Towards a science of complex systems

Complex systems, as networks of interactive entities, are studied through a rapidly increasing mass of data in all domains. At the same time, these domains share a lot of new and fundamental theoretical questions. This situation is especially favourable for developing the new science of complex systems in an interdisciplinary way. The ECCS'05 is a step towards this new science.

There are two kinds of interdisciplinarity within complex systems. The first kind begins with a particular complex system and addresses a variety of questions coming from its particular domain and points of view. The second kind addresses issues that are fundamental to complex systems in general. The first kind leads to domain-specific interdisciplinary fields such as cognitive science. The new science of complex system belongs to the second kind of interdisciplinarity. It starts from fundamental open questions relevant to many domains, and searches for methods to deal with them.

These two kinds of interdisciplinarity are complementary and interdependent: any advance in one is valuable for the other. The science of complex systems will develop through a constantly renewed process of reconstructing data from models with a permanent interaction between the two kinds of interdisciplinarity. The reconstruction of the dynamics of complex systems presents a major challenge to modern science but it is becoming increasingly accessible through an accumulating mass of data, combined with the increasing power of computers, leading to theoretical advances in understanding.

This conference follows the one organized in Torino (Italy) in December 2004 with support from the coordination actions EXYSTENCE and ONCE-CS, funded by the Future and Emerging Technologies' unit of the European Commission. ECCS'05 benefits from the same support and is the first conference in an annual series organized by the new European Complex System Society (ECSS) and its Conference Steering Committee.

We hope that the participants will appreciate the beautiful venue of the conference this year, at the Cité Internationale Universitaire de Paris.

Our special thanks to the staff at CIUP for preparing the ground to this conference. We would also like to thank the sponsors of ECCS'05 for making it possible for all the participants to share their enthusiasm and ideas in the most constructive way.

The ECCS'05 Program Committee,
The ECCS'05 Local Organization Committee,
The ECSS Conference Steering Committee.

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External Reviewers

This year, the Program Committee members were the main reviewers of all submitted papers. However, in some occasions, external reviewers were asked to review some papers, and we also want to thank here those following colleagues for their time

Gerard de Zeeuw, University of Amsterdam (Netherlands)
Peter K. Allen , Columbia University (USA)
Pierpaolo Andriani, advanced Institute of Management Research (UK),
Jannis Kallinikos, LSE (UK)

Program

Monday, November 14.

08:00-09:00 : *Registration*

09:00-09:50 : *Introduction*
Michel Rocard, Former French Prime Minister.
Georges Haddad, Director of the Higher Education Division, UNESCO.

9:50-10:20 : *Coffee break* Espace Adenauer

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Chair: Luca Cardelli
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11:10-12:00 : *Invited Speaker 2* Espace Adenauer
Chair: Luca Cardelli
The complexity from a point of view of a physicist,
Giorgio Parisi ***27***

12:00-13:30 : *Lunch*

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Chair: Michel Morvan
Reconstructing the rules of 1D cellular automata using closure systems,
José L Balcázar, Gemma C. Garriga, Pablo Díaz-López ***28***

Hiérarchies algébriques de classes d'automates cellulaires,
M. Delorme, J. Mazoyer, G. Theyssier ***29***

Parallel vs. sequential threshold cellular automata comparison and contrast,
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On stability of computations by cellular automata,
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Universality of Two Dimensional Sandpiles,
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13:30-15:10 : *Biological Modelling 1* Maison du Cambodge
Chair: Tamas Vicsek
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Modeling, inference and simulation of biological networks using Constraint Logic Programming (CLP),
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Emergent properties of metabolic systems and the effect of constraints on enzyme concentrations,

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Towards the modelling of the regulation of early haematopoiesis,
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13:30-15:10 : *Network Modelling 1* Espace Adenauer
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Weighted networks: empirical results and models,
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Lightweight centrality measures in networks under attack,
Giorgos Georgiadis, Lefteris Kirousis ***40***

Universal scaling of inter-node distances in complex networks,
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Altruism 'For Free' using Tags,
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15:10-15:40 : *Coffee break* Espace Adenauer

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Chair: Peter Schuster

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Anders Eriksson, Kristian Lindgren, Torbjörn Lundh ***46***

Reduction of complexity in dynamical systems:,
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Delay model for the mammalian circadian clock,
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Analysis and visualization of large scale networks using the k-core decomposition,
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Data stream computation for monitoring statistics of massive Webgraphs.,
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The design of an artificial society,
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Fame as an Effect of the Memory Size,
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Enabling cooperative behaviour through ICT in organisations,
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Chemotaxis-Inspired Load Balancing,
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Towards a functional formalism for modelling complex industrial systems,
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15:10-15:40 : *Coffee break* Espace Adenauer

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Combinatorial autions: From statistical physics to new algorithms,
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Statistical Physics of Boolean Control Networks,
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Flows of information as the driving force behind chemical pattern formation,
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Concentration and spectral robustness of biological networks with hierarchical distribution of time scales,
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Transition to Coherent Oscillatory Behaviour in a Route Choice Game,
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15:10-15:40 : *Coffee break* Espace Adenauer

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Chair: Vladimir Batagelj

Emergent Group-Level Selection in a Peer-to-Peer Network,
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Gabor Simon, Jozsef Steger, Peter Haga, Istvan Csabai, Gabor Vattay ***118***

Medusa, a functional model of Internet substructure,
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Mining the Inner Structure of the Webgraph,
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Chair: Wolf Singer

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Self-Organizing Communication in Language Games,
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The problem of design in complexity research,
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17:20-19:00 : *Poster Session 3*

Posters

All posters will be displayed during all 3 poster sessions

Satellite Workshops

1. Engineering with Complexity and Emergence (ECE)

Dates : Tue 15 Nov. 14h30-19h, & Wed 16 Nov. 14h30-19h

Organizers : Ozalp Babaoglu, David Hales, Mark Jelasity, Alberto Montresor, Giovanna Di Marzo, and Franco Zambonelli

Location : Maison de l'Espagne

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2. Emergent properties in natural and arificial dynamical systems (EPNADS)

Dates : Thu 17 Nov. 08h30-13h & 14h30-19h

Organizers : Michel Cotsaftis, Cyrille Bertelle, M.A. Aziz-Alaoui, Frederic Guinand, and Marc Rouff

Location : Maison Heinrich Heine

Web site : `http://www-lih.univ-lehavre.fr/~bertelle/epnads05.html`

The aim in this session is to study emergent properties arising through dynamical processes in various types of natural and artificial systems. The session is concerned with multidisciplinary approaches for getting representations of complex systems and using different methods to extract emergent structures. Equations formulation can lead to the study of emergent features such as self organization, opening on stability and robustness properties. Invariant techniques can express global emergent properties in dynamical and in temporal evolution systems. Artificial systems such as a distributed platform for simulation can be used to search emergent placement during simulation execution. Special attention is paid to population dynamics where global emergent properties can be detected.

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3. Embracing Complexity in Design

Dates : Thu 17 Nov. pm

Organizers : Jeff Johnson, Katerina Alexiou, and Theodore Zamenopoulos

Location : David Weill

Web site : `http://www.casa.ucl.ac.uk/ecid/eccs_workshop.html`

In the UK we have an EPSRC funded research cluster called 'Embracing complexity in design'. We are the leaders of this cluster. It is part of a 4 million pound initiative called 'Designing for the twenty first century'. Our cluster is having many activities investigating the impact of complex systems science on the design process and the design of artificial systems. We believe that we can put together a workshop with high quality contributions covering a range of topics covering the area. Close

4. Semiotic Dynamics and Emergence of grammar

Dates : Fri 18 Nov. 08h30-13h & 14h30-19h

Organizer : Luc Steels

Location : Maison Heinrich Heine

The emergence of grammar remains one of the most challenging puzzles of cognitive science. The key question is how there could be true level formation, i.e. how a layer of syntactic and semantic categories and constructions could arise to establish form-meaning mappings. The goal of the workshop is to present either empirical examples of the emergence of new grammatical phenomena or to present computer/robotic simulations of specific examples where this happens. Attempts will also be made to look at level formation in other complex systems (biology, economics) and to see whether a generic theory of level formation is possible.

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5. Common trends in statistical physics, information theory, and combinatorial optimization

Dates : Thu 17 Nov. 08h30-13h & 14h30-19h

Organizers : Marc Mezard (Orsay), Andrea Pagnani (ISI), Martin Weigt (ISI), and Michele Leone (ISI)

Location : Maison du Mexique

Web site : `http://isiosf.isi.it/~cospico/satellite.htm`

The task of understanding and solving hard optimization problems is fundamental in many disciplines in natural as well as in engineering sciences. The problem has also a deep interest in itself as the basic issue of the complexity theory in theoretical computer science. Recently, it has been tackled successfully with methods coming from the statistical physics of disordered systems. This new perspective has brought some new insight into the intrinsic reasons for computational hardness. Stemming from these points, a new field of research is emerging which deals, broadly speaking, with constraint satisfaction networks in systems with many simple interacting variables. It includes some key problems appearing in error correcting codes, stochastic optimization algorithms, typical case complexity and phase transitions, constraint satisfaction, statistical physics of disordered systems, and statistical inference. Researchers with different backgrounds and affiliations, including probability, physics, computer science, statistics, electrical engineering, operation research, have started to realize that many of the central problems in their own fields have similar properties and in some cases similar techniques have been developed independently in these various fields. Examples of similar problems are the satisfiability problem in complexity theory, the spin glass problem in statistical physics, and the low density parity check codes for error correction. Examples of similar techniques are the message passing algorithms, mainly belief propagation, which is heavily used in inference, in error correction and in statistical physics. These are instances of complex interacting systems where emergent properties can be studied rather in detail, and have a potential strong impact for applications. Accordingly to this presentation, the meeting will gather scientists with different backgrounds, and focus on passing messages between disciplines, with a particular focus on the state of the art of European research.

6. Peer-to-peer data management in the Complex Systems perspective

Dates : Thu 17 Nov. 08h30-13h

Organizers : Giovanni Cortese, Stefano Leonardi, Friedhelm Meyer auf der Heide, and Christian Schindelhauer

Location : David Weill

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7. Complex Time-Delay Systems

Dates : Thu 17 Nov. 08h30-13h & 14h30-19h

Organizers : Fatihcan M. Atay

Location : Maison de l'Argentine

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8. Cities and regions as collective intelligence

Dates : Thu 17 Nov. 08h30-13h & 14h30-19h

Organizers : Denise Pumain, Danièle Bourcier, and Jean-Pierre Gaudin

Location : Honnorat

Web site : `http://complexsystems.lri.fr/contents/workshopCities.htm`

Systems of cities and regions are evolutionary territorial organisations. Over hundreds of years they have changed their social content and spatial organisation, according to political and demographic events as well as economic fluctuations. They were both adapting to social change and creating this change. Due to their strong and long lasting interdependences through exchanges of information, artefacts and people, they are co-evolving in a coherent way. They have developed for long under the regulation of political states that they contributed to create and maintain. But recently they have become more and more submitted to new challenges through networks and globalisation. The multinational firms as well as the telecommunication technologies are playing new games with the territories.

The social and environmental impacts of these new pressures are tremendously threatening the sustainability of the cultural variety of urban and regional models that were historically invented in all parts of the world. Can cities and regions develop a collective intelligence for facing the difficult issues that are puzzling each of them?

A possible solution would be to shift from the former self-organisation of cities and regions into systems of cities and regions towards a conscious coordination, for a better adaptation. Discussions with experts in the science of complex systems could help in the process by sharing knowledge and experience.

