineers, Set Designers

- François Mourre (founder)  
  3D from Mars
- Patrice Bersani (CEO)  
  DreamLabs
- Vincent Monnier  
  DreamLabs
- Delphine Fabbri-Lawson (art curator)

The organizing committee of ECAL'11,

René Doursat, Hugues Bersini, Paul Bourgine, Tom Lenaerts, Mario Giacobini, Marco Dorigo

Paris
August 2011
# Week Overview

<table>
<thead>
<tr>
<th>Time</th>
<th>Monday 8</th>
<th>Tuesday 9</th>
<th>Wednesday 10</th>
<th>Thursday 11</th>
<th>Friday 12</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:00</td>
<td>registration Lobby</td>
<td>registration Lobby</td>
<td>registration Lobby</td>
<td>registration Lobby</td>
<td>registration Lobby</td>
</tr>
<tr>
<td>8:40</td>
<td>&amp; breakfast Lobby</td>
<td>&amp; breakfast Lobby</td>
<td>&amp; breakfast Lobby</td>
<td>&amp; breakfast Lobby</td>
<td>&amp; breakfast Lobby</td>
</tr>
<tr>
<td>9:00</td>
<td>Satellite workshops 1</td>
<td>Satellite workshops 1</td>
<td>Satellite workshops 1</td>
<td>Satellite workshops 1</td>
<td>Satellite workshops 1</td>
</tr>
<tr>
<td>10:00</td>
<td>coffee break, posters &amp; art Halls</td>
<td>coffee break, posters &amp; art Halls</td>
<td>coffee break, posters &amp; art Halls</td>
<td>coffee break, posters &amp; art Halls</td>
<td>coffee break, posters &amp; art Halls</td>
</tr>
<tr>
<td>10:30</td>
<td>Open coffee break 10:00-12:00 Lobby</td>
<td>Open coffee break 10:00-12:00 Lobby</td>
<td>Open coffee break 10:00-12:00 Lobby</td>
<td>Open coffee break 10:00-12:00 Lobby</td>
<td>Open coffee break 10:00-12:00 Lobby</td>
</tr>
<tr>
<td>12:10</td>
<td>Lunch, posters &amp; art Halls</td>
<td>Lunch, posters &amp; art Halls</td>
<td>Lunch, posters &amp; art Halls</td>
<td>Lunch, posters &amp; art Halls</td>
<td>Lunch, posters &amp; art Halls</td>
</tr>
<tr>
<td>13:40</td>
<td>Satellite workshops 2</td>
<td>Satellite workshops 2</td>
<td>Satellite workshops 2</td>
<td>Satellite workshops 2</td>
<td>Satellite workshops 2</td>
</tr>
<tr>
<td>14:30</td>
<td>Satellite workshops 2</td>
<td>Satellite workshops 2</td>
<td>Satellite workshops 2</td>
<td>Satellite workshops 2</td>
<td>Satellite workshops 2</td>
</tr>
<tr>
<td>15:20</td>
<td>poster pitch 1 Aden</td>
<td>poster pitch 1 Aden</td>
<td>poster pitch 1 Aden</td>
<td>poster pitch 1 Aden</td>
<td>poster pitch 1 Aden</td>
</tr>
<tr>
<td>17:30</td>
<td>Welcome reception Halls</td>
<td>Welcome reception Halls</td>
<td>Welcome reception Halls</td>
<td>Welcome reception Halls</td>
<td>Welcome reception Halls</td>
</tr>
<tr>
<td>18:00</td>
<td>poster &amp; art vernissage Halls</td>
<td>poster &amp; art vernissage Halls</td>
<td>poster &amp; art vernissage Halls</td>
<td>poster &amp; art vernissage Halls</td>
<td>poster &amp; art vernissage Halls</td>
</tr>
<tr>
<td>19:00</td>
<td>Keynote 5 Aden</td>
<td>Keynote 5 Aden</td>
<td>Keynote 5 Aden</td>
<td>Keynote 5 Aden</td>
<td>Keynote 5 Aden</td>
</tr>
<tr>
<td>20:00</td>
<td>Concert Aden François Pachet</td>
<td>Concert Aden François Pachet</td>
<td>Concert Aden François Pachet</td>
<td>Concert Aden François Pachet</td>
<td>Concert Aden François Pachet</td>
</tr>
<tr>
<td>20:30</td>
<td>Banquet Homa</td>
<td>Banquet Homa</td>
<td>Banquet Homa</td>
<td>Banquet Homa</td>
<td>Banquet Homa</td>
</tr>
</tbody>
</table>

**Monday 8**
- Satellite workshops 1

**Tuesday 9**
- Satellite workshops 1
- Open coffee break 10:00-12:00 Lobby

**Wednesday 10**
- Satellite workshops 1
- Open coffee break 10:00-12:00 Lobby

**Thursday 11**
- Satellite workshops 1
- Open coffee break 10:00-12:00 Lobby

**Friday 12**
- Satellite workshops 1
- Open coffee break 10:00-12:00 Lobby
## Day Overviews

### Monday, August 8

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:00 – 9:00</td>
<td>Registration &amp; Breakfast</td>
<td>Lobby</td>
</tr>
<tr>
<td>9:00 – 13:00</td>
<td>Satellite Workshops 1</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>AAALE(1)</strong> Alife Approaches to Artificial Language Evolution</td>
<td>[Gulb]</td>
</tr>
<tr>
<td></td>
<td>Luc Steels, Tony Belpaeme</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>BioChemIT(1)</strong> 1st COBRA Workshop on Biological and Chemical Information Technologies</td>
<td>[Cam]</td>
</tr>
<tr>
<td></td>
<td>Peter Dittrich, Zarika Khan, Martyn Amos</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>CoSMoS(1)</strong> 4th Workshop on Complex Systems Modelling and Simulation</td>
<td>[Wei]</td>
</tr>
<tr>
<td></td>
<td>Paul Andrews, Susan Stepney, Peter Welch, Carl Ritson</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>WAAT(1)</strong> Workshop on Artificial Autonomy: 20 years of practice of autonomous systems</td>
<td>[Argl]</td>
</tr>
<tr>
<td></td>
<td>Tom Froese, Matthew Egbert, Xabier Barandiaran</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>ACCS</strong> Artificial Chemical Computing Systems</td>
<td>[Sats]</td>
</tr>
<tr>
<td></td>
<td>Hideaki Suzuki, Hiroki Sayama</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>SynBioCCC(1)</strong> Workshop on the Design, Simulation, Construction and Testing of Synthetic Gene Regulatory Networks for Computation, Control and Communications</td>
<td>[Nath]</td>
</tr>
<tr>
<td></td>
<td>Nawwaf Kharma, Tams Kowalik</td>
<td></td>
</tr>
<tr>
<td></td>
<td>→ SynBioCCC(2) on Friday, August 12, 17:00</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Open Coffee Break, 10:00-12:00</td>
<td>Lobby</td>
</tr>
<tr>
<td>13:00 – 14:30</td>
<td>Lunch</td>
<td>Lobby</td>
</tr>
<tr>
<td>14:30 – 18:30</td>
<td>Satellite Workshops 2</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>AAALE(2)</strong> Alife Approaches to Artificial Language Evolution</td>
<td>[Gulb]</td>
</tr>
<tr>
<td></td>
<td>Luc Steels, Tony Belpaeme</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>BioChemIT(2)</strong> 1st COBRA Workshop on Biological and Chemical Information Technologies</td>
<td>[Cam]</td>
</tr>
<tr>
<td></td>
<td>Peter Dittrich, Zarika Khan, Martyn Amos</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>CoSMoS(2)</strong> 4th Workshop on Complex Systems Modelling and Simulation</td>
<td>[Wei]</td>
</tr>
<tr>
<td></td>
<td>Paul Andrews, Susan Stepney, Peter Welch, Carl Ritson</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>WAAT(2)</strong> Workshop on Artificial Autonomy: 20 years of practice of autonomous systems</td>
<td>[Argl]</td>
</tr>
<tr>
<td></td>
<td>Tom Froese, Matthew Egbert, Xabier Barandiaran</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>RUTSAC</strong> Research Using The Stringmol Artificial Chemistry</td>
<td>[Sats]</td>
</tr>
<tr>
<td></td>
<td>Simon Hickinbotham, Ed Clark, Adam Nellis</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>SIM-A</strong> System Immunology Models of Autopoiesis</td>
<td>[Nath]</td>
</tr>
<tr>
<td></td>
<td>Uri Hershberg, Soti Effron</td>
<td></td>
</tr>
</tbody>
</table>
### Tuesday, August 9

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:00 – 8:40</td>
<td>Registration [Lobby] &amp; Breakfast [Halls]</td>
</tr>
<tr>
<td>8:40 – 9:00</td>
<td><strong>Introduction</strong> – René Doursat, Hugues Bersini, Paul Bourgine [Aden]</td>
</tr>
<tr>
<td>9:00 – 10:00</td>
<td><strong>Keynote 1:</strong> James D. Murray – <em>On the growth of brain tumours</em> [Aden]</td>
</tr>
<tr>
<td>10:00 – 10:30</td>
<td><strong>Coffee Break, Posters &amp; Art Exhibit</strong> [Halls]</td>
</tr>
<tr>
<td>10:30 – 12:10</td>
<td><strong>Track 1A</strong> [Aden] - <strong>Evolution &amp; Games</strong> – Chair: Tom Lenaerts</td>
</tr>
<tr>
<td></td>
<td>Enea Pestelacci, Marco Tomassini and Alberto Antonioni</td>
</tr>
<tr>
<td></td>
<td>Coordination games on small worlds: Artificial agents vs. experiments</td>
</tr>
<tr>
<td></td>
<td>Francisco C. Santos, Jorge M. Pacheco and Brian Skyrms</td>
</tr>
<tr>
<td></td>
<td>Co-evolution of pre-play signaling and cooperation</td>
</tr>
<tr>
<td></td>
<td>Jorge M. Pacheco, Francisco C. Santos, Max O. Souza and Brian Skyrms</td>
</tr>
<tr>
<td></td>
<td>Evolutionary dynamics of collective action</td>
</tr>
<tr>
<td></td>
<td>Pedro Mariano and Luis Coreia</td>
</tr>
<tr>
<td></td>
<td>Evolution of partner selection</td>
</tr>
<tr>
<td></td>
<td><strong>Track 1B</strong> [CFB] - <strong>Autopoietic Systems</strong> – Chair: Barry McMullin</td>
</tr>
<tr>
<td></td>
<td>Jorge Soto-Andrade, S. Jaramillo, C. Gutiérrez and Juan-Carlos Letelier</td>
</tr>
<tr>
<td></td>
<td>Outboxes inviatores: A mathematical exploration of self-reference and metabolic closure</td>
</tr>
<tr>
<td></td>
<td>D. A. Contreras, U. Pereira, V. C. Hernandez, B. Reynaert and J.-C. Letelier</td>
</tr>
<tr>
<td></td>
<td>A loop conjecture for metabolic closure</td>
</tr>
<tr>
<td></td>
<td>A. Filippeti, A. Graudenzi, R. Serra, M. Villani, D. De Lucrezia and I. Poli</td>
</tr>
<tr>
<td></td>
<td>The role of energy in a stochastic model of the emergence of autocatalytic sets</td>
</tr>
<tr>
<td></td>
<td>Nikolaos Nanas</td>
</tr>
<tr>
<td></td>
<td>Autonomous learning in an information stream through autopoiesis</td>
</tr>
<tr>
<td>12:10 – 13:40</td>
<td><strong>Lunch, Posters &amp; Art Exhibit</strong> [Halls]</td>
</tr>
<tr>
<td>13:40 – 15:20</td>
<td><strong>Track 2A</strong> [Aden] - <strong>Language Evolution</strong> – Chair: Luc Steels</td>
</tr>
<tr>
<td></td>
<td>Luke Morehun and Ola Wikowskii</td>
</tr>
<tr>
<td></td>
<td>Devil in the details: Analysis of a coevolutionary model of language evolution via relaxation of selection</td>
</tr>
<tr>
<td></td>
<td>Jordi Arranz, Jason Noble and Eric Silverman</td>
</tr>
<tr>
<td></td>
<td>The origins of communication reinvented</td>
</tr>
<tr>
<td></td>
<td>Ryoko Uno, Keisuke Suzuki and Takashi Ikegami</td>
</tr>
<tr>
<td></td>
<td>An interactive word game as an evolution of pietro language</td>
</tr>
<tr>
<td></td>
<td>Michael Spranger</td>
</tr>
<tr>
<td></td>
<td>Recruitment, selection and alignment of spatial language strategies</td>
</tr>
<tr>
<td></td>
<td><strong>Track 2B</strong> [CFB] - <strong>Selection Dynamics</strong> – Chair: Richard Watson</td>
</tr>
<tr>
<td></td>
<td>Jeff Clune, D. Miswic, C. Ofría, R. E. Lenski, S. F. Elena and R. Sanjuan</td>
</tr>
<tr>
<td></td>
<td>Natural selection fails to optimize mutation rates for long-term adaptation on rugged fitness landscapes</td>
</tr>
<tr>
<td></td>
<td>Hywel P.T. Williams, Richard A. Boyle and Tim M. Lenton</td>
</tr>
<tr>
<td></td>
<td>Spatial structure creates community-level selection for nutrient recycling</td>
</tr>
<tr>
<td></td>
<td>Simon Powers, Christopher Heys and Richard A. Watson</td>
</tr>
<tr>
<td></td>
<td>How to measure group selection in real-world populations</td>
</tr>
<tr>
<td></td>
<td>Shelly Xiaonaow Wu and Wolfgang Banzhaf</td>
</tr>
<tr>
<td></td>
<td>Evolutionary transition through a new multilevel selection model</td>
</tr>
<tr>
<td>15:20 – 15:50</td>
<td><strong>Coffee Break, Posters &amp; Art Exhibit</strong> [Halls]</td>
</tr>
<tr>
<td>15:50 – 16:20</td>
<td><strong>Poster Pitch 1</strong> [Aden]</td>
</tr>
<tr>
<td>16:20 – 17:20</td>
<td><strong>Keynote 2:</strong> Ricard Solé – <em>Synthetic biocomputation: The possible and the actual</em> [Aden]</td>
</tr>
<tr>
<td>17:30 – 18:00</td>
<td><strong>Poster Pitch 2</strong> [Aden]</td>
</tr>
<tr>
<td>18:00 – 20:00</td>
<td><strong>Welcome Reception: Poster Inauguration &amp; Art Vernissage</strong> [Halls]</td>
</tr>
</tbody>
</table>
11th European Conference on Artificial Life (ECAL'11), Paris, August 8-12, 2011 – Program

Wednesday, August 10

8:00 – 9:00
Registration [Lobby], Breakfast, Posters & Art Exhibit [Halls]

9:00 – 10:00
Keynote 3. David Harel – Can we computerize an elephant? [Aden]

10:00 – 10:30
Coffee Break, Posters & Art Exhibit [Halls]

10:30 – 12:10
Track 3A [Aden]
Swarms – Chair: Marco Tomassini
Heiko Hamann, Thomas Schmickl and Karl Craikheim
Explaining emergent behavior in a swarm system based on an inversion of the fluctuation theorem

Alessandro Stramigi, Eliseo Ferrante, Al Emre Turgut, Vito Trianni, Carlo Pinciroli, Mauro Birattari and Marco Dorolo
Self-organized flocking with an heterogeneous mobile robot swarm

Jean-Marc Montanier and Nicolas Bredeche
Surviving the tragedy of commons: Emergence of altruism in a population of evolving autonomous agents

Arles Rodriguez Portela and Jonatan Gómez Perdomo
Programs self-healing over a termites simulator based on language games and evolutionary computing

Track 3B [CFB]
Cellular & Biochemical Networks – Chair: Christoph Flamm
Barry McMullin and James De Graeme
Evolution of self-maintaining cellular information processing networks

Joshua Payne and Jason Moore
Robustness, evolvability, and accessibility in the signal-integration space of gene regulatory circuits

Susan Khor
Why aren’t protein residue networks smaller worlds

Qinmin Pan, Christian Darabos, A. L. Tyler, J. H. Moore and J. L. Payne
The influence of whole genome duplication and subsequent diversification on environmental robustness and evolutionary innovation in gene

12:10 – 13:40
Lunch, Posters & Art Exhibit [Halls]

13:40 – 15:20
Track 4A [Aden]
Artificial Agency and Cognition – Chair: Inman Harvey
Georg Martius and J. Michael Herrmann
Tipping the scales: Guidance and intrinsically motivated behavior

Matthew Egbert and Xabier E. Barandiaran
Quantifying normative behaviour and precariousness in adaptive agency

Anne Ghoneim, Daryl L. Essam and Hussein A. Abbass
On computations and strategies for real and artificial systems

Felicia Mokom and Ziad Kobbi
A cultural evolutionary model for artificial capabilities

Track 4B [CFB]
Morphologies & Development 1 – Chair: Peter Dittrich
Lisa Schramm and Bernhard Sendhoff
An animal’s cell doctrine

S. Cussat-Blanc, N. Bredeche, H. Luga, Y. Duthen and M. Schoenauer
Artificial gene regulatory networks and spatial computation: A case study

Takuma Miyake and Kazuto Tanimura
Modelling cell division of B. subtilis using dynamic division of reaction spaces in a membrane artificial chemistry

Tadao Maekawa, Osamu Ueno, Norie Kawai, Enri Nishina, Manabu Honda and Tsutomu Cogashi
Evolutionary acquisition of genetic programs for death

15:20 – 15:50
Coffee Break, Posters & Art Exhibit [Halls]

15:50 – 17:30
Track 5A [Aden]
Agents: Mind, Motion and Evolution – Chair: Mark Bedau
Malte Schilling
Learning by seeing: Associative learning of visual features through mental simulation of observed action

Dusan Miseric, Charles Oria and Richard E. Lenski
Digital sex: Causes and Consequences

Angela Watkins, Jason Noble and C. Patrick Doncaster
An agent-based model of jaguar movement through conservation corridors

Nicholas Tomko, Inman Harvey, Andrew Philippides and Nathaniel Virgo
Many hands make light work: Group evolution and the emergent division of labour

Track 5B [CFB]
Biochemical Modelling – Chair: John McCaskill
Peter Kreyssig and Peter Dittrich
Reaction bow artificial chemistries

Nathaniel Virgo, Christiante Fernandes, Bill Bugge and Phil Husbands
The elongation catastrophe in physical self-replicators

Tomas Veloz, Bryan Reynolds, David Rujas-Camaggi and Peter Dittrich
A decomposition theorem in chemical organizations

Raphael Plasson, Kevin Montagne, Adrien Pedraz, Teruo Fuji and Yannick Ronez
A DNA toolbox for engineering in vitro life-like behaviors

17:30 – 18:00
Coffee Break, Posters & Art Exhibit [Halls]

18:00 – 20:00
Pioneers Panel Discussion – Back to the Origins of Life – Moderator: Hugues Bersini [Aden]
Mark Bedau, Takashi Ikegami, Barry McMullin, Norman Packard
Steen Rasmussen, Luc Steels, Susan Stepney
Thursday, August 11

8:00 – 9:00
Registration [Lobby], Breakfast, Posters & Art Exhibit [Halls]

9:00 – 10:00
Keynote 4: Eric Wieschaus – The mechanics of shape change in the Drosophila embryo [Aden]

10:00 – 10:30
Coffee Break, Posters & Art Exhibit [Halls]

10:30 – 12:10
Track 6A [Aden]
Complexity – Chair: Susan Stepney
Inman Harvey
Opening stable doors: Complexity and stability in nonlinear systems
Peter Wills
Life requires genetic representation and vice versa: Consequences for Aille
Tom Froese, Nathaniel Virgo and Takashi Ikegami
Life as a process of open-ended becoming: Analysis of a minimal model
M. Bedford, A. Buchanan, D. Chalmers, C. Francis, N. Passard & N. Pepper
Evidence in the patient record for the evolution of technology using citation and PageRank statistics

