ECAL2009

10th EUROPEAN CONFERENCE ON ARTIFICIAL LIFE

Darwin Meets von Neumann

International Conference on the Simulation and Synthesis of Living System

13th-16th September 2009

Budapest, Hungary

Program & Abstracts
List of Participants

Editing closed on 2 September 2009

ECAL 2009: 10th European Conference on Artificial Life

Artificial Life is an interdisciplinary enterprise investigating the fundamental properties of living systems through simulating and synthesizing biological entities and processes in artificial media. ECAL, the European Conference on Artificial Life, is a biannual meeting complementing the mostly US-based "ALife" conference series.

Over the past two decades, some of the highly speculative ideas that were discussed at the field's inception have matured to the extent that new conferences and journals devoted to them are being established: synthesising artificial cells, simulating massive biological networks, exploiting biological substrates for computation and control, and deploying bio-inspired engineering are now cutting-edge practice. In the same period, biological knowledge grew at an unprecedented rate, giving rise to entire new disciplines, such as systems biology, and witnessed the rapid advancement of modelling and quantitative methods throughout the field. ECAL209 endeavours to bring together experts of computational and other ALife methods with more "conventional" mathematical modellers, reflecting on the fact that boundaries become rapidly blurred.

The ECAL2009 conference provides an opportunity for those working across these topics to get together and exchange ideas and results. To this end, the conference presents a selection of the best current work in the field, highlight new directions for investigation, and present high-profile keynote speakers.

Papers are welcome in all areas of the field, including:

- Synthesis and origin of life, self-organization, self-replication, artificial chemistries
- Evolution and adaptation, evolutionary dynamics, evolutionary games, coevolution, major evolutionary transitions, levels of selection, ecosystems
- Development, differentiation, and regulation; generative representations
- Synthetic biology and wet artificial life
- Self-organizing technology, self-* computing and computational ecosystems
- Unconventional and biologically inspired computing
- Bio-inspired robots and embodied cognition, autonomous agents, evolutionary robotics
- Collective behavior, communication, cooperation
- Artificial consciousness; the relationship between life and mind
- Philosophical, ethical, and cultural implications
- Mathematical and philosophical foundations of Alife, new and creative syntheses

ECAL2009 is held in Budapest, Hungary, in the magnificent historical building of the Hungarian Academy of Sciences, during September 13-16, 2009.

Wishing you a good Conferernce,

The Organizing Committee of ECAL2009,

George Kampis, Eörs Szathmáry (chairs),
Chrisantha Fernando, Márk Jelasity, Ferenc Jordán, András Lőrincz, István Scheuring

Contents

Conference Information

Meeting dates and venue

ECAL2009 is being be held in Budapest, Hungary, in the magnificent historical building of the Hungarian Academy of Sciences
1051 Budapest, Roosevelt tér 9.

www.mta.hu
www.ecal2009.org

Accommodation / Conference Venue Information

Mrs Éva Jónák
congress organiser
Tensi Congress
1023 Komjádi Béla utca 1
Budapest, Hungary
Phone: +36 1 345-1553
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E-mail: ejonak@tensi.hu
www.tensi-congress.hu

Organizing Committee

George Kampis, Eörs Szathmary (chairs)
Chrisantha Fernando, Márk Jelasity, Ferenc Jordán, András Lőrincz, István Scheuring

Registration of Participants

The **registration and information desk** will be found at the Main Hall (Díszterem) of the **Hungarian Academy of Sciences**

Opening Hours

on 13th of September	15,00 – 20,00
on 14th of September	8,00 – 18,00
on 15th of September	8,00 – 18,00
on 16th of September	8,00 – 18,00

Name badge and conference kit will be provided there. Please wear your badge throughout the entire conference. The organisers can be identified by their green badges. Please do not hesitate to contact them if you need any assistance!

Presenters

Presenters are requested to submit their presentation at least one hour before the beginning of their Session to the Registration Desk. In case of morning session, delegates are encouraged to submit their presentation the preceding evening.

The preferred formats are: Microsoft Power point 2003/2007 or Adobe PDF.
The videos in the presentations should be in MPEG-1 or WMV format.
The presentations are accepted on pen drive, CD, DVD, but not in floppy.

WiFi Service

The organisers provide WiFi internet access free of charge at the venue.

Courtesies

The Organizers will provide the following courtesies for participants:

- **Lunch with two glass refreshment** during the lunch brakes and **cake , coffee and refreshment** in the coffee breaks will be provided for participants , along the entire length of the conference , i.e. from 14 to 16 September.
- The Organizing Committee welcome the participants for **a Get Together Party on 13 September from 20,00 at the restaurant of the conference venue.**
- **A facultative Gala Dinner (Conference dinner) will be organised on 16 September from 20,00 at the Királyi Borház és Pincemúzeum Restaurant** (www.kiralyiborok.com)

Cloakroom

A cloakroom will be available at the venue, from 13 September and operating during the congress hours free of charge.

Parking

Public paying parking areas can be found near to the conference venue :
- in limited numbers in front of the main entrance of the Conference site and some places in the nearby streets, called Széchenyi rakpart, Akadémia Street, and Nádor Street

Smoking policy

Smoking is allowed in the provided area in the Conference Venue's building.

First Aid

Please contact the Registration Desk, if you need any guidance.

General Information

Budapest

Budapest, the capital of Hungary, lies in the centre of Eastern Europe, on both sides of the River Danube. The dominant role of the capital is reflected in the fact that about 2 million people - every fifth Hungarian - lives in the city. The Danube sets the stage for the life of Budapest. The greener side, which is the Buda hills that involve the soft inclines of Óbuda on the left bank is sharply distinguished from the plain industrial and commercial Pest on the right bank. The Hungarian capital is revived from day to day and is transforming itself into a true "world city". The diverse and rich history, and the dynamic cultural, culinary and economic life tend to amaze visitors.

Climate

The climate of Budapest is continental. The weather in Hungary is usually sunny and pleasant in September. Temperature is usually in the range of 20-22 degrees Centigrade during the day. Rainy days may be expected.

Time

The time zone of Hungary is CET (GMT +1).

Electricity

The voltage in Hungary is 230 V, 50 Hz AC.

Tipping

There are no predetermined rules for tipping in Hungary. If you are satisfied with the service, a 10% tip is customary, particularly in a taxi, restaurant or café with table service.

Driving and Parking

Drivers should be aware that there is a zero tolerance of blood alcohol level while driving in Hungary.

If you drive a personal or rented car, always try to park at a guarded parking lot and do not leave any valuables in the car. Please note, that Budapest is divided into paying areas with parking meters. The maximum parking time duration is 2 hours, and tariffs may vary.

Stores and Shopping

The opening hours of Budapest stores are generally 10.00-18.00 on weekdays and 10.00-13.00 on Saturdays. The shopping centres are open from 10.00-21.00 from Monday to Saturday and from 10.00-18.00 on Sundays.

Public Transportation

You might use public transportation to access the conference venue. Fares can not be paid on board and there are fines for travelling without a validated ticket. Tickets can be purchased at metro stations, hotels and tobacco shops.

Emergency phone numbers

Police:	107
Ambulance:	104
Central Emergency:	112

Currency

The Forint (HUF), the official national currency, is freely convertible. Exchange rates applied in Budapest banks, official exchange offices and hotels may vary.
National Bank exchange rate: 1 Euro = ca 270 HUF in August 2009

Credit Cards

All major credit cards (VISA, EC/MC and American Express) are accepted in Hungary in places displaying the emblem at the entrance, typically restaurants, supermarkets and larger shops.

Health Requirements /Medical Treatment

- No special health precautions are necessary in Hungary.
- Tap water in Hungary is safe to drink.
- Health Insurance is just as important to cover medical expenses in case of emergency or illness.

Information technology

- **Mobile phone coverage**
  Mobile phone coverage from all Hungarian service providers is available.

Insurance

Participants are advised to take adequate personal travel insurance.

Program overview

Program overview by topics, AND = "as well as"

Talks

September 14, Monday	September 15, Tuesday	September 16, Wednesday
evo/devo AND hardware	protocells AND prebiotic systems	evolutionary computation AND linguistics
cooperation	philosophy	neuroscience
evolutionary robotics I.	group selection AND evolvability	optimization AND action selection AND all else
evolutionary robotics II.	ecosystems	systems biology

Conference Schedule

September 13. (Sunday)

15:00 – 18:00	arrival, registration
18:00	opening, get together

September 14 (Monday)

9:00 – 9:50	Plenary talk (40 minutes + 10 minutes questions)
9:50 – 10:05	Short (15 min) break-coffee break
10:05 – 11:45	5 papers (20 minutes = 15 + 5)
11:45 – 12:00	Short (15 min) break
12:00 – 13:00	3 papers (20 minutes)
13:00 – 14:00	LUNCH
14:00 – 14:50	Plenary (40 +10)
14:50 – 15:05	Short (15 min) break- coffee break
15:05 – 16:45	5 papers (20 min)
16:45 – 17:00	Short (15 min) break
17:00 – 18:40	5 papers (20 min)

September 15 (Tuesday)

9:00 – 9:50	Plenary talk (40 minutes + 10 minutes questions)
9:50 – 10:05	Short (15 min) break – coffee break
10:05 – 11:45	5 papers (20 minutes = 15 + 5)
11:45 – 12:00	Short (15 min) break
12:00 – 13:00	3 papers (20 minutes)
13:00 – 14:00	LUNCH
14:00 – 14:50	Plenary (40 +10)
14:50 – 15:05	Short (15 min) break
15:05 – 16:45	5 papers (20 min)
16:45 – 17:00	Short (15 min) break
17:00 – 18:40	5 papers (20 min)

September 16(Wednesday)

9:00 – 9:50	Plenary talk (40 minutes + 10 minutes questions)
9:50 – 10:05	Short (15 min) break –coffee break
10:05 – 11:45	5 papers (20 minutes = 15 + 5)
11:45 – 12:00	Short (15 min) break
12:00 – 13:00	3 papers (20 minutes)
13:00 – 14:00	LUNCH
14:00 – 14:50	Plenary (40 +10)
14:50 – 15:05	Short (15 min) break-coffee break
15:05 – 16:45	5 papers (20 min)
16:45 – 17:00	Short (15 min) break
17:00 – 18:40	5 papers (20 min)

September 16.

20:00 -	Conference Dinner (optional)

Keynote Speakers

Peter Hammerstein	September 14, Monday	9:00 – 9:50 a.m.
Hod Lipson	September 14, Monday	14:00 – 14:50 p.m.
Nick Barton	September 15, Tuesday	9:00 – 9:50 a.m.
Richard Watson	September 15, Tuesday	14:00 – 14:50 p.m.
Eva Jablonka	September 16. Wednesday	14:00 – 14:50 p.m.

Workshop Shedule

Note: no workshops at plenary time (14:00-14:50 each day)

Workshop 1 Sept 14, 10:00-

Levels of Selection and Individuality in Evolution: Conceptual Issues and the Role of Artificial Life Models (Simon Powers, Rob Mills, Richard Watson, Alexandra Penn and Hywel Williams)

Workshop2 Sept 15, 10:00-

Organisation, Cooperation and Emergence in Social Learning Agents (Dara Curran and Colm O'Riordan)

Workshop 3 Sept 16, 10:00-

Agent connectivity: the role of cooperation in the regulation of the behavior of animals and robots (Istvan Karsai and Thomas Schmickl)

Lectures

PROGRAM OF TALKS

September 13. (Sunday)

15:00 -18:00	arrival, registration
18:00	opening, get together

September 14 (Monday)

9:00 – 9:50	Plenary talk (40 minutes + 10 minutes questions)
9:50 – 10:05	Short (15 min) break
10:05 – 11:45	5 papers (20 minutes = 15 + 5)

Self-Organizing Biologically Inspired Configurable Circuits

André Stauffer and Joël Rossier

Ecole polytechnique fédérale de Lausanne (EPFL), Logic Systems Laboratory
CH-1015 Lausanne, Switzerland

Abstract. Inspired by the basic processes of molecular biology, our previous studies resulted in defining self-organizing mechanisms made up of simple processes. The goal of our paper is to introduce a configurable molecule able to implement these mechanisms as well as their underlying processes. The hardware description of the molecule leads to the simulation of an arithmetic and logic unit designed as a one-dimensional organism dedicated to bit slice processors.

Epigenetic Tracking: Biological Implications

Alessandro Fontana

IEEE

Abstract. "Epigenetic Tracking" is an evo-devo method to generate arbitrary 2d or 3d shapes; as such, it belongs to the field of "artificial embryology". The objective of this paper is to explore the implications of the method for some relevant aspects of biology, namely junk DNA, the "ontogeny recapitulates philogeny" theory and the process of ageing. After presenting the latest experiments performed with 3d target shapes, the mentioned aspects are investigated and the explanation provided by Epigenetic Tracking is discussed.

The Effect of Proprioceptive Feedback on the Distribution of Sensory Information in a Model of an Undulatory Organism

Ben Jones[1], Yaochu Jin[2], Bernhard Sendhoff[2], Xin Yao[1]

[1] School of Computer Science, University of Birmingham, UK
[2] Honda Research Institute Europe GmbH, Germany

Abstract. In an animal, a crucial factor concerning the arrival of information at the sensors and subsequent transmission to the effectors, is how it is distributed. At the same time, higher animals also employ proprioceptive feedback so that their respective neural circuits have information regarding the state of the animal body. In order to disseminate what this practically means for the distribution of sensory information, we have modeled a segmented swimming organism (animat) coevolving its nervous system and body plan morphology. In a simulated aquatic environment, we find that animats

artificially endowed with proprioceptive feedback are able to evolve completely decoupled central pattern generators (CPGs) meaning that they emerge without any connections made to neural circuits in adjacent body segments. Without such feedback however, we also find that the distribution of sensory information from the head of the animat becomes far more important, with adjacent CPG circuits becoming interconnected. Crucially, this demonstrates that where proprioceptive mechanisms are lacking, more effective delivery of sensory input is essential.

Emerged Coupling of Motor Control and Morphological Development in Evolution of Multi-Cellular Animats

Lisa Schramm[1] and Yaochu Jin[2] and Bernhard Sendhoff[2]

[1] Technische Universit¨at Darmstadt, Karolinenplatz 5, 64289 Darmstadt, Germany
[2] Honda Research Institute Europe, Carl-Legien-Str. 30, 63073 Offenbach, Germany

Abstract. A model for co-evolving behavior control and morphological development is presented in this paper. The development of the morphology starts with a single cell that is able to divide or die, which is controlled by a gene regulatory network. The cells are connected by springs and form the morphology of the grown individuals. The movements of animats are resulted from the shrinking and relaxation of the springs connecting the lateral cells on the body morphology. The gene regulatory network, together with the frequency and phase shifts of the spring movements are evolved to maximize the distance that the animats can swim in a given time interval. To facilitate the evolution of swimming animats, a term that awards an elongated morphology is also included in the fitness function. We show that animats with different body-plans emerge in the evolutionary runs and that the evolved movement control strategy is coupled with the body plan.

Evolution of the morphology and patterning of artificial embryos: scaling the tricolour problem to the third dimension

Michał Joachimczak and Borys Wrobel

Computational Biology Group, Department of Genetics and Marine Biotechnology
Institute of Oceanology, Polish Academy of Sciences
Powsta ´nc ´ow Warszawy 55, 81-712 Sopot, Poland

Abstract. We present a model of three-dimensional artificial embryogenesis in which a multicellular embryo develops controlled by a continuous regulatory network encoded in a linear genome. Development takes place in a continuous space, with spherical cells of variable size, and is controlled by simulated physics. We apply a genetic algorithm to the problem of the simultaneous evolution of morphology and patterning into colour stripes and demonstrate how the system achieves the task by exploiting physical forces and using self-generated morphogen gradients. We observe a high degree of robustness to damage in evolved individuals and explore the limits of the system using more complex variations of the problem. We find that the system remains highly evolvable despite the increased complexity of three-dimensional space and the flexible coding of the genome requiring from evolution to invent all necessary morphogens and transcription factors.

11:45 – 12:00 Short (15 min) break

12:00 – 13:00 3 papers (20 minutes)

Toward Minimally Social Behavior: Social Psychology Meets Evolutionary Robotics

Tom Froese and Ezequiel A. Di Paolo

CCNR, University of Sussex, Brighton, UK

Abstract. We report on a set of minimalist modeling experiments that extends previous work on the dynamics of social interaction. We used an evolutionary robotics approach to fine-tune the design of a recent psychological experiment, as well as to synthesize a solution that gives clues about how humans might perform under these novel conditions. In this manner we were able to generate a number of hypotheses that are open to verification by future experiments in social psychology. In particular, the results indicate some of the advantages and disadvantages of relying on social factors for solving behavioral tasks.

Emergence of cooperation in adaptive social networks with behavioral diversity

Sven Van Segbroeck[1,3], Francisco C. Santos[2,3], Tom Lenaerts[3] and Jorge M.Pacheco[4]

[1] COMO, Vrije Universiteit Brussel, Brussels, Belgium
[2] CoDE-IRIDIA, Universit´e Libre de Bruxelles, Brussels, Belgium
[3] MLG, Universit´e Libre de Bruxelles, Brussels, Belgium
[4] ATP-Group, CFTC & DF, University of Lisbon, Lisbon, Portugal

Abstract. Whether by nature or nurture, humans often respond differently when facing the same situation. Yet, the role of behavioral differences between individuals when immersed in their social network remains largely ignored in most problems of natural and social sciences. Here, we investigate how diversity in the way individuals assess their adverse social partners affects the evolution of cooperation. We resort to evolutionary game theory (EGT) to describe the dynamics of populations in which individuals interact according to an adaptive social network and may respond differently to unwanted social interactions. We show that increasing the number of ways of responding to adverse ties in the population always promotes cooperation. As such, adaptive social dynamics and behavioral differences benefit the entire community even though myopic individuals still act in their own interest. As defectors are wiped out, surviving cooperators maintain the full diversity of behavioral types, providing the means to establish cooperation as a robust evolutionary strategy.