A lot of information, knowledge and know-how can be shared by towns and regions: data from observatories, different kinds of inquiries under different media, discussion forums about complex issues of communalities, experiments for solving them, cultural productions. The workshop will examine in a first session how such processes of sharing

knowledge can be regulated. A second session will be devoted to the creative commons practices, whose principles could inspire new co-operations. Cities would therefore create networks of collaborative work, including their collective intelligence, as examined in the third session. The workshop is intended to bring together urban actors, social innovators, cultural entrepreneurs, policy makers and scientists.

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9. Multi-Agents for Modeling Complex Systems

Dates : Fri 18 Nov. 08h30-13h & 14h30-19h

Organizers : Salima Hassas and Giovanna Di Marzo Serugendo

Location : Maison de l'Argentine

Web site : `http://liris.cnrs.fr/salima.hassas/MA4CS/`

The multi-agents systems (MAS) paradigm is more and more used as a tool for modeling, simulating or programming complex systems, in different disciplines: mechanics, economy, urbanism, sociology, biology, computer science, etc. Researchers from Complex Systems field, study systems that exhibit complexity as a phenomenon inherent to the system' s nature. They naturally use the multi-agents pardigm as a tool for simulating or modeling such complex systems. MAS researchers focus on the study of communications languages, interaction protocols, agent architectures and MAS methodologies that facilitate the development of multiagent systems. MAS researchs are inspired by many disciplines outside of AI, including biology, sociology, economics, organization and management science, complex systems, and philosophy. This Workshop is aimed to bring together researchers from the MAS field and the complex system field, in order to cross-fertilize research being developped in both fields, and come up with theories, tools , formal operational models and methodologies for MAS approches dedicated to complex systems

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10. Industry facing the complexity

Dates : Fri 18 Nov. 08h30-13h & 14h30-19h

Organizers : Michel Morvan, Paul Bourgine, Daniel Krob, Ralph Dum, Alain Krob and Dominique Luzeaux

Location : Honnorat

Web site : `http://complexsystems.lri.fr/contents/workshopIndustry.htm]`

In modern society, complex industrial systems are just everywhere. Transportation systems or industrial equipments are typical examples of complex systems that we are using or dealing with in everyday life, sometimes without even knowing their underlying technological complexity. "Complex" can refer to the fact that the design and engineering of these industrial systems are incredibly complex and managerial operations. Complex industrial systems are indeed characterized by the intrinsic difficulty of their design, the large number of the sub-systems they involve and the big amount of different technologies and domains they imply.

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11. Dynamical processes on complex networks

Dates : Fri 18 Nov. 08h30-13h & 14h30-19h

Organizers : Alain Barrat and Marc Barthélemy

Location : Maison du Mexique

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12. Complex Chemical System Design

Dates : Fri 18 Nov. 08h30-13h & 14h30-19h

Organizers : John McCaskill and Norman Packard

Location : David Weil

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13. Reverse modeling of biological regulatory networks: expectations and limitations

Dates : Fri 18 Nov. 08h30-13h & 14h30-19h

Organizers : Florence d'Alché-Buc and François Képès

Location : Genopole Evry, (2 rue Gaston Crémieux, 91000 Evry)

Transportation : A free shuttle to Evry will leave la Cité Universitaire at 7:45AM and come back at 6:30PM.

Web site : `http://www.epigenomique.org/~dalche/reverse-modeling/index.html`

List of Abstracts

A panorama of the mathematical theory of dynamical systems

Jean-Christophe Yoccoz
Invited Speaker 1

A dynamical system consists of a phase space together with an evolution law. The goal of the theory is to understand the long term behaviour of the system. The study of stationary regimes is organized around two poles : quasiperiodic behaviour, with a rotation on a circle as paradigmatic model, and chaotic-hyperbolic behaviour, with the doubling map on the circle as paradigmatic model.

The complexity from a point of view of a physicist

Giorgio Parisi

Invited Speaker 2

In this talk I will try to express my view point on why complexity is interesting for physics and why the physical approach is interesting to complexity, A few example will be presented, stressing both the accomplished results and the the open problems, The importance of interdisciplinary research in this context will be stressed.

Reconstructing the rules of 1D cellular automata using closure systems

Gemma C. Garriga,José L Balcázar, Pablo Díaz-López

Complex Systems Methods 1

We consider the problem of identifying the rules conforming the local map of a cellular automaton; we explore the capabilities of a closure-based algorithm for this task. The algorithm has been previously proven to identify an optimal Horn-like formula true for the data, in a very precise mathematical sense.A key property of the algorithm is its ability to handle a sequential structure on the data and lift it to the Horn-like rules, thus making it apt to compare the rules it obtains with the ones that originated the data. The outcomes of the experimentation are described.

Hiérarchies algébriques de classes d'automates cellulaires

M. Delorme, J. Mazoyer, G. Theyssier

Complex Systems Methods 1

Cellular automata are a formal model of locally interacting systems. They are syntactically simple but can present extremely complex behaviors, which make them suitable to study complex systems in general. Many classifications have been proposed in literature [1], often relying on the observation of dynamics. In a first part, we present more recent approaches of algebraic nature based on notions of sub- or quotient systems. A second part is dedicated to new results concerning these algebraic tools. Actually this framework allows to set formal definitions for intuitive global notions and to prove new positive results but also, more interestingly, negative ones. More precisely, we show that modifying local rules may be more powerful in some sense than increasing the number of states; then we illustrate by the construction of an infinite lattice that dynamical universality is more powerful than usual computation universality. Our approaches are to define "natural" but tractable comparison criteria of orbits (also called space-time diagrams in the case of cellular automata) and then to derive comparison criteria of sets of orbits inducing comparisons on cellular automata themselves.

Parallel vs. sequential threshold cellular automata comparison and contrast

Tosic Predrag, Agha Gul

Complex Systems Methods 1

Cellular automata (CA) are an abstract model of a distributed dynamical system, as well as of fine-grain parallelism in computing. In a classical cellular automaton, all the nodes execute their operations in parallel and in perfect synchrony. We consider herewith the sequential version of CA, called SCA, and compare those SCA with the classical, parallel CA. In particular, we show that there are 1D CA with very simple node update rules that cannot be simulated by any comparable SCA, irrespective of the node update ordering. Consequently, the granularity of the basic CA operations and, therefore, the fine-grain parallelism of the classical, synchronous CA, insofar as the "interleaving semantics" is concerned, turns out not to be fine enough. We also study in some detail the properties of the cellular automata whose nodes update their states according to the Majority update rule. Finally, we share some thoughts on how to extend the presented results, and, in particular, we try to motivate the study of genuinely asynchronous cellular automata.

Keywords: analysis and dynamics of complex networks, cellular automata, discrete dynamical systems, configuration space properties, communication models

On stability of computations by cellular automata

Bruno Durand, Andrei Romashchenko

Complex Systems Methods 1

In this paper, we study stability of computations in the presence of random faults (noise). We focus on homogeneous models such as cellular automata. We present a new proof of stability of Toom's 2-dimensional automaton. The arguments are based on the methods from the famous "Positive Rates" paper by P.Gacs. The advantage of our construction is that it explains precisely how errors spread in the computational array and how they are stabilized. Also we show that the same technique can be used to prove correctness of a 3-dimensional fault tolerant computational array.

Universality of Two Dimensional Sandpiles

E. Goles, A. Gajardo

Complex Systems Methods 1

We present a negative result for the Universality of Sandpiles in dimension two. Universality is taken in the sense of Banks -which consists into embed a logical circuit in the cellular space. We prove that in this context it is not possible to cross information, giving by this way a strong argument to say that Sandpiles are not Universal in dimension two; at least for the usual neighborhoods. Nevertheless, if a neighborhood of radius two is used, the Universality is possible, which is proved.

Shape spaces in formal interactions

Davide Prandi, Corrado Priami, Paola Quaglia

Biological Modelling 1

In recent year formal methods from concurrency theory and process calculi have gained increasing importance in modeling complex biological systems. In this paper propension to biological interaction, as seen by the shape spaces theory, is given a linguistic interpretation. Entities from the living matter are viewed as terms of a formal concurrent language of processes with typed interaction sites. Types are strings, and interaction depends on their distance. Further, the language is associated with syntax-driven rules that permit the inference of the possible computational behaviours of the specified biological system. This approach leads to the use of all the methods and techniques developed in the context of formal languages (e.g. language translation, model checking, ...),opening new ways for studying complex biological systems.

Modeling, inference and simulation of biological networks using Constraint Logic Programming (CLP)

E. Fanchon, F. Corblin, L. Trilling

Biological Modelling 1

(1) Institut de Biologie Structurale, CNRS-CEA-U. Joseph Fourier, 41 rue J. Horowitz, 38027 Grenoble Cedex 1. (2) LSR-IMAG, U. Joseph Fourier, BP 53, 38041 Grenoble Cedex 9.

Biology is now entering a new era in which molecular components have to be integrated into a system in order to reach new levels of understanding. Our objective consists in developing a computing tool allowing on one hand to infer models from properties which can be incomplete and qualitative, on the other hand to perform simulations or predictions starting from these (partially known) models. Such a tool should allow biologists to specify a network from the available data in order to obtain a class of models consistent with the data. More generally, the tool should be highly flexible to support the exploration of model properties in the context of incomplete knowledge.

The concept of interaction network is a fundamental one in systems biology. Our work is based on the "asynchronous multivalued logic networks" proposed by R. Thomas, E. H. Snoussi et al. (1,2). This formalism has been used to model genetic, neuronal and immunological networks. Formally, it can be viewed as a discrete abstraction of a special class of Piecewise-Linear Differential Equations (PLDEs). It allows a qualitative analysis of the dynamical behavior of such differential systems. Another benefit of this type of formalism lies in the discreteness which lends itself very well to computational implementations. The interaction graph associated to the PLDE system defines the architecture of the network. The parameters characterize the strength of the (non-linear) interactions. Recently, this formalism has been extended by de Jong et al. (3) to take into account the so-called 'singular states' and 'sliding modes'. Singular states are states of reduced dimensionality located at thresholds or intersection of thresholds, and sliding modes are trajectories that slide along a threshold (or intersection of thresholds). This extended formalism is sound in the sense that every continuous trajectory of the original PLDEs is associated to a qualitative (discrete) trajectory of the discrete network.

We show that logic networks of this type can be described formally and exploited via a Constraint Logic Programming (CLP) implementation. The CLP approach rests on the cooperation of solvers on various fields (tree, list, rational, real, boolean). Its advantages are that (i) the implementation is expressed in a very similar way to the formal specification, thus guaranteeing the correctness of the implementation, (ii) it is iterative - when new information become available, new constraints can be added to reduce further the space of possible models; (iii) many different queries can easily be posed to this formal specification due to its logical form. For example, queries equivalent to simulation (parameters known / computation of behavior) as well as inference of model parameters (information on behavior / computation of parameter values). Situations that are intermediate between simulation and inference are frequent. Indeed, the experimental characterization of behaviors (trajectories in phase space) is itself often partial, and a current challenge in the field is to be able to exploit all available partial knowledge to get more precise models.

These principles are applied to the study of adhesion between human endothelial cells. The work is done in collaboration with experimental biologists (4). A submodel extracted from a larger network is presented (2 variables, 7 discrete parameters).

We explain briefly the architecture of the implementation in the declarative language prolog IV (5). A preliminary version of the tool has been published (6) which did not take into account the existence of sliding modes. This was too restrictive and a full implementation is now available. A set of logical predicates defines the discrete transition rules corresponding to the type of networks studied (asynchronous multivalued networks with singular states). A given network is described by a set of discrete equations and a set of inequalities between parameters; these entities are derived from the architecture of the given network (number of nodes/genes and pattern of interactions: activation or repression of gene gi by gene gj with threshold ij). Observational knowledge is also described by constraints (logical predicates). This can be a direct measurement of a kinetic parameter, or knowledge about the behaviour of the system, such as, for example: "when the system is perturbed and set into state Sp, it returns to stable state S0 by going through at least one state in which the concentration of such protein P is above such threshold. As illustrated in this example, this knowledge can be incomplete. It can nevertheless be formalized into a logical expression (after discretization) and exploited to make deductions about, for example, the possible values of the model parameters. As said in (ii) above, each new observation allows to add a new constraint which, in general, reduces the space of solutions. Likewise, hypotheses can be expressed as formal prolog queries in order to test their consequences. This provides a flexible tool to query model properties or, more generally, properties of a given network architecture.