Track 6B [CFB]
Evolutionary Robotics – Chair: Jordan Pollack
Yuki Sato, Hiroyuki Izuka and Takashi Ikegami
An experimental and computational approach to the dynamic body boundary problem
Michael A. Lones, Andy M. Tyrrell, Susan Stepney and Leo S. Caves
Controlling legged robots with coupled artificial biochemical network
Davis Knox and John Rieffel
Scalable co-evolution of soft robot properties and gaits
Adam Wellis and Susan Stepney
Embodied copying for richer evolution

12:10 – 13:40
Lunch, Posters & Art Exhibit [Halls]

13:40 – 15:20
Track 7A [Aden]
Systems Biology – Chair: Luis Rocha
Roman V. Belovkhin, A. Channon, E. Aston, J. Aston and C. G. Knight
Theory and Practice of Optimal Mutation Rate Control in Hamming Spaces of DNA Sequences
Jonathan Fisher and Jason Moore
Distinguishing the effects of epistasis and pleiotropy using a variant of the NK model
Carole Knibbe, David P. Parsons and Guillaume Beslon
Parsimonious modeling of scaling laws in genomes and transcriptomes
Pasquale Stano, Paolo Carrara, Tereza Souza and Pier Luigi Luisi
An update on the minimal cell project: from the physics of solute encapsulation to the experimental modeling of cell communities

Track 7B [CFB]
Robot Control – Chair: Jozef Kelemen
Keita Nakamura, Ikue Suzuki, Masahito Yamamoto and Masashi Furukawa
Virtual fluid environment on behavior ability for artificial creature
Jose Niño Perea, Porto Silva, Pedro U. Lima and Alechirio Martínol
Formulating institutions as executable Petri nets for distributed robotic systems
Sancho Oliveira, Luis Nunes and Anders Lyhne Christensen
An experiment in mixing evolving and preprogrammed robots
Eiko Matsuda, Julien Hubert and Takashi Ikegami
A robotic approach to understand the role of vicarious trial-and-error in a maze task

15:20 – 15:50
Coffee Break, Posters & Art Exhibit [Halls]

15:50 – 17:30
Track 8A [Aden]
Morphologies & Development 2 – Chair: Rene Doursat
Anais Khaurg, Guy Theraulaz, Christian Jost, Andrea Perna and J. Gautrais
Denton Cockburn and Ziad Kibbi
WASP5: A weight allocated social pressure system for the emergence of agent specialization
Navneet Bhalla, Peter Bentley, Peter Vise and Christian Jacob
Staging the self-assembly process using morphological information
Jeff Clune and Hod Lipson
Evoking three-dimensional objects with a generative encoding inspired by developmental biology

Track 8B [CFB]
Robotics – Chair: Takashi Ikegami
Emmanouil Houndras and Panos Tzimias
Computational modeling of online reaching
Hirotake Moriguchi and Hod Lipson
Learning symbolic forward models for robotic motion planning and control
Evolving robot gaits in hardware: The HyperNEAT generative encoding vs.
Pedro Santana, Ricardo Mendonça, Luís Correia and José Barata
Swans for robot vision: The case of adaptive visual trail detection and tracking

17:30 – 18:00
Coffee Break, Posters & Art Exhibit [Halls]

18:00 – 19:00
Keynote 5: Jordan Pollack – Prospects for machine embryogenesis [Aden]

19:00 – 20:00
Art Show: Louis Bec – Lipoproteinomes: a fabricated epistemology [Aden]

20:00 – 20:30

20:30 – 23:30
Conference Banquet [Horn]
Friday, August 12

8:00 – 9:00
Registration [Lobby], Breakfast, Posters & Art Exhibit [Halls]

9:00 – 10:00
Keynote 6: Jacques Demongeot – General architecture of a genetic regulation network [Aden]

10:00 – 10:30
Coffee Break, Posters & Art Exhibit [Halls]

10:30 – 12:10

Track 9A [Aden]
Ecological Modeling – Chair: Mario Giacobini
Philip Gerlee and Torbjörn Lunch
Utar: An artificial ecology platform

Robin Gras, Abbas Golestani, Meisam Hosseini Sedehi, Manara Kheter, Yasaman Majdabadi Farahani, Mortezâ Mashayekhi, Sina Mîd Ione, Elham Salehi and Ryan Scott
Selective pressures for accurate altruism targeting: Evidence from digital evolution for difficult-to-test aspects of inclusive fitness theory

Jeff Ciune, Heather Goldsby, Charles Ofria and Robert T. Pennock
Ecological and biogeographical processes networks in forest ecosystems in monsoon East Asia: Identification and interpretation

Track 9B [CFB]
Complex Networks – Chair: Andrew Wuensche
Elisabeth Zu Erbach-Schoenberg, Connor McCabe and Seth Bullock
On the interaction of adaptive timescales on networks

Joseph Litziê, Siddharth Pritam and Mikhail Prokopenko
Computational capabilities of small-world Boolean networks

Artemy Kolchinsky and Luis M. Rocha
Prediction and modularity in dynamical systems

Richard Watson, Rob Mills and Christopher Buckley
Dynamical, multi-scale optimisation in biological regulatory networks

12:10 – 13:30
Lunch, Posters & Art Exhibit [Halls]

13:30 – 17:30
Satellite Workshops 3

CS-Sports
Complex Systems in Sports
Juan Julián Merelo Guervós, Antonio Mora García, Carlos Cotta Porras
[NatH]

DDLab
Exploring Discrete Dynamics with DDLab: From Cellular Automata to Random Networks
Andy Wuensche, Andy Adamatzky, Genaro Juarez Martinez (until 17:00)
[Sats]

SynBioCCC(2)
Synthetic Gene Regulatory Networks for Computation, Control and Communications (at 17:00)

iBioMath
First International Workshop on Integral Biomathics
Piamen Simeonov, André Ehresmann, Leslie Smith
[Cam]

INCUP
Information Coding in Unconventional Computing Substrates
Jerzy Gorecki, Andy Adamatzky
[Argl]

MASmms
Workshop on Multi-Agent Systems in Biology at meso or macroscopic scales
Pascal Ballet, Marie Beuron-Aimar, Guillaume Hutzel, Bertrand Lafort
[Well]

MEW
3rd Morphogenetic Engineering Workshop
René Doursat, Hiroki Sayama
[Guib]

Open Coffee Break, 14:30-16:30 [Lobby]

(End of Conference)
**Satellite workshops**

**9:00-13:00 and 14:30-18:30, Salon Gulbenkian**

**AAALE – Alife Approaches to Artificial Language Evolution**
Luc Steels, Tony Belpaeme

AAALE discusses operational experiments in cultural artificial language evolution with embodied agents (primarily humanoid robots). Such experiments have recently reached a new level of maturity thanks to significant progress in humanoid robotics, the availability of language technologies supporting constantly evolving grammars and embodied cognitive semantics, and new insights into semiotic dynamics and cultural evolution from a complex systems point of view. The topic of language evolution has been part of Alife and SAB conferences from the very beginning, simply because language evolution is one of the most outstanding puzzles of evolutionary biology and a challenging case study of cultural evolution. Moreover, performing experiments with robots in grounded language evolution poses enormous challenges for Alife approaches to robotics. This is the first workshop ever that focuses specifically on Alife approaches to Artificial Language Evolution.

**9:00-13:00 and 14:30-18:30, Salon du Cambodge**

**BioChemIT – 1st COBRA Workshop on Biological and Chemical Information Technologies**
Peter Dittrich, Zarka Khan, Martyn Amos

BioChemIT will provide a forum to present and discuss the latest advances of Bio/Chem IT research. The workshop should foster the interaction, exchange, and communication between Bio/Chem IT research groups and projects. It should contribute to building a scientific community and providing input for a strategy and vision of Bio/Chem IT. Topics: biological/chemical information technologies; molecular and chemical computing: protocells and synthetic cells; molecular robots; integration of information processing with (bio-)chemical production; nano-bio-info interface; cellular engineering, artificial neurons, and programmable information chemistry; unconventional computing substrates.

**9:00-13:00 and 14:30-18:30, Salon David-Weill**

**CoSMoS – 4th Workshop on Complex Systems Modelling and Simulation**
Paul Andrews, Susan Stepney, Peter Welch, Carl Ritson

CoSMoS 2011 will be the fourth in a series of workshops that provide a forum for research examining all aspects of the modelling and simulation of complex systems. This year, we will place a special focus on how complex systems simulations can begin to approach the scale of real-world complex systems. We will accept both full papers (for oral presentation) and abstracts (for poster presentation), which will be peer-reviewed. We will also have at least one invited speaker, and a panel discussion to close the workshop. As for the previous 3 workshops in the series, accepted papers and abstracts will appear in proceedings published by Luniver Press. Contributing authors and the first 40 attendees will receive a copy of the proceedings free of charge.

**9:00-13:00 and 14:30-18:30, Salon de l'Argentine**

**WAAT – Workshop on Artificial Autonomy: 20 years of practice of autonomous systems**
Tom Froese, Matthew Egbert, Xabier Barandiaran

Autonomy is a system’s capacity to produce, sustain and regulate itself and its relationship with the environment it co-determines. WAAT will evaluate 20 years of practice of autonomous systems, from the first ECAL (1991) until today, and review the state of the art, future challenges and research milestones. The notions of autonomy, autopoiesis, emergence, enaction, etc., have played a central role in Artificial Life but have also experienced a relative displacement as the field has made progress in more specific and specialized research fields (from network topology to ant intelligence, from evolutionary robotics to multicellular development). We believe that increasingly specialized trends in Alife should also be compensated with renewed attempts for integrative approaches. In this sense, reviewing and recovering the visionary and pioneering notion of autonomy 20 years later provides a challenging opportunity to re-assemble Artificial Life back into the organism-centered, emergent, holistic yet mathematically and conceptually mature notion of autonomy.
9:00-13:00, Salle Satsuma

ACCS – Artificial Chemical Computing Systems
Hideaki Suzuki, Hiroki Sayama

The theme of the ACCS tutorial, Artificial Chemistry (AChem), is a research approach that implements Alife systems by taking inspiration from bio-chemical systems. In a typical AChem study, we model the behavior of biological molecules, but unlike MD (molecular dynamics) or systems biology, we minimize the computational cost by dramatically simplifying the model, and try to make self-organizing phenomena happen in a computer. Self-organization is one of the most distinctive features of bio-molecular systems, and with this AChem’s approach, we can take one of the most promising pathways towards the design of computational systems with emergent characteristics. The first half of this tutorial summarizes the fundamental methodology for the AChem design. After prerequisite conditions for a typical AChem system are presented, the chemical reaction’s rate constants are formulated under the gas and liquid phases. In the latter half of the lecture, we we take three representative AChem systems, CGA, NAC, and ATN, and see how chemical approach makes those systems rich from the computational point of view.

9:00-13:00, Salle Nathan

SynBioCCC(1) – Workshop on the Design, Simulation, Construction and Testing of Synthetic Gene Regulatory Networks for Computation, Control and Communications
Nawwaf Kharma, Taras Kowalw

SynBioCCC will be the first workshop on synthetic biology in ECAL, and it aims at providing a forum for electrical and computer science/engineering researchers, who wish to be introduced to, or present their own work in, synthetic biology. This year, we will place a special focus on the three C’s (Computing, Control & Communications). Topics: Evolutionary & automated design of gene regulatory networks (GRNs); Modeling & simulation of GRNs; Novel GRN designs for computing, control & communication; Results of implemented GRNs (in wet labs); New paradigms of computing using DNA/RNA, genes and cells.

→ SynBioCCC(2) on Friday, August 12, 17:00

14:30-18:30, Salle Satsuma

RUTSAC – Research Using The Stringmol Artificial Chemistry
Simon Hickinbotham, Ed Clark, Adam Nellis

As in an RNA World, a molecule in the Stringmol Artificial Chemistry can be both genomic and enzymic, facilitating rich interactions between the genome and the phenotype. The hands-on RUTSAC tutorial will equip attendees with the knowledge and experience necessary to set up experiments with the Stringmol Artificial Chemistry. The Stringmol system will be introduced in four stages, corresponding to four interactive tasks. Workshop attendees will participate in these tasks by running the Stringmol code and designing their own molecules via an interactive website: 1) Bootstrap design: attendees will explore molecule-molecule interactions using the web-based demonstration tool. 2) Molecular diversity in a container: moving from a single molecule design to setting up and running a simulation of a container full of molecules. 3) Container war: observing the mechanisms of container takeovers through mutation and evolution. 4) Fight to the death: finally, the attendees will pit their replicator designs against each other, to see whose molecules will win in the fight to the death for resources!

14:30-18:30, Salle Nathan

SIM-A – System Immunology Models of Autopoiesis
Uri Hershberg, Sol Efroni

Artificial life ultimately is the attempt to define the basic characteristics of living systems and emulate them in novel computational and physical means. In the past, the field has been greatly influenced by thinking in the fields of computational neuroscience and molecular evolution. We suggest that the immune system and computational immunology may be better starting points in the attempt to define the core concepts of living systems. Immune dynamics are by nature multiscale, ranging from the molecular through the cellular to the systemic. As such they embody the multicellular cooperativity of second order autopoietic machines, in which local unicellular interactions without specific control lead to emergent cooperation and individual multicellular integrity. SIM-A is intended to bring together experimentalists and computational immunologists with an emphasis on what would be the best way to create a common language between the different models that have been created over the past years and insure that experimentalists are a driving force of this computational effort.
Tuesday, August 9

8:40-9:00 Introduction, Adenauer Auditorium
René Doursat, Hugues Bersini, Paul Bourgine

9:00-10:00 Keynote 1, Adenauer Auditorium
On the growth of brain tumours: Enhancing imaging techniques, highlighting limitations of current imaging, quantifying therapy efficacy and estimating patient life expectancy
James D. Murray
The prognosis for patients with high grade brain tumours (gliomas) is grim and the various treatment protocols such as surgery, radiation and chemotherapy cannot effect a cure. I shall describe, without any technical details, a simple but very practical model which uses patient data and brain scans to quantify the spatio-temporal growth of such brain tumours. Analysis of the model shows how difficult it is to decide on the tumour volume to be treated and shows why such treatments have so little success. The model simulations can estimate life expectancy for individual patients and show how it is possible to use the patient's past record to predict the efficacy of possible treatments. Recent patient data indicates that calculating such an index of treatment efficacy is indeed a realistic aim. With the increasing discussion about cell phone use and a possible increase in brain tumours, I shall describe how to obtain an estimate for when a brain tumour started following detection.

10:30-12:10 Track 1A, Adenauer Auditorium
Evolution & Games
Chair: Tom Lenaerts

Coordination games on small-worlds: Artificial agents vs. experiments
Enea Pestelacci, Marco Tomassini and Alberto Antonioni
Effective coordination is a key social ingredient and social structure may be approximated by networks of contacts. Using Stag Hunt games, which provide socially efficient and inefficient equilibria, we compare our simulation results using artificial players and evolutionary game theory with laboratory experimental work with human subjects on small-world type networks and with theoretical results. The conclusion is that the apparently encouraging results obtained in the few human experiments in which the local interaction structure seems to promote efficient equilibria, is neither supported by simulation results nor by theoretical ones.

Co-evolution of pre-play signaling and cooperation
Francisco C. Santos, Jorge M. Pacheco and Brian Skyrms
A finite-population dynamic evolutionary model is presented, which shows that increasing the individual capacity of sending pre-play signals (without any pre-defined meaning), opens a route for cooperation. The population dynamics leads individuals to discriminate between different signals and react accordingly to the signals received. The proportion of time that the population spends in different states can be calculated analytically. We show that increasing the number of different signals benefits cooperative strategies, illustrating how cooperators may take profit from a diverse signaling portfolio to forecast future behaviors and avoid being cheated by defectors.

Evolutionary dynamics of collective action
Jorge M. Pacheco, Francisco C. Santos, Max O. Souza and Brian Skyrms
In the natural world, performing a given task which is beneficial to an entire group requires the cooperation of several individuals of that group who often share the workload required to perform the task. The mathematical framework to study the dynamics of collective action is game theory. We study the evolutionary dynamics of cooperators and defectors in a population in which groups of individuals engage in N-person, non-excludable public goods games. We analyze several N-person games imposing the existence of a threshold which must be surpassed before collective action becomes successful, and discuss the evolutionary dynamics in infinite and finite populations. The introduction of a threshold leads, in all dilemmas, to a unified behavior, characterized by two interior fixed points. Additionally, we show how the chances of collective cooperation are strongly dependent on the perception that individuals have of the collective risk of failure. In this context, we are able to show how global cooperation is better achieved within i) small groups, addressing ii) highly risky situations characterized by iii) stringent condition to meet goal.

Evolution of partner selection
Pedro Mariano and Luís Correia
Partner selection is a mechanism that promotes sustainability of cooperators in cooperative dilemmas. In this paper we investigate the conditions that favour the evolution of a particular partner selection model that can be applied to any $n$-player game. The model allows a player to select partners that satisfy his preferences or to make random selection. Model parameters are under evolutionary control. We present simulations of our model that show evidence of the evolution of partner selection.
environment, we investigate the effects on the model behaviour of changes in the rate of the energy intake. Moreover, since living systems operate with a continuous exchange of matter and energy with the constraints, devoted to the study of the emergence of autocatalytic sets, in which some of the assumptions of the already existing models have been relaxed in order to explore the possible reasons which make the emergence of autocatalytic cycles difficult or which make them unstable. These results suggest that the incorporation of metabolic closure, i.e. the systems produce themselves, into the study of metabolic networks is a promising path for a deeper understanding of living systems.

Ouroboros avatars: A mathematical exploration of self-reference and metabolic closure
Jorge Soto-Andrade, Sebastian Jaramillo, Claudio Gutiérrez and Juan-Carlos Letelier

One of the most important characteristics observed in metabolic networks is that they produce themselves. This intuition, already advanced by the theories of Autopoiesis and (M,R)-systems, can be mathematically framed in a strange looking equation, full of implications and potentialities: f(f)=f. The later equation (here referred as Ouroboros equation), can be obtained in apparently dissimilar contexts like Robert Rosen's analysis of metabolism, hyperset theory and, importantly, the untyped lambda calculus. In this paper we study the Ouroboros equation appeared in those contexts, with emphasis on Rosen's (M,R)-systems and the work of Dana Scott about reflexive domains. We envision that the ideas behind this equation, an unique kind of mathematical concept initially found in biology, would play an important role towards a true systemic theoretical biology.

A loop conjecture for metabolic closure
Diego A. Contreras, Ulises Pereira, Valentina C. Hernandez, Bryan Reynaert and Juan Carlos Letelier

Although in the last few decades a variety of theoretical tools have been developed to better understand living organisms, their impact on experimental research has been rather limited. A common element between these theories is the idea of metabolic closure, i.e. the systems produce themselves. In spite of an increasing consensus on the relevance of closure, a clear and formal definition has remained elusive. In this paper we revisit RAF sets and we give a theorem ensuring the presence of a cycle of interdependent catalysts. Furthermore, we conjecture that these cycles give stability to the network. We also presented some computer simulations supporting our point of view. Unavoidably, our point of view introduces to the purely algebraic model of RAF sets the notion of fluxes, thus, we consider necessary to use Metabolic Control Theory in addition to RAF sets to understand the temporal evolution of autocatalytic networks. The results of this work, although still preliminary, show that the incorporation of metabolic closure is a promising path for a deeper understanding of living systems.