Cooperative Behaviours with Unknown Partners by a Homeostatic Neural Controller

Hiroyuki Iizuka, Hideyuki Ando and Taro Maeda

Department of Bioinformatics Engineering, Graduate School of Information Science and
Technology, Osaka University, 2-1 Yamadaoka, Suita, Osaka 565-0871, Japan

Abstract. This study presents a new way of establishing cooperative behavior between agents with an extended homeostatic adaptation. Originally, homeostatic adaptation is proposed as a novel mechanism for a single agent to have an ability to adapt to an unseen or unexpected environment. In this paper, we will show that the mechanism can be applied to multiple agents to create a cooperative behaviour with unknown agents to achieve a task as a whole. Usually, it is a difficult problem to know how an agent should behave in response to the partners' behaviour (especially unknown partners) to create cooperation. The agent might not even know how many other agents are involved in a task. Our idea is that the homeostatic mechanism can also work in these kinds of unknown situations.

13:00 – 14:00	LUNCH
14:00 – 14:50	Plenary (40 +10)
14:50 – 15:05	Short (15 min) break
15:05 – 16:45	5 papers (20 min)

Evolving amphibian behavior in complex environment

Kenji Iwadate, Ikuo Suzuki, Masahito Yamamoto, Masashi Furukawa

Hokkaido University, Laboratory of Autonomous System Engineering.
9 Nishi, 14 Kita, Kita-ku, Sapporo, 060-0814 Japan

Abstract. In this study, we aim to evolving autonomous virtual creatures which have complex shapes in a complex environment. We implement a basic physics law and fluid influences with a virtual environment and evolve artificial creatures in plural environments (on the ground, in the water). Each model, which is evolved in a different environment, obtains an effective moving behavior in each environment (looks like walking, and swimming).

Neuro-Evolution Methods for Gathering and Collective Construction

Geoff Nitschke

Department of Computer Science, University of Pretoria, South Africa

Abstract. This paper evaluates the Collective Neuro-Evolution (CONE) method, comparative to a related controller design method, in a simulated multi-robot system. CONE solves collective behavior tasks, and increases task performance via facilitating behavioral specialization. Emergent specialization is guided by genotype and behavioral specialization difference metrics that regulate genotype recombination. CONE is comparatively evaluated with a similar Neuro-Evolution (NE) method in a Gathering and Collective Construction (GACC) task. This task requires a multi-robot system to gather objects of various types and then cooperatively build a structure from the gathered objects. This collective behavior task requires that robots adopt complementary and specialized behaviors in order to solve. Results indicate that CONE is appropriate for evolving collective behaviors for the GACC task, given that this task requires behavioral specialization.

On the dynamics of active categorisation of different objects shape through tactile sensors

Elio Tuci, Gianluca Massera, and Stefano Nolfi

ISTC-CNR, Via San Martino della Battaglia, n. 44, 00185 Rome, Italy

Abstract. Active perception refers to a theoretical approach to the study of perception grounded on the idea that perceiving is a way of acting, rather than a process whereby the brain constructs an internal representation of the world. In this paper, we complement previous studies by illustrating the operational principles of an active categorization process in which a neuro-controlled anthropomorphic robotic arm, equipped with coarse-grained tactile sensors, is required to perceptually categorise spherical and ellipsoid objects.

The Information Dynamics of Embodied Agents

Paul Williams, Randall Beer

Indiana University, United States

Abstract. Dynamical systems theory and information theory both provide powerful tools and concepts for the analysis of embodied cognitive systems. However, while dynamical analyses are primarily concerned with the temporal behavior of such systems, information-theoretic analyses typically collapse over time to apply static measures of information structure. In contrast, we demonstrate that the same basic concepts of information theory can also be used to explore the behavior of a system as it unfolds through time, giving rise to a notion of information flow. We first describe a general approach to the analysis of evolved minimally cognitive agents using the tools of information theory. The central idea of our approach is to explore how information about particular stimulus features flows through the brain-bodyenvironment system. Using standard measures such as mutual information and transfer entropy, we quantify the information that particular components of the system have as a function of time, and characterize how that information moves through the system as behavior unfolds. Next, we present results from an information-theoretic analysis of a previously reported model of relational categorization (Williams, Beer & Gasser; CogSci 2008). We demonstrate how, using techniques to characterize the structure of information flow, we can rigorously formulate and address questions such as how the agent extracts and stores information about stimulus features, and how it integrates information about multiple features. Finally, we argue that when applied in this way, informationtheoretic techniques are in fact closely related to those of dynamical systems theory, and provide a complementary picture of how the behavior of a system emerges through the specific interactions of its components.

Evolving a novel bio-inspired controller in reconfigurable robots

Jürgen Stradner, Heiko Hamann, Thomas Schmickl, Ronald Thenius[1] and Karl Crailsheim

Artificial Life Laboratory of the Department of Zoology
Karl-Franzens University Graz, Universit¨atsplatz 2, A-8010 Graz, Austria

Abstract. Evolutionary robotics uses evolutionary computation to optimize physically embodied agents. We present here a framework for performing off-line evolution of a pluripotent robot controller that manages to form multicellular robotic organisms from a swarm of autonomously moving small robot modules. We describe our evolutionary framework, show first results and discuss the advantages and disadvantages of our off-line evolution approach. In detail, we explain the single parts of the framework and a novel homeostatic hormone-based controller, which is shaped by artificial evolution to control both, the non-aggregated single robotic modules and the joined high-level robotic organisms. As a first step we present results of this evolutionary shaped controller showing the potential for different motion behaviours.

16:45 – 17:00	Short (15 min) break
17:00 – 18:40	5 papers (20 min)

Functional and Structural Topologies in Evolved Neural Networks

Joseph T. Lizier[1,2], Mahendra Piraveenan[1,2], Dany Pradhana[1], Mikhail Prokopenko[1]
and Larry S. Yaeger[3]

[1] CSIRO Information and Communications Technology Centre, Locked Bag 17, North Ryde, NSW 1670, Australia
[2] School of Information Technologies, The University of Sydney, NSW 2006, Australia
[3] School of Informatics, Indiana University, 919 E. 10th St., Bloomington, IN 47408, USA

Abstract. The topic of evolutionary trends in complexity has draw much controversy in the artificial life community. Rather than investigate the evolution of overall complexity, here we investigate the evolution of topology of networks in the Polyworld artificial life system. Our investigation encompasses both the actual structure of neural networks of agents in this system, and logical or functional networks inferred from statistical dependencies between nodes in the networks. We find interesting trends across several topological measures, which together imply a trend of more integrated activity across the networks (with the networks taking on a more "small-world" character) with evolutionary time.

Input from the external environment and input from within the body

Filippo Saglimbeni, Domenico Parisi

Institute of Cognitive Sciences and Technologies, National Research Council, Rome

Abstract. Behaviour responds to both input from the external environment and input from within the organism's body. Input from the external environment has mainly the function to regulate the execution of the organism's activities while input from the body is used to decide which activity to execute. We evolve artificial organisms which to survive and reproduce have to both eat food and drink water in equivalent quantities and therefore at any given time they have to decide whether to look for food or water. We show that in some environments the appropriate behaviour can evolve with no need for the organism's brain to know the current level of energy and water in the body while in other environments the brain needs this information from the body in the form of hunger and thirst. We discuss how the body and the body's interactions with the brain are part of the overall adaptive pattern of an organism and must co-evolve with brain and behaviour.

Towards Self-Reflecting Machines: Two-Minds in One Robot

Juan Cristobal Zagal and Hod Lipson

Computational Synthesis Laboratory, Mechanical and Aerospace Engineering,
Cornell University, Ithaca, NY 14853, USA

Abstract. We introduce a technique that allows a robot to increase its resiliency and learning skills by exploiting a process akin to self-reflection. A robot contains two controllers: A pure reactive innate controller, and a reflective controller that can observe, model and control the innate controller. The reflective controller adapts the innate controller without access to the innate controller's internal state or architecture; instead, it models it and then synthesizes filters that exploit its existing capabilities for new situations. In this paper we explore a number of scenarios where the innate controller is a recurrent neural network. We demonstrate significant adaptation ability with relatively few physical trials.

Swarm-bots to the Rescue

R. O'Grady[1], C. Pinciroli[1], R. Gro[2], A. L. Christensen[3], F. Mondada[2], M. Bonani[2] and M. Dorigo[1]

[1] IRIDIA, CoDE, Universit_e Libre de Bruxelles, Brussels, Belgium
[2] LSRO, Ecole Polytechnique Federale de Lausanne, Lausanne, Switzerland
[3] DCTI, Lisbon University Institute, Lisbon, Portugal

Abstract. We explore the problem of resource allocation in a system made up of autonomous agents that can either carry out tasks individually or, when necessary, cooperate by forming physical connections with each other. We consider a group transport scenario that involves transporting broken robots to a repair zone. Some broken robots can be transported by an individual `rescue' robot, whereas other broken robots are heavier and therefore require the rescue robots to self-assemble into a larger and stronger composite entity. We present a distributed controller that solves this task while efficiently allocating resources. We conduct a series of real-world experiments to show that our system can i) transport separate broken robots in parallel, ii) trigger self-assembly into composite entities when necessary to overcome the physical limitations of individual agents, iii) efficiently allocate resources and iv) resolve deadlock situations.

Towards an Autonomous Evolution of Non-Biological Physical Organisms

Roderich Gross, Stéphane Magnenat, Lorenz Küchler, Vasili Massaras, Michael Bonani and Francesco Mondada

LSRO, Ecole Polytechnique Federale de Lausanne, Lausanne, Switzerland

Abstract. We propose an experimental study where simplistic organisms rise from inanimate matter and evolve solely through physical interactions. These organisms are composed of three types of macroscopic building blocks floating in an agitated medium. The dynamism of the medium allows the blocks to physically bind with and disband from each other. This results in the emergence of organisms and their reproduction. The process is governed solely by the building blocks' local interactions in the absence of any blueprint or central command. We demonstrate the feasibility of our approach by realistic computer simulations and a hardware prototype. Our results suggest that an autonomous evolution of non-biological organisms can be realized in human-designed environments and, potentially, in natural environments.

September 15 (Tuesday)

9:00 – 9:50	Plenary talk (40 minutes + 10 minutes questions)
9:50 – 10:05	Short (15 min) break
10:05 – 11:45	5 papers (20 minutes = 15 + 5)

Dynamical Systems Analysis of a Protocell Lipid Compartment

Ben Blundell

Evolutionary and Adaptive Systems, University of Sussex, Brighton, BN1 9QH, UK

Abstract. This paper develops phase portraits explaining the dynamic behaviour of the lipid compartment in a recently proposed stochastic protocell model. The protocell model is being used to investigate - in a bottom-up way - the possible roots of cellular autonomy, and the lipid compartment sub-system plays an integral part in determining the cellular dynamic. Whilst motivation is to ground the early model simulation results, the analysis here also reveals an interesting _nding: simple addition of an 'osmotic bu_er' to the lipid compartment not only widens it's range of stability, but also causes a profound change in the deep dynamical structure of the whole cellular system. Relevant to the origins of life, this bifurcation increases the robustness of the compartment to perturbation and instantly grants a richer behavioural repertoire including more reliable divide cycles.

Computational identification of obligatorily autocatalytic replicators embedded in metabolic networks

Ádám Kun[1], Balázs Papp[2], Eörs Szathmáry[1]

[1] Eötvös University, Budapest, Hungary
[2] Biological Research Center, Szeged, Hungary

Abstract. If chemical A is necessary for the synthesis of more chemical A, then A has the power of replication (such systems are known as autocatalytic systems). We provide the first systems-level analysis searching for small-molecular autocatalytic components in the metabolisms of diverse organisms, including an inferred minimal metabolism. We find that intermediary metabolism is invariably autocatalytic for ATP. Furthermore, we provide evidence for the existence of additional, organism-specific autocatalytic metabolites in the forms of coenzymes (NAD+, coenzyme A, tetrahydrofolate, quinones) and sugars. Although the enzymatic reactions of a number of autocatalytic cycles are present in most of the studied organisms, they display obligatorily autocatalytic behavior in a few networks only, hence demonstrating the need for a systems-level approach to identify metabolic replicators embedded in large networks. Metabolic replicators are apparently common and potentially both universal and ancestral: without their presence, kick-starting metabolic networks is impossible, even if all enzymes and genes are present in the same cell. Identification of metabolic replicators is also important for attempts to create synthetic cells, as some of these autocatalytic molecules will presumably be needed to be added to the system as, by definition, the system cannot synthesize them without their initial presence.

The Role of the Spatial Boundary in Autopoiesis

Nathaniel Virgo, Matthew Egbert and Tom Froese

Centre for Computational Neuroscience and Robotics, University of Sussex, Brighton, UK

Abstract. We argue that the significance of the spatial boundary in autopoiesis has been overstated. It has the important task of distinguishing a living system as a unity in space but should not be seen as playing the additional role of delimiting the processes that make up the autopoietic system. We demonstrate the relevance of this to a current debate about the compatibility of the extended mind hypothesis with the enactive approach and show that a radically extended interpretation of autopoiesis was intended in one of the original works on the subject. Additionally we argue that the definitions of basic terms in the autopoietic literature can and should be made more precise, and we make some progress towards such a goal.

Chemo-ethology of an Adaptive Protocell: Sensorless sensitivity to implicit viability conditions

Matthew D. Egbert, Ezequiel A. Di Paolo and Xabier E. Barandiaran

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Abstract. The viability of a living system is a non-trivial concept, yet it is often highly simplified in models of adaptive behavior. What is lost in this abstraction? How do viability conditions appear in the first place? In order to address these questions we present a new model of an autopoietic or protocellular system simulated at the molecular level. We propose a measurement for the viability of the system and analyze the 'viability condition' that becomes evident when using this measurement. We observe how the system behaves in relation to this condition, generating instances of chemotaxis, behavioural preferences and simple (yet not trivial) examples of action selection. The model permits the formulation of a number of conclusions regarding the nature of viability conditions and adaptive behaviour modulated by metabolic processes.

On the transition from prebiotic to proto-biological membranes: from 'self-assembly' to 'self-production'

Gabriel Piedrafita[1], Fabio Mavelli [2], Federico Morán[1] and Kepa Ruiz-Mirazo [3*]

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[2] Dept. of Chemistry, University of Bari, Italy
[3] Dept. of Logic and Philosophy of Science / Biophysics Research Unit (CSIC-UPV/EHU)
University of the Basque Country, Spain

Abstract. A model is here presented to analyse how vesicles may turn into protocells that synthesize their own lipid components and the consequences that this may have on the properties of the resulting membrane (in particular, on its permeability), as well as on the overall stability of the system.

11:45 – 12:00	Short (15 min) break
12:00 – 13:00	3 papers (20 minutes)

Modeling Living Systems

Peter Andras[1]

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Newcastle upon Tyne, NE1 7RU, United Kingdom

Abstract. A fundamental issue of evolution of life is the emergence and maintenance of self-referential autocatalytic systems (e.g. living cells). In this paper the problem is analyzed from a computational perspective. It is proposed that such systems have to be infinite autocatalytic systems, which can be considered equivalent to Turing machines. The implication of this is that searching for finite autocatalytic systems is likely to not be successful, and any such finite system would be maintainable only in a highly stable environment. The infiniteness of autocatalytic systems also implies that top-down search for the simplest living system is likely to stop at relatively complex cells that are still able to provide a realization of infinite autocatalytic systems.

Facing N-P Problems via Artificial Life: a Philosophical Appraisal

Carlos E. Maldonado and Nelson Gómez

Modeling and Simulation Laboratory, Universidad del Rosario, Bogotá, Colombia

Abstract. Life as an N-P problem is a philosophical, scientific and engineering concern. N-P problems can be understood and worked out via artificial life. However, these problems demand a new understanding of engineering, since engineering is basically a way of acting upon the world. Such a new engineering is known as non-conventional engineering or also as complex systems engineering. Bio-inspired systems are more flexible and allow a higher number of degrees of freedom. As a consequence, AL enlarges our understanding of living systems in general and can be taken as a step forwards in grasping the complexity of life.

Can the map be the territory? Visualization and realisation in artificial life.

Seth Bullock

Science & Engineering of Natural Systems, School of Electronics & Computer Science, University of Southampton, UK

Abstract. In the continuing absence of a formal, consensual, definition of what it is to be a living system, artificial life has learned to make do with a mantra of "I can't define it, but I know it when I see it". An under-appreciated consequence of this position is the attendant epistemological load placed on seeing and therefore visualization. This paper considers the role of visualization within science and artificial life, specifically, reviewing its multiple distinct uses and exploring the possibility that it might sometimes play a role that is unique to the field: visualizations as realisations.

Scientific visualizations are typically taken to re-present the target phenomena of interest: a graph or chart presents data on some target system; an image from a confocal microscope is an image of some target system. Like any representation, they are typically understood to stand in some rather impoverished relation to the target system, representing it just so, capturing only a fragment of its reality—attenuating, idealising, clipping, focusing, highlighting, or otherwise differing from the real thing in itself. By contrast, when we view Craig Reynolds' Boids or Karl Sims' Blockies, we are not expected to consider the images as partial representations of some prior thing (the code, the algorithm?). They are the thing. Indeed, where typically the image offers only a glimpse of the "real" system, here the relationship is reversed. The underlying code is impenetrable, offering only a glimpse of the flocking that it gives rise to. However, is it true to claim that the flock of Boids is simply

not present in the lines of code in the same way that it is present in the image sequence? Surely there may be creatures for which viewing the image sequence, like studying the code, fails to produce the perception of a flock. Where is the locus of the "emergence" of flocking, or life, or some other complex organisational phenomena? In the code? On the screen? Within an observer's mind?

What has been termed the "synthetic methodology" offers us the promise of a new route to understanding organisational phenomena and answering systems questions through construction rather than reduction. However, where we attempt to synthesize truly new phenomena (e.g., "life-as-it-could-be") without the safety net of agreed formal category definitions, we must run the risk of relying on our (possibly raw unanalysed) visuocognitive apparatus to guide us, and will consequently be subject to its biases and idiosyncrasies. From this perspective, Ikegami and Hanczyc's oil droplets, Grey Walter's Elsie and Elmer, Langton's loops, and Ray's Tierran replicators must be regarded as denizens of the realm of ideas as much as (or perhaps more than) the realm of physical reality. They are constructs in the psychological sense as much as the engineering sense, and just as models teach us about the world only indirectly by shedding light on our ideas about the world, these artificial life systems may only change what we know of life by changing the way that we see it.