In the cell adhesion study, we exploit behavioral information resulting from the observation of the response of the cell culture after a perturbation. To illustrate the strength and the flexibility of the CLP approach, results will be commented concerning : some general properties of the model; the existence of stationary states; and the use of behavioral information to reduce the space of possible models. In particular, it is shown that imposing the existence of a path from the perturbed state to the adherent state eliminates a large number of models. If times permit, results from larger published models of developmental biology will also be presented: segmentation of the drosophila embryo (7) and the drosophila gap-gene system (8).

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Emergent properties of metabolic systems and the effect of constraints on enzyme concentrations

Delphine Sicard, Christine Dillmann, Julie Fiévet, Grégoire Talbot, Laure Grima, Dominique De Vienne

Biological Modelling 1

Cell functioning and evolution rely on complex metabolic systems constituted of many components that communicate and interact with one another through networks. Several metabolic theories have been developed to predict the emergent properties of metabolic systems. However, the effects of constraints on the properties of such systems and on their evolution under selection have been poorly studied, whereas cell necessarily functions with limited resources. Using both theoretical and experimental approaches, we have studied the effect of constraints on enzymes concentrations and their consequences on metabolic fluxes and fitness. The theoretical developments were based on the metabolic control analysis, which provides a framework linking enzymatic parameters, such as enzyme activities, to a macroscopic output of the system, the metabolic flux. We analysed the effect of competition for space and energy by introducing an overall cost for producing enzymes or by limiting the range of variation of the enzymes concentration in a pathway. In addition, we studied the effect of co-regulation by introducing correlation between enzyme concentrations. Under those conditions, our modelling revealed new emergent properties of metabolic fluxes. First, the total enzyme concentration allocated to a pathway, which is positively correlated with flux, can respond to selection. Second, competition leads to a distribution of enzyme concentrations within the pathway that maximizes metabolic flux: selection can act to increase low enzyme concentrations and to decrease high enzyme concentrations until an optimal level. Third, co-regulation leads to metabolic flux consistently lower than the one obtained with competition alone, suggesting that co-regulation may be costly. Finally, a biochemical model for hybrid vigour can be derived. In vitro reconstruction of the first part of glycolysis and in vivo analysis of various Saccharomyces cerevisiae strains were carried out to test these predictions. In vitro experiments allowed us to estimate global enzymatic parameters and confirmed that a distribution of enzyme concentrations that optimizes flux can be predicted. "Test tube genetics" performed by varying in vitro enzyme concentrations allowed us to corroborate the metabolic mechanism for hybrid vigour. Finally, proteomics and biochemical analysis of a collection of S. cerevisiae strains showed that there is genetic variability at two levels of cell integration, enzyme concentrations and glycolytic fluxes, and that selection can act to increase or decrease flux. In conclusion, taking into account constraints on enzyme concentrations allowed us to develop new modelling and in vitro tools for metabolic optimization, and gave new insight in the understanding of metabolic system evolution.

Towards the modelling of the regulation of early haematopoiesis

Sylvie Troncale, David Campard, Fariza Tahi, Abdelghani Hachami, Janine Guespin-Michel, Jean-Pierre Vannier

Biological Modelling 1

Hematopoietic stem cells (HSCs), can either remain quiescent, with a constant and low rate of self renewal, or become committed to differentiate into hematopoietic cell lineages. The switch between those two fates can be seen as the switch from one stationary state to another in a dynamic process (epigenetic switch). The control of early hematopoiesis is quite complex, involving several factors and feedback circuits. Its study needs modelling, which was not straightforward, since it requires to take into account both consumption and production of resources as well as discreet and continuous time. This was performed using Hybrid Functional Petri Nets (HFPN). The model presented simulates the results obtained in vitro, where the quiescent stem cells are rapidly lost, and shows the potentiality of HFPN to model complex systems such as the regulation of hematopoiesis. In silico simulations can now be performed to study the mechanism responsible for the epigenetic switch.

Weighted networks: empirical results and models

Marc Barthelemy, Alain Barrat,, Alessandro Vespignani

Network Modelling 1

We review the main tools which allow for the statistical characterization of weighted networks. We then present two case studies, the airline connection network and the scientific collaboration network, which are representative of critical infrastructures and social system, respectively. The main empirical results are (i) the broad distributions of various quantities and (ii) the existence of weight-topology correlations. These measurements show that weights are relevant and that in general the modeling of complex networks must go beyond topology. We propose a model which provides an explanation for the features observed in several real-world networks. This model of weighted network formation relies on the dynamical coupling between topology and weights, considering the rearrangement of weights when new links are introduced in the system. Finally, we discuss the effects of spatial constraints on the evolution of weighted networks.

Lightweight centrality measures in networks under attack

Giorgos Georgiadis, Lefteris Kirousis

Network Modelling 1

In this paper we study deliberate attacks on the infrastructure of large scale-free networks. These attacks are based on the importance of individual vertices in the network in order to be successful, and the concept of centrality (originating from social science) has been already utilized in their study with success. Some measures of centrality however, as is betweenness, have disadvantages that do not facilitate the research in this area. We show that with the aid of scale-free network characteristics such as the clustering coefficient we can get results that balance the current centrality measures, but also gain insight in the workings of these networks.

Universal scaling of inter-node distances in complex networks

J.A. Holyst, J. Sienkiewicz, A. Fronczak,, P. Fronczak,, K. Suchecki, P. Wojcicki

Network Modelling 1

Faculty of Physics and Center of Excellence for Complex Systems Research, Warsaw University of Technology, Koszykowa 75, PL-00-662 Warsaw, Poland

We have studied dependence of distances between nodes in various networks and degrees of such vertices. We have observed that the mean distance between two nodes of degrees k_i and k_j equals to l_ij=A-B log(k_i k_j). The relation holds for the following systems: Erdos-Renyi random graphs, scale-free Barabasi-Albert models, science collaboration networks, biological networks, Internet Autonomous Systems and public transport networks. A simple heuristic theory for this scaling law is presented. Corrections due to the network clustering coefficient and node degree-degree correlations are taken into account.

Behaviour as a Complex Adaptive System

Stefano Nolfi

Social Modelling 1

In this paper we will explicit the complex system and adaptive nature of behaviour. The complex system nature of behaviour derives from the fact that behaviour and behavioural properties are phenomena that occur at a given time scale and result from several non-linear interactions occur-ring at a smaller time scale. Interactions occur in time (i.e. consists of a sequence events in which future interactions are constrained by preceding interactions) and might eventually consists of a vector of concurrent interactions. Moreover we argued that behaviour might involve several emergent dynamical processes, hierarchically organized, that affect each others bottom-up and top-down. The adaptive system nature of behaviour derives from the fact that, due to the very indi-rect relationship between the properties of the interacting elements and the emergent results of the interactions, behavioural systems can hardly be designed while can be effectively synthesized on the basis of a self-organization process (in which properties emerging from interactions can be discovered and retained through an adaptive process based on exploration and selection). These two claims will be demonstrated in two concrete examples involving mobile robots in which non-trivial individual and collective behaviour have been synthesized through an evolutionary tech-nique.

On the Dynamics of Communication and Cooperation in Artificial Societies

A.E Eiben, M.C. Schut, N. Vink

Social Modelling 1

This paper compares two fundamental building blocks of complex interaction-based systems: communication and cooperation. We investigate the effectiveness of communication in an environment where the need for cooperation is scalable as well as the available resources. Several aspects of communication are considered: firstly, we compare a centralised with a decentralised communication protocol; secondly, we compare a population that always communicates with one where the entities can (evolutionary) learn to communicate. This work is part of a larger project whose main goal is to investigate the emergence of cooperation and communication in response of (scalable) environmental challenges. Our application context is an artificial society, i.e., a simulation of a societal system that was inspired by the classical SUGARSCAPE that embodies a bottom-up approach to investigate complex effects that do not necessarily have complex causes.

Altruism 'For Free' using Tags

David Hales

Social Modelling 1

A number of recent models have shown how "tags" [11] (arbitrary observable phenotypic markers) can produce altruistic behaviour between initially selfish individuals in an evolving system [15, 19, 20, 23]. These models tend to use tag and tolerance values associated with each individual and non-standard "donation games". Here we outline a simpler approach in which individuals play the single round Prisoner's Dilemma (PD) game. Contrary to previous tag models [18, 19, 23], altruism is demonstrated in the single round game without forced altruism between those with identical tags or knowledge of previous interactions. The system is reverse-scalable (the more individuals in the population the quicker altruism emerges) and robust to noise. This "altruism for free" property has already been adapted and applied into robotic scenarios [21], peer-to-peer networks [22] and implemented in deployed agent-based platforms [25].

Invariant grids: method of complexity reduction in reaction networks

A Gorban, I Karlin, A Zinovyev

Biological Modelling 2

Complexity in the description of big chemical reaction networks has both structural (number of species and reactions) and temporal (very different reaction rates) aspects. A consistent way to make model reduction is to construct the invariant manifold which describes the asymptotic system behavior. In this paper we present a discrete analog of this object: an invariant grid. Invariant grid is introduced independently from the invariant manifold notion and can serve itself to represent the dynamic system behavior as well as to approximate the invariant manifold after refinement. The method is designed for pure dissipative systems and widely uses their thermodynamic properties but allows also generalizations for some classes of open systems. The method is illustrated by two examples: the simplest catalytic reaction (Michaelis-Menten mechanism) and the hydrogen oxidation.

War of attrition with implicit time cost

Anders Eriksson, Kristian Lindgren, Torbjörn Lundh

Biological Modelling 2

Many animals have a formidable arsenal of teeth, hooves or horns, and violent fights among these animals often result in death or serious injury. It is thus perhaps not surprising that there is a wide variety of ways in which animals settle disputes over food, mates or territory without resorting to violence. A common theme in such contests, is that the animals display until one of them gives up, leaving the prize to the animal that endured. It is then safe to assume that a cost can be associated with the length of the display, since otherwise animals would wait indefinitely.

Maynard Smith and Price (1974, J. Theor. Biol., 47, p. 209) pioneered the waiting-game as a model of wars of attrition. In this game, there is a prize worth one unit of fitness, that goes to the winner of the contest. For instance, the prize could be a desirable territory, and the fitness is then the expected number of offspring in the territory. The loser has to settle for a less attractive territory, which entails $k < 1$ fitness units. It is assumed that the contest costs c fitness units per unit of time, and both contestants pay the cost until one of them gives up, losing the contest. Making standard assumptions of the mating structure of the population, e.g. abundance of waiting-times in the population obey the replicator dynamics, this model has been thoroughly investigated in the literature.

The standard waiting-game assumes that all individuals in the population play the same number of games per unit of time. We investigate the co-evolutionary dynamics of a population where players engage in wars of attrition, where the time cost is not explicitly given, but instead depends implicitly on the strategies of the whole population (Eriksson *et al.* 2004, J. Theor. Biol., 230, p. 319). Each player participates in a series of games, where those prepared to wait longer win with higher certainty but play less frequently. The players in the population can be in one of two states: either they are involved in a contest with another player, or they are available for entering a new contest. The activity of the players in the population, during a generation, is modelled as a process that randomly selects pairs of available players to engage in contests. This leads to an implicit time cost, which is higher for players involved in longer games.