The role of energy in a stochastic model of the emergence of autocatalytic sets
Alessandro Filisetti, Alex Graudenzi, Roberto Serra, Marco Villani, Davide De Luzezia and Irene Poli

In most theories concerning the origin of life autocatalytic sets are supposed to play an important role in the phase transition between non-living and living matter. Although several theoretical models describe this phase transition, it is very hard to recreate the experimental conditions in the wet lab. We here introduce a stochastic model of catalytic reaction networks with energy constraints, devoted to the study of the emergence of autocatalytic sets, in which some of the assumptions of the already existing model are relaxed in order to explore the possible reasons which make the emergence of autocatalytic cycles difficult or which make them unstable. Moreover, since living systems operate with a continuous exchange of matter and energy with the environment, we investigate the effects on the model behaviour of changes in the rate of the energy intake.

Autonomous learning in an information stream through autopoiesis
Nikolaos Nanas

Nootropia is a complex, self-organizing system, inspired by the Theory of Autopoiesis and successfully applied so far to the challenging problem of profiling a user's interests. In this paper, we study Nootropia for the first time in the context of Artificial Life, as an autonomous system that learns to identify relevant information without human intervention. A series of experiments demonstrate that Nootropia can learn to identify documents belonging to a specific topic with minimal training. This is achieved through a deterministic process of self-organization, which, when coupled with a complex and dynamic information environment, gives rise to rich and unpredictable behavior. Nootropia is open to its environment and operates far from equilibrium, while it tries to maintain its identity within an information stream. Our exploration of the dynamics behind Nootropia’s autonomous learning capabilities lead to interesting insights, which may extend beyond its successful application to the problem of profiling and towards a new research stream that uses Nootropia as a means for studying computational autopoiesis.

13:40-15:20 Track 2A, Adenauer Auditorium
Language Evolution
Chair: Luc Steels

Devil in the details: Analysis of a coevolutionary model of language evolution via relaxation of selection
Luke McCrohon and Olaf Witkowski

In recent years computational modeling has become an important tool in the study of language evolution. For researchers faced with limited access to historical data and an inability to experiment directly with their subject matter this trend is hardly surprising. Models have been used not only to test particular hypotheses, but also as a source of data on the nature of interactions between various processes assumed to have played a role during language evolution. One particular area in which such modeling has been used is in the study of the interaction of biology and culture during evolution; so called gene-culture coevolution. In this paper we take an in depth look at one recent model from this area (Yamauchi and Hashimoto, 2010) and show that a set of behaviors observed in the model, which are claimed to be significant, are in fact artifacts produced by the design of the model. We describe how the agent “geography” is responsible for producing these behaviors, and show that it is something other coevolutionary models are also likely to be susceptible to.
The origins of communication revisited
Jordi Arranz, Jason Noble and Eric Silverman
Quinn (2001) sought to demonstrate that communication between simulated agents could be evolved without pre-defined communication channels. Quinn’s work was exciting because it showed the potential for ALife models to look at the real origin of communication; however, the work has never been replicated. In order to test the generality of Quinn’s result we use a similar task but a completely different agent architecture. We find that qualitatively similar behaviours emerge, but it is not clear whether they are genuinely communicative. We extend Quinn’s work by adding perceptual noise and internal state to the agents in order to promote ritualization of the nascent signal. Results were inconclusive; philosophical implications are discussed.

An interactive wall game as an evolution of proto language
Ryoko Uno, Keisuke Suzuki and Takashi Ikegami
A new interactive “wall game” is proposed in which two human players alternatively configure a pattern to communicate. A pattern consists of 3x3 sites, on which a player can place one of three symbols. The two major findings in this paper are i) the subjects mainly communicated in two modes. Either the subjects changed the pattern by watching the pattern as it is (dynamical mode) or by having narrative reflection (metaphorical mode). ii) Subjects switched between these two modes. Most of the experiments in evolutionary linguistics are based on “task-oriented communication” and they observe the emergence of lexical items. In contrast, our experiment explores whether “communication without purpose” leads to the emergence of complex rules such as linguistic grammar. We argue that the switching between the two modes observed in our experiment can be seen as a grammatical process in the sense that it is a procedure to take an internal state outside using the media (i.e., patterns in the wall game). Under this hypothesis, the players’ exploration of the media becomes a crucial step in the emergence of language and grammar.

Recruitment, selection and alignment of spatial language strategies
Michael Spranger
All languages of the world have a way to talk about space and spatial relations of objects. Cross-culturally, immense variation in how people conceptualize space for language has been attested. Different spatial conceptualization strategies such as proximal, projective and absolute have been identified to underly peoples conception of spatial reality. This paper argues that spatial conceptualization strategies are negotiated in a cultural process of linguistic selection. Conceptualization strategies originate in the cognitive capabilities of agents. The ecological conditions and the structure of the environment influence the conceptualization strategy agents invent and which corresponding system of lexicon and ontology of spatial relations is selected for. The validity of these claims is explored using populations of humanoid robots.

13:40-15:20 Track 2B, CFB Auditorium
Selection Dynamics
Chair: Richard Watson

Natural selection fails to optimize mutation rates for long-term adaptation on rugged fitness landscapes
Jeff Clune, Dusan Misevic, Charles Ofria, Richard E. Lenski, Santiago F. Elena and Rafael Sanjuán
The rate of mutation is central to evolution. Mutations are required for adaptation, yet most mutations with phenotypic effects are deleterious. As a consequence, the mutation rate that maximizes adaptation will be some intermediate value. This abstract summarizes a previous publication in which we used Avida, a well-studied artificial life platform, to investigate the ability of natural selection to adjust and optimize mutation rates. Our initial experiments occurred in a previously studied environment with a complex fitness landscape (Lenski et al. Nature, 423, 2003) where Avidians were rewarded for performing any of nine logic tasks. We assessed the optimal mutation rate by empirically determining which unchanging mutation rate produced the highest rate of adaptation. Then, we allowed mutation rates to evolve and we evaluated their proximity to the optimum. Although we chose conditions favorable for mutation rate optimization (asexual organisms not yet adapted to a new environment), the evolved rates were invariably far below the optimum across a wide range of experimental parameter settings (Fig. 1). We hypothesized that the reason mutation rates evolved to be suboptimal was the ruggedness of fitness landscapes. To test this hypothesis, we created a simplified ‘counting ones’ (a.k.a. ‘onemax’) landscape without any fitness valleys and found that, in such conditions, populations evolved near-optimal mutation rates (Fig. 2, top row). In contrast, once moderate fitness valleys were added to this simple landscape, the ability of evolving populations to find the optimal mutation rate was lost (Fig. 2, bottom two rows). Additional experiments revealed that lowering the rate at which mutation rates evolved did not preclude the evolution of suboptimal mutation rates (see original manuscript). We conclude that rugged fitness landscapes can prevent the evolution of mutation rates that are optimal for long-term adaptation because of the short-term costs of traversing fitness valleys. This finding has important implications for evolutionary research in both biological and computational realms.

Spatial structure creates community-level selection for nutrient recycling
Hywel T.P. Williams, Richard A. Boyle and Tim M. Lenton
Nutrient cycling is a ubiquitous feature of ecosystems at all scales, allowing productivity to rise beyond the limits set by external nutrient inputs. Nutrient cycling occurs as a side-effect of the metabolism of a diverse set of species that each performs a step in the recycling loop. Recycling loops can be large and involve many steps. At each step the possibility exists for ‘side-reactions’ in the form of species with metabolisms that consume an intermediate metabolite but do not create the product needed to complete the recycling loop. Also, at least some of the biochemical reactions in any closed recycling loop must be endergonic (energy-consuming) and thus recycling loops may be vulnerable to invasion or parasitism by species that consume intermediates but do not produce costly products needed to close the loop. The possibility of such destabilising side-reactions appears to conflict with the apparent stability and ubiquity of nutrient recycling in nature. Here we propose that the ecosystem-level autocatalysis provided by nutrient
How to measure group selection in real-world populations
Simon Powers, Christopher Heys and Richard A. Watson

Multilevel selection and the evolution of cooperation are fundamental to the formation of higher-level organisation and the evolution of biocomplexity, but such notions are controversial and poorly understood in natural populations. The theoretic principles of group selection are well-developed in idealised models where a population is neatly divided into multiple semi-isolated sub-populations. But since such models can be explained by individual selection given the localised frequency-dependent effects involved, some argue that the group selection concepts offered are, even in the idealised case, redundant and that in natural conditions where groups are not well-defined that a group selection framework is entirely inapplicable. This does not necessarily mean, however, that a natural population is not subject to some interesting localised frequency-dependent effects - but how could we formally quantify this under realistic conditions? Here we focus on the presence of a Simpson's paradox where, although the local proportion of cooperators decreases at all locations, the global proportion of cooperators increases. We illustrate this principle in a simple individual-based model of bacterial biofilm growth and discuss various complicating factors in moving from theory to practice of measuring group selection.

Evolutionary transition through a new multilevel selection model
Shelly Xiaonan Wu and Wolfgang Banzhaf

Most multilevel selection models in the literature focus on addressing the evolution of cooperation. Another aspect of multilevel selection theory is that it might be able to provide explanations for evolutionary transitions, which involve the creation of higher level complexes out of simpler elements. Here, we propose a multilevel selection model to support evolutionary transitions. This model employs a new operator called “cooperation” to build the hierarchical structure used in multilevel selection theory, and applies two types of multilevel selection to achieve transitions. We demonstrate by experiments on an extended N-player Prisoner’s Dilemma game that groups with all required features emerge from a population of independent individuals, no matter whether features are equally rewarded or not. Our experiments confirm that both types of multilevel selection mentioned are relevant to evolutionary transitions.
Wednesday, August 10

9:00-10:00 Keynote 3, Adenauer Auditorium

**Can we computerize an elephant?**

David Harel

The talk shows how techniques from computer science and software engineering can be applied beneficially to research in the life sciences. We discuss the idea of comprehensive and realistic modeling of biological systems, where we try to understand and analyze an entire system in detail, utilizing in the modeling effort all that is known about it. I will address the motivation for such modeling and the philosophy underlying the techniques for carrying it out, as well as the crucial question of when such models are to be deemed valid, or complete. The examples will be from among the biological modeling efforts my group has been involved in: T cell development, lymph node behavior, organogenesis of the pancreas, and fate determination in the reproductive system of the C. elegans nematode worm. The ultimate long-term “grand challenge” is to produce an interactive, dynamic, computerized model of an entire multi-cellular organism, such as the C. elegans, which is complex, but well-defined in terms of anatomy and genetics.

10:30-12:10 Track 3A, Adenauer Auditorium

**Swarms**

Chair: Marco Tomassini

- **Explaining emergent behavior in a swarm system based on an inversion of the fluctuation theorem**
  Heiko Hamann, Thomas Schmicl and Karl Crailsheim

  A grand challenge in the field of artificial life is to find a general theory of emergent self-organizing systems. In this paper we try to explain the emergent behavior of a simulated swarm by applying methods based on the fluctuation theorem. Empirical results indicate that the swarm is able to produce negative entropy within an isolated sub-system due to ‘frozen accidents’. Individuals of the swarm are able to locally detect fluctuations of the global entropy measure and store them, if they are negative entropy productions. By accumulating these stored fluctuations over time the swarm as a whole is producing negative entropy and the system ends up in an ordered state. We claim that this indicates the existence of an inverted fluctuation theorem for emergent self-organizing dissipative systems. This approach bears the potential of general applicability.

- **Self-organized flocking with an heterogeneous mobile robot swarm**
  Alessandro Stranieri, Eliseo Ferrante, Ali Emre Turgut, Vito Trianni, Carlo Pincioli, Mauro Birattari and Marco Dorigo

  Individuals living in animal groups show a great variation due to several factors such as age, experience, and morphology. This variation results in behavioral differences among the individuals. These differences cause observable and rich collective dynamics of the group when they are on the move. Robot swarms are also heterogeneous in nature due either to physical differences (hardware capabilities, battery level, and wear) or to behavioral differences intentionally imposed by the designers. In this paper, we study the coordinated motion of a group composed of behaviorally heterogeneous robots. Being inspired by the animal groups in Nature, we study self-organized flocking in a mobile robot swarm consisting of aligning and non-aligning robots. Aligning robots are capable of communicating their own orientation, or alternatively, of sensing their neighbors orientation, in order to agree on a common heading direction. Conversely, non-aligning robots lack this capability. Through systematic physics-based simulations, we show that a group of aligning and non-aligning robots can achieve cohesive, ordered and fast coordinated motion towards a common direction. Furthermore, we show that the performance is affected not only by the proportion of aligning robots, but also by the way they integrate information about their neighbors and also by heterogeneity in the way robots implement their movement.

- **Surviving the tragedy of commons: Emergence of altruism in a population of evolving autonomous agents**
  Jean-Marc Montanian and Nicolas Bredeche

  In this paper, we are interested in the tragedy of commons: a situation where selfish individuals may be the cause of the extinction of the whole population. The motivation is to study how a fixed-size population of autonomous agents (e.g. a group of virtual creatures or robots) may overcome this problem by learning to display altruistic behaviors through evolutionary adaptation. Experiments show that the proposed evolutionary adaptation algorithm favors the emergence of altruistic behavior under some assumptions regarding genome relatedness. In-depth experimental studies explore the relation between genotypic diversity and degree of altruism as well as the exact nature of the evolutionary adaptation process.

- **Programs self-healing over a termites simulator based on language games and evolutionary computing**
  Arles Rodríguez Portela and Jonatan Gómez Perdomo

  This paper presents a mechanism of programs self-healing in an environment of agents looking for food. The failure system is defined based on initial failures that each agent (termite) has on their programs. By using language games concepts and the Q-learning algorithm, termites diagnose failures on their programs. Termites also have enough information to determine if their programs are failing based on a simple voting system that is the result of language games of diagnosis. The proposed self-healing mechanism was tested on virtual worlds with 100, 200 and 500 termites and different failures per termite. The results show that the proposed approach is capable, from local interactions, of building a set of very specific diagnosis questions, allowing the system to diagnose more than one type of failure at the same time, while the accounted number of diagnosis questions for instructions with low failure probability is reduced. By using the voting system and storing a ranking of possible missing code lines, mutations are induced on the code and the system is capable of recovering the programs.
Robustness, evolvability, and accessibility in the signal-integration space of gene regulatory circuits

Joshua Payne and Jason Moore

Gene expression is commonly modulated by a set of regulating gene products, which bind to a gene's cis-regulatory region. This region encodes an input-output function, referred to as signal-integration logic, that maps a specific combination of regulatory signals (inputs) to a particular gene expression state (output). The space of all possible signal-integration functions (genotypes) is vast and highly redundant: for the same set of inputs, many functions yield the same expression output (phenotype). Here, we exhaustively characterize signal-integration space within a computational model of genetic regulation. Our goal is to understand how the inherent redundancy of signal-integration space affects the relationship between robustness and evolvability in regulatory circuits. Among a number of results, we show that robust phenotypes are (i) evolvable, (ii) easily identified by random mutation, and (iii) mutationally biased toward other robust phenotypes. We then explore the implications of these results for mutation-based evolution by conducting an ensemble of random walks between randomly chosen source and target phenotypes. We demonstrate that the time required to identify the target phenotype is independent of the properties of the source phenotype.

Why aren’t protein residue networks smaller worlds

Susan Khor

The principles underlying protein folding remains one of Nature’s puzzles with important practical consequences for Life. An approach that has gathered momentum since the late 1990’s, looks at protein hetero-polymers and their folding process through the lens of complex network analysis. Consequently, there is now a body of empirical studies describing topological characteristics of protein macro-molecules through their residue contact networks and linking these topological characteristics to protein folding. A common feature exhibited by such protein residue networks (PRNs) is the small-world property, i.e. they are heavily clustered at the local level, but have inter-nodal ties that effectuate short diameter and average path lengths (APL) at the global level. The relative short APLs of PRNs is believed to be an important topological feature facilitating interaction cooperativity crucial for rapid and correct protein folding. In this paper, in silico experiments are performed to investigate why PRNs, i.e. networks induced by spatial contacts between amino acid residues of a protein, do not have shorter APLs in spite of their importance to protein folding. We find that shorter average inter-nodal distances does not necessarily imply better search performance, i.e. more successful protein folding. Search performance of a zero-temperature Metropolis style hill-climber was not significantly improved by randomizing only the long-range links of PRNs even though such randomization significantly reduces APLs of PRNs while retaining much of the clustering and positive degree-degree correlation inherent in PRNs. However, this result is contingent upon the optimization function. We found that the optimization function which places PRNs in a favorable spot in the space of possible network configurations considered in this paper parallels an existing view in protein folding theory that neither short-range nor long-range interactions dominate the protein folding process. These findings suggest the existence of explanations, other than the excluded volume argument, beneath the topological limits of PRNs.

The influence of whole genome duplication and subsequent diversification on environmental robustness and evolutionary innovation in gene regulatory networks

Qinxin Pan, Christian Darabos, Anna L. Tyler, Jason H. Moore and Joshua L. Payne

In biological systems, whole genome duplication and subsequent diversification constitute powerful mechanisms for the discovery of new phenotypes and for the protection of these phenotypes against environmental perturbation. Here, we use Random Boolean Networks to investigate the influence of these genetic mechanisms on the relationship between evolutionary innovation and environmental robustness in gene regulatory networks. We find that whole genome duplication is highly deleterious in ancestral environments, but provides fitness advantages in novel environments, which come at the cost of reduced environmental robustness. We then show that the subsequent diversification of duplicated networks, via the loss of regulatory interactions, can partly negotiate this trade-off, improving evolutionary innovation and environmental robustness. We conclude by discussing the implications, limitations, and future directions of our research.
Learning algorithm in a control task and demonstrate its remarkable scalability with respect to the degrees of freedom of the system.

The individual is placed into a physics simulation environment and the distance it swims in a defined time is evaluated.

from the intrinsic exploratory movements rather than imposed by a control command. The learning paradigm is a form of guided self-organization and is complementary to both active and intrinsically motivated learning. We present a systematic analysis of the learning algorithm in a control task and demonstrate its remarkable scalability with respect to the degrees of freedom of the system.

An animat's cell doctrine
Lisa Schramm and Bernhard Sendhoff

We present a developmental model to simulate swimming digital organisms following an animat's cell doctrine. Morphology and control are encoded in one genome concurrently using artificial cells as the basic building blocks for both. Each individual starts with one cell in the middle of a computational environment, and its development is controlled by a gene regulatory network. The cells can differentiate into central pattern generators that control the movements of the resulting individual. After the developmental process, the individual is placed into a physics simulation environment and the distance it swims in a defined time is evaluated.
Contrary to most existing models, one genome for both, morphology and control is used and the CPGs representing the dynamic control contribute to the morphology of the organism.

Artificial gene regulatory networks and spatial computation: A case study
Sylvain Cussat-Blanc, Nicolas Bredeche, Hervé Luga, Yves Duthen and Marc Schoenauer
This paper explores temporal and spatial dynamics of coupled Genetic Regulatory Networks (GRN). In order to so, a GRN model is spatially distributed to solve a multi-cellular Artificial Ontogeny problem, and Evolutionary Computation is used to optimize the developmental sequences. An in-depth analysis is provided and show that such coupled GRNs display strong spatial behaviors. We present an agent-based model of jaguars (Panthera onca), scaled for fragmented habitat in Belize where proposals are used and the CPGs representing the dynamic control contribute to the morphology of the organism.

Artificial gene regulatory networks and spatial computation: A case study
Sylvain Cussat-Blanc, Nicolas Bredeche, Hervé Luga, Yves Duthen and Marc Schoenauer
This paper explores temporal and spatial dynamics of coupled Genetic Regulatory Networks (GRN). In order to so, a GRN model is spatially distributed to solve a multi-cellular Artificial Ontogeny problem, and Evolutionary Computation is used to optimize the developmental sequences. An in-depth analysis is provided and show that such coupled GRNs display strong spatial behaviors.