13:00 – 14:00	LUNCH
14:00 – 14:50	Plenary (40 +10)
14:50 – 15:05	Short (15 min) break
15:05 – 16:45	5 papers (20 min)

Investigations of Wilson's and Traulsen's Group Selection Models in Evolutionary Computation

Shelly X. Wu and Wolfgang Banzhaf

Computer Science Department, Memorial University of Newfoundland, St John's, Canada, A1B 3X5

Abstract. Evolving cooperation by evolutionary algorithms is impossible without introducing extra mechanisms. Group selection theory in biology is a good candidate as it explains the evolution of cooperation in nature. Two biological models, Wilson's trait group selection model and Traulsen's group selection model are investigated and compared in evolutionary computation. Three evolutionary algorithms were designed and tested on an n-player prisoner's dilemma problem; two EAs implement the original Wilson and Traulsen models respectively, and one EA extends Traulsen's model. Experimental results show that the latter model introduces high between-group variance, leading to more robustness than the other two in response to parameter changes such as group size, the fraction of cooperators and selection pressure.

The Evolution of Division of Labor

Heather J. Goldsby, David B. Knoester, Jeff Clune, Philip K. McKinley, Charles Ofria

Department of Computer Science and Engineering, Michigan State University, East Lansing, Michigan 48824

Abstract. We use digital evolution to study the division of labor among heterogeneous organisms under multiple levels of selection. Although division of labor is practiced by many social organisms, the labor roles are typically associated with different individual fitness effects. This fitness variation raises the question of why an individual organism would select a less desirable role. For this study, we provide organisms with varying rewards for labor roles and impose a group-level pressure for division of labor. We demonstrate that a group selection pressure acting on a heterogeneous population is sufficient to ensure role diversity regardless of individual selection pressures, be they beneficial or detrimental.

A Sequence-to-Function Map for Ribozyme-catalyzed Metabolisms

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[2] University of Vienna, Institute for Theoretical Chemistry, Währingerstr. 17, 1090 Vienna, Austria

Abstract. We introduce a novel genotype-phenotype mapping based on the relation between RNA sequence and its secondary structure for the use in evolutionary studies. Various extensive studies concerning RNA folding in the context of neutral theory yielded insights about properties of the structure space and the mapping itself. We intend to get a better understanding of some of these properties and especially of the evolution of RNA-molecules as well as their effect on the evolution of the entire molecular system. We investigate the constitution of the neutral network and compare our mapping with other artificial approaches using cellular automatons, random Boolean networks and others also based on RNA folding. We yield the highest extent, connectivity and evolvability of the underlying neutral network. Further, we successfully apply the mapping in an existing model for the evolution of a ribozyme-catalyzed metabolism.

Can Selfish Symbioses Effect Higher-level Selection?

Richard A. Watson, Niclas Palmius, Rob Mills, Simon Powers, Alexandra Penn.

Natural Systems group, University of Southampton, U.K.

Abstract. The role of symbiosis in macro-evolution is poorly understood. On the one hand, symbiosis seems to be a perfectly normal manifestation of individual selection, on the other hand, in some of the major transitions in evolution it seems to be implicated in the creation of new higher-level units of selection. Here we present a model of individual selection for symbiotic relationships where individuals can genetically specify traits which partially control which other species they associate with – i.e. they can evolve species-specific grouping. We find that when the genetic evolution of symbiotic relationships occurs slowly compared to ecological population dynamics, symbioses form which canalise the combinations of species that commonly occur at local ESSs into new units of selection. Thus even though symbioses will only evolve if they are beneficial to the individual, we find that the symbiotic groups that form are selectively significant and result in combinations of species that are more cooperative than would be possible under individual selection. These findings thus provide a systematic mechanism for creating significant higher-level selective units from individual selection, and support the notion of a significant and systematic role of symbiosis in macro-evolution.

The effect of group size and frequency-of-encounter on the evolution of cooperation

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[2] Manchester Business School, University of Manchester, UK

Abstract. We introduce a model of the evolution of cooperation in groups which incorporates both conditional direct-reciprocity ("tit-for-tat"), and indirect-reciprocity based on public reputation ("conspicuous altruism"). We use ALife methods to quantitatively assess the effect of changing the group size and the frequency with which other group members are encountered. We find that for moderately sized groups, although conspicuous altruism plays an important role in enabling cooperation, it fails to prevent an exponential increase in the level of the defectors as the group size is increased, suggesting that economic factors may limit group size for cooperative ecological tasks such as foraging.

16:45 – 17:00 Short (15 min) break
17:00 – 18:40 5 papers (20 min)

Evolutionary and environmental triggers for nonlinear change in simulated ecosystems

Hywel T. P. Williams & Timothy M. Lenton

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Abstract. Throughout Earth history, life has coevolved with its physical environment. There have been many occasions where key transitions in evolutionary history have been causally linked to transitions in Earth history, highlighting the existence of complex feedbacks between life and its environment (Lenton et al, 2004). In the current period of rapid climate change, understanding the evolutionary response of ecosystems to environmental forcing is of key importance. Ecosystems are complex adaptive systems (Levin, 1998) that integrate nutrient and energy cycles through trophic structure and physical processes. Predicting ecosystem level responses to perturbation requires consideration of the lower level responses of constituent species, as well as species-species and species-environment interactions. The responses of ecosystems to environmental change are varied. In some cases, linear forcing can lead to a nonlinear response, such as when a bistable ecological system is tipped into a different attractor state (Scheffer et al, 2001). This kind of rapid nonlinear change (or "catastrophic regime shift") may suggest a mechanism to explain some large coupled transitions in evolutionary and Earth history. However, most theoretical work has focused on understanding purely ecological systems and the response of evolving ecosystems is poorly understood. Evolution introduces a new internal source of perturbation, in the form of novel species resulting from evolutionary adaptation, that can potentially have a radical disruptive effect. Here we use an individual based evolutionary simulation model to analyse nonlinear changes in global ecosystem state resulting from internal (novel species) and external (environmental forcing) perturbations. We show that local adaptation and speciation can trigger sudden change across the ecosystem, when new traits allowing rapid growth of biomass cause abrupt environmental change, driving incumbent species extinct (Williams & Lenton, 2009). Similarly extreme disruptions can be caused by external forcing of the environment, which can overcome the stabilising tendency of an established community and push key variables beyond resilience thresholds (Williams & Lenton, in prep). In both scenarios, the perturbation may result in ecosystem collapse, followed by recovery to an alternate stable state, or even system wide extinction. We analyse the internal and external triggers for ecosystem collapse and examine possible methods for their prediction. We find that the impacts of newly evolved species on an ecosystem (measured in terms of environmental change, productivity, and species turnover) follow a power law distribution, suggesting interesting parallels with the power law distribution of extinction event sizes in the fossil record (Sole & Manrubia, 1996). We hypothesise that the perturbation caused by novel species, amplified by environmental feedbacks on growth, may offer a new mechanism to explain some mass extinction events in evolutionary history.

Towards formalising the theory of Dual Phase Evolution

Greg Paperin and Suzanne Sadedin

Clayton School of Information Technology, Monash University, Vic. 3800 Australia

Abstract. Complex adaptive and evolutionary systems exhibit sustained diversity, far-from equilibrium dynamics, and permanent novelty and adaptation in the absence of a global controller. Previously, we have shown that many of such properties may be a result of Dual Phase Evolution (DPE) - a widespread family of natural processes in which complex systems adapt and self-organise by alternating between two phases. During one phase, the system is highly connected and interactions among components occur at a global scale; during the other phase, connectivity is low and interactions are predominantly localised.

Previous work demonstrates that DPE processes can lead to the emergence of perpetual novelty and complex diversity in spatially distributed ecosystems. Phases of different connectivity lead to well-defined periods of balance and variation, while repeated switching between these regimes facilitates continual reorganisation and innovation within these ecosystems [5]. Patterns arising from DPE are evident at a range of temporal and spatial scales, including ecological state transitions due to fire spread, and adaptive radiation events triggered by climate change and mass extinctions.

Insights into both the processes that underlie the emergence of complex network structures, and the effects of such structures, are necessary to understand the properties that characterise adaptive evolutionary systems. Studies show that DPE can give rise to important network topologies previously attributed to other processes. For instance, DPE can lead to the emergence of small world and scale-free topologies in networks of constant size . Modular network topologies are poorly understood and present a topic of much recent research. Studies show that such structures can also arise through DPE processes. These models along with a growing body of empirical data suggest a need to further refine and formalise the DPE theory. We present on-going modelling work that demonstrates the occurrence of DPE in various artificial and natural adaptive systems. We then concentrate on refining the DPE theory within the context of established formalisms for complex systems.

Embodiment of Honeybee's Thermotaxis in a Mobile Robot Swarm

Daniela Kengyel[1], Thomas Schmickl[2], Heiko Hamann[2] and Karl Crailsheim[2]

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[2] Artificial Life Laboratory of the Department of Zoology, Karl-Franzens University Graz, Universitätsplatz 2, A-8010 Graz, Austria

Abstract. Searching an area of interest based on environmental cues is a challenging benchmark task for an autonomous robot. It gets even harder to achieve if the goal is to aggregate a whole swarm of robots at such a target site after exhaustive exploration of the whole environment. When searching gas leakages or heat sources, swarm robotic approaches have been evaluated in recent years, which were, in part, inspired by biologically motivated control algorithms. Here we present a bio-inspired control program for swarm robots, which collectively explore the environment for a heat source to aggregate. Behaviours of young honeybees were embodied on a robot by adding thermosensors in `virtual antennae'. This enables the robot to perform thermotaxis, which was evaluated in a comparative study of an egoistic versus a collective swarm approach.

Novel approaches to engineering complex microbial communities

Alexandra Penn, Richard Watson, Tim Conibear, Lex Kraaijeveld and Jeremy Webb

University of Southampton, UK.

Abstract. Bacteria in complex microbial communities constitute the majority of individuals, biomass and diversity present in the biosphere. Interaction with and control of such communities presents an enormous challenge and is key in vital issues such as climate change, bioenergy, bioremediation and chronic infections. In addition, the recent upsurge in biologically-based and biologically-inspired technologies has created new engineering challenges which can be usefully related to the management of such communities. Problems in both these areas demand a better ability to understand and manage complex biological systems than is currently available.

Conventional approaches to working with biological systems are, for the most part, "brute force", attempting to effect control in an input and effort intensive manner and are often insufficient when dealing with the inherent non-linearity and complexity of such systems. Biological systems, by their very nature, are dynamic, adaptive and resilient. Our novel, "light-touch", engineering approach which aims to exploit rather than fight those properties, presents a more efficient and robust alternative. The essence of this approach is what I will call "equilibrium engineering", manipulating

systems' own self-organisation and evolution so that the evolutionarily stable group or community species and genetic composition corresponds to a community function which we require. In this talk I will describe and explore this approach and it's utility. I will focus on one particular aspect : manipulating systems' adaptive trajectories so that the evolutionarily stable strategy in a given scenario corresponds to a system behaviour that suits our purposes. Specifically we consider changing the context of selection by either manipulating or imposing the effective "level of selection" within the system. Particular levels of selection will produce particular types of community composition. For example, higher-level selection will promote co-operation and interspecies synergy useful for efficient bioremediation, whereas encouraging lower-level selection might allow us to engineer a "tragedy of the commons" in problematic bacterial communities. This approach can be applied in a variety of different ways, ranging from straightforward imposition of higher-level selection, to indirectly manipulating parameters of the selective process such as effective group size which alter the outcome of selection in certain ways. I will illustrate these ideas both conceptually and using methodology and preliminary results from ongoing experimental work with bacterial biofilms of Psuedamonous aeruginosa in which direct or indirect manipulation of parameters affecting group structure and dispersal mechanisms modify the effective level of and hence response to selection. I will describe approaches to increase the robustness of the engineered community by promoting the genetic canalisation of an appropriate level of selection by co-evolution (via artificial selection) of group structure and dispersal with other community functions. Finally I will contrast this methodology with imposition of higher-level selection to encourage co-operative or synergistic behaviour illustrated via current work on soil ecosystem selection under way in the Biosphere 2 research facility.

Breaking Waves in Population Flows

George Kampis[1,2] and Istvan Karsai[3]

[1] Collegium Budapest, Institute for Advanced Study, Budapest, Hungary
[2] Eötvös University, Department of Philosophy of Sciece, Budapest, Hungary
[3] Department BISC, East Tennessee State University, Johnson City, TN, USA.

Abstract. The effects of fragmentation and corridors on the dynamics of coexistence are explored via an agent based model. Based on the analogy of wave breakers, the spatio-temporal fluctuations of a simple prey and predator system are measured and analyzed. In an unfragmented habitat, predator populations show massive waves and the fragmentation of the habitat usually results in the extinction of the predators. However, connected fragmented systems decrease oscillations and save the predators from prey overexploitation and extinction. Corridors allow the prey to escape temporally from the predators and to colonize territories commonly left without predators. Later, predators also find these sub-habitats, but this delay and the many parallel processes in the different sub-habitats result in a stable coexistence dynamics.

September 16 (Wednesday)

9:00 – 9:50	Plenary talk (40 minutes + 10 minutes questions)
9:50 – 10:05	Short (15 min) break
10:05 – 11:45	5 papers (20 minutes = 15 + 5)

HybrID: A Hybridization of Indirect and Direct Encodings for Evolutionary Computation

Jeff Clune[1], Benjamin E. Beckmann[1], Robert T. Pennock[1,2] and Charles Ofria[1]

1 Department of Computer Science and Engineering
2 Department of Philosophy and Lyman Briggs College, Michigan State University, East Lansing, MI, USA

Abstract. Evolutionary algorithms typically use direct encodings, where each element of the phenotype is specified independently in the genotype. Because direct encodings have difficulty evolving modular and symmetric phenotypes, some researchers use indirect encodings, wherein one genomic element can influence multiple parts of a phenotype. We have previously shown that Hyper-NEAT, an indirect encoding, outperforms FT-NEAT, a direct-encoding control, on many problems, especially as the regularity of the problem increases. However, HyperNEAT is no panacea; it had difficulty accounting for irregularities in problems. In this paper, we propose a new algorithm, a Hybridized Indirect and Direct encoding (HybrID), which discovers the regularity of a problem with an indirect encoding and accounts for irregularities via a direct encoding. In three different problem domains, HybrID outperforms HyperNEAT in most situations, with performance improvements as large as 40%. Our work suggests that hybridizing indirect and direct encodings can be an effective way to improve the performance of evolutionary algorithms.

An Analysis of Lamarckian Learning in Changing Environments

Dara Curran and Barry O'Sullivan

Cork Constraint Computation Centre, Department of Computer Science, University College Cork, Ireland

Abstract. It is widely recognised that many species adapt to complex and dynamic environments, but it is no longer accepted that an organism passes characteristics acquired during its lifetime to its offspring. However, in evolutionary computation such Lamarckian inheritance can be useful. Simulations of the benefits of Lamarckian inheritance have been reported in the literature. However, in this paper we present the first formal proof that Lamarckian inheritance can dominate more traditional individual (non-inheritable) learning.We present a parameterised model that can demonstrate conditions in which different inheritance types perform best, which we empirically validate.

Linguistic Selection of Language Strategies: A Case Study for Colour

Joris Bleys[1] and Luc Steels[1,2]

[1] Artificial Intelligence Laboratory, Vrije Universiteit Brussel, Brussels, Belgium
[2] Sony Computer Science Laboratory, Paris, France

Abstract. Language evolution takes place at two levels: the level of language strategies, which are ways in which a particular subarea of meaning and function is structured and expressed, and the level of concrete linguistic choices for the meanings, words, or grammatical constructions that instantiate a particular language strategy. It is now reasonably well understood how a shared language strategy enables a population of agents to self-organise a shared language system. But the origins and evolution of strategies has so far been explored less. This paper proposes that linguistic selection, i.e. selection driven by communicative success and cognitive effort, is relevant and shows a concrete case study for the domain of colour on how different language strategies may cooperate and compete for dominance in a population.

The Microbial Genetic Algorithm

Inman Harvey

Evolutionary and Adaptive Systems Group, Centre for Computational Neuroscience and
Robotics, Department of Informatics, University of Sussex, Brighton BN1 9QH, UK

Abstract. We analyse how the conventional Genetic Algorithm can be stripped down and reduced to its basics. We present a minimal, modified version that can be interpreted in terms of horizontal gene transfer, as in bacterial conjugation. Whilst its functionality is effectively similar to the conventional version, it is much easier to program, and recommended for both teaching purposes and practical applications. Despite the simplicity of the core code, it effects Selection, (variable rates of) Recombination, Mutation, Elitism ('for free') and Geographical Distribution.

Robots That Say 'No'

Frank Förster, Chrystopher L. Nehaniv, and Joe Saunders

Adaptive Systems Research Group, School of Computer Science
University of Hertfordshire,College Lane, Hatfield, AL10 9AB.United Kingdom

Abstract. This paper reports on foundational considerations for experiments into the acquisition of human-like use and understanding of negation in linguistic utterances via a developmental robotics approach. For this purpose different taxonomies of negation in early child language are analysed in order to show the large variety of communicative functions that these different types of negation have. Requirements for robotic systems that aim at acquiring these utterances in a linguistically unconstrained human-robot dialog are derived from this analysis.

11:45 – 12:00	Short (15 min) break
12:00 – 13:00	3 papers (20 minutes)

Transfer of Spike Timing Patterns by Theta Phase Synchrony

Daniel Bush[1,2], Chrisantha Fernando[1,2], Eors Szathmary[1] and Phil Husbands[2]

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Abstract. Auto-associative neural network models represent an established computational framework for the study of mammalian learning and declarative memory function. Biological correlates of these models – consisting of recurrently connected networks which exhibit extensive synaptic plasticity – have been proposed to exist in the CA3 region of the hippocampus and layers 2/3 of the neo-cortex. Both of these brain regions are modulated by inhibitory theta oscillations during mnemonic processing, and the magnitude and direction of changes in synaptic strength induced by standard protocols in the hippocampus has been shown to vary significantly within each theta cycle. Furthermore, phase synchrony between neocortical and hippocampal networks increases with mnemonic load, which suggests that one function of theta may be to mediate a dynamic link between the distributed network of pre-frontal, mediotemporal and visual cortices during learning, recall and decision making.

Here, we present an abstract model of cortico-hippocampal interaction that consists of two bi-directionally connected auto-associative networks, the neural and synaptic dynamics of which are modulated by independent theta frequency oscillations in a biologically realistic manner. This configuration allows externally applied patterns of temporally-coded activity to be learned by either network, and subsequently transferred between the networks at will by manipulating the synchrony of respective theta oscillations. This model therefore provides a biologically inspired mechanism for the selective copying of established cell assemblies between disparate neural networks. This research is

particularly relevant to the neuronal replicator hypothesis, which posits that a process akin to Darwinian evolution may operate within the brain; and theories of declarative memory consolidation, which posit that mnemonic traces are transferred between complementary learning systems in the hippocampus and cortex.