The model is characterised by the ratio of the winner's score to the loser's score, in a single game. The fitness of a player is determined by the accumulated score from the games played during a generation. We derive the stationary distribution of strategies under the replicator dynamics. When the score ratio is high, we find that the stationary distribution is unstable, with respect to both evolutionary and dynamical stability, and the dynamics converge to a limit cycle. When the ratio is low, the dynamics converge to the stationary distribution. For an intermediate interval of the ratio, the distribution is dynamically but not evolutionarily stable.

We find that our model has immediate implications for two earlier models that takes implicit costs into account. Hines (1977, J. Theor. Biol., 67, p. 141) proposed a model in which animals forage for food. When an animal finds a piece of food, with a given probability it may consume the food undisturbed, otherwise it enters a war of attrition for the food parcel. Here, it is assumed that engaging in competitions prevents foraging, so that there is a trade-off between the probability of winning a contest and the time spent foraging. It turns out that we can capture the evolutionary dynamics of this model within our model (assuming replicator dynamics), although the original model has four parameters and our model only has one. Cannings and Whittaker (1994, J. Theor. Biol.,

167, p. 397) studied a modification of the model by Maynard Smith, similar to the one we present. They suggest a mechanism that implies more games for players that finish faster, but keep the explicit time cost. Unlike our model, their approach is restricted to positive integer waiting-times. Here, we are able to apply our results in the limit of long games and to calculate the stationary distribution analytically.

Finally, we note that the dynamics of the population during a generation modelled here can be useful for studies of game-theoretic problems in general; one example could be the study of the Prisoner's Dilemma game with refusal in which a player may quit a repeated game when encountering a deviation from cooperation. Here, the threat to abandon is equivalent to an outside option, where the value of the option is again implicit: it depends on the composition of the population.

Reduction of complexity in dynamical systems:

Tri Nguyen-Huu, Pierre Auge, Christophe Lett, Jean-Christophe Poggiale

Biological Modelling 2

Realistic ecological models must take into account processes which are going on in different levels: the individual, the population, the community level. This leads to mathematical models involving many variables and parameters, which are usually difficult to handle. In many cases, the time scales associated to processes going on at each level are different. At the individual level, the time scale is typically the day, at the population level, the year and at the community level, the evolutionary time scale. Aggregation methods take advantage of these time scales to build a reduced model governing a few global variables at a slow time scale. We present an application to a spatial model of a host-parasitoid community. We consider a square two-dimensional grid of spatial patches. The initial model (complete model) is described by a huge number of equations (20000 for a 100x100 square grid). We show that when the dispersal process becomes fast in comparison with local interactions, the dynamics of the metapopulation can be described by a two-equation model governing the total insect population densities on the grid (aggregated model). We present numerical simulations of both models. Our results show a good agreement between asymptotic behaviour of the complete model and the aggregated model for small differences in time scales. This allows using the aggregated model to make valid predictions about global host-parasitoid spatial dynamics.

Delay model for the mammalian circadian clock

K. Sriram, Gilles Bernot,, François Képès

Biological Modelling 2

A circadian rhythm is an oscillation with a period of approximately 24 hr, which exhibits entrainment to environmental light dark (LD) cycles and shifting of phase by light stimulation. Even though many theoretical models with ordinary differential equation (ODE) have been proposed based on the biochemical mechanisms for circadian rhythms [1], relatively few studies have been carried out with delay differential equations (DDE) [2, 3, 4, 5]. Delayed feedbacks are common and occur naturally in many biological systems and in particular, the regulatory networks of circadian rhythms. Here, we propose a delay model for the circadian rhythm of the mammals [6] with three dynamical variables that has three delayed positive and negative feedback loops.

On Small-World generating Models

Michael Kaufmann, Katharina A. Lehmann, Hendrik Post

Network Modelling 2

What exactly is a small-world? Watts and Strogatz define every network with a high clustering coefficient and a low diameter to be a small-world. We will show here that for this classic definition there are some counter-intuitive examples where either false-negative or false-positive classifications of network models occur.

To bring forth a new definition for small-world generating network models, we will first introduce a slightly varied small-world network model. This model is based on a regular grid graph and an added G(n,p) random graph. We will then give an upper bound for the diameter of the generated networks dependent on p and n. This upper bound is generalized to combinations of a so-called 'locally clustered' graph family with a G(n,p) graph. On the basis of this general method we propose a new definition for small-world generating models.

Counting loops in random graphs and real-world networks

E. Marinari, R. Monasson, G. Semerjian

Network Modelling 2

Data gathering in fields as diverse as social sciences, biology or Internet measurements, has provided an impressive amount of knowledge on the topology of the underlying interaction networks (i.e. graphs) in these domains. A crucial direction of research is now to identify characteristic features of these networks, in particular in view of(in)validating proposed modelings.

These features can be roughly classified in two categories. "Local"ones, for instance the connectivity distribution and the clustering coefficient, can be efficiently computed on any graph, even if very large. However the most distinguishing features might be "global",involving large patterns of the network. Identifying and counting these patterns becomes a very demanding task when their sizes increase, prohibiting in general the use of exact counting algorithms. Among these global features, a very natural one is the distribution of the lengths of the circuits (closed loops) in the graphs. Whereas it is quite easy to measure the number of short loops (triangles for instance), this becomes very hard when the loops studied have a length of the order of the size of the network.

We have developed an alternative approach to this counting problem, based on its reformulation in terms of a statistical mechanics model, which is treated within the Bethe approximation. The outcomes of this method are of two types. On the one hand, it yields an efficient approximate counting algorithm based on a message passing procedure, with a computational cost linear in the size of the graph. On the other hand, we have also obtained results on the typical number of long circuits in ensembles of random graphs, in particular in situations where usual probabilistic methods fail because of large fluctuations in these numbers.

Analysis and visualization of large scale networks using the k-core decomposition

Ignacio Alvarez-Hamelin, Luca Dall'Asta, Alain Barrat, Alessandro Vespignani

Network Modelling 2

In recent times the informatics revolution has allowed the systematic gathering and handling of data sets on several large scale networks, leading to the large scale analysis of their detailed structure features. In particular, mapping projects of the WWW and the physical Internet offered the first chance to study the topology and traffic of large-scale networks. Gradually other studies followed describing population networks of practical interest in social science, critical infrastructures and epidemiology. Large scale networks, however, face us with unprecedented scientific challenges. The uncovering of the basic hierarchies present in networks is particularly difficult because of the entangled nature of their structure. The identification of the backbones and the central elements of the systems is hindered by the complex interplay of connectivity patterns, traffic flows and geographical, social and economical attributes of the network's elements. For these reasons, a large research effort is tackling the challenge of providing effective visualization and analysis tools for very large scale networks.

Here, having in mind as primary focus the Internet at various granularity level, we use the k-core decomposition in order to provide insights on the hierarchical structure of large scale networks. The k-core decomposition is obtained by recursively removing all the nodes of degree less than k, until the degree of all nodes is larger than or equal to k. Nodes can be therefore assigned a coreness number indicating the value k at which the node is removed. This procedure defines sets of nodes with coreness k. The larger the coreness and the larger is the degree as well as the centrality of the node in the network. We use the k-core decomposition to define subgraphs that progressively uncover the most interconnected and central region of the original network. The method can be used to study the variation under this transformation of the topological and correlation properties of the subgraphs. Strikingly, we observe for scale-free graphs such the Internet at the Autonomous System and Router level a global invariance of the statistical distributions characterizing degree and betweenness, and of the correlation and clustering spectrum. The k-core decomposition appears therefore as a suitable way to define a pruning procedure equivalent to a change of scale preserving the statistical properties of graphs.

Motivated by the previous observation we propose a visualization algorithm based on k-core decomposition. The running time of the algorithm grows only linearly with the size of the network, which allows to visualize very large networks, e.g. a network of 1M vertices and 650 000 edges is processed in lees than 4 minutes on an AMD Athlon(TM) XP 2800+ at 2GHz. The obtained visualization tool is used to perform a graphical analysis of several real and computer generated large scale networks. The k-core visualization allows the identification of different classes of networks as well as the understanding of the hierarchical arrangement of networks. The distinction between networks with seemingly similar properties is simply achieved by looking at the generated layout of the visualization algorithm. The proposed visualization algorithm thus appears as a convenient method for the general analysis of complex large scale networks and the study of their architecture.

Keywords: network analysis, k-cores, Internet, visualization

Data stream computation for monitoring statistics of massive Webgraphs.

Luciana S. Buriol,, Debora Donato, Stefano Leonardi, Tobias Matzner

Network Modelling 2

Computing statistical and topological properties of large graphs can be a time consuming task if the graph does not fit in main memory. The webgraph, the graph generated by the link structure of Web pages, is an example of such massive graphs. Performing measures on large graphs consuming little time and memory can be prohibitive if exact results are required. Data stream algorithms seems to provide a good trade-off between quality of results and system requirements, as time and space. Moreover, in some applications, we require the dynamic update of the results according to the link information seen so far, rather than merely returning the final computation. In this work we report on data stream algorithms for monitoring statistical properties of the webgraph. We started computing the indegree distribution of a graph obtained as a stream of edges. More specifically, we maintain the indegree rarity of the graph, that is the ratio between the number of nodes that have a given indegree over the total number of different nodes seen in the stream so far. We implement a rarity algorithm proposed in the literature and show experimentally that the results approximate very well the real value with very limited use of memory and time. Moreover, we show an improved approximation by using a different family of hash functions. When considering some structure in the stream, other properties can be computed. For example, reading the stream as an adjacency list of edges, the same rarity algorithm is used for enumerating important classes of motifs, such as small bipartite cliques. We present experimental results for the distribution of indegree and bipartite cliques of size three. We estimate the quality of the results by comparing with the exact values provided by an optimal implementation. We test our algorithms on crawls of the Web collected by the consortium and by other international projects, and on important networks living in the Web such as the graph of the Wikipedia database, the distributed on-line Encyclopidia.

Distributed Algorithms for Data Propagation in Deeply Networked Wireless Sensor Devices

Ioannis Chatzigiannakis, Sotiris Nikoletseas, Paul Spirakis

Network Modelling 2

Wireless sensor networks are comprised of a vast number of ultra-small fully autonomous computing, communication and sensing devices, with very restricted energy and computing capabilities, which co-operate to accomplish a large sensing task. Such networks can be very useful in practice in applications that require fine-grain monitoring of physical environment subjected to critical conditions (such as inaccessible terrains or disaster places).

Very large numbers of sensor devices can be deployed in areas of interest and use self-organization and collaborative methods to form deeply networked environments. Features including the huge number of sensor devices involved, the severe power, computational and memory limitations, their dense deployment and frequent failures, pose new design and implementation aspects. The efficient and robust realization of such large, highly-dynamic, complex, non-conventional environments is a challenging algorithmic and technological task.

In this work we consider certain important aspects of the design, deployment and operation of distributed algorithms for data propagation in wireless sensor networks and discuss some characteristic protocols, along with an evaluation of their performance.

Heterogeneity and predictability of global epidemics

V. Colizza, A. Barrat,, M. Barthelemy,, A. Vespignani

Social Modelling 2

We investigate the role of the large scale properties of the airline transportation network in determining the global diffusion pattern of emerging disease. We study a stochastic epidemic modeling framework that considers the complete International Air Transport Association 2002 database complemented with census population data. We adopt measures used in information theory to analyze quantitatively the level of heterogeneity and predictability of the epidemic pattern and its relation with the network's structure. The level of spatio-temporal heterogeneity of the spreading pattern is globally characterized and found to be a direct consequence of the network statistical complexity. The epidemic pattern predictability is quantitatively determined and traced back to the occurrence of epidemic pathways defining a backbone of dominant connections in the disease spreading. The presented results provide a general framework for the analysis of containment policies and epidemic risk forecast.