Modeling cell division of B. subtilis using dynamic division of reaction spaces in a membrane artificial chemistry
Takuma Miyake and Kazuto Tominaga
Localization of molecules in a natural cell plays important roles in interesting behavior of organisms like cell division and morphogenesis. Such localization is mostly formalized in a continuous space or lattice. This paper takes another approach using an artificial chemistry with membranes; we propose a dynamic division of reaction spaces to deal with molecular localization. As an application of the method, we modeled the cell division of B. subtilis. We executed the model on a simulator and observed the intended results.

Evolutionary acquisition of genetic program for death
Tadao Maekawa, Osamu Ueno, Norie Kawai, Emi Nishina, Manabu Honda and Tsutomu Oohashi
As part of our research on programmed self-decomposition, we formed the hypothesis that originally immortal terrestrial organisms evolve into ones that are programmed for autonomous death. We then conducted simulation experiments in which we examined this hypothesis using an artificial ecosystem that we designed to refer to a terrestrial ecosystem endowed with Artificial Chemistry (AChem). Our findings suggest that, in the case of a mortal organism appearing among a population of immortal organisms as a mutant which evolutionarily acquires a genetic program for death by means of self-decomposition, this organism and its surviving offspring surpass immortal organisms and eventually prosper with adaptive divergence under various environmental conditions within a certain probability.

15:50-17:30 Track 5A, Adenauer Auditorium
Agents: Mind, Motion and Evolution
Chair: Mark Bedau

Learning by seeing: Associative learning of visual features through mental simulation of observed action
Malte Schilling
Internal representations employed in cognitive tasks have to be embodied. The flexible use of such grounded models allows for higher-level function like planning ahead, cooperation and communication. But at the same time this flexibility presupposes that the utilized internal models are interrelating multiple modalities. In this article we present how an internal body model serving motor control tasks can be recruited for learning to recognize movements performed by another agent. We show that—as the movements are governed by an equal underlying internal model—it is sufficient to observe the other agent performing a series of movements and that there is no supervised learning necessary, i.e. the learning agent does not require access to the performing agents postural information (joint configurations). Instead, through the shared underlying dynamics the mapping can be bootstrapped by the observing agent from the sequence of visual input features.

Digital sex: Causes and consequences
Dusan Misevic, Charles Ofria and Richard E. Lenski
Many existing theories try to explain the evolution of sex, but the question remains unanswered due to scarcity of compelling and comprehensive empirical tests. Here we summarize the results of two of our published studies investigating evolution of sex using digital organisms. We used these evolving computer programs to test the hypothesis that sexual reproduction is advantageous in changing environments. We found that sex evolved to be the dominant mode of reproduction only when the environment was changing rapidly and substantially. Additionally, we measured the effects of sexual reproduction on genetic architecture, specifically modularity and epistasis. We found that sex profoundly influences genome organization, increasing modular organization and decreasing interactions between individual mutations organisms may experience. Our studies advanced the understanding of causes and consequences of sexual reproduction while also demonstrating the efficacy and power of in silico approaches to the study of the evolution of sex.

An agent-based model of jaguar movement through conservation corridors
Angela Watkins, Jason Noble and C. Patrick Doncaster
Wildlife corridors mitigate against habitat fragmentation by connecting otherwise isolated regions, bringing well-established benefits to conservation both in principle and practice. Populations of large mammals in particular may depend on habitat connectivity, yet conservation managers struggle to optimise corridor designs with the rudimentary information generally available on movement behaviours. We present an agent-based model of jaguars (Panthera onca), scaled for fragmented habitat in Belize where proposals already exist for creating a jaguar corridor. We use a least-cost approach to simulate movement paths through alternative possible landscapes. Six different types of corridor and three control conditions differ substantially in their effectiveness at mixing agents across the environment despite relatively little difference in individual welfare. Our best estimates of jaguar movement behaviours suggest that a set of five narrow corridors may out-perform one wide corridor of the same overall area. We discuss the utility of ALife modelling for conservation management.
Many hands make light work: Group evolution and the emergent division of labour
Nicholas Tomko, Inman Harvey, Andrew Philippides and Nathaniel Virgo

Most standard genetic and evolutionary algorithms (GAs) are unable to evolve cooperative solutions to problems where there is a division of labour among genetically different component parts. This is because standard GAs evaluate and select all individuals on the same task which leads to genetic convergence within the population. The goal of evolutionary niching methods is to enforce diversity in the population so that this genetic convergence is avoided. One drawback with some of these niching methods is that they require a priori knowledge or assumptions about the specific fitness landscape in order to work. Another issue is that many of these niching methods are not set-up to work on cooperative tasks where fitness is only relevant at the group level. In this paper we present the Group GA which is a group based evolutionary algorithm that can evolve cooperative solutions to problems using emergent niching with minimal a priori assumptions. We demonstrate this novel GA on an immune system matching task and explain why we think this type of GA has the potential to effectively solve a wide range of problems that would benefit from being solved cooperatively.

15:50-17:30 Track 5B, CFB Auditorium

Biochemical Modeling
Chair: John McCaskill

Reaction flow artificial chemistries
Peter Kreyssig and Peter Dittrich

Artificial chemistries have been analysed mostly under the precondition of a well-stirred reaction vessel. In other words, the localisation of molecules is ignored for simplicity. Here we drop this assumption and replace it with a spatial distribution of molecules given by a flow, i.e., molecules move according to a given vector field. This can be seen as a particular type of dynamics. It also gives additional parameters to the control over the development of the chemistry over time. In particular, the modelling of membranes and transport processes which occur in cells, for example, can be described using continuous vector fields instead of giving a discrete formulation. We give some examples and ideas for analysing such chemistries via a stochastic simulation, a PDE and chemical organisations.

The elongation catastrophe in physical self-replicators
Nathaniel Virgo, Chrisantha Fernando, Bill Bigge and Phil Husbands

An insufficiently appreciated paradox in the origin of life is that there is no template replication without specific ligation, but no specific ligation without template replication. We investigate this problem by building a physical model of self-replication out of specifically shaped plastic pieces with embedded magnets, which float around on an air-hockey type table. Non-catalysed ligation is ligation in which complementary oligomers or monomers are joined together without a template catalyst, i.e. spontaneously generated. Template directed ligation is ligation that is catalysed by hybridization upon a template strand. Homologous ligation is template directed ligation that does not result in elongation at a staggered end. It was shown previously in simulations and chemical experiments that non-enzymatic template replication suffers from the elongation catastrophe caused by excess free-ligation and only partially homologous ligation. The spontaneous generation of de novo sequences rather than the replication of existing sequences transforms evolution by natural selection into mere random search. Non-homologous ligation results in sequences being trapped in elongating strands. The extant solution for avoiding these fates is the use of highly evolved protein ligases. The chicken and egg question is how to achieve specific ligation without complex enzymes that require template replication in the first place? By building a real physical model of template replication a new answer to this question is suggested. We propose that early pre-biotic monomers required structural specializations that reduced the rate of non-catalysed ligation and of partially homologous ligation without the need of an external enzyme.

A decomposition theorem in chemical organizations
Tomas Veloz, Bryan Reynaert, David Rojas-Camaggi and Peter Dittrich

The Chemical Organization Theory (COT) is an abstract reaction network model that has a deep connection to autopoiesis as they share the same central topic: Organization. The main characteristic of autopoietic systems is that they preserve their own organization; this constitutes their identity. In terms of COT, organizations are special reaction networks which are closed and self-maintaining. Organizations compose the majority of stable behaviours of a reaction network, in particular every fixed point can be mapped to an organization. Obtaining the set of organizations of a network is a central objective in COT, but it is usually a complex computational task. This work intends to reveal the underlying mathematical structure of organizations. We state a theorem of decomposition for organizations to understand the difficulties of verifying if a set of molecular species is an organization. This suggests a step towards the development of more efficient algorithms and the classification of reaction networks in terms of how complex it is to obtain its set of organizations. We also discuss the consequences of this theorem in relation to autopoietic systems.

A DNA toolbox for engineering in vitro life-like behaviors
Raphaël Plasson, Kevin Montagne, Adrien Padirac, Teruo Fujii and Yannick Rondelez

We developed a modular toolbox based on a simple biochemical machinery, for designing arbitrary experimental chemical networks. As a proof of concept, we successfully assembled an autocatalytic unit with a negative feedback loop, generating a predictable chemical oscillator. This can be used to construct other life-like functions (bistable, gradient responsive switches, logical gates, boolean networks). Compartimentalization of these systems may provide a good platform for designing protocols.
18:00-20:00 Pioneers Panel Discussion, Adenauer Auditorium

**Back to the Origins of ALife**

Moderator: Hugues Bersini

**Mark Bedau, Takashi Ikegami, Barry McMullin, Norman Packard, Steen Rasmussen, Luc Steels, Susan Stepney**

_Do we need a theory in the era of massive data flow?_

**Takashi Ikegami**

Massive Data Flow (MDF) is everywhere these days; from data about neural cells, social insects and genetic networks, to Lifelog (digital storage of a person’s visual and audio life log) and SNS (Social network service) data streams. Current web and device technology has made it possible for us to record detailed and massive data flows of artificial and real living systems.

But how can we analyze and understand MDF? Can a simple toy model based on a plausible narrative and simulation still tell us something? Concepts like “the edge of chaos” and “self-organized criticality” once helped us to understand living systems, but we do not know whether the same concepts can be useful to MDF.

I think studies of artificial life in MDF need larger models, because we need the strength of models that overcomes MDF. Possible larger models do not have to mimic existing living creatures but can be larger, in the sense of novel invention and utilization of space and time. In other words, to understand the complexity of MDF is to recast and reconfigure it into a larger artificial model. Indeed, I myself made a large model called “MTM” (Mind Time Machine) in 2010 that ran for three months in an open space, receiving massive visual data from the environment with 15 cameras, processed by internal neural dynamics with a learning capability, and showing sustainable complex adaptive dynamics.

We need a theory to make large artificial life models and to take them out into the real world.

**A review of one approach to bottom up assembly of minimal life**

**Steen Rasmussen**, Pierre-Alain Monnard, Martin Hanczyc, Anders Albertsen, James Boncella, Eva Bonzli, Filippo Caschera, Mark Dorr, Harold Fellermann, Maik Hadorn, Wendie Jørgensen, Philipp Loffler, Sarah Maurer, Kent Nielsen, Pernille Pedersen, Carsten Svaneborg, Michael Wamborg, Rafal Wieczorek and Hans Ziock.

When seeking to assemble minimal life from the bottom up in wet carbon chemistry, the critical properties of life apparently emerge from the interconnected functions of three subsystems: information, metabolism and container. Such interconnected supramolecular systems, so-called protocells, are under the right circumstances able to mimic the main functions of a living cell although in a very simplified manner.

Seeking to create minimal life from the top down leads us to a somewhat different picture, where construction of synthetic / streamlined genomes becomes the critical scientific issue. How to integrate the knowledge we obtain from the top down- and the bottom up approaches is a great challenge for our and related communities and a good problem to discuss at this meeting.

In technical terms, our bottom up team explores ruthenium-based photocatalysis as metabolism, fatty acids vesicles, oil droplets and reverse micelles as containers and lipophilic XNA as minimal informational systems. Based on our experimental, computational and theoretical work we review protocell feeding, growth, division, motility, and information controlled metabolic production of containers.

Finally, we demonstrate preliminary integration of biochemical- and microelectromechanical (MEMS) systems where life-like information processing and material production occur and interact in different media and as such form an exciting frontier for the study of artificial life.

**ALife: a tension between biology and software engineering**

**Susan Stepney**

Biological systems are insanely complicated. If we look at the details of plant growth, of the vertebrate adaptive immune system, of bacterial horizontal gene transfer (to pick three areas with which I have a soupçon of familiarity), it is all insanely complicated, on every level, from top to bottom. When a feature is this ubiquitous, it may just be necessary. It is at least telling us something important.

One of the guiding principles of ALife is studying, understanding, and creating life from the bottom up. Since our only current exemplar, biological life, is insanely complicated, even at the bottom, what does this tell us about in silico implementations?

Everything we are taught in Software Engineering is about reducing, constraining, containing, and managing complexity. Well-defined small stable interfaces. Formally specified requirements. Rigorous development of correct code. And all this known and documented before the code is deployed in the field.

Life however exhibits open-ended evolution, continual novelty: not only new organisms, but new species, new families, new phyla, new kinds of life. Evolution evolves. The code of life writes itself.

Object-oriented agent-based simulations running inside an evolutionary algorithm, no matter how bio-inspired the genetic operators, nor how bio-inspired the developmental stage, are closed. They cannot escape their small pre-specified box in possibility space. They cannot exhibit open-ended evolution. If we want life in silico, we have to allow the code to write itself.

I am not suggesting that we throw up our hands in despair, pour assembly language into a big bucket and just let it trample all over itself, in the hope that life will emerge after several billion CPU years. We can use bio-inspiration at the whole simulation level, to develop code that can self-adapt and self-modify in ways plausibly analogous to bio-evolutionary processes. Hand-in-hand with our sophisticated understanding of biology, we need to use more sophisticated computer science, including self-modification through computational reflection.
Thursday, August 11

9:00-10:00 Keynote 4, Adenauer Auditorium

The mechanics of shape change in the Drosophila embryo

Eric F. Wieschaus, Adam C. Martin, Bing He, Matthias Kaschube, Oleg Polyakov

With the first three hours of development, the Drosophila embryo establishes a precise pattern of transcription factors that divides the blastoderm into groups of cells destined to form different organs and tissues in the adult. Along the dorsal ventral axis, the first and perhaps most important of these cell fate decisions is the establishment of mesoderm controlled by expression of the Twist and Snail transcription factors. These cell fates decisions are immediately translated in changes in the shapes and physical properties of the 800 mesodermal cells and result in the formation of the furrow that translocates them to the interior. Although at the cellular level these changes involve a re-organization of the cytoskeleton, adhesion and motor activities to achieve distinct shape we are interested in the underlying physical parameters that govern behavior.

In my talk I will discuss the relationship between the initial transcription profiles and a novel pulsating reorganization of the Actin/Myosin cytoskeleton in the apical region of cells that will make the ventral furrow. We show that the resultant contractile pulses drive cell shape changes in the entire mesodermal primordium. The individual contractions appear to be unpolarized but they result in polarized wedge-like constrictions because global tension in the sheet is polarized along the AP axis. We analyze the force distributions in the mesodermal primordia using a combination of genetics and RNAi to lower adhesive strengths between cells, and laser dissections to locally disrupt the cytoskeleton.

We have developed analytical tools that allow tracking surface areas and volumes of all 800 mesodermal cells during the process of furrow formation. We find that cell volume is essentially constant during the process and that global cell shape changes are pulsed in synchrony with the Actin/Myosin contractions in the apical surface. We envision that force generated apically is transmitted over large distances by the non-compressible nature of the cytoplasm and suggest that similar mechanism that may underlie many morphogenetic movements.

10:30-12:10 Track 6A, Adenauer Auditorium

Complexity

Chair: Susan Stepney

Opening stable doors: Complexity and stability in nonlinear systems

Inman Harvey

Generic complex systems of many interacting parts can model both natural and artificial systems, and the conditions for their stability are of interest. Two influential papers (Gardner and Ashby, 1970; May 1972) laid down a mathematical framework suggesting that, without some specific constraints on the interactions, such systems are very likely to be unstable as they increase in size and connectance. We draw attention to a programming error and to flaws and omissions in reasoning that discredit such conclusions when applied to nonlinear systems. With nonlinearity the role of ‘ambiguous’ functions, where the sign of an interaction varies between plus and minus according to context, is highlighted as increasing the number and variety of equilibria. Unimodal ‘hat-functions’ are a very basic class of ambiguous function. In Daisyworld models they serve to model a viability range for a species in a biota-environment system that results in an extended range of stable equilibria. It is concluded that the flaws in the traditional framework make it unsuitable for understanding generic complex nonlinear systems, and that opening up to the use of these ambiguous functions increases the prospects for finding stability.

Life requires genetic representation and vice versa: Consequences for Alife

Peter Wills

It is inconceivable that complex networks of physico-chemical processes displaying levels of specificity typical of molecular biological systems could possibly be controlled in an integrated fashion without the creation of some mode of informational representation in molecular form – what we call genes. It is equally inconceivable that DNA sequences could attain any representational meaning of biological significance except through their natural selection as parts of systems which express the information in them. Nothing worthy of the designation “Artificial Life” will exist until an information-interpreter/constructor coupling of the sort that emerged at life’s origin on our planet is recapitulated in the laboratory. Current motivation for attempting to achieve such a goal is highly questionable.

Life as a process of open-ended becoming: Analysis of a minimal model

Tom Frosse, Nathaniel Virgo and Takashi Ikegami

We argue that the phenomenon of life is best understood as a process of open-ended becoming and that this potentiality for continuous change is expressed over a variety of timescales, in particular in the form of metabolism, behavior, development, and evolution. We make use of a minimal synthetic approach that attempts to model this potentiality of life in terms of simpler dissipative structures, using reaction-diffusion systems to produce models that exhibit these characteristics. An analysis of the model shows that it exhibits some instances of these kinds of changes, but we do not consider it open-ended enough to be called alive. Accordingly, the model sheds light on the possible origins of life on earth and, due to its practical limitations, on the role of the genetic system in the subsequent evolution of life.
Evidence in the patent record for the evolution of technology using citation and PageRank statistics
Mark A. Bedau, Andrew J. Buchanan, Devin W. Chalmers, C. Cooper Francis, Norman H. Packard and Noah M. Pepper
We examine evidence for the evolution of technology using citation and PageRank statistics of the US patent record, as well as data produced by a number of simple models serving as null hypotheses. We study three classes of models, driven respectively by what we term random, preferential, and a priori attachment. We make qualitative and quantitative comparisons of the cumulative citation curves produced by the patents and the three models. We find that random, a priori, and preferential attachment models fail to explain certain significant patterns in the patent record.

10:30-12:10 Track 6B, CFB Auditorium
Evolutionary Robotics
Chair: Jordan Pollack
An experimental and computational approach to the dynamic body boundary problem
Yuki Sato, Hiroyuki lizuka and Takashi Ikegami
In this paper, we propose an experimental and computational model to challenge the dynamic body boundary problem, as seen in the rubber hands illusion and phantom limbs. Our strategy examines an agent’s “attention shift”. A computational model (lizuka & Ikegami, 2005) was used to explore how a body and sensor can be made inseparable. A model agent was required to determine the number of vanes on a windmill by touching the windmill blindly with a stick. By adding an additional windmill to the first one, we investigated the agent’s shift of attention, i.e. the agent could either determine the vanes on the first windmill, or the second windmill by using the first one as a tool. In other words, an agent’s body image can shift from its arm tip to the boundary between the first and second windmill. We then introduced an experiment with a real windmill model to test the hypothesis shown by the theoretical model. Subjects were tasked with determining the number of vanes on the second windmill. We found that sensory-motor correlations between their actions and perceptions of the movement of the windmills had an important role in extending their body boundaries.

Controlling legged robots with coupled artificial biochemical network
Michael A. Lones, Andy M. Tyrrell, Susan Stepney and Leo S. Caves
Artificial biochemical networks (ABNs) are computational architectures motivated by the organisation of cells and tissues at a biochemical level. In previous work, we have shown how artificial biochemical networks can be used to control trajectories in discrete and continuous dynamical systems. In this work, we extend the approach to the control of a hybrid dynamical system: a legged robot. Taking inspiration from biological cells, in which complex behaviours come about through the interaction of different classes of biochemical network, we develop the notion of a coupled artificial biochemical network, in which an artificial genetic network controls the configuration of an artificial metabolic network. Using a higher-level robotic control task, we show how the coupled network finds solutions which can not be readily expressed using the artificial genetic network or artificial metabolic network alone. Our results also show the important role that non-linear maps can play as a natural source of complex dynamics.