Memory-Based Cognitive Framework: a Low-Level Association Approach to Cognitive Architectures

Paul Baxter[1] and Will Browne[1]

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Abstract. At its most fundamental, cognition as displayed by biological agents (such as humans) may be described as being the manipulation and utilisation of memory. A low-level approach to the associative sensory-motor development of cognition is then appropriate, rather than the more common higher-level functional approach. A novel theoretical framework – the memory-based cognitive framework (MBCF) – is proposed based upon these considerations. A computational architecture based on the MBCF is implemented on a mobile robot platform, and experimental results are presented to demonstrate the functionality of the architecture. It is shown that this low-level, bottom-up, approach can produce adaptive behaviours, which may ultimately form the foundation of cognitively flexible agents.

Modelling Coordination of Learning Systems: A Reservoir Systems Approach to Dopamine Modulated Pavlovian Conditioning

Robert Lowe[1], Francesco Mannella[2], Tom Ziemke[3] and Gianluca Baldassarre[4]

[1;3] University of Skovde, Informatics Research Centre, Cognition & Interaction Lab
[2;4] Consiglio Nazionale delle Ricerche, Istituto di Scienze e Tecnologie della Cognizione
Laboratory of Computational Embodied Neuroscience

Abstract. This paper presents a biologically constrained reward prediction model capable of learning cue-outcome associations involving temporally distant stimuli without using the commonly used temporal difference model. The model incorporates a novel use of an adapted echo state network to substitute the biologically implausible delay chains usually used, in relation to dopamine phenomena, for tackling temporally structured stimuli. Moreover, the model is based on a novel algorithm which successfully coordinates two sub systems: one providing Pavlovian conditioning, one providing timely inhibition of dopamine responses to salient anticipated stimuli. The model is validated against the typical profile of phasic dopamine in first and second order Pavlovian conditioning. The model is relevant not only to explaining the mechanisms underlying the biological regulation of dopamine signals, but also for applications in autonomous robotics involving reinforcement-based learning.

13:00 – 14:00	LUNCH
14:00 – 14:50	Plenary (40 +10)
14:50 – 15:05	Short (15 min) break
15:05 – 16:45	5 papers (20 min)

Agent-based toy modeling for comparing distributive and competitive free market

Hugues Bersini

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Abstract. Is a competitive free market the most efficient way to equally allocate rare resources among economical agents ? Many economists tend to think it is the case. This paper presents a preliminary attempt through a very Alife like model to tackle this question. Agents which are alternatively producer, seller, buyer and consumer participate in a free market to increase their welfare. The simulation is organized and presented in a UML class diagram and two types of economy, competitive and distributive, are compared.

Swarm Cognition and Artificial Life

Vito Trianni and Elio Tuci

Institute of Cognitive Sciences and Technologies (ISTC), National Research Council (CNR), Rome, Italy

Abstract. Swarm Cognition is the juxtaposition of two relatively unrelated concepts that evoke, on the one hand, the power of collective behaviours displayed by natural swarms, and on the other hand the complexity of cognitive processes in the vertebrate brain. Recently, scientists from various disciplines suggest that, at a certain level of description, operational principles used to account for the behaviour of natural swarms may turn out to be extremely powerful tools to identify the neuroscientific basis of cognition. In this paper, we review the most recent studies in this direction, and propose an integration of Swarm Cognition with Artificial Life, identifying a roadmap for a scientific and technological breakthrough in Cognitive Sciences.

Life Engine - creating artificial life for scientific and entertainment purposes

Gonçalo Marques[1], Lorena António[1], Tânia Sousa[1], Tiago Domingos[1] and Kooijman Bas[2]

[1] Instituto Superior Técnico, Portugal
[2] Vrije Universiteit, Netherlands

Abstract. The Dynamic Energy Budget (DEB) theory has become a fundamental tool in modeling the metabolic behaviour of organisms. On the other hand, the videogame industry is striving for more realism in its products. The DEB group in IST has joined Biodroid, a game developing company, in the Life Engine project to build a game engine for metabolic modeling using DEB. Our goal is not only to have a module to be used in games but also a module for scientific purposes.

DEB theory (http://www.bio.vu.nl/thb/deb/) is a general mathematical theory at the organism level applicable to all taxonomic groups with implications at the sub- and supra-organism levels. Since DEB is a non-species specific theory, we can describe all types of organisms, from bacteria to trees, with the same computational framework. Each species is characterized in DEB theory by a set of parameter values and DEB theory predicts how these parameter values change as a function of the maximum size of the species. Apart from the evident economy in coding, this DEB engine provides also an enormous potential for realistic and unexpected complexity.

DEB theory is based on simple mechanistic rules for the uptake of energy and nutrients and the consequences of these rules for physiological organization along the life cycle of organisms. It has many empirical models as special cases, such as Droop's model for the nutrient limited growth of

algae, von Bertalanffy's model for the growth of animals or Kleiber's law for respiration. The large collection of empirical support for all these empirical models that accumulated in the literature and the bits of evidence that people working with DEB accumulated during the 30 years of DEB research makes DEB theory probably one of the best tested theories in biology. It has already several practical applications, namely in toxicology (where its use is recommended by ISO and OECD), environmental engineering and biological engineering.

The present project will have two main lines of research and implementation. The first one comprises the increase of complexity at the individual level. We will start from the organism of the Standard DEB model, defined by having one reserve (which receives the products of assimilation and fuel all processes in the organism, but have no maintenance needs) and one structure (which establishes the size of the organism and has maintenance needs), and extend it. The second axes will be in biological organization levels. We will start by focusing on an IBM (Individual-Based Model) approach, modeling each individual separately. We will also introduce structured populations and we will study the transition between IBMs and structured populations. We hope to develop a set of rules to make a useful and smooth transition between the two approaches.

This first implementation of the DEB engine follows the development of a large number of individuals (IBM) in a cradle to grave perspective. These organisms have the capacity to eat, mature, grow, reproduce and die. They are also capable of simple interactions, such as mating and predation.

An Analysis of New Expert Knowledge Scaling Methods for Biologically Inspired Computing

Jason M. Gilmore, Casey S. Greene, Peter C. Andrews, Jeff Kiralis, and Jason H. Moore

Dartmouth College, Lebanon, NH. USA

Abstract. High-throughput genotyping has made genome-wide data on human genetic variation commonly available, however, finding associations between specific variations and common diseases has proven difficult. Individual susceptibility to common diseases likely depends on gene-gene interactions, i.e. epistasis, and not merely on independent genes. Furthermore, genome-wide datasets present an informatic challenge because exhaustive searching within them for even pair-wise interactions is computationally infeasible. Instead, search methods must be used which efficiently and effectively mine these datasets. To meet these challenges, we turn to a biologically inspired ant colony optimization strategy. We have previously developed an ant system which allows the incorporation of expert knowledge as heuristic information. One method of scaling expert knowledge to probabilities usable in the algorithm, an exponential distribution function which respects intervals between raw expert knowledge scores, has been previously examined. Here, we develop and evaluate three additional expert knowledge scaling methods and find parameter sets for each which maximize power.

Impoverished Empowerment: `Meaningful' Action Sequence Generation through Bandwidth Limitation

Tom Anthony, Daniel Polani, Chrystopher L. Nehaniv

Adaptive Systems Research Group, University of Hertfordshire, UK

Abstract. Empowerment is a promising concept to begin explaining how some biological organisms may assign a priori value expectations to states in taskless scenarios. Standard empowerment samples the full richness of an environment and assumes it can be fully explored. This may be too aggressive an assumption; here we explore impoverished versions achieved by limiting the bandwidth of the empowerment generating action sequences. It turns out that limited richness of actions concentrate on the „most important" ones with the additional benefit that the empowerment horizon can be extended drastically into the future. This indicates a path towards and intrinsic preselection for preferred behaviour sequences and helps to suggest more biologically plausible approaches.

16:45 – 17:00 Short (15 min) break
17:00 – 18:40 5 papers (20 min)

Are cells really operating at the Edge of Chaos ? A case study of two real-life regulatory networks

Christian Darabos[1,2], Mario Giacobini[2,4], Marco Tomassini[1], Paolo Provero[2,3] and
Ferdinando Di Cunto[2,3]

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[2] Computational Biology Unit, Molecular Biotechnology Center, University of Torino, Italy
[3] Department of Genetics Biology and Biochemistry, University of Torino, Italy
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Abstract. It has been suggested that the cells of living organisms are functioning in a near chaotic regime called critical, which offers a trade-off between stability and evolvability. Abstract models for regulatory networks such as Kauffman's Random Boolean Networks certainly point in that direction. In this work, we applied the essence of these models to investigate the dynamical behavior of two real-life genetic regulatory networks, deduced in two different organisms. Moreover, a novel, more biologically accurate, way individual genes respond to activation signaling is investigated. We perform numerical simulation and successfully identify contexts in which our model's response can be interpreted as critical, thus most biologically plausible. We also discover that results are comparable in both studied organisms.

Cotranslational protein folding with L-systems

Gemma B. Danks[1,2], Susan Stepney[2], and Leo S. D. Caves[2]

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Abstract. A protein molecule adopts a specific 3D structure, necessary for its function in the cell, through a process of folding. Modelling the folding process and predicting the final fold from the unique amino acid sequence remain challenging problems. We have previously described the application of L-systems, parallel rewriting rules, to modelling protein folding using two complementary approaches: a physics-based approach, using calculations of interatomic forces, and a knowledge-based approach, using data from fragments of known protein structures. Here we describe a model combining these two approaches creating an adaptive stochastic open L-systems model of protein folding. L-systems were originally developed to model growth and development. Here we also describe extensions of our L-systems models to investigate cotranslational protein folding, i.e. folding during protein biosynthesis on the ribosome, which is increasingly thought to play an important role. We demonstrate that cotranslational folding fits very naturally into the L-systems framework.

Molecular microprograms

Simon Hickinbotham[1], Edward Clark[1], Susan Stepney[1], Tim Clarke[2], Adam Nellis[1],
Mungo Pay[2], Peter Young[3]

Departments of Computer Science[1], Electronics[2], Biology[3], University of York, UK

Abstract. Bacteria offer an evolutionary model in which rich interactions between phenotype and genotype lead to compact genomes with efficient metabolic pathways. We seek an analogous computational process that supports a rich artificial heredity. These systems can be simulated by stochastic chemistry models, but there is currently no scope for open-ended evolution of the molecular species that make up the models. Instruction-set based Artifical Life has appropriate

evolutionary properties, but the individual is represented as a single executing sequence with little additional physiology. We describe a novel combination of stochastic chemistries and evolvable molecule microprograms that gives a rich evolutionary framework. A single organism is represented by a set of executing sequences. Key to this approach is the use of inexact sequence matching for binding between individual molecules and for branching of molecular microprograms. We illustrate the approach by implementation of two steady-state replicase RNA analogues that demonstrate "invasion when rare".

Identifying Molecular Organic Codes in Reaction Networks

Dennis Görlich and Peter Dittrich

Bio Systems Analysis Group, Jena Centre for Bioinformatics (JCB) and Department of Mathematics and Computer Science, Friedrich-Schiller University Jena, D-07743 Jena, Germany

Abstract. Studying semantics is strongly connected to studying codes that link signs to meanings. Here we suggest a formal method to identify organic codes at a molecular level. We define a molecular organic code with respect to a given reaction network as a mapping between two sets of molecular species called signs and meanings, respectively, such that (a) this mapping can be realized by a third set of molecular species, the codemaker and (b) there exists alternative sets of molecular species, i.e., alternative codemakers, implying different mappings between the same two sets of signals and meanings. We discuss theoretical implications of our definition, demonstrate its application on two abstract examples, and show that it is compatible to Barbieri's definition of organic codes. Our approach can be applied to differentiate the semantic capacity of molecular sub-systems found in the living world. We hypothesize that we find an increasing capacity when going from metabolism to protein networks to gene regulatory networks. Finally we hypothesize that during the chemical and Darwinian evolution of life the capacity for molecular organic codes increased by the discovery and incorporation of those reaction systems that contain many molecular organic codes.

September 16. (Wednesday)

20:00 -	Conference Dinner (optional)

POSTERS

ECAL 2009 poster size is maximum 900 x 1400 mm (practically, this is ISO A0 size plus some leg room). There will be pegs and other paraphernalia to fix your poster.

Each poster is assigned a presentation day. Posters are to be set up in the afternoon/evening before the day they are presented. Posters will hang out the whole day.

Day 1

Positively versus Negatively Frequency-Dependent Selection

Robert Morris and Tim Watson

Faculty of Technology, De Montfort University

Abstract. Frequency-dependent selection (FDS) refers to situations where individual fitnesses are dependent (to some degree) on where the individual's alleles lie in the proximate allele frequency distribution. If the dependence is negative – that is, if alleles become increasingly detrimental to fitness as they become increasingly common at a given locus – then genetic diversity may be maintained. If the dependence is positive, then alleles may converge at given loci.

A hypothetical evolutionary model of FDS is here presented, in which the individuals themselves determined – by means of a gene – whether their fitnesses were positively or negatively frequency-dependent. The population ratio of the two types of individual was monitored in runs with different parameters, and explanations of what happened are offered.

Gene Regulatory Network Properties Linked to Gene Expression Dynamics in Spatially Extended Systems

Costas Bouyioukos and Jan T. Kim

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Abstract. Gene expression levels within a cell are determined by the network of regulatory interactions among genes. In spatially extended systems of multiple cells, gene expression levels are also affected by activity in neighbouring cells. This interplay of a genetic regulatory network and interactions among neighbouring cells may qualitatively alter the dynamics of gene expression and is at the core of biological pattern formation.

In this study, we investigate the effects of the topology of a regulatory network on its pattern formation potential. We score networks by comparing the heterogeneity of gene expression levels generated on a lattice to that of the levels generated in a well stirred reactor as a null model, and assess the correlation of this score to characteristics of topology, such as density or centrality measures.

Density is strongly correlated to the potential to generate gene expression heterogeneity. For some networks that produce high heterogeneity on lattices, centrality and membership in cycles are indicative of the impact which deleting a gene has on the level of heterogeneity produced.

Visualising Random Boolean Network Dynamics: effects of perturbations and canalisation

Susan Stepney

Department of Computer Science, University of York, UK

Abstract. We have proposed a simple approach to visualising the time behaviour of Random Boolean Networks (RBNs). Here we demonstrate the approach in a variety of cases: examining the effect of state and structure mutations, and examining the effect of canalising functions for $K > 2$ networks.

An Open-Ended Computational Evolution Strategy for Evolving Parsimonious Solutions to Human Genetics Problems

Casey S. Greene, Douglas P. Hill, and Jason H. Moore

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Abstract. In human genetics a primary goal is the discovery of genetic factors that predict individual susceptibility to common human diseases, but this has proven difficult to achieve because these diseases are likely to result from the joint failure of two or more interacting components. Currently geneticists measure genetic variations from across the genomes of individuals with and without the disease. The association of single variants with disease is then assessed. Our goal is to develop methods capable of identifying combinations of genetic variations predictive of discrete measures of health in human population data. "Artificial evolution" approaches loosely based on real biological processes have been developed and applied, but it has recently been suggested that "computational evolution" approaches will be more likely to solve problems of interest to biomedical researchers. Here we introduce a method to evolve parsimonious solutions in an open-ended computational evolution framework that more closely mimics the complexity of biological systems. In ecological systems a highly specialized organism can fail to thrive as the environment changes. By introducing numerous small changes into training data, i.e. the environment, during evolution we drive evolution towards general solutions. We show that this method leads to smaller solutions and does not reduce the power of an open-ended computational evolution system. This method of environmental perturbation fits within the computational evolution framework and is an effective method of evolving parsimonious solutions.

Modeling self-organizing traffic lights with elementary cellular automata

Carlos Gershenson and David Rosenblueth

UNAM, Mexico

Abstract. We extend a simple highway traffic model based on elementary cellular automata (rule 184) to a city grid and improve a self-organizing method for controlling traffic lights adaptively.

In our model, most cells follow rule 184. We employ two more rules around a red light: Rule 252 for cells immediately before the light and 136 for those immediately after. The nearest neighbors of intersections switch between either rule 252 or 136 (red light) and rule 184 (green light). An intersection always follows rule 184, but the two nearest neighbors determining an intersection's next state vary, and are the ones following rule 184 at that moment.

We use flow as a measure of system performance, which can be mapped into velocity, percentage of stopped vehicles, and average waiting time. Our model is computationally cheap and reproduces the main properties of traffic flow.

We first performed simulations of a single intersection and observed two phase transitions. One from free flow (v=1) to "intermittent" (vehicles wait behind red light) at a density rho=0.25. Another one at rho=0.75 from intermittent to "interfered" (the queue of one street grows and blocks the intersection around the torus).

We then performed simulations of a 10x10 Manhattan-style street environment, with streets alternating directions. We compared two traffic light controllers:

1. The green-wave method, used in many cities, is able to allow free flow for two directions for low densities, but the other two directions face anti-correlated traffic lights. We found only two phases: intermittent and gridlock (v=0), with a transition at rho=0.25. The queues on directions opposite to the green wave grow and block intersections upstream, leading to gridlocks at medium densities.

2. A self-organizing method (improved from Gershenson, 2005). This simply gives preference to streets with higher demand. With five rules, traffic lights promote the formation of platoons and vehicles flow freely at low densities. Traffic lights only communicate via vehicles travelling between lights. We found five phases: free flow, intermittent, interfered, self-interfered (the queques of streets propagate to intersections upstream and affect the original traffic light), and gridlock. The transitions were at rho=~0.1, ~0.55, ~0.65, 0.75. The flow averaged over all densities for the green wave method was 0.2 and for our self-organizing method 0.5 (150% improvement). Averaging only densities < 0.25, flow for green-wave is 0.7 and for self-organizing 0.95 (35% improvement).

There are several advantages of simple traffic models. They are easy to implement and reproduce and are computationally cheap. Also, by abstracting most details from real traffic, one can observe properties more clearly. For example, the phase transitions we found were not visible in our previous, more realistic multi-agent simulations. The phases can be identified, but the details of those models smoothened the transitions, which are difficult to find analytically. Finally, with this simple model it was possible to find better explanations of why the green-wave method is not efficient and why the upgraded self-organizing method delivers such a great improvement.