The design of an artificial society

Nigel Gilbert, Stephan Schuster, Lu Yang

Social Modelling 2

The New and Emergent World models Through Individual, Evolutionary and Social learning (NewTies) project is concerned with emergence and complexity in socially-inspired artificial systems. It is developing a large computational system consisting of an environment and a population of agents. The main goal of the project is to realize an evolving artificial society whose members are capable of exploring the environment and developing their own images of this environment and the society through interaction and cooperation. A subsidiary objective is to develop the system so that it can be used as an experimental testbed to examine hypotheses originally formulated as explanations of phenomena observed in human societies.

In this presentation, we shall consider what is involved in designing this system of agents and environment. The design problem comes from the need to steer between, on the one hand, producing a system which attempts to simulate so many of the characteristics of humans that understanding the system is impossible or, on the other hand, designing a system that is so simplistic that any inference to human societies is at best tenuous. The issue is made more difficult by our prior assumption that most features of human societies are emergent from social interaction, and that interaction itself is only achieved through the social evolution of the means of communication.

Our solution has been to design an environment containing rather few different types of object, each with carefully chosen properties (e.g. building blocks with which agents can construct either 'roads' to ease their mobility, or 'walls' to provide fortifications) and to give the agents a small number of primitive actions (e.g. move, pick up object, talk). The expectation is that agents will be able to create a rich behavioural repertoire by composing the primitive actions, and that, despite there being only a few different types of object, the environment will be complex enough to encourage the agents to exercise this repertoire.

The presentation will describe the environment and the agents' abilities and explain how and why they were designed in this way. In order to show how the system could eventually be used to examine social theories about human societies, examples will also be given of 'scenarios' that can be created that emulate the circumstances in which 'simple' societies have lived, as described by social anthropologists.

Fame as an Effect of the Memory Size

Haluk Bingol

Social Modelling 2

This paper investigates the effect of the memory size to fame. A population of individuals of the same memory size is considered. A simple recommendation model is defined based on the memory of the individuals, the social network and the population memory. Recommendation process changes the content of the memory. As the ratio of memory size to population size decreases, a self-organized pattern emerged in who-knows-who graph. Majority of the people become unknown yet a few become very famous. This could be a model for fame and memory.

The evolution of free/libre and open source software contracts : a dynamic model

Jean-Batiste Soufron, Jean Sallantin

Social Modelling 2

There has been an increasing interest from lawyers and social scientists for the development of legal tools adapted to share knowledge. To this end, several contractual tools have been proposed for allowing the best uses of intellectual property law, notably Free/Libre Open Source Software Licenses (or FLOSS Licenses). The legal applicability of these Licenses have been well studied but there has been no model proposed to explain their creation and their evolution. In this view, it is of utermost interest to propose tools enabling people to understand the processes at work and use them for their best interest in contractual negotiations. Existing approaches in community findings are either based on expert systems or on classical contractual approach. There has been roughly no attempt to link different Licenses between them under a dynamic model. Actually, the various study of FLOSS often concentrates on a very small number of Licenses. We give a formal framework for understanding the creation of these contracts and their evolution, using a model based on the realistic approach that contracts are legal answers to problems raised by users, and that new contracts are obtained by combining the clauses of ancient ones or by creating new ones. Suggesting that this leads to the emergence of a legal domain throught the abduction of its terms and the induction of the constraints linking them, we eventually propose to precise this model to help people to better negotiate Licenses and contracts. Our main source of data is Sourceforge, the world's largest Open Source software online repository providing free hosting to nearly 100 000 projects. This data is summarized and publicly accessible on their website but we precise our study using the various mailing-lists associated with the projects. Eventually we add some data from external FLOSS sources when it is available.

Enabling cooperative behaviour through ICT in organisations

Jostein Engesmo

Social Modelling 2

This paper addresses a new way of making sense of behaviour in organisations mediated by information and communication technology (ICT). By studying micro-level interactional processes and relating this to macro-level patterns of interaction, mutually influencing each other, I suggest the importance addressing these issues in projects with the intention of changing behaviour through the employment of ICT.

The empirical case studies are from the Norwegian hospital sector, where the electronic patient records (EPR) is employed in organisational change projects. The first case is a project of moving from oral face-to-face nursing hand-over to hand-over employing EPR for asynchronous communication. The second case is a project of introducing a module of EPR for nurses to document plans, actions and evaluations in their practical work. Both cases have been followed over a period of 10 months. During this time 42 semi-structured interviews with different stakeholders have been carried out. In addition participant observation of everyday practice and different meetings has been carried out comprising approximately 300 hours.

To conceptualize how one actor is interconnected with other actors in the complex social system of organisations, the theory of symbolic interaction and in particular the thoughts of Mead on the fundament of human interaction, is employed [1,2,3]. Behaviour of the individual is constructed taking into account other actors in a continuous and dynamic process. Using ICT, I argue that actors taken into account are distributed in the time and space dimensions. Hence, the interactional processes that are so strong in face-to-face interaction are not absent when it comes to interaction through ICT. This perspective needs empirical investigation, it is argued. From the cases, it is shown that when EPR is employed for nursing hand-over, actors reflect more on the needs of the next nurse reading it than before, therefore including more information, and spending more time documenting. Further, even if these micro-level interactional processes are characterized of local situatedness and unpredictability [4], patterns of interaction emerge that are orderly and random at the same time [5,6].

In ICT change projects behaviour is usually seen through lenses of system theory, controlled through system design, e.g. syntax or sequences for processing information. Here, the action of the individual is connected to other individuals from the perspective of designers and planners of the system. In contrast, in this paper it is argued that it should be realised that the action of the individual is not possible to control, nor is it desirable to do so. The interconnections of actors in complex systems is not something that designers or managers prescribe from the outside, but something that "exists" in the minds of the individual actors continually aligning their actions and interactions, as argued above. This cooperative behaviour is not locked to some definite system, but remains adaptive for further modifications in connection with other agents in the social system. Accordingly, change is seen as being enabled, as through the lenses of complexity theory [7,8,9].

Through the case studies I discuss and show how individual and cooperative behaviour can be understood based on the premise of 'taking others into account' and how the employment of ICT leads to changing patterns of interaction on an overall level working back on the micro level interaction. Further, I show how the failure of addressing these issues jeopardized the success of the projects.

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An electronically controlled microfluidics approach towards artificial cells

Uwe Tangen,, Patrick F. Wagler, Steffen Chemnitz, Goran Goranovic,, Thomas Maeke, John S. McCaskill

Bio Inspired Methods 1

This work focuses on the application of on-line programmable microfluidic bioprocessing as a complementation vehicle towards the design of artificial cells. The electronically controlled collection, separation and channel transfer of the biomolecules are monitored by a sensitive fluorescence setup. Two different physical effects, electrophoresis and electro-osmotic-flow, are used to allow for a detailed micro-control of fluids in micro-reaction environments. A combination of these basic electronically controlled two input reaction chambers makes combinatorial fluidic-networks and indefinitely sustained biochemical or chemical reaction-networks feasible. Experimental data showing the power of this approach is presented. Not only does this processing power pave the way towards the development of artificial cells (using a technology to complement not yet established autonomous metabolic or replication capabilities) but it also opens up new processes for applications of combinatorial chemistry and lab-on-a-chip biotechnology todrug discovery and diagnosis.

Chemotaxis-Inspired Load Balancing

Geoffrey Canright,, Andreas Deutsch,, Tore Urnes

Bio Inspired Methods 1

We present an approach to the problem of load balancing on networks of nodes. Our approach is inspired by the phenomenon of negative chemotaxis in living systems. We use a diffusing signal (which is emitted by load, and moves faster than the load) to guide the movement of load towards the balanced state. Our reference system (for comparison) is unguided, diffusing load, moving at the same speed. Our tests show that the chemotaxis system can give large improvements over the reference system in convergence speed, as well as showing much reduced sensitivity to variations in network topology and in initial load distribution.

Container growth and replicator dynamics in pre-biotic chemistry

Olof Görnerup, Martin Nilsson Jacobi, Steen Rasmussen

Bio Inspired Methods 1

At the transition from non-living to living matter, the distinction between genotype and phenotype, as well as genome replication and ontogeny, is not clearly defined. In primitive organisms, without central control of genome replication, a conflict between selfishly reproducing genes and genes useful for the replication of the whole organism occurs. This raises the question of how, and when, such systems can evolve into contemporary organisms with well-defined separation between the genotype and phenotype, and a coordinated replication.

We study the evolutionary dynamics of systems consisting of self-assembling container aggregates that contain populations of self-replicating information carrying molecules: proto-genes. The aggregates can be viewed at primitive proto-organisms. Their genome consists of an evolving population of proto-genes, which in a steady state may form a quasi-species. The aggregates themselves grow by successively incorporating new building blocks. Eventually the aggregates become unstable and spontaneously divide, whereby a replication of the proto-organism has occurred. The production of new building blocks (e.g. amphiphilic polymers) is controlled by the proto-genes (e.g. through an electron charge transfer process). A strain's ability to self-replicate and its chemical properties critical to the growth of the aggregate are assumed to be uncorrelated. Certain strains of proto-genes are efficient as self-replicators, whereas other strains are more active in the production of new building blocks, and thereby contribute to the reproduction of the container. The evolution of the system as a whole is then characterized by a conflict reminiscent of group selection. The central question is under which conditions selections favors co-existence of selfish genomes and genomes that are active in the growth of the aggregate.

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Uncovering the overlapping community structure of complex networks

Tamas Vicsek
Invited Speaker 3

Many complex systems in nature and society can be described in terms of networks capturing the intricate web of connections among the units they are made of. A fundamental question of great current interest is how to interpret the global organisation of such networks as the coexistence of their structural sub-units (communities) associated with more highly interconnected parts. Identifying these unknown building blocks (e.g., functionally related proteins, industrial sectors, groups of people) is crucial to the understanding of the structural and functional properties of networks. The existing deterministic methods used for large data sets find separated communities, while most of the actual networks are made of highly overlapping cohesive groups of nodes. Here we introduce an approach to analyse the main statistical features of the interwoven sets of overlapping communities making a much needed step towards the uncovering of the modular structure of complex systems.

After defining a set of new characteristic quantities for the statistics of communities, we apply an efficient technique to explore overlapping communities on a large scale. We find that overlaps are indeed very significant, and the distributions we introduce reveal novel universal features of networks. Our studies of collaboration, word association, and protein interaction graphs demonstrate that the web of communities has highly non-trivial correlations and specific scaling properties.

*This works has been carried out in collaboration with G. Palla, I. Derenyi and I. Farkas

Biological Systems as Reactive Systems

Luca Cardelli

Invited Speaker 4

Systems Biology is a new discipline aiming to understand the behavior of biological systems as it results from the (non-trivial, "emergent") interaction of biological components. We discuss some biological networks that are characterized by simple components, but by complex interactions. The components are separately described in stochastic pi-calculus, which is a "programming language" that should scale up to description of large systems. The components are then wired together, and their interactions are studied by stochastic simulation. Subtle and unexpected behavior emerges even from simple circuits, and yet stable behavior emerges too, giving some hints about what may be critical and what may be irrelevant in the organization of biological networks.

Modular Robotic Systems as Complex Systems

Henrik Lund
Inviter Speaker 5

This talk presents the robotic building block concept in which processing and physical aspects of robotic artefacts is distributed. The technological concept of physical building blocks with processing, input, output (incl. communication) is derived from embodied artificial intelligence that emphasises the role of interplay between morphology and control. The building block concept is exemplified with a variety of applications in toys, self-assembling robots, and playware. Playware is the use of intelligent technology to create the kind of leisure activities we normally label play, i.e. intelligent hard- and software that aims at producing play and playful experiences among users. We developed the modular tangible tiles as components for a new kind of playground, on which children can experience immediate feedback on their motions. Hence, this kind of playground allows implementation of games and plays that demand physical activity amongst the users, and thereby contribute as a new tool in the fight against obesity. The tangible tiles are homogenous robotic building blocks, which gives assembly, substitution and production advantages. Also, studies show that using neural networks it may be possible to classify children's behaviour, and use such classification to develop adaptive playgrounds

Is selection optimal for scale-free small worlds?