Scalable co-evolution of soft robot properties and gaits
Davis Knox and John Rieffel
One of the outstanding challenges in soft robotics is the chicken-and-egg problem of body/brain design: generation of locomotion is predicated on the existence of a locomotion-capable body, and generation of body plans is predicated upon the existence of effective locomotion. This problem is compounded by the high degree of coupling between the material properties of a soft body (such as stiffness or damping coefficients) and the effectiveness of a gait. In this work we describe a means by which the material properties of a simulated soft body co-evolve alongside locomotive gaits. Improvements in simulation time, with no loss of overall fitness, are obtained by incrementally increasing mesh density over the course of evolution.

Embodied copying for richer evolution
Adam Nellis and Susan Stepney
We address the process of copying in Artificial Life organisms. Copying is a source of mutations, a crucial component in evolution. We propose that rich copying mechanisms, and thereby rich evolutionary systems, can be obtained by embodying the copying process in a lower-level simulation. We demonstrate an embodied copying process that allows the system to alter its own mutation rate, without having the concept of a mutation rate parameter explicit in the system.

13:40-15:20 Track 7A, Adenauer Auditorium
Systems Biology
Chair: Luis Rocha
Theory and practice of optimal mutation rate control in Hamming spaces of DNA sequences
Roman V. Belavkin, Alastair Channon, Elizabeth Aston, John Aston and Christopher G. Knight
We investigate the problem of optimal control of mutation by asexual self-replicating organisms represented by points in a metric space. We introduce the notion of a relatively monotonic fitness landscape and consider a generalisation of Fisher's geometric model of adaptation for such spaces. Using a Hamming space as a prime example, we derive the probability of adaptation as a function of reproduction parameters (e.g. mutation size or rate). Optimal control rules for the parameters are derived explicitly for
reported here have been published in Mol. Biol. Evol., Biosystems and Alife XII.

network (number of nodes and links) thus reproducing parsimoniously a large panel of known biological properties. The results
phenomenon concerns genome size and content (non-coding DNA, presence of operons, number of genes) as well as gene
undergoing high spontaneous rearrangement rates show more compact structures than individuals undergoing lower rates. This
insights into Kauffman's complexity catastrophe.

Parsimonious modeling of scaling laws in genomes and transcriptomes
Carole Knibbe, David P. Parsons and Guillaume Beslon
We report here the use of Aevol, a software developed in our team to unravel the indirect selective pressures (i.e. pressures for
robustness and/or evolvability) that act on the genome and transcriptome structures. Using Aevol, we have shown that these
structures are under strong -- although indirect -- pressure due to the mutagenic effect of chromosomal rearrangements. Individuals
undergoing high spontaneous rearrangement rates show more compact structures than individuals undergoing lower rates. This
phenomenon concerns genome size and content (non-coding DNA, presence of operons, number of genes) as well as gene
network (number of nodes and links) thus reproducing parsimoniously a large panel of known biological properties. The results
reported here have been published in Mol. Biol. Evol., Biosystems and Alife XII.

An update on the minimal cell project: From the physics of solute encapsulation to the experimental modeling of cell
communities
Pasquale Stano, Paolo Carrara, Tereza Perreira de Souza and Pier Luigi Luisi
The minimal cell (MC) project aims at understanding the emergence of cellular life by constructing experimental models of cells,
according to a synthetic (constructive) biology approach. Our strategy -- also known as the semi-synthetic one -- is based on the
encapsulation of the minimal number of biomolecular components inside lipid vesicles (liposomes). Being interested in studying the
key step for constructing semi-synthetic cells, namely the physical entrapment of the solutes, we have recently reported that the
mechanism of vesicle formation can bring about to a spontaneous local concentration of proteins inside vesicles (Luisi et al.,
ChemBioChem 2010, 11, 1989-1992). In particular, it was shown that the protein ferritin can reach intravesicle concentration of at
least one order of magnitude higher when compared to the bulk (external) concentration. This self-organization phenomenon might
give a rational account for the formation of functional cell from diluted solutions, and therefore help to understand the origin of
metabolism. The effective encapsulation of solutes, however, is only one of the ways for achieving functional cells. The second
route is fusion of vesicles or the exchange of solutes among vesicles (Caschera et al., J. Coll. Inter. Sci. 2010, 345, 561-565). Both
processes allow the combination of different solutes to give compartments that can exhibit improved reactivity. Aiming at developing
a realistic model for cooperative interactions among vesicles, we have recently developed a cell colony model. This is based on the
formation of lipid vesicles clusters adherent to a solid substrate, representing a minimal model of cell communities. Here we
summarize the most significant aspects of our recent activities.

13:40-15:20 Track 7B, CFB Auditorium
Robot Control
Chair: Jozef Kelemen

Virtual fluid environment on behavior ability for artificial creature
Keita Nakamura, Ikuo Suzuki, Masahito Yamamoto and Masashi Furukawa
An environment plays an important role in behaviors acquisition for artificial creatures. Thus, the environment must obey the
physical laws. In this paper, it is examined how the behavior differences appear when the artificial creature autonomously behaves
in some fluid environments. We construct the approximate virtual fluid environment with low computing costs to simulate the
behavior acquisition for artificial creatures. Also we propose a simulation method for artificial creatures in consideration of effects
from the virtual fluid environment based on physics modeling. As a result of simulation, we verify that it is possible for the creature
to acquire adaptive behaviors in different environments. After evolution, the creature behaves autonomously by leveraging
effectively fluid forces in each virtual environment.

Formalizing institutions as executable Petri nets for distributed robotic systems
José Nuno Pereira, Porfírio Silva, Pedro U. Lima and Alcherio Martinoli
Institutional Robotics is a new approach to the coordination of distributed robotic systems, drawing inspiration from social sciences.
It aims to provide a comprehensive strategy for specifying social interactions among robots in the form of institutions. In this paper,
we present a formalism for institutions in the Institutional Robotics model. We apply this formalism to two case studies. The first is
concerned with a distributed swarm of simple robots which has to maintain wireless connectivity. The second is concerned with role
allocation in a robotic team to improve coordination and performance in a given task.
An experiment in mixing evolving and preprogrammed robots
Sancho Oliveira, Luis Nunes and Anders Lyhne Christensen

Artificial evolution of robot behavior is commonly conducted in environments containing a single robot or multiple robots that are all controlled by evolving behavioral logic. In this paper, we take a novel approach and study how the presence of preprogrammed robots affects the evolutionary process and the solutions evolved. We evolve behavioral control that enables robots to forage. The robots are situated in an environment that contains a nest and a number of prey. The robots must either push or carry the prey to the nest. We analyze the behaviors evolved in mixed setups in which one or more preprogrammed robots are present. We compare these behaviors to behaviors evolved in non-mixed setup in which no preprogrammed robots are present. The results show that the evolving robots learn to collaborate with the preprogrammed robots, and that the performance of some of the solutions evolved in the mixed setup are higher than those obtained by homogeneous groups of robots.

A robotic approach to understand the role of vicarious trial-and-error in a T-maze task
Eiko Matsuda, Julien Hubert and Takashi Ikegami

Vicarious trial-and-error (VTE) is a type of conflict-like behavior, observed in route selection tasks (Tolman (1939)). Studies of VTE have shown a correlation between the number of VTEs exhibited by a system with its learning efficiency. At the onset of learning a task, the number of VTEs increases, and when the learning reaches its plateau, it decreases. The question we explore in this paper concerns the role of VTE. Basing ourselves on a model developed by Bovet and Pfeifer (2005), we ran robotic experiments to compute the number of VTEs during the learning of a T-maze task. Our results first show that what has been found in rats can be replicated in artificial systems. Furthermore, by changing the connectivity pattern of the original model, we discovered that the connection between VTEs and learning efficiency might not be necessarily true as our results show that two models exhibiting the same performance can possess a different pattern of VTEs. By comparing the robustness of the two models under varied conditions, we propose that VTEs are connected to the adaptivity of a system to environmental changes.

15:50-17:30 Track 8A, Adenauer Auditorium
Morphologies & Development 2
Chair: René Doursat

A computational model of ant nest morphogenesis
Anais Khuong, Guy Theraulaz, Christian Jost, Andrea Perna and Jacques Gautrais

The nests of social insects are not only impressive because of their sheer complexity, but also because they are built from much smaller agents whose work is not centrally coordinated. A central question is therefore how this coordination can lead to such large scale structures. In this paper we present an individual based nest construction model from experimentally inspired rules. The coordination of the building process is achieved through three main ingredients: 1) stigmergy, which implies that the local configuration of the structure is the stimulus which determines how to continue, 2) body template, where the interaction between the ant's body and the growing structure determines the proportions of the emerging pattern, and 3) a construction pheromone, a chemical compound capable of triggering building actions. Our simulations show that this simple set of coordination rules can reproduce the key features observed experimentally in the ant Lasius niger, notably the emergence of mushroom-like pillars and layered structures. A sensitivity analysis on the evaporation rate of the construction pheromone shows that a large range of architectures, from dynamic multilayered nests to compact sponge-like structures, can be produced with the same behavioural rules by simply modifying evaporation rate. We discuss the relevance of these results with respect to the variety of nest architectures found in social insects.

WASPS: A weight-allocated social pressure system for the emergence of agent specialization
Denton Cockburn and Ziad Kobti

Division of labour, or specialization, is common in many types of insect colonies. It emerges in some of these societies as a result of age polyethism, whereby the division of labour is tied to the age of the individuals. One known method that explains this is social inhibition. Individuals release pheromones when they interact with other agents. The strength of their pheromones is tied to their age. These pheromones inhibit the desire of other agents to perform the same task. Using social inhibition, individual agents can be allocated among the available tasks to be performed related to the colony. We apply a variation of this approach to the problem domain where agents can divide their time among multiple tasks. While age is not a factor, agents differ in their skill at performing each task. We create a weight-allocated social inhibition approach whereby more skilled agents inhibit the desire of less skilled agents to perform a task. We are able to see that this approach drives agents toward tasks where they have comparative advantages. This leads to an increase in the division of labour within the population. While inspired by social insects, this approach is easily applicable to agents in other domains.

Staging the self-assembly process using morphological information
Navneet Bhatta, Peter Bentley, Peter Vize and Christian Jacob

One of the practical challenges facing the creation of self-assembling systems is being able to exploit a limited set of fixed components and their bonding mechanisms. Staging addresses this challenge by dividing the self-assembly process into time intervals, and encodes the construction of a target structure in the staging algorithm itself and not exclusively into the design of components. Previous staging strategies do not consider the interplay between component physical features (morphological information). In this work we use morphological information to stage the self-assembly process, with the benefit of reducing assembly errors and leveraging bonding mechanism with rotational properties. Four experiments are presented, which use heterogeneous, passive, mechanical components that are fabricated using rapid prototyping. Two orbital shaking environments are used to provide energy to the components, and to investigate the role of morphological information with component movement in
Evolutionary computer programs can be a powerful way to evolve complex, interesting objects, which should be of use in fields as diverse as art, engineering, and biology.

**Evolving three-dimensional objects with a generative encoding inspired by developmental biology**

Jeff Clune and Hod Lipson

This paper introduces an algorithm for evolving 3D objects with a generative encoding that abstracts how biological morphologies are produced. Evolving interesting 3D objects is useful in many disciplines, including artistic design (e.g. sculpture), engineering (e.g. robotics, architecture, or product design), and biology (e.g. for investigating morphological evolution). A critical element in evolving 3D objects is the representation, which strongly influences the types of objects produced. In 2007 a representation was introduced called Compositional Pattern Producing Networks (CPPN), which abstracts how natural phenotypes are generated. To date, however, the ability of CPPNs to create 3D objects has barely been explored. Here we present a new way to create 3D objects with CPPNs. Experiments with both interactive and target-based evolution demonstrate that CPPNs show potential in generating interesting, complex, 3D objects. We further show that changing the information provided to CPPNs and the functions allowed in their genomes biases the types of objects produced. Finally, we validate that the objects transfer well from simulation to the real-world by printing them with a 3D printer. Overall, this paper shows that evolving objects with encodings based on concepts from biological development can be a powerful way to evolve complex, interesting objects, which should be of use in fields as diverse as art, engineering, and biology.

**15:50-17:30 Track 8B, CFB Auditorium**

**Robotics**

Chair: Takashi Ikegami

**Computational modeling of online reaching**

Emmanouil Houndakis and Panos Trahanias

Humans are able to perform an unlimited repertoire of reaching movements with high accuracy. The skillfulness with which we carry out a giving reaching task suggests that there are fundamental control policies that allow us to move our body. In the current paper we examine how an adaptive reach policy can be established, using biologically inspired techniques. The developed model, after an initial imitation phase, can replicate any given trajectory with very good performance.

**Learning symbolic forward models for robotic motion planning and control**

Hirotaka Moriguchi and Hod Lipson

Physiological studies suggest that humans have internal dynamics models for both themselves as well as their environment, which are integral components in motion planning and control. Although robotic systems rely on similar models, a primary constraint for robotic applications is how such models are acquired and developed. Traditionally human engineers derive the dynamics models for robots; this approach is not scalable for increasingly complex designs. As a result, there is growing interest in model inference methods, which automate the modeling process and extends the design range of robots. This paper proposes a novel method that infers dynamics models as mathematical expressions via Symbolic Regression and applies them for robotic motion planning and control tasks. The advantage of this expression is not only the accuracy but also the computational efficiency. Experimental results on underpowered pendulum domains validate that our inferred models enable fast accurate motion planning and rapid real-time re-planning, with significantly superior results over Support Vector Regression and Gaussian Process Regression.

**Evolving robot gaits in hardware: The HyperNEAT generative encoding vs. parameter optimization**

Jason Yosinski, Jeff Clune, Diana Hidalgo, Sarah Nguyen, Juan Cristobal Zagal and Hod Lipson

Creating gaits for legged robots is an important task to enable robots to access rugged terrain, yet designing such gaits by hand is a challenging and time-consuming process. In this paper we investigate various algorithms for automating the creation of quadruped gaits. Because many robots do not have accurate simulators, we test gait-learning algorithms entirely on a physical robot. We compare the performance of two classes of gait-learning algorithms: locally searching parameterized motion models and evolving artificial neural networks with the HyperNEAT generative encoding. Specifically, we test six different parameterized learning strategies: uniform and Gaussian random hill climbing, policy gradient reinforcement learning, Nelder-Mead simplex, a random baseline, and a new method that builds a model of the fitness landscape with linear regression to guide further exploration. While all parameter search methods outperform a manually-designed gait, only the linear regression and Nelder-Mead simplex strategies outperform a random baseline strategy. Gaits evolved with HyperNEAT perform considerably better than all parameterized local search methods and produce gaits nearly 9 times faster than a hand-designed gait. The best HyperNEAT gaits exhibit complex motion patterns that contain multiple frequencies, yet are regular in that the leg movements are coordinated.

**Swarms for robot vision: The case of adaptive visual trail detection and tracking**

Pedro Santana, Ricardo Mendonça, Luís Correia and José Barata

Previous work has shown that a pheromone-based visual saliency map can be computed by a swarm of simple agents inhabiting the robot's input image. It was also shown that, with a proper set of behaviours controlling the agents, the saliency map can be used to localise trails present in the robot's visual field. Under the assumption that the robot starts its autonomous operation already on the trail, this paper extends that work by enabling the agents to learn on-line an appearance model of the trail. The learned model is then used to increase the level of pheromone deployed in the regions of the input image that are more probable of belonging to the trail. This is motivated by the well-known importance that a priori object knowledge has to improve visual search. The outcome of this extension is a self-organising behaviour capable of detecting trails in 98% of the evaluated situations, outperforming the original work. The agents being simple their computation is fast, resulting in a 12Hz performance. Thus, by
introducing a parsimonious learning mechanism, this paper contributes to increase robustness of swarm-based robot vision systems.

18:00-19:00 Keynote 5, Adenauer Auditorium

Prospects for machine embryogenesis

Jordan Pollack

In Nature, the embryogenesis process proceeds from a single fertilized cell through division, migration, specialization and apoptosis. Although a lot is known about development, we still have a long way to go from theories of pattern formation towards understanding the intelligence within an unsupervised manufacturing process which robustly assembles complex biological forms.

Our approach has been to co-evolve bodies and brains in simulation and then convert them into reality using commercial manufacturing technology. I will review several generations of robots which were automatically designed using co-evolutionary techniques. The goal has been the fully automated design and construction of artificial lifeforms.

The first generation was based on genetic programming and a simulation of LEGO rod adhesion. The second generation used direct evolution on an iterative simulation of truss structures and used 3D printing for the output. A third generation was based on generative representations using L-systems.

In each of these cases, we assumed a perfect factory which could accept an evolved specification and then manufacture the desired result. In reality, there is no perfect factory, except for the science fiction Star Trek replicator. All manufacturing and assembly systems are subject to error. Each primitive manufacturing action results not in a deterministic new state, but a probability distribution of outcomes.

In later work, we replaced the idea of a perfect factory with one subject to noise and error. Even the smallest bit of error ruins the outcome of deterministic construction plans. We first evolved construction plans which could overcome errors through redundancy, and then this led to a new model for machine embryogenesis as a process which continuously optimizes assembly processes in a game against Nature.

19:00-20:00 Art Show, Adenauer Auditorium

Upokrinomenes: A fabulated epistemology

Louis Bec

Zoosystemician Louis Bec forces us to question the validity of each claim by reformulating and staging scientific discourse. His reasoning possesses all the marks of scientific assertiveness, combining scientific jargon with scholarly neologisms. Questioning life and our inability to understand it through traditional investigative methods, he founded the field of Upokrinomenology. It is a theory of life using models based on computer science, robotics, video and other interactive devices, where irony holds a significant place. By putting scientific discourse into perspective, he challenges us to investigate, unravel and interpret the propositions that he makes. In this research, scientific discourse becomes poetic and Louis Bec becomes a storyteller. Founder of the Scientific Institute of Paranaturalistic Research, he invites us to discover a life we did not know existed, one that looms at the border between shapes, language and behavior [after C. Beaugrand & A. Charre, Reinventing the museum]. His presentation will be followed by 7p., cuis., s. de b., … à saisir (6BR, kitch., bath., … selling now), a short film by Agnès Varda featuring Louis Bec.

20:00-20:30 Pre-Banquet Concert, Adenauer Auditorium

The Continuator project: Playing with virtual musicians

François Pachet

François Pachet (guitar player) and Jeff Suzda (professional sax player) will perform a short Jazz concert with their band “Quintet of Two”. They comprise the two human musicians in the group, performing alongside three “software” musicians. The goal of this project is to play “standard” jazz using virtual instruments intimately controlled by the human players. The technologies employed, developed at Sony CSL, involve Markov chains, constraint programming, signal processing, and a great degree of musical tuning. The performance is still exploratory, but we hope to convey a sense of the direction we are heading to: enhance musical expressivity through controllable machines.

20:30-23:30 Conference Banquet, Salon Honnorat
Friday, August 12

9:00-10:00 Keynote 6, Adenauer Auditorium

**General architecture of a genetic regulation network: Applications to embryologic and immunologic control**

*Jacques Demongeot*

The general architecture of a genetic regulation network consists of strong connected components of its interaction graph, to which are attached three kinds of sub-structures:

- a set of up-trees, issued from the sources of the interaction graph of the network, made either of small RNAs (like the microRNAs or mitomiRs, translational inhibitors respectively of the messenger RNAs and of the tRNAs), or of genes repressors and/or inductors, self-expressed without any other genes controlling them
- a set of circuits in the core (in graph sense) of the strong connected components of the interaction graph. These circuits are unique or multiple, reduced to one gene or made of several ones, negative (having an odd number of negative interactions) or positive, and disjoint of intersected;
- a set of down-trees going to the sinks of the interaction graph, i.e., to genes controlled, but not controlling any other genes.