Applying weak equivalence of categories between partial maps and pointed sets to the 2-arm bandit problem with changing conditions

Takayuki Niizato andYukio Gunji

Kobe University, Japan

Abstract. We usually think that there is a clear cut between known facts and unknown facts. In category theory, this can be expressed as equivalence of categories for partial map and pointed set. If this analogy is accepted, the difference of “before” and “after encoding” is destined to be ignored. The observer who ignores this difference never leans a new thing that he never knows in advance. To distinguish between “before” and “after observing”, the observer should make up the entire world at each moment that he observes it. We therefore admit this discrepancy and propose the system implementing the weak condition of equivalence of categories for partial map and pointed set, and show the advantage of our system in learning or cognitive systems. Especially we apply our system to 2-arms bandit problem so as to estimate the property of our system in terms exploitation and exploration. This problem is well known for reinforcement learning. When the agent decides the answer in finite time, it gives rise to the problem that is trade-off between exploring and exploiting. This problem never arises given enough time. The agent must decide answer from his imperfect information under the finite time condition. Recently, the heuristic model is attracted to approach this problem (Shinohara et. 2008). We proposed different approach for 2-arms bandit problem. For the model of weak equivalence of categories that we proposed, the agent can change dynamically his knowledge and adapt the environment. Moreover, we check the changing condition of the problem, for example, changing the probability of the machine, and show that our model can also adapt under the changing condition.

Creative Agency: A Clearer Goal for Artificial Life in the Arts

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Abstract. One of the goals of artificial life in the arts is to develop systems that exhibit creativity. We argue that creativity per se is a confusing goal for articial life systems because of the complexity of the relationship between the system, its designers and users, and the creative domain. We analyse this confusion in terms of factors affecting individual human motivation in the arts, and the methods used to measure the success of artificial creative systems. We argue that an attempt to understand

creative agency as a common thread in nature, human culture, human individuals and computational systems is a necessary step towards a better understanding of computational creativity. We define creative agency with respect to existing theories of creativity and consider human creative agency in terms of human social behaviour. We then propose how creative agency can be used to analyse the creativity of computational systems in artistic domains.

Agent Based Modelling of Auxin Transport Canalisation

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The plant hormone auxin is known to be a key regulator of many plant developmental processes. Auxin transport canalisation is of particular interest because it describes how auxin organises and promotes its own transport through cells. Auxin canalisation is therefore an interesting target for computer simulation as it can be thought of as a self-organising process where auxin in cells promotes its own transport between cells. In the case of vascular tissue formation the transport goes from an area where auxin is accumulating, to a sink elsewhere in the tissue. The narrow transport path that forms between these two sites is known as an auxin canal. Established auxin canals can differentiate into the vascular tissue of the plant. There are a number of factors that are thought to be important in canalisation. Auxin is a weak acid and it is able to enter a cell passively from the acidic apoplast. However the cytoplasm is neutral and therefore cytoplasmic auxin is largely deprotonated and unable to re-cross the membrane to leave a cell. For most of the cytoplasmic auxin, the only route out of a cell is via active transport. often dependent on PIN proteins. A second important feature is that auxin is thought to promote the production and membrane localisation of PINs. As such, PIN concentration at the membrane increases with auxin concentration. The combination of these effects causes the efficiency of auxin transport to increase as the concentration of auxin in the cells of the canal increase.

One of the important missing links in this process is the regulation of the positioning of the PIN proteins on the cell membrane. During canalisation, PIN proteins are observed to be polarised in the direction of auxin flux. This could be by targeted removal or targeted insertion of PIN proteins causing them ultimately to become polarly localised on the cell membrane in the correct location to pump auxin towards the sink. To investigate canalisation in the hope that we can direct future wet laboratory work, we have developed a flexible agent based modelling framework to allow for testing of different hypotheses about how PIN localisation might be being regulated. The models are built by putting agents representing auxin, and proteins including PIN, into a tissue consisting of a number of cells. The agents are programmed with simple behaviours directing how they interact with each other and there environment. We then look for the global behaviour of canalisation as an emergent property of these simple interactions.

Adding Vertical Meaning to Phylogenetic Trees by Articial Evolution

Francesco Cerutti[1,2], Luigi Bertolotti[1,2], Tony L. Goldberg[3] and Mario Giacobini[1,2]

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Faculty of Veterinary Medicine, University of Torino, Italy
2 Molecular Biotechnology Center, University of Torino, Italy
3 Department of Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin-Madison, USA

Abstract. Phylogenetic trees are the most commonly used method for representing the relationships among living organisms. Additive trees are often used to show evolutionary features, based on models of molecular evolution. In this case, information in the tree is contained only in the root-to-node direction or, in other words, in its topology. Indeed, in a typical left-to-right phylogram, the vertical order of taxa is

meaningless, and the degree of similarity between taxa is reflected by the branch path between them. In an effort to make unresolved trees more informative, we applied a (1+1) Evolutionary Algorithm to find the best graphical tree representation that includes vertical information. The order of taxa linked to polytomic nodes is defined using data from distance matrices created from different features of taxa, such as genetic, temporal or geographical data. In this way, the vertical ordering of taxa on a phylogenetic tree can be used to represent non-genetic features of interest.

Niche Particle Swarm Opitmization for Neural Network Ensembles

Camiel Castillo and Geoff Nitschke and Andries Engelbrecht

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Abstract. This research investigates a swarm intelligence based multiobjective optimization algorithm for optimizing the behavior of a group of Artifcial Neural Networks (ANNs), where each ANN specializes to solving a specific part of a task, such that the group as a whole achieves an effective solution. Niche Particle Swarm Optimization (NichePSO) is a speciation technique that has proven effective at locating multiple solutions in complex multivariate tasks. This research evaluates the efficacy of the NichePSO method for training a group of ANNs that form a neural network ensemble (NNE) for the purpose of solving a set of multivariate tasks. NichePSO is compared with a gradient descent method for training a set of individual ANNs to solve different parts of a multivariate task, and then combining the outputs of each ANN into a single solution. To date, there has been little research that has compared the effectiveness of applying NichePSO versus more traditional supervised learning methods for the training of neural network ensembles.

An application of category theory to systems biology

Taichi Haruna

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Abstract. We discuss (i) a new analytical tool for directed networks and (ii) a new hypothesis on network motifs, through category theory. A network represented by a directed graph consists of a set of function-less nodes and a set of arcs between nodes. However, in real networks, nodes are not really function-less. For example, in transcription regulation networks or neuronal networks, we can find information processing in each node. It would be useful for further understanding of the real network structure if we succeed to obtain a formal representation including a function of a node such as information processing, which is usually neglected. Here we simply represent a function of a node as a directed graph representing information flow within nodes. In addition, we prepare another directed graph corresponding to an arc to represent how functions of nodes are related. Incorporating these materials into the Grothendieck construction in category theory, we obtain a graph transformation that transforms a network to its functional network. This transformation is a functor from the category of directed graphs to itself, denoted by L. L has its dual R (called the right adjoint to L in category theory). R is a transformation of forgetting function. We performed the transformation L to various real networks in the literature. We found a distinguishing global structure common in the functional networks for the real networks by comparing them to suitable ensembles of random networks. Moreover, we obtained the condition when a directed graph G satisfies RL(G)=G. This equation means that all functional constraint appeared in L(G) is already incorporated in G itself. We make a new hypothesis on a network motif called bi-fan through this condition and our data analysis. Network motifs are local patterns found in real networks significantly more often than suitable ensembles of random networks. Among them, bi-fan is ubiquitously found in various real networks and is most over-represented. In the previous work, network motifs are considered locally both in their structures and functions. However, we discuss the possibility that the ubiquitous nature of bi-fan is explained in relation to the global feature of real networks by combining our data analysis and the mathematical condition RL(G)=G.

Robustness of Market-based Task Allocation in a Distributed Satellite System

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Abstract. The perceived robustness of multi-agent systems is claimed to be one of the great benefits of distributed control, but centralised control dominates in space applications. We propose the use of market-based control to allocate tasks in a distributed satellite system. The use of an artificial currency allows us to take the capabilities, energy levels and location of individual satellites, as well as significant communication costs into account. Simulation is used to compare this approach to centralised allocation. We find the market-based system is more efficient and more robust to satellite failure, due to the adaptive allocation of tasks.

An optimisation-driven method to discriminate Gene Regulatory Network topologies

Anyela Camargo and Jan T. Kim

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Abstract. The genes of a genome are organised into a gene regulatory network (GRN) in which the expression level of each gene is controlled by the expression levels of its regulator genes. Many computational simulations of GRNs can be subdivided into network topology, which is often part of a hypothesis or otherwise assumed to be known or fixed, and a set of dynamical parameters, which frequently are largely. Gene expression levels can be empirically measured by (postgenomic, high-throughput) techniques such as microarrays. Using such empirical data to validate and develop computational GRN models is a current challenge of ALife and Systems Biology. We address this challenge by presenting a method to determine which topology is most consistent with a given set of gene expression data.

We present a method that uses an optimisation heuristic to discriminate candidate topologies based on their ability to produce gene expression dynamics that are similar to empirical measurements. This technique provides high discriminatory resolution at noise levels typical of current microarray technology, and it is operable even at noise levels up to two orders of magnitude in excess of that.

Origins of Scaling in Genetic Code

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[2] Department of Computer Science, University of Hertfordshire, Hatfeld, UK

Abstract. The principle of least effort in communications has been shown, by Ferrer i Cancho and Solé, to explain emergence of power laws (e.g., Zipf's law) in human languages. This paper applies the principle and the information-theoretic model of Ferrer i Cancho and Sol ´e to genetic coding. The application of the principle is achieved via equating the ambiguity of signals used by "speakers" with codon usage, on the one hand, and the effort of "hearers" with needs of amino acid translation mechanics, on the other hand. The re-interpreted model captures the case of the typical (vertical) gene transfer, and confirms that Zipf's law can be found in the transition between referentially useless systems (i.e., ambiguous genetic coding) and indexical reference systems (i.e., zero-redundancy genetic coding). As with linguistic symbols, arranging genetic codes according to Zipf's law is observed to be the optimal solution for maximising the referential power under the effort constraints. Thus, the model identifies the origins of scaling in genetic coding – via a trade-off between codon usage and needs of amino acid translation. Furthermore, the paper extends the model to multiple inputs, reaching out toward the case of horizontal gene transfer (HGT) where multiple contributors may share the same genetic coding. Importantly, the extended model also leads to a sharp transition between ambiguous HGT and zero-redundancy HGT. Zipf's law is also observed to be the optimal solution in the HGT case.

Implications of the social brain hypothesis for evolving human-like cognition in digital organisms

Suzanne Sadedin and Greg Paperin

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Abstract. Data show that human-like cognitive traits do not evolve in animals through natural selection. Rather, human-like cognition evolves through runaway selection for social skills. Here, we discuss why social selection may be uniquely effective for promoting human-like cognition, and the conditions that facilitate it. These observations suggest future directions for artificial life research aimed at generating human-like cognition in digital organisms.

A Chemical Model of the Naming Game

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Abstract. A key feature of many biological distributed systems is that they have the capacity to behave in highly coordinated ways. In the domain of language, such coordination dynamics have been studied within the framework of language games. As yet however, a fundamental understanding that goes beyond the simplest cases is still missing.

In this paper, a novel approach is proposed for investigating coordination problems. I illustrate the approach for a simple but well studied case called the naming game. I will therefore bring together a number of ideas from Artificial Chemistry and Chemical Reaction Network Theory, Semiotic Dynamics and Immunology, and conclude by arguing why the proposed approach provides a good starting point for tackling more complex coordination problems as well.

Influence of Promoter Length on Network Convergence in Genetic Regulation Network based Evolutionary algorithms

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Abstract. Genetic Regulation Networks (GRNs) are a model of the mechanisms by which a cell regulates the expression of its different genes depending on its state and the surrounding environment. These mechanisms are thought to greatly improve the capacity of the evolutionary process through the regulation loop they create.

Some Evolutionary Algorithms have been designed to offer improved performance by taking advantage of the GRN mechanisms. A recent hypothesis suggests a correlation between the length of promoters for a gene and the complexity of its activation behavior in a given genome. This hypothesis is used to identify the links in in-vivo GRNs in a recent paper and is also interesting for evolutionary algorithms. In this work, we first confirm the correlation between the length of a promoter (binding site) and the complexity of the interactions involved on a simplified model. We then show that an operator modifying the length of the promoter during evolution is useful to converge on complex specific network topologies. We used the Analog Genetic Encoding (AGE) model in order to test our hypothesis.

Guiding for Associative Learning : How to Shape Artificial Dynamic Cognition

Kristen Manac'h and Pierre De Loor

UEB – ENIB-CERV – LISyC, Brest – France

Abstract. This paper describes an evolutionary robotics experiment, which aims at showing the possibility of learning by guidance in a dynamic cognition perspective. Our model relies on Continuous Time Recurrent Neural Networks and Hebbian plasticity. The agents have the ability to be guided by stimuli and we study the in?uence of a guidance on their external behavior and internal dynamic when faced with other stimuli. The article develops the experiment and presents some results on the dynamic of the systems.

Adaptive Walk on Fitness Soundscape

Reiji Suzuki and Takaya Arita

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Abstract. We propose a new IEC for musical works based on an adaptive walk on a fitness landscape of sounds. In this system, there is a virtual plane that represents the genetic space of possible musical works called fitness soundscape. The user stands on the soundscape, and hears the multiple sounds that correspond to one's neighboring genotypes at the same time. These sounds come from different directions that correspond to the locations of their genotypes on the soundscape. By using the human abilities for localization and selective listening of sounds, the user can repeatedly walk toward the direction from which more favorite sounds come. This virtual environment can be realized by a home theater system with multiple speakers creating "surrounded sound". We report on the basic concept of the system, a simple prototype for musical composition with several functional features for improvement of evolutionary search, and preliminary evaluations of the system.

Dual Coding in an Auto-associative Network Model of the Hippocampus

Daniel Bush and Andrew Philippides and Phil Husbands and Michael O'Shea

University of Sussex, United Kingdom

Abstract. Electrophysiology studies in a range of mammalian species have demonstrated that the firing rate of single pyramidal neurons in the hippocampus encodes for the presence of both spatial and non-spatial cues. The phase of place cell firing, with respect to the theta oscillation that dominates the hippocampal EEG during learning, is also correlated with the exact location of an animal within the corresponding place field. Importantly, it has been demonstrated that the rate and phase of neural activity can be dissociated, and may thus encode information separately and independently. Here we present a neural network model which is, to our knowledge, the first to utilise a dual coding system in order to learn and recall associations between both temporally-coded (spatial) and rate-coded (non-spatial) activity patterns.

Our model consists of a spiking auto-associative network with a novel STDP rule that replicates a BCM-type dependence of synaptic weight upon mean firing rate. The scale of external input, recurrent synaptic currents and synaptic plasticity are each modulated by a theta frequency oscillation. Place cell activity is represented by a compressed temporal sequence of neural firing within each theta phase, while the presence of a non-spatial 'object' is represented by neural bursting at the trough of the theta phase. We simulate the network moving along a circular track of 50 overlapping place fields with non-spatial cues present at 5 equidistant locations. Following learning, we demonstrate that:

1. The external stimulation of any place cell generates the sequential recall of upcoming place fields on the learned route.

2. The external stimulation of any place cell generates the recall of any object that was previously encountered at that place.
3. The external stimulation of cells which encode an object generates recall of both the place at which that object was observed, and the upcoming place fields on the learned route.
4. The network performs pattern completion, meaning that only a subset of cues is required for this recall activity to be generated.

This model provides the first known demonstration of an asymmetric STDP rule mediating rate-coded learning in a spiking auto-associative network that in inspired by the neurobiology of the CA3 region. Furthermore, the dual coding system utilised can integrate both dynamic and static activity patterns, and thus unify the disparate (spatial and episodic) mnemonic functions ascribed to the hippocampus. This research therefore provides the foundations for a novel computational model of learning and memory in the medial temporal lobe and beyond.

Adaptation in Tissue Sustained by Hormonal Loops

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Abstract. When faced with the requirements for the design of an autonomous adaptive system, many aspects of the system organisation need be addressed. In living systems, the co-evolution with the environment has provided the solution for such challenges in a form of inherent mechanisms which are employed when the environmental fluctuation occurs leading to the organism achieving adaptation through some adaptive process. In this paper we investigate such mechanisms, more precisely the priniples on which their operation is based. In particular, the focus is set on endocrine system within homeostatic processes. We postulate that adaptation to a fluctuating environment can be achieved if initiated and sustained by the hormone flow loops. Such statement is further supported by simulations. Based on the recognised advantages of the system organisation endowed with the ability to form hormonal loops, the avenues of research are identified for further work.

A loosely symmetric model of cognition

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Abstract. Cognitive biases and heuristics explaining human deviation from formal logic have been broadly studied but the general formalism is still missing. We here try to give one, introducing a probabilistic formula for causal induction. It has prominent symmetries reflecting human cognitive biases and shows extremely high correlation with the experimental data. When it is applied to deductive or abductive tasks (n-armed bandit problems), searching for the best cause for the objective result, an optimal property breaking the usual trade-o? is shown.

Cellular Automata Evolution Of Leader Election

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Abstract. The leader election problem is a crucial problem in the theory of distributed algorithms, multi-agent systems as well as in sociobiology. In this paper we investigate one-dimensional binary state cellular automata with an intention to track self-organizational mechanisms that finally enable a global leader to be elected. Since our model is anonymous and uniform we also have to deal with

a problem of symmetry that in great majority of cases is broken by inhomogeneity of arbitrary initial configurations. Our approach to the problem is based on the evolution of cellular automata by genetic algorithms and the methodology of computational mechanics. The presented new solution of the leader election reaches remarkably high performance of 94 - 99%. The analysis shows a sophisticated collective computation demonstrated by so called particles and their interactions. Due to the simplicity of our model, presented approach is general and universal enough to be applicable even at the level of primitive biological or artificial societies.

A framework for identifying communication - when should we call an interaction between robots a communication?

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Abstract. "Communication" is a term used in many different disciplines and with different meanings. The spectrum ranges from a concept that only applies to specific interactions among conscious humans over the transmission of some bit string through a channel to the interaction between plants using certain chemicals.

In this article, we wish to identify some aspects of communication some of which are shared by all those notions, whereas others can serve to distinguish between them and formalize their differences.