Zs. Palotai,, Cs. Farkas, A. Lorincz

Network Modelling 3

The 'No Free Lunch Theorem' claims that for the set of all problems no algorithm performs better than random search and thus, selection can be advantageous only on a limited set of problems. In this paper we investigate how the topological structure of the environment influences algorithmic efficiency. We study the performances of algorithms, using selective learning, reinforcement learning, and their combinations, in random, scale-free, and scale-free small world (SFSW) environments. The learning problem is to search for novel, not-yet-found information. We ran our experiments on a large news site and on its downloaded portion. Controlled experiments were performed on this downloaded portion: we modified the topology, but preserved the publication time of the news. Our empirical results show that the selective learning is the most efficient in SFSW topology. In non-small world topologies, however, the combination of the selective and reinforcement learning algorithms performs the best.

Bounded Rationality and Repeated Network Formation

Sylvain Béal, Nicolas Quérou

Network Modelling 3

We define a finite-horizon repeated network formation game with consent, and study the differences induced by different levels of individual rationality. We prove that perfectly rational players will remain unconnected at the equilibrium, while nonempty equilibria are possible when, following Neyman (1985), players are assumed to behave as finite automata. We define two types of equilibria, namely the Repeated Nash Network (RNN), in which the same network forms at each period, and the Repeated Nash Equilibrium (RNE), in which different networks may form. We state a sufficient condition under which a given network may be implemented as a RNN. Then, we provide structural properties of RNE. For instance, players may form totally different networks at each period, or the networks within a given RNE may exhibit a total order relationship. Finally we investigate the question of efficiency. We characterize efficient outcomes and prove that the sets of Bentham and Pareto efficient outcomes are identical.

A generative model of power law distributions with optimizing agents with constrained information access

Laszlo Gulyas

Network Modelling 3

Power laws are of special interest to complex systems studies. A number of general, abstract mechanisms and generative models have been proposed to explain the occurrence of power law distributions, independent of the particular domain they may occur in. These models make different assumptions of the system, its actors and their dynamics. In this paper a new generative model is presented, based on utility maximizing behavior of agents using limited local information. This model is capable of generating power law distributions given sufficient heterogeneity is present in the distribution of information among the agents. The model is related to the city formation model of Simon [12][13] that has become more widely known in its variant by Albert and Barabási, the 'preferential attachment' model. [1][2] The main difference between these models and the one presented in this paper is that the former models require global access to information (i.e., the arriving new agent or node has to assess the distribution of links/size of the whole pre-existing population), while our model operates with limited information and utility maximization subject to this set of information.

A theory-based dynamical model of innovation processes

David Lane, Roberto Serra,, Marco Villani, Luca Ansaloni

Social Modelling 3

We present an agent-based model of innovation processes, based upon a theory of innovation by Lane and Maxfield. The theory inspires and constrains the features of the model, thus reducing the embarasse de richesse that is one of the major methodological problems of agent-based modeling. Artefacts are produced by agents using recipes; the basic dynamics, absent innovation, is one of production and sales, where the external world supplies "raw materials" and external demand. Depending upon the initial conditions, self-sustaining cycles of production and exchange can emerge among the agents. Innovation – that is, the generation of new recipes, in particular desired directions, called "goals" – results in substantial modification of the system dynamics. Two innovation regimes are introduced: a "lonely" mode, in which each agent tries to introduce new products by itself, and a "relational" mode, in which two agents can improve their reciprocal knowledge and can decide to try to jointly develop a new artifact.

Modeling Firm Skill-Set Dynamics as a Complex System

Edoardo Mollona, David Hales

Social Modelling 3

The article explores emergence and survival of human resource management strategies and organisational types in a knowledge-based job market. The analysis considers a dynamic environment in which skill requirements change rapidly. We built an agent-based model to simulate a market where firms post job offers to fill vacancies and decide how to select and reward employees; employees, bearing skills, select firms comparing job offers. Taking an evolutionary approach, we explore how hiring strategies, which guarantee survival, emerge from interconnected variation, selection and retention processes. The simulation experiments suggest that, as the rate of change of the environment increases, long-term employment and firm-specific knowledge building emerge as the survival strategy.

Metamimetic games : Modeling Social Cognition

David Chavalarias

Social Modelling 3

Imitation is fundamental in the understanding of social system dynamics but the diversity of imitation rules employed by modelers proves that the modeling of mimetic processes cannot avoid the traditional problem of endogenization of all the choices, including the one of the mimetic rules. Starting from the remark that human reflexive capacities are the ground for a new class of mimetic rules, I propose a formal framework, metamimetic games, that enable to endogenize the distribution of imitation rules while being human specific. The corresponding concepts of equilibrium - counterfactually stable state - and attractor are introduced. Finally, I give an interpretation of social differentiation in terms of cultural co-evolution among a set of possible motivations that departs from the traditional view of an optimization process indexed to criteria that exist prior to the activity of agents.

Towards a functional formalism for modelling complex industrial systems

D. Krob, S. Bliduze

Social Modelling 3

This paper is devoted to the presentation of the main lines of a unified functional formalism for modelling complex industrial systems, that is to say systems that typically mix a big number of different software and physical devices. Our approach is based on a discrete non standard representation of time. It captures both the hierarchical architecture and the temporal and data multi-scale structures of a complex industrial system. We show in particular in this paper how our formalism allows to recover in an totally unified way various sorts of simple systems such as Turing Machines, elementary conservative physical systems and low level software/physical interfaces (sampler, modulator).

Production networks and failure avalanches

Gérard Weisbuch, Stefano Battiston

Social Modelling 3

Although standard economics textbooks are seldom interested in production networks, modern economies are more and more based upon suppliers/customers interactions. One can consider entire sectors of the economy as generalised supply chains. We will take this view in the present paper and study under which conditions local failures to produce or simply to deliver can result in avalanches of shortage across the whole network. The integrated economic consequences of these local failures will be our main concern.

Noise sensitivity of portfolio selection under various risk measures

I. Kondor, S. Pafka, G. Nagy

Social Modelling 3

The theory of portfolios, initiated by Markowitz, has suffered from the "curse of dimensions" from the very outset. Whereas the computational difficulties associated with the selection of the optimal portfolio have been greatly alleviated by the progress of information technology, the fundamental problem of insufficient input data and the resulting estimation error remain serious stumbling blocks. Even if we disregard the notoriously difficult problem of estimating returns and focus exclusively on the minimal risk portfolio, the amount of information contained in the available finite-length time series is typically far below the amount of information necessary for the reliable determination of the optimal portfolio. As for a portfolio of size N and time series of length T, the number of input data is NT, whereas the number of data needed for the construction of the covariance matrix is $O(N^2)$, we expect that the quality of the estimate essentially depends on the ratio N/T and that the error goes to zero only in the limit of very small N/T. Now the problem is that for typical bank portfolios N/T is never sufficiently small, in fact, it may well be larger than unity, the threshold value where the covariance matrix becomes singular and the portfolio selection problem meaningless. Over the past decades a large number of different techniques have been developed to tackle this problem and reduce the effective dimension of large bank portfolios, but the efficiency and reliability of these procedures are hard to assess or compare. In this paper we propose a model (simulation)- based approach which can be used for the systematic testing of all these dimensionality-reduction (filtering) techniques [1]. To illustrate the usefulness of our framework, we develop several toy models (including a single-index or market model and a market plus sectors model) that display some of the main characteristic features of empirical correlations and generate artificial time series from them. Then, we regard these time series as empirical data and reconstruct the corresponding correlation matrices which will inevitably contain a certain amount of noise, due to the finite length of the time series. For multivariate normal portfolios and asymptotically large N and T with N/T fixed we derive a simple analytic formula for the relative error in the portfolio. Now we apply several correlation matrix estimators and dimensionality-reduction techniques introduced in the literature and/or applied in practice. As in our artificial world the only source of error is the finite length of the time series and, in addition, the "true" model, hence also the "true" correlation matrix, are precisely known, we can meaningfully compare the performance of the various noise-reduction techniques. One of our recurrent observations [2] is that the recently introduced filtering technique based on random matrix theory (RMT) [3] performs consistently well in all the investigated cases. Based on this experience, we believe that our simulation-based approach can also be useful for the systematic investigation of several related problems of current interest in finance. In addition to correlated Gaussian returns, we also consider non-stationary time series of the IGARCH(1,1) type, closely related to the exponentially weighted moving average technique implemented in RiskMetrics [4]. In order to be able to apply the RMT-based filtering technique in this context, we have derived the spectrum of a random covariance matrix where the returns are exponentially weighted with time [5]. Applying this method to empirical data we find that the effect of risk depends on the weight factor, whose optimal value corresponds to the trade off between discarding too many past data, thereby destroying the statistics, or retaining too many, hence including non-stationary effects. We determine the optimal weight factor and find that it is consid-

erably larger than the value advocated in RiskMetrics. As a further attempt to go beyond the classical mean-variance framework, we have also studied the effect of noise on portfolio selection under some alternative risk measures. In particular, we have studied the case of mean absolute deviation (MAD), as described in ref. [6]. The level surfaces of risk under MAD are polyhedrons (instead of the ellipsoidal iso-risk surfaces corresponding to variance), and this leads to an increased sensitivity to noise. We observe a similar effect under the use of expected shortfall (ES) or conditional value at risk which is strongly promoted in the academic literature as the simplest of the coherent risk measures [7]. In addition, portfolio optimization under this measure has been shown to be reducible to linear programming [8] which might, in principle, allow one to optimize extremely large portfolios at a relatively light computational cost. As we show here, the downside is a strongly increased sensitivity to noise. One might think that this is due to the fact that ES, as a kind of conditional expectation, omits a large amount of input data by concentrating only on those above a (typically high) confidence level. A systematic study of the problem reveals, however, that the enhanced sensitivity remains true even for as low confidence levels as 60where ES can be compared with semi-variance. The fundamental reason of this high noise-sensitivity of ES is not understood at present. At the other extreme, for confidence levels approaching 100have a risk measure that can be called worst loss (WL). Although over-pessimistic, this still has the virtue of coherence. Not surprisingly, WL is found to be very sensitive to noise again. In the course of our studies of the noise-sensitivity of the risk measures ES and WL we have observed a striking phenomenon. As we have already mentioned, the portfolio selection problem within the mean-variance framework becomes meaningless for $N/T > 1$. The same is true for all the other risk measures studied in this paper. On the other hand, for $N/T < 1$, optimization under the variance and also under MAD always has a solution, even if it may be strongly influenced by noise for N/T not small enough. In contrast to this, the optimization under ES and WL does not necessarily have a solution even under the threshold $N/T = 1$, instead, the existence of a solution becomes a probabilistic issue: it depends on the sample. We have studied this remarkable phenomenon both analytically and numerically. In the case of Gaussian-distributed (or, more generally, elliptically distributed) assets and under the WL risk measure we have been able to derive a closed formula for the probability of the optimization problem to have a solution and found that this probability goes to unity only for N/T going to zero. Similar behaviour is observed in numerical simulations for the ES measure for the entire range of confidence levels we have studied. This puzzling phenomenon is absent if short selling is excluded, which may be the reason why it had not been observed by previous authors.

On the Complexity of Physical Problems and a Swarm Algorithm for k-Clique Search in Physical Graphs

Yaniv Altshuler, Arie Matsliah, Ariel Felner

Bio Inspired Methods 2

As the complexity of systems increases, so does the need of examining the nature of complexity itself. This work discusses the domain of physical swarm problems, in which a swarm of mobile agents is employed for solving physical graph problems (where a certain amount of travel effort in required for every movement along the graph's edges).