The various state configurations it is possible to observe in the above sub-structures correspond to different dynamical behaviours. We show that these dynamics have in general a small number of attractors, corresponding to the functions of the tissue they represent in the Delbrück's paradigm. Examples of such dynamics will be given in embryology (feather morphogenesis in chicken, gastrulation and wings morphogenesis in Drosophila) as well as in immunology (rearrangements of the genes of the TCR receptors in mice).

10:30-12:10 Track 9A, Adenauer Auditorium

**Ecological modeling**

Chair: Mario Giacobini

*Urdar: An artificial ecology platform*

Philip Gerlee and Torbjörn Lundh

Cross-feeding interactions are a common feature of many microbial systems, such as colonies of *E. coli* grown on a single limiting resource. We have studied this phenomenon from an abstract point of view by considering artificial organisms which metabolise binary strings from a shared environment. The organisms are represented as simple cellular automaton rules and the analog of energy in the system is an approximation of the Shannon entropy of the binary strings. Only organisms which increase the entropy of the transformed strings are allowed to replicate. This system exhibits a large degree of species diversity, which increases when the flow of binary strings into the system is reduced.

*EcoSim: An individual-based platform for studying evolution*

Robin Gras, Abbas Golestani, Meisam Hosseini Sedehi, Marwa Khater, Yasaman Majdabadi Farahani, Morteza Mashayekhi, Sina Md Ibne, Elham Salehi and Ryan Scott

To study the evolutionary process and the emergence of species, we have conceived an individual-based evolving predator-prey ecosystem simulation. One major and unique contribution of this simulation is that it combines a behavioral, an evolutionary and a speciation mechanism. This is the only simulation modeling the fact that individual behaviors affect evolution and speciation. We have already obtained some very interesting and promising results from our simulation on species abundance distribution, study of chaotic patterns or population spatial distribution.

*Selective pressures for accurate altruism targeting: Evidence from digital evolution for difficult-to-test aspects of inclusive fitness theory*

Jeff Clune, Heather Goldsby, Charles Ofria and Robert T. Pennock

Inclusive fitness theory predicts that natural selection will favor altruist genes that are more accurate in targeting altruism only to copies of themselves. We use digital evolution to support this prediction by competing multiple altruist-targeting mechanisms that vary in their accuracy. We compete altruism-targeting mechanisms based on (i) kinship (kin targeting), (ii) genetic similarity at a level greater than that expected of kin (similarly targeting), and (iii) perfect knowledge of the presence of an altruist gene (green beard targeting). Natural selection always favored the most accurate targeting mechanism available. Our investigations also revealed that evolution did not increase altruism levels when all green beard altruists used the same phenotypic marker. The green beard altruism levels stably increased only when mutations that changed the altruism level also changed the marker (e.g. beard color), such that beard color reliably indicated the altruism level. For kin- and similarly-targeting mechanisms, we found that evolution was able to stably adjust altruism levels. Our results confirm that natural selection favors altruist genes that are increasingly accurate in targeting altruism to only their copies. Our work also emphasizes that the concept of targeting accuracy must include both the presence of an altruist gene its level of altruism.

*Ecohydrologic and biogeochemical process networks in forest ecosystems in monsoon East Asia: Identification and interpretation*

Joon Kim, Juyeol Yun, Jewoo Hong, Hyojung Kwon and Junghwa Chun

Forest ecosystems play a critical role in the cycles of carbon and water from local to global scales. These cycles and their variability, in turn, play an important role in the non-trivial emergent and self-organizing interactions between forest ecosystems and their...
environment. Observational evidence, based on micrometeorological eddy covariance measurements, suggests that heterogeneity and disturbance (both human and natural) in forest ecosystems in monsoon East Asia may facilitate to build resilience for adaptation to change. Yet, the principles that characterize the role of variability in these interactions remain elusive. A process network is defined as a network of feedback loops and the related time scales, which describe the magnitude and direction of the flow of energy, matter, and information between the different variables in a complex system. We attempt to delineate and interpret such process networks by analyzing multivariate ecohydrologic and biogeochemical time series data based on information flow statistics.

10:30-12:10 Track 9B, CFB Auditorium

**Complex Networks**

Chair: Andrew Werncseh

*On the interaction of adaptive timescales on networks*

Elisabeth Zu Erbach-Schoenberg, Connor McCabe and Seth Bullock

The dynamics of real-world systems often involve multiple processes that influence system state. The timescales that these processes operate on may be separated by orders of magnitude or may coincide closely. Where timescales are not separable, the way that they relate to each other will be important for understanding system dynamics. In this paper, we present a short overview of how modellers have dealt with multiple timescales and introduce a definition to formalise conditions under which timescales are separable. We investigate timescale separation in a simple model, consisting of a network of nodes on which two processes act. The first process updates the values taken by the network's nodes, tending to move a node's value towards that of its neighbours. The second process influences the topology of the network, by rewiring edges such that they tend to more often lie between similar individuals. We show that the behaviour of the system when timescales are separated is very different from the case where they are mixed. When the timescales of the two processes are mixed, the ratio of the rates of the two processes determines the system's equilibrium state. We go on to explore the impact of heterogeneity in the system's timescales, i.e., where some nodes may update their value and/or neighbourhood faster than others, demonstrating that it can have a significant impact on the equilibrium behaviour of the model.

*Computational capabilities of small-world Boolean networks*

Joseph Lizier, Siddharth Pritam and Mikhail Prokopenko

We discuss an ensemble investigation of the computational capabilities of small-world networks as compared to ordered and random topologies, using random Boolean functions to provide dynamics of the nodes. We find that the ordered phase of the dynamics (low activity in dynamics) and topologies with low randomness are dominated by information storage, while the chaotic phase (high activity in dynamics) and topologies with high randomness are dominated by information transfer. Information storage and information transfer are somewhat balanced near the small-world regime, providing quantitative evidence that small-world networks do indeed have a propensity to “combine” comparably large information storage and transfer capacity.

*Prediction and modularity in dynamical systems*

Artemy Kolchinsky and Luis M. Rocha

The predictive power of statistical models depends on their complexity. When provided with only a limited amount of data, complex models will often generate worse predictions than simple ones. We apply this principle to the analysis of modularity in complex dynamical systems. We show that finite data imposes a bottleneck-like trade-off between predictive accuracy and difficulty of learning parameters. This trade-off is then used to derive a method to generate optimal multi-scale decompositions of dynamical networks into weakly-coupled, simpler subsystems.

*Transformations and multi-scale optimisation in biological adaptive networks*

Richard Watson, Rob Mills and Christopher Buckley

The natural energy minimisation behaviour of a dynamical system can be interpreted as a simple optimisation process, finding a locally optimal resolution of constraints between system variables. In human problem solving, high-dimensional problems are often made much easier by inferring a low-dimensional model of the system in which search is more effective. But this is an approach that seems to require top-down domain knowledge; not one amenable to the spontaneous energy minimisation behaviour of a natural dynamical system. However, in recent work (Adaptive Behaviour, 2011) we investigated the ability of distributed dynamical systems to improve their constraint resolution ability over time by self-organisation. Using a ‘self-modelling’ Hopfield network with a particular type of associative connection we illustrated how slowly changing relationships between system components results in a transformation into a new system, a low-dimensional caricature of the original system, in which the energy minimisation behaviour is significantly more effective at globally resolving system constraints. This uses only very simple, and fully-distributed positive feedback mechanisms that are relevant to other ‘active linking’ and adaptive networks. Here we overview the implications of this neural network model for understanding transformations and emergent collective behaviour in various non-neural adaptive networks such as social, genetic and in particular, ecological networks.

12:10-12:40, Adenauer Auditorium

**ECAL’13 bid: Proposals for the 2013 European Conference on Artificial Life**

As ECAL’11 is drawing to a close, we are glad to announce a bid process for the organization of the next ECAL in 2013. We invite anyone interested in hosting this event to prepare a 1- or 2-page PDF proposal. This flyer should specify the venue and date and contain the most relevant information highlighting your proposal. Please email your ECAL’13 flyer to Hugues Bersini, Paul Bourgine and René Doursat by Thursday, August 11 at the latest. You should also prepare a 5-10mn slideshow to present during this bid session. The final decision will be made the same day through a voting procedure among the board members of the International Society of Artificial Life (ISAL), together with the main organizers of previous Alife and ECAL conferences present at ECAL’11.

40
Satellite workshops

13:30-17:30, Salle Nathan
CS-Sports – Complex Systems in Sports
Juan Julián Merelo Guervós, Antonio Mora García, Carlos Cotta Porras

The main topic of CS-Sports is the intersection between complex systems and sports, for instance the application of complex networks to the description and analysis of team sports, and its application to the prediction of team performance and outcome. The workshop is addressed to computer, social and sports scientists, interested in unraveling the dynamics and emergent patterns of games in team sports. A complex systems approach can also be applied to the evolution of robots playing sports such as Robosoccer. The format is preferably peer reviewed papers, but can also include poster sessions and panel discussions. In addition, the organizers may give an introductory talk to present the main topics and current state of the art in this scope; a round table may close the workshop with brainstorming on the topic of how to apply complex systems to sports analysis and prediction.

13:30-17:00, Salle Satsuma
DDLab – Exploring Discrete Dynamics with DDLab: From Cellular Automata to Random Networks
Andy Wuensche, Andy Adamatzky, Genaro Juárez Martínez

Discrete dynamical networks (DDN), which include cellular automata (CA) and random Boolean networks (RBN), are at the very core of complexity and emergent self-organisation, and provided the inspiration for the founding ideas of Artificial Life, notably by Chris Langton. Discrete Dynamics Lab (DDLab) is an open-source interactive graphics software able to explore a huge diversity of behaviour, space-time patterns, and basins of attraction representing the convergent flow in state-space. The latest version of DDLab is documented in the book *Exploring Discrete Dynamics*, which has just been published. The workshop will include a tutorial to demonstrate DDLab and try out your own experiments (please bring your laptop), and an opportunity for a 10mn presentation of your work involving DDLab. Selected papers will be published in a special issue of the Journal of Cellular Automata (JCA). See www.ddlab.org for the compiled software, source code, and documentation.

17:00-17:30, Salle Satsuma
SynBioCCC (2) – Workshop on the Design, Simulation, Construction and Testing of Synthetic Gene Regulatory Networks for Computation, Control and Communications

13:30-17:30, Salon du Cambodge
iBioMath – First International Workshop on Integral Biomathics
Plamen Simeonov, André Ehresmann, Leslie Smith

Are we nearly there yet? (This is a common question asked by small children in the back of the car.) Are the definitions of what is life (Schrödinger, Varela), life itself (Rosen) and more than life itself (Louie) convergent? Did we really expect a discovery such as the arsenic-incorporated Mono lake bacteria to start redefining our concept of life? Are not life forms inevitable in the evolution of the Universe? Where is the boundary between the machine and the organism? Is there such a boundary at all? Are our theories of living and cognitive systems strong enough? Does our underlying understanding of computation and cognition, of the difference between living, non-living and synthetic systems, of sensing and action suffice for building systems that really can mimic living systems, for building systems that really can cope with the vagaries of real environments, of real sensors, and real actuators that don't always behave quite as model systems do. Or is there a theoretical (or even not so theoretical) underlying area that is still missing? These are some of the basic questions posed by the emerging discipline of Integral Biomathics we wish to address in iBioMath’11.

13:30-17:30, Salon de l'Argentine
INCUP – Information Coding in Unconventional Computing Substrates
Jerzy Gorecki, Andy Adamatzky

A conventional computing medium is a cleverly prepared semiconductor structure, where two different potential levels represent the logical TRUE and FALSE states. As it is well known, this approach is highly successful and modern society cannot exist without silicon-based computers. An unconventional computer, whether physical, chemical or a living substrate, solves problems in a natural way, i.e. as the result of the time evolution that proceeds according to the laws of physics. Information coding is the translation of system state into a string belonging to a formal language. We know many types of computing medium like self-assembling nanoparticles, chemical far-from-equilibrium systems, interacting microfluids or living organisms. The application of a photosensitive Belousov-Zhabotinsky reaction for direct image processing is a beautiful example. INCUP aims to bring together physicists, mathematicians, chemists, biologists and engineers to discuss what the optimal representation of information for unconventional computing could be.
Multi-agent modeling concerns the study and conception of systems composed of autonomous entities (the agents) in interaction with each other or with their environment. Multi-Agent Systems (MAS) have the capability to simulate complex phenomena and allow to design their distributed solutions by a collectivity of agents. Many domains in computer science, distributed artificial intelligence, software engineering; but also physics, mathematics and, obviously, biology are concerned by multi-agent modeling at the cellular and subcellular level. MASmms aims at organizing interactions among the members of the recently emerging MAS community that works on biological problems at meso or macroscopic scales using in silico experiments. Another aim of this workshop will be to meet European researchers involved in similar topics.

On the one hand, phenomena of spontaneous pattern formation are generally random and repetitive, whereas, on the other hand, complicated heterogeneous architectures are the product of human design. Biological organisms are rather unique examples of natural systems that are both self-organized and architectured. Can we export their precise self-formation capabilities to technological systems? To address this issue, MEW 2011 proposes a new field of research called "Morphogenetic Engineering", which explores the artificial design and implementation of autonomous systems capable of developing complex, heterogeneous morphologies. Particular emphasis is set on the programmability and controllability of self-organization, properties that are often underappreciated in complex systems science—while, conversely, the benefits of self-organization are often underappreciated in engineering methodologies.
1) Evolutionary attributes of simulated prebiotic metabolic networks
Omer Markovitch and Doron Lancet
A metabolism-first scenario for the origin of life entails that as early as replicating entities have emerged prebiotically, they must have constituted relatively complex molecular networks, arising via spontaneous accretion of assemblies of simpler organic molecules. While it is widely accepted that self-catalysis is a prerequisite for life, considerably less attention has been devoted to network-based mutual-catalysis and its effect on evolution. To remedy this, we have used the graded autocatalytic replication domain (GARD) model, previously shown to capture essential features of reproduction, mutation and evolution in compositional molecular assemblies. We simulated a large ensemble of GARD rate-enhancement networks, thus allowing one to better study the crucial network properties of the implicated molecular assemblies. We found, with high statistical power, that high prevalence of mutual-catalysis is required for the emergence of appreciable diversity and evolvability of the assemblies, as well as for them to have significant selection attributes. We suggest that only minimal self-catalysis capabilities are needed to facilitate evolution-like behavior, and that excess self-catalysis may drive a population towards an evolutionary ‘dead-end’.

2) A complex systems approach to education in Switzerland
Regina Frei
The insights gained from the study of complex systems in biological, social, and engineered systems enables us not only to observe and understand, but also to actively design systems which will be capable of successfully coping with complex and dynamically changing situations. The methods and mindset required for this approach have been applied to educational systems with their diverse levels of scale and complexity. Based on the general case made by Yaneer Bar-Yam, this paper applies the complex systems approach to the educational system in Switzerland. It confirms that the complex systems approach is valid. Indeed, many recommendations made for the general case have already been implemented in the Swiss education system. To address existing problems and difficulties, further steps are recommended. This paper contributes to the further establishment complex systems approach by shedding light on an area which concerns us all, which is a frequent topic of discussion and dispute among politicians and the public, where billions of dollars have been spent without achieving the desired results, and where it is difficult to directly derive consequences from actions taken. The analysis of the education system's different levels, their complexity and scale will clarify how such a dynamic system should be approached, and how it can be guided towards the desired performance.

3) Reflecting on open-ended evolution
Susan Stepney and Tim Hoverd
We describe a computationally reflective object-oriented architecture suitable for incorporating open-ended innovation and emergent entities into simulations. This allows emergent properties to be reified into objects. This requires modifying the model, and the metamodel, by incorporating novel classes and metaclasses dynamically. The classes and metaclasses are modified by including them in the model through reflection. We argue that such computationally reflective introduction of novelty is necessary for true open-ended simulations.

4) An improved transfer entropy method for establishing causal effects in synchronizing oscillators
James Thornley
A number of studies have proposed that the analysis of spatio-temporal information flow may help to understand cognitive behaviour in biological and artificial agents. A specific case of interest is the study of synchronization of CPG oscillators in embodied systems. Pitti et al. used simulated biped walkers to demonstrate a correlation between task success and measured transfer entropy from the body to the neural oscillator. This suggests it may be possible to use transfer entropy to help understand, control and improve the behaviour of limbed robots. This paper presents a novel method of analysing synchronizing oscillators with transfer entropy, which it is hoped will lead to advances in controlling such systems. The necessary discretization of continuous time oscillator observations is performed via a stroboscopic analysis that preserves the information of interest and allows a natural interpretation of the results. Unlike some previous studies, this method addresses the tendency of naïve transfer entropy calculations to over-estimate causal relationships in a significant and non-trivial way. It is shown that causal links influencing synchrony may be detected between unperturbed systems with chaotic dynamics using transfer entropy. It is hoped further development will lead to a method of guiding self organization in a modular robotic system.

5) Non-template molecules designed for open-ended evolution
Chris Gordon-Smith
Theories of the Origin of Life can be categorised as 'template replication first' and 'metabolism first'. A key question for metabolism first theories is whether metabolic systems can support open-ended evolution; this is related to the number of possible persistent states of such a system. Earlier work has demonstrated that artificial chemical systems can have memory; an essential requirement for inheritance. The current paper extends this, taking a 'proof of concept' approach to the question of the number of persistent states. It shows an artificial chemical network forming a ‘memory bank’ with many possible states. It also makes the link between chemical network structure and molecular structure, and provides a design for a set of artificial molecular species for the memory bank network. Preliminary simulation results from the SimSoup artificial chemistry simulator are included, confirming the operation of an initial set of 'memory units'. The work supports the view that open-ended evolution can begin without requiring highly complex template molecules.
6) Embodied genomes and metaprogramming
Simon Hickinbotham, Susan Stepney, Adam Nellis, Tim Clarke, Ed Clark, Mungo Pay and Peter Young [Fiona Polack]
We model some of the crucial properties of biological novelty generation, and abstract these out into minimal requirements for an ALife system that exhibits constant novelty generation (open ended evolution) combined with robustness. The requirements are an embodied genome that supports runtime metaprogramming (‘self modifying code’), generation of multiple behaviours expressible as interfaces, and specialisation via (implicit or explicit) removal of interfaces. The main application of self modifying code to date has been top down, in the branch of Artificial Intelligence concerned with "learning to learn". However, here we take the bottom up Artificial Life philosophy seriously, and apply the concept to low level behaviours, in order to develop emergent novelty.

7) Feeding the beast: Can computational demographic models free us from the tyranny of data?
Eric Silverman, Jakub Bijak and Jason Noble
Since its inception, ALife has moved from producing large numbers of highly-idealised, theoretical models towards greater integration with empirically collected data. In contrast, demography — the interdisciplinary study of human populations — has been largely following the principles of logical empiricism, with models driven mainly by data, and insufficient attention being paid to theoretical investigation. Such an approach reduces the ability to produce micro-level explanations of population processes, which would be coherent with the phenomena observed at the macro level, without having to rely on ever-increasing data demands of complex demographic models. In this paper we argue that by bringing ALife-inspired, agent-based methods into demographic research, we can both develop a greater understanding of the processes underlying demographic change, and avoid a limiting over-dependence on potentially immense sets of data.