1. Communication is a form of interaction between a sender and one or several receivers.
2. Communication takes place via a channel mediating the interaction between sender and receiver, i.e. an action of the sender can be interpreted as a signal carrying information about something external to the receiver.
3. The transmitted signal is informative for the receiver in the sense that it causes a response or has an effect. That effect may simply consist in, but does not have to be restricted to, a change of the internal state of the receiver. Thus the signal establishes a coupling between the state of the sender and the receiver.
4. The response of the receiver is not determined by the physical properties of the signal and, moreover, depends also on the internal state of the receiver. Even if an established meaning exists (see 6.) the receiver might "understand" the signal differently or not react at all.
5. The sender can control when to emit a signal and what signal to send, wanting the receiver to understand the message in the sense that a certain effect is produced.
6. In a communication situation both the sender and receiver have to take into account that the other could use the signal differently, as described in 4 and 5. This double contingency is resolved by a convention establishing the communicative meaning of the signal.

While points 1-3 apply to many mediated interactions, points 4-6 require contingencies and therefore new degrees of freedom on both the sides of the sender and the receiver. In many biological systems these degrees of freedom do not exist for the organisms themselves but only at the evolutionary scale. The same applies also for many examples of robot communication. We therefore operationalize these criteria in a way that they can be tested empirically. We describe the systems and their environment as a stochastic process with corresponding random variables. By formalizing "intentions" and "expectations" using this description we are able to formulate testable conditions for the points 1-6.

Finally we discuss a point that is most prominent in human communication compared to animal signalling:

7. Communications can build upon other communications, instead of simply referring to a state of the outside world. Thus, the communication process may become selfreferential.

In order to do so, both the sender and the receiver understand the conventional aspect of their communication and can thus base further conventions on the existing ones. If the necessary contingencies only exist at the level of evolution it is hard to imagine how a sophisticated self-referential communication system could be established.

Multi-Agent Model for Simulation at the Subcellular Level

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Abstract. From the beginning of biological modeling, simulations were an efficient way to understand local mechanisms linked to whole system behaviors. Cellular automata and more recently Multi-Agent Systems (MAS) are currently used to model ecological systems. Virus dissemination through population or insect collaborations are well known examples of how simple interactions between entities (agents) are able to build a complex situation at the level of the whole population. But use of MAS to design biological system at the cellular or subcellular level, mainly for enzymatic reactions, is a relatively new application of the agent paradigm. In fact, agents used for ecology simulations are 'non-physical' agents, i.e. in general they do not have any explicit representation of their geometry, their space bulk or the articulated movements of their body parts. These characteristics are essential in enzymatic behaviors. The three dimension structure and movements of this structure condition the realisation of the reaction that can be stopped or conversely favored by specific conformations. In order to simulate subcellular biological processes, we defined agents capable of simulating molecular conformational changes. These agents integrate molecular modeling data, for conformational change methods, and biological ontology data, for conformational change conditions. As some biological entities are motor of the enzymatic reactions while others are simple partners, we defined two agent subtypes, active and passive agents. As a proof of concept, we applied our model to the simulation of enzymatic oxydo-reduction reactions.

Combining different interaction strategies reduces uncertainty when bootstrapping a lexicon

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Abstract. When bootstrapping a new language, the agents in a population need to be able to agree on the meaning of the individual words. In order to do so, they need to overcome the problem of referential uncertainty, which captures the idea that the meaning of words can not realisticly be transferred directly between agents nor through the environment. One way to reduce the amount of uncertainty, is to allow the agents, based on their current knowledge of the language system and the environment, to choose the interaction script they play based on a motivational system. We show the impact of this idea through a computational model on the time needed for a population of agents to converge on a shared language system and how the motivational system allows the agents to self-regulate this process.

A Local Behavior Identification Algorithm for Generative Network Automata Configurations

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Abstract. Relation between the part and the whole is investigated in the context of complex discrete dynamical systems. For that purpose, an algorithm for local behavior identification from global data described as Generative Network Automata model configurations is developed. It is shown that one can devise a procedure to simulate finite GNA configurations via Automata Networks having static rule-space setting. In practice, the algorithm provides an automated approach to model construction and it can suitably be used in GNA based system modeling effort.

An Ant-Based Rule for UMDA's Update Strategy

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Abstract. This paper investigates an update strategy for the Univariate Marginal Distribution Algorithm (UMDA) probabilistic model inspired by the equations of the Ant Colony Optimization (ACO) computational paradigm. By adapting ACO's transition probability equations to the univariate probabilistic model, it is possible to control the balance between exploration and exploitation by tuning a single parameter. It is expected that a proper balance can improve the scalability of the algorithm on hard problems with bounded difficulties and experiments conducted on such problems with increasing difficulty and size confirmed these assumptions. These are important results because the performance is improved without increasing the complexity of the model, which is known to have a considerable computational effort.

Extending the Critical Brain Hypothesis to Rate Dynamics: A Case Study of the Antennal Lobe of the Moth

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Abstract. The hypothesis that biological systems exhibit dynamics critically poised at the boundary between order and chaos has been the subject of investigation within ALife for almost 20 years now [1,2]. It has been suggested, that the idea of the brain exhibiting dynamics at the boundary of order and chaos may perhaps even be older going back as far as Alan Turing [3]. Recently, Beggs et. al. demonstrated the presence of a power law distribution of neuronal avalanche sizes in slices of rat cortex. These observations are thought to constitute the first experimental evidence for the criticality hypothesis in the brain [4]. Furthermore, a plethora of computational models exists that posit critical dynamics as a partial but parsimonious explanation of information transmission [4], storage [5] and computational [6] properties of the nervous system.

To date, the majority of computational models of critical brain dynamics have focused on excitatory networks of excitable spiking neurons [3]. This may be due to the perception that this model class is an adequate description of the cerebral cortex [3] but it is also may be because it has allowed researcher to make formal comparisons to second order phase transitions in 'stick slip' and Ising models. It is not clear a priori how the notion of critical brain dynamics can be extended to neural subsystems that include inhibitory pathways. Indeed, in mammalian olfactory system some authors have suggested the presence of gap junctions in otherwise completely inhibitory networks to resolve this issue [7]. Other authors have studied critical dynamics has been studied in more abstract neural networks [6,8]. While this work accommodates the notion of inhibition it has, however, generally focused on thresholded, discrete time, recurrent neural networks which sit more comfortably with connectionist systems rather than biologically more plausible neural models.

Here, we develop the notion of criticality in a biological plausible model of the Macro Glomerular Complex (MGC), the core of the pheromone detection system in the antennal lobe of the male moth. The MGC comprises a set of recurrent networks of inhibitory neurons and hence is not directly amenable to existing neuronal criticality models. We begin by constructing a spiking model that describes the dynamics of the MGC. We go on to construct a formally equivalent rate model that is analytically tractable and show that the dynamics can be understood in terms of a transient 'winner takes all' system. We describe the presence of critical dynamics in terms of spike rates and develop an expression for critical point in terms of the network parameters. We conjecture that critical rate dynamics may play a role in the maximization of dynamic range and the sensitivity of the MGC to pheromone. We conclude by discussing the generality of our results and their wider implications for critical rate dynamics in the nervous system.

Learning in Minority Games with Multiple Resources

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Abstract. We study learning inMinority Games (MG) with multiple resources. The MG is a repeated con?icting interest game involving a large number of agents. So far, the learning mechanisms studied were rather naive and involved only exploitation of the best strategy at the expense of exploring new strategies. Instead, we use a reinforcement learning method called Q-learning and show how it improves the results on MG extensions of increasing difficulty.

A Genetic Programming Approach to an Appropriation Common Pool Game

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Abstract. We investigate the performance of agents co-evolved using genetic programming techniques to play an appropriation common pool game. This game is used to study behaviours of users participating in scenarios with shared resources or interests eg. fisheries. We compare the outcomes achieved by the evolved strategies to that of human players as reported by [6]. Results show that genetic programming techniques are suitable for generating strategies in a repeated investment problem. We find that by using co-evolutionary methods, populations of strategies will quickly converge to nash equilibrium predicted by game theoretic analysis, but also lose many adaptive behaviours. Further, by evolving against a set of naive strategies, we show the creation of diverse and adaptive behaviours that play similarly to humans as described in previous experiments.

Moderate contact between sub-populations promotes evolved assortativity enabling group selection

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Abstract. Group selection is easily observed when spatial group structure is imposed on a population. In fact, spatial structure is just a means of providing assortative interactions such that the benefits of cooperating are delivered to other cooperators more than to selfish individuals. In principle, assortative interactions could be supported by individually adapted traits without physical grouping. But this possibility seems to be ruled-out because any 'marker' that cooperators used for this purpose could be adopted by selfish individuals also. However, here we show that stable assortative marking can evolve when sub-populations at different evolutionarily stable strategies (ESSs) are brought into contact. Interestingly, if they are brought into contact too quickly, individual selection causes loss of behavioural diversity before assortative markers have a chance to evolve. But if they are brought into contact slowly, moderate initial mixing between sub-populations produces a pressure to evolve traits that facilitate assortative interactions. Once assortative interactions have become established, group competition between the two ESSs is facilitated without any spatial group structure. This process thus illustrates conditions where individual selection canalises groups that are initially spatially defined into stable groups that compete without the need for continued spatial separation.

Evolving Central Pattern Generators with Varying Number of Neurons

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Abstract. Central pattern generator (CPG) is a kind of neural circuit which can be observed in many animals showing rhythmic patterns of actions. The CPG neural circuit can produce complex rhythmic patterns by receiving only simple signals from the brain. Generally, the CPG neural models can be applied to solve robotic problems, or to understand the underlying neural mechanism for rhythmic animal behaviours. In this paper, we focus on how a small number of neurons generate the variable frequencies and phase of motor actions, and inspect what is the capacity of a varying number of neurons as a CPG model. The performance measure consists of frequency variability, input/output response rate, and phase shift. We have used evolutionary computation to measure the best performance for each number of CPG neurons ranging from two to eight neurons, and the result shows that four neurons or more can easily generate variable frequencies and anti-phase difference for left and right motor actions.

Landmark Navigation Using Sector-Based Image Matching

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Abstract. Many insects return home by using their environmental landmarks. They remember the image at their nest and find the homeward direction, comparing it with the current image. There have been robotic researches to model the landmark navigation, focusing on how the image matching process can lead an agent to return to the nest, starting from an arbitrary spot. According to Franz's navigation algorithm, an agent estimates the changes of image for its own movement, and evaluates which directional movement can produce the image pattern most similar to the snapshot taken at the nest. Then it finally chooses the best image-matching direction. Based on the idea, we suggest a new navigation approach where the image is divided into several sectors and then the sector-based image matching is applied. It checks the occupancy and the distance variation for each sector. As a result, it shows better performance than Franz's algorithm.

Transient Perturbations on Scale-Free Boolean Networks with Topology Driven Dynamics

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Abstract. Taking into account the topology of genetic regulatory networks and abstracting recent finndings about them, we investigate the behavior of a new, more biologically plausible, variation of the original Random Boolean Network paradigm. We study the dynamics of Boolean networks with scale-free structures, that evolve in time using a semi-synchronous topology-driven update scheme. Simulating statistical ensembles of networks, we discuss the attractors of the dynamics, and analyze in depth the fault-tolerance of the proposed model. Results are encouraging, as our model shows comparable and usually better performance and resilience to perturbations than the original one and is closer in spirit to real-life networks.

Day 2

Networks of Artificial Social Interactions

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Abstract. Evolution of cooperation is a fundamental question of socio-biology. Intrinsic factors like kinship play an important role in cooperation among selfish individuals. External factors like uncertainty and the structure of the social interaction network also contribute significantly to the evolution of cooperation. Here I use agent-based simulations to generate artificial social networks. I show that some of these networks have similar scale-free structure as real social networks. The analysis shows that having agents with memory and with the ability to share their memory through gossiping does not have a significant effect on the scale-free nature of simulated social networks. However the presence of high uncertainty in the cooperation games played by the agents is required for the generation of scale-free social interaction networks.

Why Gaia Theory is a load of hot air: a thermodynamic account of planetary homeostasis

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Abstract. The original Gaia Hypothesis proposed that life, the atmosphere, oceans and crust of the Earth are elements of a homeostatic system that maintains certain environmental conditions to within the range required for widespread life (Lovelock, 1979, Gaia: a new look at life on Earth, OUP). It will be argued that thermodynamics may provide an explanatory framework for such homeostasis as certain systems will respond to perturbations in such ways as to tend to return to high entropy production states. This can explain how negative feedback processes arose and are maintained at a planetary level.

The Second Law of thermodynamics states that the entropy of an isolated system will increase over time. This explains the observation that ordered systems will `run down' and become increasingly disordered. An interesting feature of some open systems, is that their entropy can decrease over time. Open systems can extract work from energy gradients and put that work to use in maintaining order. By literally feeding off energy gradients, biological organisms are able to maintain high levels of organisation. An individual organism is able to decrease internal entropy and flourish under the presence of the Second Law by exporting higher entropy to the rest of the universe. The high entropy `waste' produced by organisms is greater than the reduction in internal entropy, so that the Second Law is not contravened.

It will be shown that the Earth shares an important characteristic with living organisms: the maintenance of low entropy states. The sun pours radiation onto its surface. The Earth `feeds' off this energy and exports entropy to the rest of the universe. The Maximum Entropy Production Principle (MEPP) proposes that open, dissipative systems such as the Earth's climate are in states of maximum entropy production (Paltridge, 1975, The steady-state format of global climate systems, Q. J. Roy. Met. Soc. 927-945). Studies have used the MEPP in order to accurately predict atmospheric states on Earth as well as other planets. It will be shown that ongoing research uses the MEPP in order to increase our understanding of geological forces. The role of life in these entropy producing processes will be highlighted. For example it has been argued that life significantly increased the rate of continental crust formation (Rosing et al, 2006, The rise of continents - an essay on the geological consequences of photosynthesis, Palaeogeography, Palaeoclimatology, Palaeoecology, 232:99-113). This would have had a major impact on entropy production via geological heat flux. It will be shown that these processes may exhibit negative feedback and so reduce the effects of perturbations. Consequently, planetary homeostasis may emerge largely as a consequence of the maximisation of entropy production.

Acquisition of Adaptive Behavior for Virtual Modular Robot Using Evolutionary Computation

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Abstract. In areas such as evolutionary robotics and artificial life, simulating artificial robots and organisms are significant challenges to acquire their proper behaviors that achieve given tasks. This study proposes Animated Robot ("Anibot"), which can behave by obeying physical laws in a virtual 3D environment. Especially, we aim to obtain a control system in evolution which makes it possible to behave "Anibot" autonomously. This paper focuses on a virtual modular robot with a flexible structure and simulating it for learning and controlling. The experimental results show that the modular robot can move toward a light source as its goal in different circumstances. In addition, we discuss an adaptive ability in the different circumstances and a motion mechanism of an obtained behavior.

Acquisition of Swimming Behavior on Artificial Creature in Virtual Water Environment

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Abstract. The environment greatly influences acquirement of the behavior on the artificial life creature (AC) and artifact object (AO). However, the conventional studies like Karl Sims' ones have not accurately considered in an environmental influence. Instead, these influences are considered by replacing them into a simple environment. In this study, we accurately model the under-water environmental influence. And we propose a simulation method for artificial creature swimming in consideration of buoyancy and water drags as a virtual water environment. As a result of simulation, we verify that it is possible for AC and AO to acquire swimming behavior in the under-water environment. Additionally we show the analysis of the acquired swimming behavior.

Agent-based toy modeling for comparing distributive and competitive free market

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Abstract. Is a competitive free market the most efficient way to equally allocate rare resources among economical agents? Many economists tend to think it is the case. This paper presents a preliminary attempt through a very Alife like model to tackle this question. Agents which are alternatively producer, seller, buyer and consumer participate in a free market to increase their welfare. The simulation is organized and presented in a UML class diagram and two types of economy, competitive and distributive, are compared.

Evolving Virtual Fireflies

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Abstract. In this paper, we present a study in the evolution of cooperative behavior, specifically synchronization, through digital evolution and multilevel selection. In digital evolution, a population of self-replicating computer programs exists in a user-defined computational environment and is subject to instructionlevel mutations and natural selection. Multilevel selection links the survival of the individual to the survival of its group, thus encouraging cooperation. Previous approaches to designing synchronization algorithms have taken inspiration from nature: In the well-known firefly model, the only form of communication between agents is in the form of "flash" messages among

neighbors. Here we demonstrate that populations of digital organisms, provided with a similar mechanism and minimal information about their environment, are capable of evolving algorithms for synchronization, and that the evolved behaviors are robust to message loss. Moreover, analysis of the dominant genome reveals that the evolved solution utilizes an adaptive frequency strategy strikingly similar to that observed in fireflies.

RBN-World: A Sub-Symbolic Artificial Chemistry

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Abstract. We describe a composable dynamical system that uses the emergent properties of coupled random Boolean networks (RBNs) as a basis for a sub-symbolic artificial chemistry. The approach shows potential for open-ended emergent properties and may lead to a foundation for artificial life.

Selection of Cooperative Partners in n-Player Games

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Abstract. We address the problem of finding the appropriate agents to interact with in n-player games. In our model an agent only requires knowledge about the payoff and identification of its partners. This information is used to update a probability distribution over candidate partners. As such, our model is applicable in any situation, be it a cooperative dilemma or a game where a Nash Equilibrium is equal to a Pareto Optimal profile.

Heterarchy-model for Functionally Class 4

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Abstract. Class 4 automata are considered to exhibit the essential feature of biological systems that a system is divided into stably periodic parts which can interact with each other. Turing machines can also be implemented by using a non-diffusive particle known as “glider” in class 4 behaviors, which can be used as a device for logical gates, shifts, delays and reflections. Robust but dynamic biological systems in nature are assumed to be hierarchical, while class 4 automata have no hierarchical structure. Whether simple or complex, behaviors can be reduced to transition rules, and even class 4 behavior is not an exception from this generalization. In examining a biochemical network or an immune system, hierarchy can be functionally lost in the interaction between the layers, while structural hierarchy is found to be robust. The notion of hierarchy itself is self-referential and ambiguous, and these properties have been recently reflected in the term “heterarchy”. If a heterarchical structure is implemented in ECA, the question arises whether class 4 and/or more complex behaviors can emerge in such a system. In other words, here we propose a model for class 4 behavior as heterarchy, which is constructed as follows. First, we analyze the macroscopic properties of class 3 ECA by using an algebraic structure based on the lattice derived by rough set analysis. Next, a virtual algebraic structure which characterizes class 1 or 2 ECA which cannot be derived from class 3 rules is assumed in the same ECA, and we seek modifications in the rules to reveal such a virtual algebraic structure. This results in the superposition of the middle layer transition which can intermediate the microscopic ECA transition and the virtual algebraic structure. Finally, we obtain a recipe which can produce class 3 ECA exhibiting class 4 behavior.