A new kind of complexity scheme, suitable for this domain, is discussed by examining a central problem of this domain - the physical k-clique problem. In this problem, a swarm comprising of mobile agents travels along the vertices of a physical graph G, searching for a clique of size k. Thus, the complexity of the problem is measured in travel efforts (instead of in computation resources).

In order to share information between the agents, two communication models are discussed - a complete knowledge sharing (referred to as centralized shared memory) and a distributed shared memory model, where the mobile agents can store and extract information using the graph's vertices.

The work presents a search algorithm for the agents, and discusses its performance under each communication model. The major contribution of this work is demonstrating the strength of the distributed shared memory model. Although this model is much easier to implement and maintain, is highly fault tolerant and has high scalability, the quality of the results it produces is very high, compared to the strongest model of complete knowledge sharing.

The POEtic Electronic Tissue and its Role in the Emulation of Large-Scale Biologically Inspired Spiking Neural Networks Models

Manuel J. Moreno, Yann Thoma, Eduardo Sanchez, Jan Eriksson, Javier Iglesias, Alessandro Villa

Bio Inspired Methods 2

One of the major obstacles found when trying to construct artefacts derived from principles observed in living beings is the lack of actual dynamic hardware with autonomous capabilities. Even if programmable devices offer the possibility of modifying the functionality implemented in the device, they rely on external hardware and software elements to provide its physical configuration. In this paper we shall present a new family of electronic devices, called POEtic, whose architecture has been derived from the basic properties that can be extracted from the three major organisation principles present in living beings: phylogenesis, ontogenesis and epigenesis. We shall demonstrate that the capabilities present in these new programmable devices make them an ideal candidate for the real-time emulation of large-scale biologically inspired spiking neural networks models.

Evolving artificial 'brains': a biomimetic Evolutionary Neuro-

P. Ittzés, Z. Szatmáry, S. Számadó, E. Szathmáry

Bio Inspired Methods 2

The evolution of autonomous communicating agents is a hot area in recent research. We have developed a software framework, called ENGA, to evolve flexible neuronal networks capable of solving first simple but then more and more complicated communication tasks. We took a biomimetic approach, that is, the design of the system was inspired by important biological phenomena such as brain ontogenesis, neuron morphologies, and indirect genetic encoding. We exposed our neuronal networks to simple coordination and task-allocation games to test the potential of the system. Neuronal networks were selected and were allowed to reproduce as a function of their performance in the given task. The selected neuronal networks in all scenarios were able to solve the communication problem they had to face. Although this result tells little about the full potential of the biomimetic approach, it is a promising start, on which we intend to build by introducing our neuronal networks to more and more complicated communication scenarios. The most striking feature of the model is that it works with highly indirect genetic encoding–just as brains do.

Traffic dynamics in scale-free networks

Attila Fekete, Gabor Vattay, Ljupco Kocarev, , ,

Information Tech. Modelling 1

We study traffic dynamics in growing scale-free networks. Both the scale-free structure of the network and the adaptive nature of the dynamics which controls traffic in the network are considered in the model. The model is investigated with computer simulations and analytically for the case of scale-free tree. For the scale-free tree, an exact formula and its power law approximation of the complementary cumulative distribution function (CDF) of link load (edge betweenness) is presented. We examine whether the scaling properties of the network affect the performance of the transport mechanism and estimate the average number of competing transport mechanisms at bottlenecks. We find that bottlenecks tend to appear on the periphery of the network as the performance increases. Various bandwidth allocation strategies are compared. We show that the best performance is achieved when capacity is distributed proportionally to the expected load of links. We demonstrate that it is necessary to study both the topology and the dynamics of the transport mechanism to understand the whole system.

Sampling of networks with traceroute-like probes

Alain Barrat, Ignacio Alvarez-Hamelin, Luca Dall'Asta, Alexei Vazquez, Alessandro Vespignani

Information Tech. Modelling 1

A large part of the recent development of the interest in complex networks has been triggered by the observation of particular characteristics of real world networks, such as the small-world properties or the heavy-tailed distributions of degrees. Many datasets are however the result of an incomplete sampling of the underlying real networks, and it has been argued that sampling procedures might introduce uncontrolled biases in the statistical properties of the sampled graph. In this paper, we explore this issue in the case of the Internet, which is generally mapped from a limited set of sources by using `traceroute`-like probes. The origin of the biases introduced by such a sampling process is investigated and related with the global topological properties of the underlying network. We complement the analytical discussion with a throughout numerical investigation of simulated mapping strategies in network models with different topologies.

A Simulation Study of Network Discovery Strategies

F. Eberhard, T. Erlebach, A. Hall

Information Tech. Modelling 1

Due to its fast, dynamic, and distributed growth process, it is hard to obtain an accurate map of the Internet. In many cases such a map (representing the structure of the Internet as a graph with nodes and links) is a prerequisite when investigating properties of the Internet. A common way to obtain such maps is to make certain local measurements at a small subset of the nodes and then to combine these in order to discover (an approximation of) the actual graph. Each of these measurements is potentially quite costly. It is thus a natural objective to minimize the number of measurements which still discover the whole graph. We consider this problem for a specific type of measurements and compare four simple greedy strategies in an experimental analysis. Our results show that one can discover accurate information about the structure of large and complex networks using a surprisingly small number of queries.

Message passing algorithms for non-linear nodes and data compression

Stefano Ciliberti, Marc Mezard, Riccardo Zecchina

Complex Systems Methods 2

The use of parity-check gates in information theory has proved to be very efficient. In particular, error correcting codes based on parity checks over low-density graphs show excellent performances. Another basic issue of information theory, namely data compression, can be addressed in a similar way by a kind of dual approach. The theoretical performance of such a Parity Source Coder can attain the optimal limit predicted by the general rate-distortion theory. However, in order to turn this approach into an efficient compression code (with fast encoding/decoding algorithms) one must depart from parity checks and use some general random gates. By taking advantage of analytical approaches from the statistical physics of disordered systems and SP-like message passing algorithms, we construct a compressor based on low-density non-linear gates with a very good theoretical *and* practical performance.

Combinatorial autions: From statistical physics to new algorithms

Michele Leone, Mauro Sellitto, Martin Weigt

Complex Systems Methods 2

In a combinatorial auction, a bidder is not interested in buying single objects, but whole packets of objects, and he is willing to pay a certain price for the complete packet only. For the auctioneer, the ćombinatorial auction problem(CAP) consists in selecting winning bids maximizing his total revenue. There are, however, hard constraints to this selection: No object can be sold twice, i.e. no two bidders with packets sharing one or more objects can buy simultaneously. These constraints make the CAP a NP-hard problem. With the uprise of internet auctions, the interest in combinatorial auctions has recently increased, and the need for efficient heuristic algorithms is steadily growing.

A statistical-mechanics approach allows for a detailed statistical analysis of the properties and organization of optimal solutions to a CAP. We find, e.g., a phase transition between a simply solvable phase for relatively few buyers and/or small packets to a complex, clustered and thus hard-to-solve region. The used method can be reformulated and used as a fast heuristic algorithm even in this hard phase, where it outperforms local search methods.

Combinatorial auctions are also interesting in the context of the new field of complex-networks research. The CAP can be graphically represented by its ´conflict network´: The nodes are given by the bidders, links represent conflicting interests, i.e. non disjoint packets. This network naturally owns properties like clustering and short average distances. The interplay between the topological structure of this network and the solutions of the CAP can also be clarified by the statistical-physics approach.

A spin glass model of human logic systems

Fariel Shafee

Complex Systems Methods 2

In this paper, we discuss different models for human logic systems and describe a game with nature. Godel's incompleteness theorem is taken into account to construct a model of logical networks based on axioms obtained by symmetry breaking. We start by saying that although an agent is rational, the axioms defining different agent's logic systems need not be the same although they might have a large degree of overlap. This can be seen as each agent being coupled to a higher dimensional world by means of his perception where the couplings produce slightly different projections of the higher dimensional world to each agent. The different projections would produce slightly different concepts about the "world" to each agent and hence create a slightly differing set of axioms that each agent would use to act logically. Then we place the agents in an interacting logical network, where these axioms can be treated as spins that can be flipped as agents interact with each other and with the environment in which they are placed. Agents, who would share a common material world that they wish to use or change by using different or conflicting sets of axioms will try to flip the other agent's axioms (This can be seen by observing that as one agent acts to interact with his world as followed by his axiom, another agent's world changes as well, and the change might be contradictory to the second agent's "axioms" or "optimal world". We define an equation that allows an axiom to be flipped into an "anti axiom (the opposite or conflicting axiom)" as agents interact. All agents share an "existence" axiom by means of which they strive to perpetuate themselves or the network. The agents acquire more information that can act as an underlying axiom as they play against nature to perpetuate themselves while nature vies to increase entropy or disorder. Each agent has only a finite amount of "time" or "energy" to spend against nature and against other agents when they compete. Spurious axioms are fabricated in order to keep the existence axiom from flipping, providing agents with a "meaning". Spurious axioms can be traded among agents in exchange of another agent's time and energy. We then introduce teh idea of probabilistic axioms that allows an agent to choose one decision over anotehr with a certain probability.

Statistical Physics of Boolean Control Networks

L. Correale, M. Leone, A. Pagnani, M. Weigt, R. Zecchina

Complex Systems Methods 2

We explore the static behavior of large Boolean control networks with methods recasting the Boolean regulation problem into a constraint satisfaction problem. Our analysis includes a modified version of the leaf-removal procedure as well as results coming from the belief and survey propagation algorithms. This allows to explore the complex solution-space structure of the problem. We find a phase transition from simple to complex regulatory control, and identify relevant regulatory variables which select the fixed points of the network within the global solution space.

In the last two decades a large wealth of new data about the organization of gene-regulatory networks (RNs) is being collected It has become clear that in many cases biological functions cannot be identified at the level of single genes and proteins. Constructing a detailed biochemical model of an entire cell by analyzing each gene and its interactions with others one by one appears to be a formidable task. Even in the case of a relatively simple cell like yeast, the number of genes is of the order of 6000. To make progress in the understanding of the combinatorial aspects of genes regulation it appears crucial to model these systems on a coarse-grained level, and to encode the interactions in a so-called RNs: nodes of this network represent individual genes, and directed connections genetic interactions. Such models can be expected to give insight into the collective large-scale behavior of the gene as well as more general regulatory mechanism, and to infer emergent cooperative phenomena which cannot be understood at the level of single components.

A possible way of (coarse grain) modeling RNs is to consider them as bipartite factor graphs made of N genes that are regulated by a set M function nodes. Gene expression is modeled by variables taking a discrete set of activity levels x_i in level set 0,1,...,q. A function node directed from K input factors I(i) = i_1,..,i_k (genes, proteins, regulatory regions, etc.) to factor "i" in the graph implies that the first K factors play some regulatory role in the transcription process of "i": the function F_i(x_j in I(i)) determines the expression level x_i. One function node regulates one gene. External inputs (chemical concentrations, extracellular signals...) can be modeled by variables of in-degree zero, appearing only as regulating variables. The binary case of q=1 is well-known as Boolean networks (or Kauffman networks) and has been repeatedly applied to mimic the dynamical behavior of many kinds of biological regulation mechanisms, from the already cited transcription to metabolic and to protein-protein interaction networks.

Despite the large wealth of work on the subject, which however mainly addressed the behaviour of boolean control networks under rather artificial updating dynamics, the issue of fully understand the nature, organization, stability and accessibility of the fixed points of this problem is still a largely open question, since so far numerical techniques have been based mainly on exhaustive enumeration or monte-carlo approaches. The first allowing only for the study of much smaller regulatory subnetworks, the latter failing to extensively explore the solution space structure. The fixed points problem can however be exactly mapped in a Constrained Satisfaction problem, and studied with techniques explicitly developed and optimized in the fields of combinatorial optimization and Bayesian inference.