8) An innovative bio-inspired fault tolerant unitronics architecture
Mohammad Samie, Gabriel Dragffy, Tony Pipe and Paul Bremner
This paper describes a unique bio-inspired electronic system, that we term Unitronics (Unicellular Electronics). It is a programmable cellular FPGA-like system inspired by unicellular bacterial organisms, and transposes self-healing and fault tolerant properties of nature to electronics systems. An e-puck robot controller was built to demonstrate all the underlying theories of our research, the validity of the bio-inspired model and the capabilities of the Unitronics architecture that it facilitated. The robot successfully demonstrated that it was able to cope with multiple, simultaneously occurring faults. Integrity of the system is continuously monitored on-line, and if a fault is detected its location is automatically identified. Detection will trigger a self-repair mechanism and only when it is complete will normal system operation resume.

9) Detecting emergent processes in cellular automata with excess information
David Balduzzi
Many natural processes occur over characteristic spatial and temporal scales. This paper presents tools for (i) flexibly and scalably coarse-graining cellular automata and (ii) identifying which coarse-grainings express an automaton’s dynamics well, and which express its dynamics badly. We apply the tools to investigate a range of examples in Conway’s Game of Life and Hopfield networks and demonstrate that they capture some basic intuitions about emergent processes. Finally, we formalize the notion that a process is emergent if it is better expressed at a coarser granularity.

10) Embodied reaction logic in a simulated chemical computer
Fintan Nagle and Simon Hickinbotham
This work uses an ALife simulation to explore the implementation of embodied reaction logic in a chemical computer. Chemical systems have potential for computation. There are properties of a logical system that are desirable in any computational system, such as the ability of the system to change state in response to some input. An issue in chemistry is that the molecules must have some physical embodiment, which must somehow represent state, and state is then interpreted as the presence or absence of certain molecular configurations in the system. The design of a chemical logic gate is a means of showing that a chemical system can change state appropriately and demonstrate that the information encoded in the molecules is available to be processed as information. This paper compares two simulated chemical computing systems, Bindworld (a simple illustrative example) and StringMol (a fully implemented complex DNA-inspired evolutionary computing framework). The problems and design decisions involved in creating a NOT gate in each system are compared, showing that designed computational systems require a certain complexity and flexibility to be useful to human operators. Finally we discuss general extensions to the StringMol reaction chemistry that would simplify the process of information processing in embodied systems.

11) Recovering hidden swarm parameters using a simulated “Robofish”
Richard Coates and Simon Hickinbotham [Paul Andrews]
Swarming is behaviour which emerges from the action of individual agents. Models of swarm behaviour impose fixed model parameters on the agents comprising the swarm. This paper evaluates the possibility of extracting the parameters of a swarm model from the swarm. The approach was inspired by work on so-called "robofish" by Faria et al. If we assume that the collective dynamics of wild animals can be modelled, it would be desirable to recover the dynamics of the model via interaction with them. In this paper, we demonstrate that it is possible to recover the parameters of a shoaling model used by a swarm. This can be achieved by evolving the parameters of a single agent that interacts with the swarm. We present an evaluation of this approach, using a genetic algorithm to drive the learning process. The experiments also reveal information about the effects of varying the parameters of the model on swarm dynamics.
12) On the emergence of structure in behaviours evolved through embodied imitation in a group of robots
Mehmet D. Erbas and Alan F. T. Winfield
In this research, we have used real robots to model social interactions between embodied artificial agents (robots). We show that variations that arise from embodiment allow certain behaviours, those that are more robust to the processes of embodied imitation, to emerge and evolve during multiple cycles of imitation.

13) Artificial organelle for energy production in artificial cell
Yuutetsu Kuruma, Toshiharu Suzuki, Masasuke Yoshida and Takuya Ueda
Autonomous production of biological energy is one of the primal processes in living cells. In cells, adenosine triphosphate (ATP) is produced by ATP synthase, which is located on lipid membrane. For instance, in mitochondria, proton potential across the membrane drives FoF1-ATP synthase (FoF1). On the other hand, bacteriorhodopsin (bR) is known as a proton pump that generates the proton potential due to light stimulation. Therefore, if the bR and FoF1 were synthesized on a liposome membrane, the resulting liposome is able to generate ATP. Our recent results show that FoF1 and bR were synthesized in a cell-free protein synthesis system in the presence of liposomes and supplemental factors. Fo complex, the membrane integrated part of FoF1, was synthesized in situ and formed the desired FoF1 complex in combination with a supplied F1. The FoF1 complex was fully functional, by showing ATPase driven H+ translocation activity. Additionally, the bR is also co-synthesized with the subunit proteins of Fo complex. These results imply that the bottom up construction of an artificial organelle, which is capable of generating the bioenergy, is experimentally feasible. We believe that our bR-FoF1 liposomes will be essential machinery for constructing artificial cells.

14) Using statistical inference for designing termination conditions ensuring convergence of evolutionary algorithms
David Roche, Deboara Gil and Jesus Giraldo
A main challenge in Evolutionary Algorithms (EAs) is determining a termination condition ensuring stabilization close to the optimum in real-world applications. Although for known test functions distribution-based quantities are good candidates (as far as suitable parameters are used), in real-world problems an open question still remains unsolved. How can we estimate an upper-bound for the termination condition value ensuring a given accuracy for the (unknown) EA solution? We claim that the termination problem would be fully solved if we defined a quantity (depending only on the EA output) behaving like the solution accuracy. The open question would be, then, satisfactorily answered if we had a model relating both quantities, since accuracy could be predicted from the alternative quantity. We present a statistical inference framework addressing two topics: checking the correlation between the two quantities and defining a regression model for predicting (at a given confidence level) accuracy values from the EA output.

15) Walking, hopping and jumping: A model of transcription factor dynamics on DNA
David J. Barnes and Dominique Chu
We present a model of how transcription factors scan DNA to find their specific binding sites. Following the classical work by Berg, our model assumes two modes of transcription factor dynamics. Adjacent moves, where the proteins make a single step movement to one side, or short walks where the transcription factors slide along the DNA several binding sites at a time. The purpose of this article is twofold. Firstly, we discuss how such a system can be efficiently modelled computationally. Secondly, we analyse how the mean first binding times of transcription factors to their specific time depend on key parameters of the system.

16) How to prevent intolerant agents from high segregation?
Philippe Collard and Salma Mesmoudi
In the framework of Agent-Based Complex Systems we examine dynamics that lead individuals towards spatial segregation. Such systems are constituted of numerous entities, among which local interactions create global patterns which cannot be easily related to the properties of the constituent entities. In the 70’s, Thomas C. Schelling showed that an important spatial segregation phenomenon may emerge at the global level, if it is based upon local preferences. Moreover, segregation may occur, even if it does not correspond to agent preferences. In real life preferences regarding segregation are influenced by individual contexts as well as social norms; in this paper we will propose a model which describes the dynamic evolution of individuals tolerance. We will introduce heterogeneity in agents’ preferences and allow them to evolve over time. We will show that it is possible to dynamically get a distribution of tolerance over the agents with a low average and in the same time to deeply limit global aggregation. As the Schelling’s model showed that individual tolerance can nevertheless induce global aggregation, this paper takes the opposite view showing that intolerant agents can avoid segregation in some extent.

17) Energy as a driver of diversity in open-ended evolution
Tim Howerd and Susan Stepney
We investigate the consequences of introducing an energy model into open ended evolutionary simulations. We propose a metamodel for simulations that incorporate an energy model and apply that model by extending Turk’s Sticky Feet model. We show that introducing an energy model produces simulations with measurably increased diversity of the simulated population.

18) Genetic transposition inspired incremental genetic programming for efficient coevolution of locomotion and sensing of simulated snake-like robot
Tüze Kuyucu, Ivan Tanev and Katsunori Shimohara
Genetic transposition (GT) is a process of moving sequences of DNA to different positions within the genome of a single cell. It is recognized that the transposons (the jumping genes) facilitate the evolution of increasingly complex forms of life by providing the creative playground for the mutation where the latter could experiment with developing novel genetic structures without the risk of damaging the already existing, well-functioning genome. In this work we investigate the effect of a GT-inspired mechanism on the efficiency of genetic programming (GP) employed for coevolution of locomotion gaits and sensing of the simulated snake like robot
(Snakebot). In the proposed approach, the task of coevolving the locomotion and the sensing morphology of Snakebot in a challenging environment is decomposed into two subtasks, implemented as two consecutive evolutionary stages. At first stage we employ GP to evolve a pool of simple, sensorless bots that are able to move fast in a smooth, open terrain. Then, during the second stage, we use these Snakebots to seed the initial population of the bots that are further subjected to coevolution of their locomotion control and sensing in a more challenging environment. For the second phase the seed is used as it is to create only part of a new individual, and the rest of the new individual’s genetic makeup is created by a mutant copy of the seed. Experimental results suggest that the proposed two-staged GT inspired incremental evolution contributes to significant increase in the efficiency of the evolution of fast moving and sensing Snakebots.

19) From egocentric systems to systems allowing for theory of mind and mutualism
Holk Cruse and Malte Schilling
Simple artificial agents representing more or less elaborated Braitenberg vehicles, usually adopt an egocentric view. One example is Walknet, a biologically inspired neural network controlling hexapod walking. Here we show how such a controller can be expanded to be able to interpret observed behaviours that are performed by other individuals, i.e. the system shows properties of a mirror system. This allows to further expand the network to become an “allocentric” system that might implement subjective feelings which could be attributed to other individuals, i.e. the system implements a Theory of Mind. As a last expansion we introduce a two-body model, or we-model, which may allow for mutualism. Application of we-models allows for what often has been called the third person’s view. The different steps proposed can be interpreted as corresponding to an evolutionary development.

20) Evolutionary dynamics of GAs in a simple model with dynamical environment and neutrality
Yoshiaki Katada
Biological organisms have various mechanisms of coping with the dynamical environments in which they live. Recent papers in computational biology show that individuals reside in different regions of neutral networks according to environmental variation. This work investigated evolutionary dynamics of GAs in dynamical environments with neutrality using a simple model. The evolutionary dynamics observed were consistent with those observed in the experiments of biological evolution, confirming that the genotype distributions change depending on the rates of environmental variation as well as mutation.

21) Global structure of directed networks emerging from a category theoretical formulation of the idea “objects as processes, interactions as interfaces”
Taichi Haruna
A system of interacting elements can be represented by a directed network so that elements are nodes and interaction between two elements is an arc. Conventionally, each node is just a point, each arc represents some kind of interaction between two nodes and nothing more after the system is mapped to a directed network. However, in many real systems, each element has its own intra-node process and interaction between two elements can be seen as an interface between two intra-node processes. We can formalize this idea “objects as processes, interactions as interfaces” within the framework of category theory. We show that a new notion of connectedness called ‘lateral connectedness’ emerges as a canonical structure obtained from the idea. Lateral connectedness is not defined on the nodes of a directed network, but on the set of arcs. By its definition, it may be associated with functional commonality between arcs emerging from shared input or output. As a first application, we examine significance of lateral connectedness in the neuronal network of the nematode (Caenorhabditis elegans) by comparing the partition of the set of arcs induced by the connectedness and the partitions based on neuron functions. Lateral connectedness can capture a part of functional segregation of the neuronal network above a certain interaction strength level.

22) Bondable cellular automata
Mark Hatcher, Wolfgang Banzhaf and Tina Yu
We present the Bondable Cellular Automata model, which uses simple 1-dimensional, binary cellular automata as the base atomic elements of an artificial chemistry. Reactions are dependent upon an emergent, ‘resolution independent’ observable, measurable for individual or composite cellular automata structures. We discuss the rationale behind our choice of observable, ‘mean polarity’, and behind the choice of a bonding mechanism based on this observable. From simple experimentation we observe that using cellular automata as the underlying dynamical system coupled with using mean polarity as the reaction success criterion shows potential to support sustainable emergent behaviour.

23) Artificial cells as reified quines
Lance R. Williams
Cellular automata were initially conceived as a formal model to study self-replicating systems. Although reproduction by biological cells is characterized by exponential population increase, no population of self-replicating machines modeled as a cellular automaton has ever exhibited such rapid growth. We believe this is due to the inability of cellular automata to model bonded complexes of reified actors undergoing random independent motion. To address this limitation, we introduce a model of parallel distributed spatial computation which is highly expressive, infinitely scalable, and asynchronous. We then use this model to define two examples of self-replicating kinemetic automata. These machines assemble copies of themselves from components supplied by diffusion and increase in number exponentially until the supply of components is depleted. Because they are both programmable constructors and self-descriptions, we call them reified quines.

24) Measuring information storage and transfer in swarms
X. Rosalind Wang, Jennifer M. Miller, Joseph T. Lizier, Mikhail Prokopenko and Louis F. Rossi
Spatial aggregation of animal groups give individuals many benefits that they would not be able to obtain otherwise. One of the key questions in the study of these animal groups, or “swarms”, concern the way in which information is propagated through the group. In this paper, we examine this propagation using an information-theoretic framework of distributed computation. Swarm dynamics is
interpreted as a type of distributed computation. Two localized information-theoretic measures (active information storage and transfer entropy) are adapted to the task of tracing the information dynamics in a kinematic context. The observed types of swarm dynamics, as well as transitions among these types, are shown to coincide with well-marked local and global optima of the proposed measures. Specifically, active information storage tends to maximize as the swarm is becoming less fragmented and the kinematic history begins to strongly inform an observer about the next state. The peak of transfer entropy is observed to lag behind the peak of active information storage, showing most markedly at the final stages of merging of swarm fragments, near the “edge of chaos” where the system actively computes its next stable configuration. Both measures tend to minimize for either unstable or static swarm configurations.

25) Simulation of cell-like self-replication phenomenon in a two-dimensional hybrid-cellular automata model
Takeshi Ishida
Understanding the generalized mechanism of self-reproduction is considered fundamental for application in various fields such as the mass-production of molecular machines in nanotechnology. We developed a model for simulating cellular self-reproduction in a two-dimensional cellular automaton. We demonstrated that the following three functions could be realized: (1) formation of a border similar to cell membrane, (2) self-replication while maintaining a carrier containing information, and (3) division of the cell membrane while maintaining the total structure. Furthermore, we constructed a hybrid cellular automaton model. To reduce the number of transition rules, we considered not only the state transition rules but also the concentration diffusion of the Gray Scott model, in which the self-reproduction phenomenon emerges with certain parameters.

26) Behavioral acquisition of complicated locomotion for artificial elastic robot using decentralized behavior composed
Keisuke Yoneda, Ikuo Suzuki, Masahito Yamamoto and Masashi Furukawa
A virtual elastic robot is proposed which has a body with multiple degrees of freedom. It is capable of fitting its body to the given surrounding environment. This study focuses to allow the elastic robot to adapt to various environments. The intended robot is modeled by rigid objects connected by spring joints in a circular structure. Its control system manipulates spring actuators to realize elastic movements. This paper aims to acquire its control system for the robot to behave autonomously. A behavior acquisition is implemented as an optimization problem by the use of Evolutionary Computation. A physical simulation on the computer is carried out to achieve given tasks for the virtual elastic robot. The task is set to achieve a locomotion which moves toward a destination on a flat ground. Simulation results show that the elastic robot acquires a locomotion. Moreover, we assume a complicated circumstance in which obstacles are placed. In order to allow the robot to adapt to a complicated circumstance, we propose “Behavior Composed” to design a complicated behavior from several simple behaviors. These experimental results prove that the robot is capable of acquiring an adaptive locomotion in specific circumstances.

27) Embodied swarming based on back propagation through time shows water-crossing, hourglass and logic-gate behaviors
Yukio-Pegio Gunji, Hisashi Murakami, Takayuki Niizato, Andrew Adamatzky, Yuta Nishiyama, Koichiro Enomoto, Masashi Toda, Toru Moriyama, Tetsuya Matsui and Kojiro Iizuka
A flock, school, and swarm are collective behaviors that can be compared to a human consciousness or body. Through recent developments in image analysis and model simulation, it has been found that the collective behavior of animals can, as a whole, show characteristics of a single “body”. It has also been found that intrinsic noise can positively contribute to swarming and/or flocking. Motivated by field observations of soldier crabs, Mictyris guinotae, we propose a swarm model based on inherent noise and back propagation in time that mimics mutual anticipation. A swarm generated by this model is characterized by flexible, dynamical and robust behavior containing inherent turbulence. We demonstrate that the model can produce water-crossing, hourglass and logic gate behaviors, which are also found in real soldier crabs. We describe how a sense of ownership and a sense of agency of the “body” arise in our model, and we propose that the concept of a body should be verified in terms not of stability but of robustness.

28) Multi-agent systems and heterogeneous scales interactions: Application to pharmacokinetics of vitamin K antagonists
Sébastien Le Yaoaug, Pascal Redou, Christophe Le Gal, Jean-François Abgrall and Jacques Tisseau
The study of complex systems consists in considering entities submitted to interactions which define the dynamics of the system. Virtual reality opens the way to interactive simulation of complex systems, so called the in virtuo experimentation. For that purpose we use multi-interactions systems, based on the reification of interactions and multi-agent systems, in a phenomenological approach. Interaction agents represent the modeler understanding of the relations between the constituents of the system. Such descriptive models lead us to define parameters a priori. Moreover these parameters can be fluctuant, or even unknown, during a simulation in relation to the system dynamics or user interventions. To respond to this problem, we expose in this paper a redundant multiscale architecture which rests upon the fact that we can establish models of a same phenomenon at heterogeneous time and space scales. Heterogenous Multiscale Methods provide a general framework to mix levels of description of a system. Our intention is to implement this framework in multi-interactions systems by means of a Scale-Interaction agent. Then we illustrate our architecture through a pharmacokinetics application. Indeed biochemical kinetics abounds of parametric phenomena. Finally we discuss about some questions raised by this methodology, such as synchronicity, organization detection and genericity.

29) Local information maximisation creates emergent flocking behaviour
Christoph Salge and Daniel Polani
The three boids rules of alignment, separation and cohesion, introduced by Reynolds to recreate flocking behaviour have become a well known standard to create swarm behaviour. In this paper we want to demonstrate how similar flocking behaviour can be created by a local, agent based model, following a principle of information maximisation. The basis for our model is an extension of Vergassola’s infotaxis model, where agents determine their actions based on the highest expected reduction of entropy. We
adapted this approach to a grid world-based search task, and extended the agents abilities so they could not only perform a Bayesian update with information gained from the environment, but also with information gained from other agents. The resulting global flocking behaviour is then analysed in regard to how well it resembles the basic boids rules.

30) Promoting meme diversity and transmission fidelity in artificial proto-cultures
Andrew Guest, Andrew Sapeluk, Alan Winfield and James Bown [Mehmet D. Erbas]
Cultural evolution occurs through the transmission of cultural traits, and we consider the meme as the unit of cultural transmission. We construct an agent-based model representing the processes by which cultural transmission occurs and to link these to the community-scale phenomena arising from agent interactions. We base our model on small communities of e-Puck robots, and following work on movement-based memes, consider sound as the medium of cultural transmission. Our architecture affords (re)production of memes, variation in meme production and a range of meme selection and meme memory strategies. Through these processes, we identify the meme complexities, meme memory strategies, meme selection strategies and e-Puck movement speeds that promote and inhibit both meme diversity and reproductive fidelity.

31) Application of small-world mutation topologies to an artificial life system
Alastair Droop and Simon Hickinbotham
The mutation networks observed in biological systems have the properties of small-world networks. These properties of short average path length and high transitivity confer a favourable exploration of mutation space. Any evolvable string-based ALife system (for example stringmol, typogenetics, Tierra or Avida) uses a substitution network either implicitly or explicitly. Current ALife simulations use either regular or random mutations schemes. We have previously discussed the requirement for small-world substitution networks (Droop and Hickinbotham, 2011) for ALife simulations. In this paper, we explore the effects of rewiring the stringmol mutation lattice on the evolution of a self-replicating molecule.