A new approach for auto-organizing a groups of artificial ants

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Abstract. We present in this paper a new combined clustering algorithm based on two biomimetic models : artificial ants and self-organizing map (SOM). We describe the main principles of our method that aims at auto-organizing a group of homogeneous ants (data's). We show how these principles can be applied to the problem of data clustering.

Update Dynamics, Strategy Exchanges and the Evolution of Cooperation in the Snowdrift Game

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Abstract. We verify through numerical simulations that the influence of the update dynamics on the evolution of cooperation in the Snowdrift game is closely related to the number of strategy exchanges between agents. The results show that strategy exchanges contribute to the destruction of compact clusters favorable to cooperator agents. In general, strategy exchanges decrease as the synchrony rate decreases. This explains why smaller synchrony rates are beneficial to cooperators in situations where a large number of exchanges occur with synchronous updating. On the other hand, this is coherent with the fact that the Snowdrift game is completely insensitive to the synchrony rate when the replicator dynamics transition rule is used: there are almost no strategy exchanges when this rule is used.

56 Feasibility of biomimetic classification on NVIDIA® CUDA™

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Abstract. Both the brain and modern computing architectures rely on massive parallelism for solving demanding tasks, like the critical problem of pattern recognition, in a fast and efficient way. In this paper we present a parallel classification scheme, inspired by the insect olfactory system, and its implementation on modern parallel hardware, i.e., in the NVIDIA® CUDA™ framework on a NVidia® Tesla™) S1070 device. We apply the algorithm to the benchmark MNIST dataset of handwritten digits and show that the parallel implementation of the bio-inspired classification provides 6-30fold speedup, compared to a standard serial implementation on a modern PC (with AMD® Phenom™ 9600 quad-core processor at 2.3 GHz and 4 GB of RAM). Our results suggest that modern parallel computing architectures and bio-mimetic algorithms are a natural match, hence it may well be the right time to go "bio-parallel".

Local Ultrastability in a real system based on Programmable Springs

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Abstract. A way to move gradually towards an objective is by making sure at every step that there is as little deviation as possible while adapting to obstacles. This has inspired us to model a local strategy to eventually attain viability (equilibrium) in a real complex dynamical system, amidst perturbations, using ultrastability to make sure that the path to viability itself is viable. We have tested this approach on a real actuator powered by a technology called "programmable springs" that allows for real-time non-linear programmable actuation. Our experiment involves a problem in adaptation similar to the polebalancing problem. To solve it, we use ultrastability in a novel way, looking at the viability of dynamical transitions of the system in its phase space, to tweak the local properties of the actuator. Observations show that our approach is indeed effective in producing adaptive behaviour although it still requires further testing in other platforms, thus supporting the original hypothesis that ultrastability can be an effective adaptive mechanism [3] and laying a foundation for a promising new perspective in ultrastable robotics.

Investigations of Attractor Behavior over the Decay of Modular RBNs

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Abstract. When is it safe to approximate a complicated random Boolean network (RBN) as a simplified, easier to model RBN? When can static measures of network structure be reliably used to infer the network's dynamics? This simple experiment tests the ability of disjoint modular RBNs to approximate the dynamics of progressively more interconnected RBNs, while characterizing the performance of both static and dynamic measures of modularity as both break down. We find that, at least in the small networks investigated, the Newman 2004 [1] measure of static modularity performs as well as a more complex dynamic measure of modularity, and that the progressively increasing failure of one tracks that of the other. The dynamic measure is based on the Hamming distance of attractor schemata in rewired networks from those in perfectly modular networks. This result holds for a range of p-values.

For Corvids together is better. A model of cooperation in Evolutionary Robotics

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Abstract. In this paper we describe a model of cooperation in evolutionary robotics (ER) derived by animal research on Corvids. In recent years many researchers have proposed models of ER which are bioinspired. The main source of inspiration has come from social insects, such as ants. Inspiration may come also from other representatives in the animal kingdom such as primates or corvids, thus producing different models that can address different issues. The work presented here starts from works inspired by social insects and then describes an ER model inspired by tasks in corvids, that addresses the evolution of cooperation, showing how different bio-inspired models can be useful to study different issues.

Simulating Swarm Robots for Collision Avoidance Problem Based on a DBN

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Abstract. This paper presents a simulator for the behaviors of swarm robots based on a Dynamic Bayesian Network (DBN). Our task is to design each robot's controller which enables the robot to patrol as many regions as possible without collisions. As the first step, we use two swarm robots, each of which has two motors each of which is connected to a wheel and three distance-measurement sensors. To design the controllers of these robots, we must determine several parameters such as the motor speed and thresholds of the three sensors. The simulator is used to reduce the number of real experiments in deciding values of such parameters. We fist performed measurement experiments for our real robots in order to get probabilistic data of the DBN. The simulator based on the DBN revealed appropriate values of a threshold parameter and interesting phase transitions of their behaviors in terms of the values.

Evolving Group Coordination in an N-Player Game

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Abstract.The evolution of coordination is an important consideration in living systems. Throughout the natural world examples of coordination can be found. These include fish schooling, birds flocking and animals hunting in packs. This paper examines the issue of coordination and how groups can coordinate their actions in a competitive setting. A number of existing game theoretic representations of coordination have been proposed. Much of the existing research has studied two player coordination games. This paper will investigate the emergence of coordination through an n-player game. The use of signalling, communication and norms is common when attempting to address the topic of coordination, yet in this paper we will not apply any of these approaches. This paper investigates the effect of group structures on the evolution of coordination in a population of self interested individuals. The results will demonstrate the importance of these group structures when attempting to evolve coordinated actions.

Solving a Heterogeneous Fleet VRPTW with the Asynchronous Situated Coevolution Algorithm

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Abstract. In this work we present the practical application of the Asynchronous Situated Coevolution (ASiCo) algorithm to a special type of vehicle routing problem, the heterogeneous fleet vehicle routing problem with time windows (HVRPTW). It consists in simultaneously determining the composition and the routing of a fleet of heterogeneous vehicles in order to serve a set of time-constrained delivery demands. The ASiCo algorithm performs a situated coevolution process inspired on those typical of the Artificial Life field that has been improved with a strategy to guide the evolution towards a design objective. This strategy is based on the principled evaluation function selection for evolving coordinated multirobot systems developed by Agogino and Tumer. ASiCo has been designed to solve dynamic, distributed and combinatorial optimization problems in a completely decentralized way, resulting in an alternative approach to be applied to several engineering optimization domains where current algorithms perform unsatisfactorily.

Development of Abstract Categories in Embodied Agents

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Abstract. In this paper we demonstrate how a neuro-robot situated in an environment containing parallelepiped objects that vary in shape, size, and orientation can develop an ability to recognize and label the category of the objects and generalize to new objects. The analysis of the dynamical system constituted by the robot and the environment in interaction allowed us to understand how adapted agents solve the categorization problem at the level of the detailed mechanisms and at the level of the general strategy.

Evolving Social Behavior in Adverse Environments

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Abstract. Cooperative behaviors are pervasive in the natural world. How organisms evolve stable cooperative strategies, specifically how selection can favor such costly behaviors, is a difficult problem for which several theories exist. In this work, we use digital evolution to explore the evolution of the production of a public resource that enables populations of organisms to survive in an adverse environment. Kin selection and limited dispersal are shown to promote cooperative acts, and evolved organisms stave off invasion by cheaters and survive in increasingly-adverse environments. Further, we observe how populations react to the disappearance and later re-emergence of adversity in the environment.

Hybridizing River Formation Dynamics and Ant Colony Optimization

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Abstract. River Formation Dynamics (RFD) is an evolutionary computation method based on copying how drops form rivers by eroding the ground and depositing sediments. In a rough sense, this method can be seen as a gradient-oriented version of Ant Colony Optimization (ACO). Several experiments have shown that the gradient orientation of RFD makes this method solve problems in a different way as ACO. In particular, RFD typically performs deeper searches, which in turn makes it find worse solutions than ACO in the first execution steps in general, though RFD solutions surpass ACO solutions after some more time passes. In this paper we try to get the best features of both worlds by hybridizing RFD and ACO, in particular by using a kind of ant-drop hybrid and considering both pheromone trails and altitudes in the environment.

All in the same boat: A "situated" model of emergent immune response

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Abstract. Immune systems provide a unique window on the evolution of individuality. Existing models of immune systems fail to consider them as situated within a biochemical context. We present a model that uses an NK landscape as an underlying metabolic substrate, represents organisms as having both internal and external structure, and provides a basis for studying the coevolution of pathogens and host immune responses. Early results from the model are discussed; we show that interaction between organisms drives a population to optima distinct from those found when adapting against an abiotic background.

The universal constructor in the DigiHive Environment

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Abstract. The paper describes an universal constructor model realized in artificial environment called DigiHive. The environment is a two dimensional space, containing stacks of hexagonal tiles being able to moving, colliding, and making bonds between them. On the higher level of organization a structure of tiles specifies some function whose execution affects other tiles in its neighborhood. After short description of the DigiHive the paper describes design of an universal constructor and discusses possibilities of simulating self-replicating strategies in the environment.

To grip, or not to grip: Evolving coordination in autonomous robots

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Abstract. In evolutionary robotics, as in the animal world, performing a task which is beneficial to the entire group demands the coordination of different individuals. Whenever time-dependent dynamic allocation of roles is needed and individual roles are not pre-defined, coordination can often be hard to achieve. In this paper, we study the evolution of role allocation and self-assembling strategies in a group of two homogeneous robots.We show how robot coordination and individual choices (who will grip whom) can be successfully restated in terms of anti-coordination problems, showing how conventional game theoretical tools can be used in the interpretation and design of evolutionary outcomes in collective robotics. Moreover, we highlight and discuss striking similarities between the way our physical robots allocate roles and the way animals solve conflicts. Arguably, these similarities suggest that evolutionary robotics may offer apart from automatic controller design for autonomous robots a viable alternative for the study of biological phenomena.

Metamorphosis and Artificial Development: An Abstract Approach to Functionality

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Abstract. An artificial developmental process may reflect the principle of a process starting with a zygote which develops to a multicellular organism. An organism goes through an interwoven process of shaping the form and behaviour. Metamorphosis is a stage in the development of many species, e.g. insects, which include a large variation of phenotypic shape and behaviour in the life-time of the organism. Here principles from metamorphosis are included as a developmental stage that can be exploited by evolution to produce artificial organisms with variation in behaviour at different developmental stages. The target developmental system is a cellular system close to a non-uniform cellular automaton. As such, Darwin's discovery is exploited for evolving genomes for the construction (development) of von Neumann's cellular machines, Darwin meets von Neumann.

Evolving adaptive behavior that adapts: Flexible deployment of contingent motor resources in evolved model agents

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Abstract. A common challenge faced by biological organisms and mobile robots alike is the need to adjust motor activity in response to unreliable effectors so as to robustly achieve some behavioral goal. When motor actions fail to produce their desired consequences–when a wheel slips or, in more extreme cases, when an entire motor apparatus becomes disabled–an agent must adaptively reorganize its behavior to meet the changing circumstances and accomplish its objective. Can simple model agents be evolved to exhibit this kind of behavioral robustness and flexibility? If so, what kinds of control strategies will they employ? Here we present results from an evolutionary agents study offering an initial exploration of these important questions.

In this study, agents equipped with two effectors–a leg and a pair of pure force effectors or "wheels"–were evolved to catch circular objects falling towards them from above. The effectors were chosen to require qualitatively different patterns of control, so that it is nontrivial for a single controller to operate them both. During evolution, each agent is evaluated in three different

conditions. In the first, the agent is required to catch objects while both of its effectors are available for use. Then, in each of two lesion conditions, one or the other of the agent's effectors is disabled, and the agent must catch objects using only its one remaining effector. Thus, the agent must adapt its motor output in each condition to compensate for the variable reliability of its effectors. Additionally, the agent is not provided with any explicit indication of the current status of its effectors, so it must determine the appropriate behavior based solely on the differing patterns of feedback that its effectors produce.

We present results from several experiments investigating the behavior of the best evolved agent. First, we describe a series of experiments which demonstrate that the agent produces qualitatively distinct motor patterns in each of the three conditions. Next, we examine the ability of our evolved agent to flexibly adapt its behavior in two previously unseen situations. First, we show that the agent can redirect its motion to catch objects that change horizontal position, even when the change occurs very late in the trial. Second, we show that the agent is able to robustly switch between the use of any combination of its effectors—for example, switching from using both effectors to only its leg—at any point during a trial.

Finally, we present evidence demonstrating that the agent's behavior is governed primarily by the different patterns of feedback through the body and environment that the effectors produce in each condition. Interestingly, Izquierdo and Buhrmann (ALife XI, 2008) report a similar finding for an agent evolved to exhibit two qualitatively distinct behaviors, and also observe a similar ability of their agent to flexibly switch behaviors. Thus, we conclude by suggesting that the ability to flexibly switch between distinct behavioral dynamics may be a powerful and general feature of control strategies that rely on continuous transient feedback through the brainbody-environment system.

Distance Discrimination of Weakly Electric Fish with a Sweep of Tail Bending Movements

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Abstract. Weakly electric fish use active electrolocation to identify objects. They generate electric field by the electric organ discharge and perceive the distortion of electric image with existence of certain object. There have been many researches to comprehend the electrolocation mechanism of electric fishes. It is known that the ratio between the maximal slope of electric image and its maximal amplitude can discriminate object distances, regardless of object size and conductivity. In this paper, we suggest that the temporal pattern with tail bending is another cue to discriminate object distances. As a result, the electric field pattern for a specific electroreceptor shows consistency, regardless of object size and conductivity, when the distance is constant. Also, the lateral location of an object significantly changes the temporal pattern of electric image.

Day 3

Artificial cells for information processing: Iris Classification

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Abstract. This paper presents a model in the Artificial Embryogene (AE) framework. The presented system tries to model the main functions of the biological cell model. The main part of this paper describes the Gene Regulatory Network (GRN) model, which has a similar processing information capacity as Boole's Algebra. This paper also describes how to use it to perform the Iris Classification problem which is a pattern classification problem. The aim of this work is to show that the model can solve this kind of problems.

Artificial Life, The Universe and Everything

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Abstract. In the Hitchiker's Guide to the Galaxy, Douglas Adams concluded that the answer to the greatest question - the question of life, the universe and everything - was 42. Artificial life is well posed to consider certain theoretical aspects of what is arguably one of the greatest scientific questions of the current age: is the Earth unique as the only home to life in the universe or does life exist elsewhere in the cosmos? Considering under what circumstances life may exist on other planets has the potential to considerably inform our understanding of life on Earth, in particular how has life persisted for billions of years despite calamities such as climate changing volcanoes, asteroid impacts and solar variance.

Typically, it is assumed that estimating the number of biospheres in the universe will be some function of the probability of abiogenesis and the number of worlds on which life may arise. For example, the probability of life arising may be very small. However, if there are a very large number of rocky worlds on which life may arise, then life elsewhere in the universe may exist.

It is possible that we will never know how life on Earth arose as it may be impossible to have a sufficiently accurate understanding of the pre-biotic Earth. One interesting property of all life on Earth is that it appears related. This is evidence for a single act of abiogenesis or multiple abiogenesis events with all forms of life apart from a single `germ line' going extinct at some point very early in its evolution, or 'alien' life forms as yet undetected on Earth. Despite a wide range of shocks, stresses and perturbations, widespread life has returned and the biosphere has continued to flourish. Is this persistence of life on Earth simply a lucky coincidence? Can this be seen as support for weak or stronger versions of the anthropic cosmological principle (Barrow, Tipler, 1986, The anthropic cosmological principle, OUP)? Or is there something about the Earth's biosphere that makes it inherently robust to perturbations, so that its continued existence is a manifestation of some self-regulating property?

It will be argued that when considering the possibility of, and searching for, life on other planets, we should consider how robust and resilient life on Earth is. This idea is related to the Gaia Hypothesis: that life, in interacting with the Earth's oceans, crust and atmosphere, forms a homeostatic system that maintains certain environmental conditions to within the bounds necessary for widespread life (Lovelock, 1979, Gaia: a new look at life on Earth, OUP). Abiogenesis may be very improbable. However, if once a biosphere is established it effectively regulates against otherwise deleterious perturbations, then life may be more widespread than initial estimates would suggest. A critical component of this argument is that Gaian regulation is not necessarily homeostatic in the sense of environmental stasis. The Earth has evolved and environmental conditions have significantly changed.

It will be argued that homeorhesis is a more appropriate concept as the Earth's biosphere has maintained particular trajectories along which life evolves, which in turn affects such trajectories. This reinforces the importance of viewing life and environment as a coupled co-evolving system. In that respect, artificial environments may be as important as artificial life when considering life as it is and as it could be.

Building the Mind's Consciousness from the Bottom Up

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Abstract. A multi-cellular organism consists of a collection of cells, but it presents itself to the outside world as a unified entity. How? The natural development of multiple scales is commonly restricted to carbon-based covalent-bonded systems – to living organisms. In a naturally evolving system, these scales are not independent: their multiplication corresponds to the emergence of a differentiated entity in the yet higher dimension of hyperscale. An entity is its hyperscale: hyperscale provides identity, and in a multiply-autonomous organism there are even a number of different 'identities' related to its different scales and regional autonomies.

The key to an organism's evolutionary survival is the ability to anticipate danger and avoid its consequences. Anticipative capability is therefore central to the evolution which has led to our species' mental development. Consequently the evolutions of survivability, anticipation, consciousness, the mind, intelligence, wisdom and evolution itself are broadly equivalent. Successful anticipation depends on the creation of transparent internal models of external environmental features and phenomena. However, it also necessitates the extension of these models to include the organism itself, and so the creation of an internal transparent environmental model is automatically and intimately associated with the creation of an internal transparent self-model. The birational complementary character of environmental- and self-modeling has evolved in the brain to the mind's logical-emotional pairing of conscious and unconscious processing.

An organism's continually changing awareness of multiple external events focuses attention on those which are judged to be the most relevant to survival or of greatest current interest, and other more static phenomena become neglected. The degree to which we pay attention to deviations from anticipated events or conditions reduces with their future distance, and this exacerbates stasis-neglect, and strengthens attention's long-term 'complementary ecosystem' of 'neglected' stasis. This phenomenon of 'stasis neglect' has the important effect of making it possible for repeated actions to be transferred out of regions of the brain which consciousness 'keeps track of' and for them to become quasi-automatic.

Metzinger's 'transparent self' hypothesis provides a credible model for the independence of the mind. Metzinger does not, however, provide us with any clue as to 'where' we can 'find' the 'self-model', or how it has been generated over the aeons of evolution. We believe that unification-maintaining hyperscalar survivalist sapient behavior has resulted in long-term evolution of the high-level transparent self-model Metzinger refers to. Matsuno's self-consistent view of 'reality' is based on the interpretation of observation as a mutual measurement. The recursive inter-correlation of the two sapiences of a birational hierarchy provides an excellent example of 'mutual self-measurement'. The 'phenomenon' of self 'resides' in truncation by stasis neglect of this infinite self-observational sequence. We conclude that the construction of a natural birational hierarchy leads automatically to the generation of mind and consciousness.

SimSoup: Artificial Chemistry Meets Pauling

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Abstract. Theories of the Origin of Life can be categorised as `template replication first' and `metabolism first'. A key question for metabolism first theories is the mechanism for transfer of inherited information. Earlier work presented a mechanism based on catalytic cycles, along with supporting results from the SimSoup artificial chemistry simulator[1]. The current paper presents an enhanced SimSoup model that is closer to real chemistry and more open ended. Molecules and the types of Interactions between them are constructed by the model itself using simple rules based on valence theory. Results of a preliminary run of the model are presented. Most of the Molecules produced are of a few simple types with low molecular weight. There is a `long tail' of many low frequency Molecules, many of which are more complex with high molecular weight.

Prediction vs. Adaptation in Science

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Abstract. Since the days of Galielo, Newton, Laplace, and Descartes, classical science has aimed at predicting the world around us. This has been very useful and great developments in science and technology have been made with this approach. However, the assumption that all phenomena are predictable has been put into question in recent decades for two main reasons. First, systems presenting deterministic chaos may not be predictable in practice due to sensitivity to initial conditions. Still, chaos does not threaten the predictability assumption, since in theory systems could be predictable, we just do not have enough precision. Also, techniques for controlling chaos have been developed and can contribute to force a chaotic system into a predictable pattern. Second, complexity implies that systems cannot be reduced to the behavior of their parts. This is because the interactions between them are relevant to determine the future state of the elements. This implies that novel relevant information is generated as the system develops. In other words, we cannot make a priori statements. We need to observe the evolution of a particular state of a system (e.g. a type IV cellular automaton) before we can predict a future state. In other words, we need to "run the tape and see". In many cases, complex interactions imply a "non-stationary state space" (or phase space for continuous models), as the novel information generated by the interactions modify the state space. Using the classical method, we can attempt at predicting where the system will be (an attractor), or find an optimal solution for a problem. However, if the state space is changing, prediction will give obsolete solutions. This forces us to change the approach from prediction to adaptation. Even when prediction is more desirable, it must be acknowledged that in many complex systems prediction is not enough to find solutions, as the problem is not specified beforehand. Adaptation complements prediction by constantly finding solutions in a changing state space. Living systems are rich in adaptation, since the solution to their problem (survive and propagate) changes constantly with their environment. Artificial Life has taken inspiration in the adaptability of living systems to build technological systems capable of adapting to a dynamic environment, i.e. a non-stationary state space. Given the increasing complexity of our environments, the ALife approach should be propagated into all scientific disciplines. Instead of attempting to predict our world, and building systems based on this assumption, we should try to be adaptable to our changing world, and build systems able to adapt to the unforeseen. This shift demands more than a change of methodology, it requires a change of worldview.

Observer Based Emergence of Local Endo-Time in Living Systems: Theoretical and Mathematical Reasoning

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Abstract. In this paper, we analyze the temporal dimension of the problem of emergence of functional networks in living systems and give an abstract mathematical framework for dealing with those issues without considering the structure of the particular mappings or the resulting dynamics. We found that formal structures equivalent to emergence of local ordering and local chronologies can be defined within the framework of topological relations based on local observers. By using category theory, we further represented higher levels of transformations (between closures), with a special focus on observer turnover.

Life and its Close Relatives

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Abstract. When driven by an external thermodynamic gradient, non-biological physical systems can exhibit a wide range of behaviours usually associated with living systems. Consequently, Artificial Life researchers should be open to the possibility that there is no hard-and-fast distinction between the biological and the physical. This suggests a novel field of research: the application of biologists' methods for studying organisms to simple \near-life" phenomena in non-equilibrium physical systems. We illustrate this with some examples, including natural dynamic phenomena such as hurricanes and human artefacts such as photocopiers. This has implications for the notion of agency, which we discuss.

Using Pareto Front for a Consensus Building, Human Based, Genetic Algorithm

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Abstract. We present a decision making procedure, for a problem where no solution is known a priori. The decision making procedure is a human powered genetic algorithm that uses human beings to produce variations and evaluation of the partial solution proposed. Following [1] we then pick the pareto front of the proposed partial solutions proposed, eliminating the dominated ones. We then feed back the partial results to the human beings, asking them to find a alternative proposals, that integrate and synthesize the solutions in the pareto front. The algorithm is right now being implemented, and some preliminary results are being presented. Some possible variations on the algorithm, and some limits of it, are also discussed.

Elongation Control in an Algorithmic Chemistry

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Abstract. Algorithmic chemistries intended as computation models seldom model energy. This could partly explain some undesirable phenomena such as unlimited elongation of strings in these chemistries, in contrast to nature where polymerization tends to be unfavored. In this paper, we show that a simple yet sufficiently accurate energy model can efficiently steer resource usage, in particular for the case of elongation control. A string chemistry is constructed on purpose to make strings grow arbitrarily large. Simulation results show that the addition of energy control alone is able to keep the molecules within reasonable length bounds, even without mass conservation, and without explicit length thresholds. A narrow energy range is detected where the system neither stays inert nor grows unbounded. At this operating point, interesting phenomena often emerge, such as clusters of autocatalytic molecules, which seem to cooperate.

Flying over Mount Improbable

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Abstract. Using Chemical Organisation Theory [1] we present here an analysis of two classical models of artificial chemistries: a system equivalent to AlChemy [2], and the Automata Chemistry [3]. We show that Chemical Organisation Theory is able to explain why AlChemy was unable to evolve, while the Automata Chemistry would produce a stream of novelty that would on the one side explore the space of the possible molecules (and organisations) and on the other build upon the previous findings of the system. We relate to Suzuki's et al. [4] ten necessary conditions for the evolutions of complex forms of life, by adding an 11th one.

The Synthetic Production of Antibiotics by Protocells

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Abstract. Wet Artificial Life (wet ALife) studies biological systems in vitro, focused on understanding life. One of its main subjects is the study of protocells (Rasmussen et al., 2008) which intend to recreate natural cells in a simpler form.

There is a thin – almost unnoticeable – boundary between living and non-living systems. We know that living organisms are an ensemble of non-living ones. But at which point life emerges? How can we reach an operational definition of life? These and many other questions regarding the origins of life have been asked by many people for centuries, and in recent years great scientists have opened paths towards the answers.

In this work we review the protocell literature. Protocells are simple artificial forms of life. Their origins, developments, state-of-the-art, and its prospects are exposed. A potential application of protocells in biotechnology is exposed, in an attempt to use protocells as workers, exploiting their autopoietic nature. Specifically, the cheap and efficient production of antibiotics by protocells is explored.

A simulation is presented where protocells self-assemble from free molecules. The simulation implements a simplified model to illustrate the potential production of an antibiotic (fosfomycin) by protocells, describing the steps that should be taken. The simulation starts with populations of free lipids, nucleotides, and two types of genes: one that produces an antibiotic precursor, and another that uses the precursor to generate the antibiotic. Membranes self-assemble from lipid molecules. They can absorb genes and nucleotides. When there are enough nucleotides to match the sequences found in the genes, the protocell reproduces by division. Once protocells have both genes, they can synthetize the antibiotic and release it into the environment. For different abundance of resources, the dynamics of the antibiotic production are studied.

The implications of protocell research and applications are discussed. We believe that there will be an impact not only on the life sciences, but also on society and philosophy of science. Moreover, protocell research will contribute not only to ALife, but also to the development of a "general biology" (Kauffman, 2000), where living systems are studied beyond the carbon-, DNA-, cell-based life that we know. This should bring a better understanding of what life is.

A Kinematic Model of a Self-Replicating Programmable Constructing Machine

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Abstract. To date, research into the implementation of autonomous self-replicating systems has focused either on highly abstract logical models, or on physical systems that are deliberately engineered in some way so as to make the problem more tractable [1]. There are also several system-level proposals for physical self-replicating systems.

A simulation environment is presented at a level of abstraction that supports motion, connection and disconnection of parts, and which enforces the conservation of matter. This level of abstraction lies somewhere between cellular automaton models and real physical systems.

The simulation environment is a 3D kinematic automaton in which cubic parts can be placed into a discrete space and connected together to make machines. The environment supports six part types:

A *wire part* receives a boolean input value at its base and propagates this value to all five of its outputs after one time unit.

A *nor-gate part* receives boolean input values from all five of its inputs, and propagates the logical NOR of these values to its output after one time unit.

A *slide part* receives a boolean input value from its input. If this value is true, then one time unit later it will move any part directly opposite its input.

A *rotate part* receives a boolean input value from its input. If this value is true then one time unit later it will rotate any part directly opposite its input.

A *connect part* receives a boolean input value from its input. If this value is true then one time unit later it will connect together the part lying opposite its input to a neighbouring part.

A *disconnect part* receives a boolean input value from its input. If this value is true then one time unit later it will disconnect the part lying opposite its input from a neighbouring part.

The simulation environment has previously been described in [2].

A self-replicating programmable constructing machine (SRPC) with an architecture similar to that in [3] has been implemented in this environment. The machine can take a disorganised collection of parts as its input and construct machines from these parts according to a sequence of instructions. As a special case, it can be programmed to construct a replica of itself. The machine is made from 59,504 parts, of which 49,152 make up the machine's memory.

By demonstrating that an SRPC can be implemented in this environment, it is shown that some of the results already obtained about SRPCs in cellular automaton environments can be extended into the domain of kinematic systems, and also that consideration of the kinematical concepts of motion and connectivity along with the conservation of matter does not introduce any barrier to the existence of such machines.

Simulations of Abstract Autopoietic Machines

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Abstract. Some artificial life works aimed at simulating artificial autopoiesis. Generally, the purpose is to maintain a topological organization of automata. At the opposite, we esteem that simulation can override topological aspects because topology has no significance in the computational domain. Consequently, we present a model of an Abstract Autopoiesis Machine which resists of abstract perturbations. It is a short paper and the final presentation will present the result of some simulations of this system.

Digital Organ Cooperation: Toward the Assembly of a Self-feeding Organism

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Abstract. In Nature, the intrinsic cooperation between organism's parts is capital. Most living systems are composed of organs, functional units specialized for specific actions. In our last research, we developed an evolutionary model able to generate artificial organs. This paper deals with the assemby of organs. We show, through experimentation, the development of an artificial organism composed of four digital organs able to produce a self-feeding organism. This kind of structure has applications in the mophogenetic-engineering of future nano and bio robots.

A Life in the Galapagos: migration effects on neuro-controller design

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Abstract. The parallelization of evolutionary computation tasks using a coarse-grained approach can be efficiently achieved using the island migration model. Strongly influenced by the theory of punctuated equilibria, such a scheme guarantees an efficient exchange of genetic material between niches, not only accelerating but also improving the evolutionary process. We study the island model computational paradigm in relation to the evolutionary robotics methodology. We let populations of robots evolve in different islands of an archipelago and exchange individuals along allowed migration paths. We show, for the test-case selected, how the exchange of genetic material coming from different islands improves the overall design efficiency and speed, effectively taking advantage of a parallel computing environment to improve the methodology of evolutionary robotics, often criticized for its computational cost.

Algorithmic Feasibility of Entity Recognition in Artificial Life

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Abstract. Observations are an essential implicit component of the simulation based artificial-life (ALife) studies by which entities are identified and their behavior is observed to uncover higher-level "emergent" phenomena. Building upon the axiomatic framework of Henz&Misra [2], we analyze computational complexity bounds for the algorithmic implementation of an observation process for an automated discovery of the life-like entities in arbitrary ALife models. Among other results of such analysis is the conclusion that the problem of entity recognition in a simulation using syntactic constraints is a NP-hard problem and therefore cannot always be solved in polynomial number of steps. The computational complexity bounds are established distinguishing further between those ALife models which allow entities with overlapping structures to coexist in a state and others which do not.

Chaotic patterns in crowd simulation

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Abstract. We have developed a model of crowd based on social agents and swarm intelligence. The model takes the form of a randomly generated directed graph where nodes represent individuals locked in a room where a fire occurs. Each individual follows connected individuals,

called the references. There are two special individuals, the firegfihters, situated at the two exits from the room: exit T or true and exit F or false. The agents are directed at targets T and F in a computer animation implemented in Netlogo. They come into conflict of over-information when they receive contradictory information from their references.

We studied experimentally the influence of the following mechanisms of conflict resolution: follow the mode or the anti-mode, random resolution and the effect of excluding the own opinion. We found that these mechanisms lead people following the mode to unanimously choose one of the options, flocking towards the selected goal. In the case of anti-mode, the population oscillates between the two options. The number of references is critical to this behavior and following one or two references with exclusion of the own state leads the system to chaotic patterns of convergence.

Synchronization Waves in a 2D Grid of Pulse-Coupled Oscillators

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Abstract. A model of a cellular automaton on a 2D grid is studied where each cell periodically enters a firing state. Firing of a cell is sensed by other cells in a circular vicinity of radius R. As a result the sensing cell may change it’s firing rate. The interaction strength between a firing and a sensing cell is inversely proportional to the square of the distance between the two cells. Under most starting conditions waves of synchronized firing cells emerge in the cell array. Simulation data indicates that for certain parameter values the emergence of synchronization waves occurs only if there is dispersion in the intrinsic firing frequencies of the cells.

Symbiosis Enables the Evolution of Rare Complexes in Structured Environments

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Abstract. We present a model that considers evolvable symbiotic associations between species, such that one species can have an influence over the likelihood of other species being present in its environment. We show that this process of ‘symbiotic evolution’ leads to rare and adaptively significant complexes that are unavailable via non-associative evolution.

Hierarchical Behaviours: Getting the Most Bang for your Bit

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Abstract. Hierarchical structuring of behaviour is prevalent in natural and artificial agents and can be shown to be useful for learning and performing tasks. To progress systematic understanding of these benefits we study the effect of hierarchical architectures on the required information processing capability of an optimally acting agent. We show that an information-theoretical approach provides important insights into why factored and layered behaviour structures are beneficial.

Evolution of Individual Group Size Preference can Increase Group-level Selection and Cooperation

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Abstract. The question of how cooperative groups can evolve and be maintained is fundamental to understanding the evolution of social behaviour in general, and the major transitions in particular. Here, we show how selection on an individual trait for group size preference can increase variance in ?tness at the group-level, thereby leading to an increase in cooperation through stronger group selection. We are thus able to show conditions under which a population can evolve from an initial state with low cooperation and only weak group selection, to one where group selection is a highly effective force.

Agent-based model of Dengue Disease Transimission by *Aedes aegypti* Populations

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Abstract. This paper presents an agent based model of the *Aedes aegypti* mosquito showing not only population dynamics but also the Dengue disease propagation in both the vector and host populations (mosquitoes and humans, respectively); this study will focus on the latter aspect. The agents model the main aspects of the mosquito's ecology and behavior, while the environmental components are implemented as a layer of dynamic elements obeying to physical laws. Model verication was performed through examination of simulation parameters variation and qualitative assessment with existing models and simulations. The agent based modeling and simulation platform used was the LAIS simulator.

Embodiment of the Game of Life

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Abstract. In this paper, an expression of embodiment on computation and its effect are explored. By introducing the notion of latent state space, embodiment is formalized as an extension of state space and its projection process and resulting misidentification of states. Implementing this structure in the game of life, we investigate the relationships between the original system and misidentification of states by means of informational structures. As a result, we observe that, in particular case, misidentification affects the system's behavior and is relevant to maintain the property of the original system.

Invariants of Behavior

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Abstract. It may at first seem like a paradox that in nervous systems extreme variability may peacefully coexist with conspicuous constancy. Variability and constancy are present in substrate (what is it made of), structure (how is it organized) and function (what it can do). For any identifiable dimension one chooses to quantify, be that in morphology or in behavior, one finds simultaneously spreads of measures and consistent means. In neural systems this interplay finds its most impressive expression. How is the system able to display constancy in behavior, despite the variations in the

structure of networks and connections? I employ recurrent neural networks, artificially evolved to control the behavior of robots, to understand the interplay between structure variation and behavioral constancy. The paradigm is neurodynamics, which views the body, the neural systems and the environment as coupled dynamical systems.

I have asked the question "why can different networks solve embodied problems similarly?". The answer is framed within a neurodynamics paradigm, with which I studied the dynamical reservoirs (attractor landscapes) of recurrent neural networks produced by evolutionary robotics methods controlling robots. I have shown how an evolutionary procedure causes evolutionary convergence towards behavioral function (with two case studies, one in active tracking in which a pan-tilt camera tracks a moving object, and one in which a robot freely follows moving objects in a dynamical environment). Equivalent behavior appears despite variability in structures. It can be said that a given behavioral function will define an equivalence class of structures that are able to deploy that ability equivalently. Invariance in this case is not respective to transformations of network structures, but to the kinds of dynamics that may subserve particular behavioral functions, as seen in the dynamical reservoir of networks, the attractor landscapes.

Behaviors of A Chemical Reactions with A Small Number of Molecules

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Abstract. Living systems are composed of biochemical reactions and many of them involves a small number of molecules. We investigate the behaviors of chemical reactions of the Lotka-Volterra model with small number of molecules by using Abstract Rewriting System on Multisets, ARMS; ARMS is a stochastic method of simulating chemical reactions and it is based on the reaction rate equation. We confirmed that the magnitude of fluctuations on periodicity of oscillations becomes large, as the number of involved molecules is getting smaller and the dynamical characteristics is changed. We investigate the coarse grained state space of ARMS and show that the mechanism of fluctuations occur in the chemical reactions involved a small number of molecules.

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