32) Emergence of temporal and spatial synchronous behaviors in a foraging swarm
Sylvain Chevallier, Nicolas Bredeche, Hélène Paugam-Moisy and Michèle Sebag
Populations of living systems exhibit complex behaviors, achieving efficiently a large number of tasks, without any central control. Synchronization of behavior is an important property for improving the population performance. The adaptation of this emergent synchronization for division of labor is of a prime interest for swarm robotics. This contribution describes a microscale model of an autonomous agent accounting for a self-organized synchronized division of labor at the macroscale of a swarm. The model relies on coupled spiking neurons competing with one another to modelize the decision making process, requiring only limited capabilities on the agent side. On a population level, three regimes of synchronization emerge depending on two control parameters, related to the coupling and the connectivity of the population. A study is conducted, in a 2D simulator of robotic environment, in order to evaluate the impact of synchronized behaviors for a foraging task. It can be observed that synchronized agents moving together are less likely to collide in each others, thus resulting in a more efficient task fulfillment.

33) Modeling and simulating crowdsourcing as a complex biological system: Human crowds manifesting collective intelligence on the internet
Thierry Buecheler, Rocky Lonigro, Rudolf M. Füchslin and Rolf Pfeifer
Crowdsourcing, a real-life instance of human collective intelligence, is a phenomenon that changes the way organizations use the Internet to collect ideas, solve complex cognitive problems, and build high-quality repositories (e.g., Wikipedia) by self-organizing agents around data and knowledge. Many recent studies have highlighted the factors and the small sets of parameters that play a role when a large crowd interacts with an organization. However, no comprehensive simulation has yet been developed to incorporate all these parameters, investigate “Alife” phenomena such as emergence and self-organization and potentially generate predictive power. Based on a presentation at ALIFE XII, this paper describes the development of a simulator for human crowds performing collective problem solving in a Crowdsourcing scenario. It details the mechanics of a multi-agent system (MAS) by building on insights from empirical science in several disciplines. The simulator allows running sensitivity analyses of multiple parameters as well as simulation of analytically irreducible interactions of complex networks of irrational agents. In addition, the paper provides a review of Crowdsourcing and human collective intelligence literature structured from an Alife point-of-view.

34) Cognitive conditions to the emergence of sign interpretation in artificial creatures
Angelo Loula, Ricardo Gudwin and João Queiroz
Although the emergence of communication has been the topic of various Artificial Life experiments, the study of underlying representational processes remains a key issue. We have previously differentiated between symbolic and indexical interpretation and proposed that symbolic interpretation may act as a shortcut to cognitive traits already acquired. Here we evaluate conditions of this acquired cognitive trait for the emergence of different modalities of sign interpretation. Results show that symbolic processes may act as a cognitive shortcut to a previous acquired cognitive competence even if minimally functional or initially not available.

35) A checkpoint-orientated model to simulate unconstrained proliferation of cells
Jonathan Pascalle, Valérie Lobnjois, Hervé Luga, Bernard Ducommun and Yves Duthen
In this paper we propose a new computational model of cell cycle to study the dynamics of cells population in 2-D monolayer culture. Whereas most of the models are phase-orientated our model deals with a checkpoint orientated paradigm and uses the phase orientation as an output to provide to the biologists a relevant view of the simulation result. Through this paper we will present the genericity of our model, able to reproduce the exponential growth phase of different cellular processes.
36) Landmark vector model with quantized distance for homing navigation
Seung-Eun Yu and DaeEun Kim
Inspired by the astonishing navigation ability of insects and other animals, there have been many robotic approaches for homing navigation. In this paper, we present a landmark vector model with quantized distance information. The method is highly successful to return home only with visual information, and it provides better performance than the conventional navigation algorithms. This work has been published in the paper (Yu and Kim, 2011).

37) Identifying species by genetic clustering
Jamie Murdock and Larry S. Yaeger
Complex artificial life simulations can yield substantially distinct populations of agents corresponding to different adaptions to a common environment or specialized adaptations to different environments. Here we show how a standard clustering algorithm applied to the artificial genomes of such agents can be used to discover and characterize these subpopulations. As gene changes propagate throughout the population, new subpopulations are produced, which show up as new clusters. Cluster centroids allow us to characterize these different subpopulations and identify their distinct adaptation mechanisms. We suggest these subpopulations may reasonably be thought of as species, even if the simulation software allows interbreeding between members of the different subpopulations, and provide evidence of both sympatric and allopatric speciation in the Polyworld artificial life system. Analyzing intra- and inter-cluster fecundity differences suggests that this effect alone may support sympatric speciation in artificial and biological ecosystems.

38) Homologous and illegitimate rearrangements: Interactions and effects on evolvability
David P. Parsons, Carole Knibbe and Guillaume Beslon
By using Aevol, a simulation framework designed to study the evolution of genome structure, we investigate the effect of homologous rearrangements on the course of evolution. We designed an efficient model of rearrangements based on an intermittent search algorithm. Then, using experimental in silico evolution, we explore the effect of rearrangement rates on the genome structure. We show that the effect of homologous rearrangements is quite complex. At first glance they appear to be dangerous enough to trigger an indirect selective pressure leading to short genomes when the rearrangement rate is high. However, by analyzing the successful lineage in the best runs, we found that there is a positive correlation between the number of homologous rearrangements and the fitness improvement in these lineages. Thus the impact of homologous rearrangements on evolution is rather complex: Dangerous on the one hand but necessary on the other one to ensure a sufficient evolvability level to the organisms. Moreover, our results show that the spontaneous rate of small mutations influences the relative proportions of homologous versus illegitimate rearrangements.

39) Degeneracy enriches artificial chemistry binding systems
Ed Clark, Adam Nellis, Simon Hickinbotham, Susan Stepney, Tim Clarke, Mungo Pay and Peter Young
We assert that degeneracy in the components of an artificial chemistry (AChem) facilitates the complexity of the system as a whole. We introduce definitions of degeneracy and redundancy and show how these quantities can be calculated for the binding system of an AChem. In order to support our assertion, we present a case study using the AChem Stringmol. We detail parasite evasion in Stringmol and hypothesize that it is the binding system that Stringmol uses which enables Stringmol simulations to survive the introduction of a parasite. To test our hypothesis, we demonstrate that the binding system in Stringmol has degeneracy and create a deliberately poor variant: ‘sticky-Stringmol’, that has a binding system with no degeneracy. Results from these simulations support our hypothesis as sticky-Stringmol is unable to evade a parasite. We also note the loss of many other simulation artifacts that have been used as evidence of the complexity of Stringmol, such as emergent macro-mutations and hypercycles. These results are evidence that degeneracy in the components of an AChem facilitates the complexity of the system as a whole.

40) Clustering behavior of a bio-inspired decentralized aggregation scheme
Nikolaos Vlassopoulos and Nazım Fates [Olivier Bouré]
This note reviews a bio-inspired scheme for aggregating autonomous agents in the absence of global communication or coordination, a problem that is known as Decentralized Gathering. We present results on the clustering behavior of the agents, as we vary the main parameter that controls the agent aggregation. Our observations show that there exist two phenomenologically different behaviors, characterized by a different evolution of the number of clusters with time. We relate these different behaviors to different scales of significance of the fluctuations that appear in the model.

41) Clever creatures: Case studies of evolved digital organisms
Laura M. Grabowski, David M. Bryson, Fred C. Dyer, Robert T. Pennock and Charles Ofria
We present in-depth analysis of three digital organisms—self-replicating computer programs—that evolved in three different experimental environments in the Avida platform. The ancestral environments required the evolving organisms to use memory in different ways as they gathered information from the environment and made behavioral decisions. Each organism exhibited a behavior or algorithm of particular interest: 1) simple step-counting odometer; 2) clever low-level computation; 3) pronounced modularity in both program structure and program functionality. We focus our analysis of the case study organisms on the structure and operation of the evolved algorithms that produce the individuals' adaptive behaviors.

42) A gene regulatory network implementing a asynchronous single-input delay flip-flop
Imad Hoteit, Nawwaf Kharma and Luc Varin
We present a fully detailed design of the very first asynchronous single-input delay flip-flop (or BioD) implemented as a gene regulatory network in Escherichia coli (E. coli). The device has one data input (trans-acting RNA), one clock input (far-red light) and two complementary outputs that report the state of the device using a green fluorescent protein (GFP). The proposed (simulated but not synthesized) device builds on the toggle switch of (Gardner et al., 2000) to provide a more sophisticated device that can be
synchronized with other devices in/out of the same cell, and which requires only one input. We provide the first results of a deterministic simulation of a mathematical model of the new device, one which provides evidence that the device is likely to work as required when actually synthesized.

43) Social learning and evolution in a structured environment
Daniel Jones and Tim Blackwell
We survey the relationships between evolution, individual learning and social transmission within mixed and structured environments. With a novel individual-based simulation, we determine the regimes under which each mode of learning dominates, in terms of the environment's relative complexity and its rate of change. We show that social learning can give rise to a particularly potent form of the "Baldwin effect", wherein an organism develops an innate trait having first acquired it socially. We demonstrate that social learning is of increased significance in a structured environment.

44) Critical mutation rate has an exponential dependence on population size
Alastair Channon, Elizabeth Aston, Charles Day, Roman Belavkin and Christopher Knight
Populations of individuals exist in a wide range of sizes, from billions of microorganisms to fewer than ten individuals in some critically endangered species saved on the brink of extinction. In any evolutionary system, there is significant evolutionary pressure to evolve sequences that are both fit and robust; at high mutation rates, individuals with greater mutational robustness can outcompete those with higher fitness, a concept that has been referred to as survival-of-the-flattest. Previous studies have suggested that population size does not influence the size of mutation rate that can be tolerated before fitter individuals are outcompeted by those that have a greater mutational robustness. However, using a genetic algorithm with a simple two-peak fitness landscape, we show that the size of mutation rate at which the high, narrow peak and the lower, broader peak are lost for increasing population sizes can be approximated by an exponential function (where a peak was considered to be lost when there were no individuals present anywhere in its range). In addition, there is evidence for a continuum of mutation rates representing a transition from survival-of-the-fittest to survival-of-the-flattest. This identifies a critical mutation rate representing the start of the transition, which is defined as the highest mutation rate where survival-of-the-fittest is still the predominant outcome, but where the population is no longer able to maintain the fittest peak indefinitely. The effect of population size on the critical mutation rate is shown to be particularly noticeable in small populations with 100 individuals or less. This provides new insight into the factors that can affect survival-of-the-flattest in small populations, and has implications for populations under threat of local extinction.

45) A schematic representation of autopoiesis using a new kind of discrete spatial automaton
Jean Sirmaji
Autopoiesis, or one's ability to renew oneself, is a meaningful concept for the study of life. Modeling of autopoiesis would permit its analysis in relation with other biological properties such as feeding, breeding, being ill, healing, dying, etc. Here, we report the design of a "morphoautomaton," a new kind of discrete spatial automaton able to represent within the same space an unlimited number of various complex interacting forms. Assuming that functions are encoded only by the represented forms, this automaton can use a simple, single effective formalism to describe the movements, transports, and transformations of those forms. This representation can be made consistent with the laws of thermodynamics and conservation and thus may be used to model significant features of macromolecular solutions chemistry. We use it here to represent, define, and describe an autopoietic individual within its environment. Using this representation, the modeling of other biological properties in relation with autopoiesis should now be possible. These models should allow future comparisons, definition, and classification of these biological properties. Comparison with other studies using equivalent formalisms should also be useful. Finally, a strategy for complete structural and functional analysis of real simple systems is proposed.

46) Coming phase to phase with surfactants
Stuart Bartlett and Seth Bullock
We introduce a fast cellular automata model for the simulation of surfactant dynamics based on a previous model by Ono and Ikegami (2001). Here, individual lipid-like particles undergo stochastic movement and rotation on a two-dimensional lattice in response to potential energy gradients. The particles are endowed with an internal structure that reflects their amphiphilic character. Their head groups are weakly repelled by water whereas their hydrophobic tails cannot be readily hydrated. This leads to the formation of a variety of structures when the particles are placed in solution. Phases including micelles, bilayers and monolayers are all reproduced. The model in its current form compels a myriad of potential self-organisation experiments. Heterogeneous boundary conditions, chemical interactions and an arbitrary diversity of particles can easily be modelled within this simple framework.

47) A biomimetic robot controller based on minimizing the unpredictability of the environment: allostatic control revised
Martí Sánchez-Fliba, Armin Duff, Ulysses Bernardet and Paul F.M.J. Verschure
Rodents are optimal real-world foragers that regulate internal states, such as security, arousal, energy, etc., maintaining a dynamic stability with their surroundings. Free exploration is an interesting scenario as rodents display behavioral patterns that are very different from being random, even in the absence of reward. Our aim is to understand foraging behavior by implementing an artificial rat that behaves as real ones do. We depart form the hypothesis that rodents, when performing free exploration, may be minimizing the unpredictability of the environment in terms of internally mapping its structure and discovering all the actions that it can afford. This drive for exploration is counterbalanced by a drive for security. Building from a self-regulation model based on the Distributed Adaptive Control architecture (DAC), we implement a biomimetic control that uses this predictability principle to generate behavior. We validate the controller by solving a benchmark task in which the agent learns to displace a movable obstacle to discover unexplored areas of an arena.
48) Polyethism in a colony of artificial ants
Chris Marriott and Carlos Gershenson
Polyethism in a colony of artificial ants We explore self-organizing strategies for role assignment and strategy selection in a foraging task carried out by a colony of artificial agents. Foraging strategies are selected by strategies inspired by various mechanisms of division of labor (polyethism) observed in eusocial insects like ants, termites, or bees. Specifically we instantiate models of 'emph' (polyethism) and 'emph' (temporal polyethism) to evaluate the benefits to foraging in a dynamic or unknown environment. We focus on the ability of division of labor mechanisms to self-organize individual strategy selection based on the environment.

49) Autonomy of the internet: Complexity of flow dynamics in a packet switching network
Takashi Ikegami, Mizuki Oka and Hirotake Abe
Autonomy of the internet (web system) is studied by running an NS-2 simulator. A web system consists of three layers, they are the network, the transport and the application layer and an network simulator called NS-2 can simulate the transport layer of the web as a packet switching network (PSN). This paper reports on the complexity of mutually crossing packet flows which are comparable to other autonomous complex networks, such as real Hippocampus slices, Izhikevich neural networks, or the game of life. One unique feature common in all these systems is the coexistence of several synchronised patterns that we think of as the underlying mechanism of autonomy. In the case of PSNs, adaptive window sizes of each packet flow show synchronisation but only locally, and often chaotic behavior is displayed when congestion occurs. Also considering the packet flow in PSNs as gliders, this congestion allows gliders to bifurcate. We thus propose PSNs as a new experimental testbed for discussing the autonomy and adaptability of living systems.

50) Encouraging networks modularity by seeding motifs
Shuguang Li, Jianping Yuan and Juan Cristóbal Zagal
We propose a motifs seeding method to encourage the emergence of modular structure during network evolution. Previous studies fail to trigger modularity on freeform evolving ANNs either when varying environmental factors or the evolutionary process itself. We extracted statistical profiles of 3-node and 4-node motifs from evolved networks, and then generated new networks by seeding the most useful 3-node motif (ID:38). A series of retina recognition experiments was conducted using the seeded networks. The performance of different algorithms was measured. Our results indicate that modularity could be encouraged under certain conditions. We were able to build networks meeting a desired Z-score.

51) Grounding synthetic knowledge: An epistemological framework and criteria of relevance for the scientific exploration of life, affect and social cognition
Luisa Damiano, Antoine Hiolle and Lola Cañamero.
In what ways can artificial life contribute to the scientific exploration of cognitive, affective and social processes? In what sense can synthetic models be relevant for the advancement of behavioral and cognitive sciences? This article addresses these questions by presenting the case study of an interdisciplinary cooperation between developmental robotics and developmental psychology in the exploration of attachment bonds. Its main aim is to show how the synthetic study of cognition, as the synthetic study of life, can find in autopoietic cognitive biology a grounding framework able to generate general criteria of relevance for synthetic models, that is, criteria (a) valuable for the three main branches of artificial life (soft, hard, and wet artificial life), and (b) useful to define the significance of their models for the scientific exploration of natural living and cognitive processes. On the basis of the formulation of this criteria, the article proposes a range of different forms of relevance that synthetic models of living and cognitive processes can express with regard to the inquiries of biological, behavioural and cognitive sciences.

52) Discovering and maintaining behaviours inaccessible to incremental genetic evolution through transcription errors and cultural transmission
James Borg, Alastair Channon and Charles Day
Abstract In this work the question of whether learning by imitation enables the evolution of behaviours inaccessible to incremental genetic evolution is assessed. To answer this question we implement a neural network model using a hybrid of two different networks: one capable of demonstrating reactive qualities, the other controlling deliberative goal selecting behaviours. Animats using this model are evolved in an adaptation of the novel environment proposed by Robinson et al. (2007) to solve an increasingly difficult task, this task requiring the demonstration of complex behaviours. Evolution in this work is by means of incremental genetic evolution, characterised by a ‘species adaptation genetic algorithm’ using an initially converged population. Tests are run on populations with and without learning by imitation to assess the relative success of each strategy, leading to the conclusion that populations with learning by imitation will successfully demonstrate the more complex behaviour, which is empirically found to be inaccessible to non learning populations.

53) Effective calibration of artificial gene regulatory networks
Davide Agostini, Jole Costanza, Vincenzo Cutello, Luca Zammarato, Natalio Krasnogor, Mario Pavone and Giuseppe Nicosia
Knowing all single components of biological systems is not enough to determine and understand the complexity of the system but rather becomes crucial understand how these components interact. It is not important a knowledge of genes and proteins, but rather know their structures, their dynamics, and primarily their parameters governing their dynamics, often unknown and impossible to measure directly. Gene Regulatory Networks explain exactly how genomic sequence encodes the regulation of expression of the sets of genes that progressively generate developmental patterns and execute the construction of multiple states of differentiation. Their main aim is to represent the regulation rules underlying the gene expression. In this research work we have designed the CMA-ES algorithm to inferring the parameters in the S-system model of a gene regulatory network. It is a well-known mathematical model whose structure is rich enough to capture many relevant biological
dynamics, and can modeling more complicated genetic network behaviour. CMA-ES was compared with 7 state-of-the-art algorithms to evaluate its efficiency in optimization, and its robustness. From a general point of view, analyzing all experiments done appear to be clear how CMA-ES is able to estimating in a better way the parameters target with respect to the state-of-the-art, either in order to the success rate and in term of euclidean distance. Finally, in this research paper has been also included a study on the convergence process of CMA-ES through Time-To-Target plots, which are a way to characterize the running time of stochastic algorithms; and a global sensitivity analysis method (the Morris method), which evaluate the effect of a parameter while all other parameters are varied simultaneously.

54) Quantifying evolutionary dynamics of swarm chemistry

Hiroki Sayama and Chun Wong

We developed two simple measurements to quantify the degrees of evolutionary exploration and macroscopic structuredness of swarm populations observed in Swarm Chemistry. Evolutionary exploration was quantified by counting the number of new colors that appeared in a simulation snapshot at a specific time point for the first time. Macroscopic structuredness was quantified by measuring a Kullback-Leibler divergence of a pairwise particle distance distribution from that of a homogeneous case. These measurements were designed so that they can be easily calculated a posteriori from a sequence of snapshots in past simulation runs. We first applied these measurements to two experimental conditions studied before: one with low mutation rates and static environments, and the other with high mutation rates and dynamical exogenous perturbations. Results showed that the latter promotes continuous evolutionary exploration, yet it tends to destroy macroscopic structures by allowing swarms to evolve toward simpler, homogeneous forms. We found a technical problem in the original collision detection mechanism that possibly destroyed macroscopic structures, so we made a minor modification to it and ran a new set of simulations. Measuring evolutionary dynamics of the new results showed that the model revision successfully maintained macroscopic structures at the minor cost of evolutionary exploration.