We extensively explored the fixed points phase space of the K=1, K=2, K=3 and mixed models, in the case of large random regulatory networks with poissonian and scale-free outgoing link degree distributions. For certain Boolean nodes types (namely the XOR boolean function in the K=2 case and all but pure AND and OR functions in the K = 3

case), a region in the phase space is present where the space of solution clusterizes in a large number of well separated thermodynamical states.

The onset of this region cam be studied in some particularly simple cases with a modified leaf-removal procedure, but a correct characterization of it can only be done exploiting a multi-state clustering hypothesis for the phase space, that can be efficiently studied with the Survey Propagation algorithm. The nature of this clusterized phase and the reasons why some boolean functions show a more dramatic behaviour than others with this respect is quantified and explained.

A precise hierarchy of nodes exhibiting this behaviour is presented and justified. Some conjectures on the universality of the clustering phenomenon are presented and fortified with numerical results.

The meaning of the clustering phenomenon in terms of (biological) control properties is proposed through the application of previous theoretical results to real large gene networks.

Flows of information as the driving force behind chemical pattern formation

Kristian Lindgren, Anders Eriksson

Complex Systems Methods 2

Keywords: self-organisation, information theory, pattern formation, second law, information flow

Pattern formation in chemical systems is a dynamical process that has been extensively studied in the litterature since the original work by Turing. Thermodynamic analysis of this type of self-organising systems is of importance in order to understand some of the constraints that self-organisation meets, primarily the need of free energy as a driving force behind formation of spatial patterns.

We have developed an information-theoretic framework that goes one step further in the analysis of physical constraints in chemical pattern formation (see Lindgren et al in ALife 9 proceedings 2004). The formalism is based on a thermodynamic information quantity (via statistical mechanics), and this makes it possible to connect an information-theoretic characterisation of a spatial pattern with the free energy driving the system. In this way, a consistent picture of the pattern formation process in terms of free energy being transformed into information in a spatial pattern and eventually destroyed by entropy production when reactions and diffusion processes tries to bring the system towards equilibrium.

In our analysis the information in the pattern is decomposed into contributions from both different positions and different length scales. The overall picture we get is an inflow of information at large length scales, due to the inflow of chemical free energy. Information then flows down in length scale (and also across space), where accumulation at certain positions is connected with the pattern formation. Information is lost from the system at the finest length scales. The whole process is summarised in a continuity equation for information.

In the present paper we investigate the possibility to use this formalism to make predictions on how pattern formation may depend on the structure of the driving force, i.e., the inflow of free energy. Preliminary results indicate that the information flow is generally going in the direction described above – from larger to smaller length scales – which may be viewed as generalised "second law" of information destruction. If the characteristic length scale of the free energy inflow is reduced below the length scale of the patterns in the system, the flow will not be able to support the structures built up and neither will new structure emerge unless that happends on a smaller length scale. In the same way as ambient heat has too low energy quality to drive a physical process, a chemical free energy inflow of too low length scale characteristics may be insufficient to support pattern formation.

Complex Qualitative Models in Biology: a new approach

P. Veber, M. Le Borgne, A. Siegel, S. Lagarrigue, O. Radulescu

Biological Modelling 3

We advocate the use of qualitative models in the analysis of large biological systems. We show how qualitative models are linked to theoretical differential models and practical graphical models of biological networks. A new technique for analyzing qualitative models is introduced, which is based on an efficient representation of qualitative systems. As shown through several applications, this representation is a relevant tool for the understanding and testing of large and complex biological networks.

Dynamics and pattern formation in invasive tumor growth

Evgeniy Khain, Leonard M. Sander

Biological Modelling 3

One of the most common and clinically aggressive forms of primary brain tumor is Glioblastoma Multiforme (GBM). Despite major advances in the fields of molecular biology and cellular biology, the overall prognosis still remains very poor. One of main reasons for such a high mortality and low success in medical treatment is the fact that GBMs are highly invasive. In-vitro experiments show that a growing tumor consists of two zones: an inner dense proliferative region and an outer less dense invasive region. This is the invasive nature of malignant gliomas that makes treatment to be a very difficult and challenging task.

Malignant brain tumors are complex self-organized multicellular biological systems. Experiments with different types of cells show qualitatively different behavior. For wild type cells, the invasive region grows faster, and tumor remains spherically symmetric. On the other hand, the invasive region grows slower for mutant type cells, and there are indications of symmetry-breaking of spherically symmetric growth. We formulate a continuum model that captures these experimental findings, using two coupled reaction-diffusion equations for cells and nutrient concentrations. When the ratio of nutrient and cell diffusion coefficients exceeds some critical value, the plane propagating front becomes unstable with respect to transversal perturbations. The instability threshold and the full phase-plane diagram in the parameter space are determined. Based on our model, we can explain different patterns by different diffusion constants and proliferation rates of wild and mutant cells: wild type cells diffuse faster, but have lower proliferation rate, compared to mutant type cells.

87.18.Ed Aggregation and other collective behavior of motile cells 87.18.Hf Spatiotemporal pattern formation in cellular populations

Self-organisation and other emergent properties in a simple biological system of microtubules.

James Tabony, James Tabony

Biological Modelling 3

In biological systems, emergent properties may develop due to numerous individual molecular elements in a population being strongly coupled in a non-linear manner. Under suitable conditions, the formation in vitro of a population of microtubules, a major component of the cellular skeleton (cytoskeleton), behaves as a complex system and develops a number of emergent phenomena. These preparations, which initially contain just two molecular species, a nucleotide and a protein, self-organise by reaction and diffusion and the morphology that develops is determined at a critical moment early in the process by weak external factors such as gravity and magnetic fields. The process also results in other emergent phenomena; namely, replication of form, generation of positional information, and collective transport and organisation of colloidal sized particles. Microtubules are responsible both for cellular organisation and the transport of sub-cellular particles from one part of the cell to another. Frequently, this behaviour is triggered by some weak internal or external factor. The in vitro observations outlined thus illustrate how in a simple biological system, a complex behaviour may give rise to emergent phenomena that outwardly resemble major biological functions.

Concentration and spectral robustness of biological networks with hierarchical distribution of time scales

A.N. Gorban, O. Radulescu

Biological Modelling 3

We discuss here the robustness of the relaxation time using a chemical reaction description of genetic and signalling networks. First, we obtain the following result for linear networks: for large multiscale systems with hierarchical distribution of time scales the variance of the inverse relaxation time (as well as the variance of the stationary rate) is much lower than the variance of the separate constants. Moreover, it can tend to 0 faster than 1/q, where q is the number of reactions. We argue that similar phenomena are valid in the nonlinear case as well. As a numerical illustration we use a model of signalling network that can be applied to important transcription factors such as NFκB or TGFβ.

Keywords: Complex network; Relaxation time; Robustness; Signalling network; Chemical kinetics; Limitation; Measure concentration

Spreading on networks: a topographic view

Geoffrey S Canright, Kenth Engø-Monsen

Network Modelling 4

We apply our previously developed method of "topographic" analysis of networks to the problem of epidemic spreading. We consider the simplest form of epidemic spreading, namely the "SI" model. We argue that the eigenvector centrality of a node is a good indicator of that node's spreading power. From this we develop seven specific predictions. In particular, we predict that each region (as defined by our approach) will have its own S curve for cumulative adoption over time, and we describe the various phases of the S curve in terms of motion of the infection over the region. Our predictions are well supported by simulations. In particular, the significance of regions to epidemic spreading is clear. Finally, we develop a mathematical theory, giving partial support to our picture. The theory includes a precise quantitative definition of the spreading power of a node, and some approximate analytical results for epidemic spreading.

Correlation Model of Worm Propagation on Scale-Free Networks

Nikoloski Zoran, Deo Narsingh, Kucera Ludek

Network Modelling 4

The problem of network worms is worsening despite increasing efforts and expenditure on cyber security. Worm propagation is a random process that creates a complex system of interacting agents (worm copies) over the propagation medium—a scale-free graph, representing real-world networks. Understanding the propagation of network worms on scale-free graphs is the first step towards devising effective techniques for worm quarantining. After presenting the drawbacks of existing mean-field models, we develop a pair-approximation (correlation) model of worm propagation that employs the salient network characteristics—order, size, degree distribution, and transitivity. Inclusion of the transitivity shows significant improvement over existing pair-approximation models. The validity of the model is confirmed by comparing the numeric solution of the model to results from our individual-based simulation. Our model demonstrates that the network structure has considerable impact on the propagation dynamics when the worm uses local propagation strategies.

Variability of the infection time in scale-free networks

Pascal Crépey, Fabian Alvarez, Marc Barthélemy

Network Modelling 4

Recent studies suggest that a large number of natural and artificial networks are characterized by very large degree fluctuations. This result means that a non-negligible number of nodes are extremely well connected while the majority just have a few links. The effect of such large fluctuations can be dramatic as illustrated by the fact that infectious agents can spread on these networks even for a very small value of the transmission probability.

Another consequence is that random immunization is inefficient for this kind of networks. Consequently, containment protocols and vaccination of traced contacts become our only defense but are unfortunately difficult to use at a large scale and in this context, an efficient method for detecting epidemics during their early stage becomes imperative. These efforts, now broadly labeled as "syndromic surveillance" are the centers of attention of public health agencies concerned with bioterrorism-related diseases. More precisely, an important point is to be able to determine and characterize specific nodes in the network which display interesting features in regards of an early detection system. In the present work, we focus on two specific features: (i) a small average infection time t_inf and (ii) low fluctuations around that time t_inf.

We analyze and compare the behaviors of the infection time obtained for the usual random Erdos-Renyi graph and the Barabasi-Albert scale-free network. We first compare the patterns obtained on both kind of networks and we then describe the variations of the infection time with the degree and with the topological distance to the initially infected node.

The complexity of genotype-phenotype maps and its consequences for evolution

Peter Schuster

Invited Speaker 6

Genotype-phenotype mappings are indispensable for a comprehensive understanding of evolutionary optimization. At the current state of the art only one example of a genotype-phenotype map is sufficiently well known in order to use it as a basis for modeling evolution: The sequence-structure map of RNA molecules, which can be investigated also experimentally, for example through the evolutionary design of RNA aptamers using the SELEX technique. Several evolutionarily relevant features of this mapping from sequence space into a space of structures, representing the phenotypes in RNA evolution experiments, have been discovered in the past: (i) High degree of neutrality leading to connected neutral networks spanning whole sequence space, (ii) shape space covering predicting that each common RNA structure can be reached from (almost) everywhere in sequence space through a fairly small number of point mutations, and (iii) the intersection theorem, which states that there exists at least one sequence for any arbitrarily chosen pair of structures that can fold into both. Modeling evolutionary optimization by computer simulation of replication, mutation, and selection of RNA molecules in a flow reactor revealed several characteristic features, among them: (i) The optimization process occurs in steps rather than continuously because fast adaptive phases are interrupted by long quasi-stationary epochs of neutral evolution, (ii) the evolution of a population in the stationary epochs corresponds to a diffusion process on a neutral network, and (iii) the exploration of sequence space by replication and mutation can be interpreted as a kind of primitive learning at the population level. This learning process has many features in common with the foraging strategies of ant colonies. The simple scenario assigning one structure to a given sequence becomes more realistic and more complex through considering suboptimal structures and explicit folding kinetics of RNA molecules. Comparing the set of suboptimal structures with the set of structures in the one-error neighborhood of a neutral network, called the shadow, allows for modeling the evolution of Boltzmann ensembles at different temperatures. Interaction between RNA molecules through cofolding provides another dimension of higher complexity within the RNA model. Several examples of multi-conformational RNA molecules will be presented. Such molecules have been designed and occur also in nature where they have important regulatory properties in molecular genetics.

Multi-net analysis and nonlinear dynamics: some methods and results in complexity science

Douglas White
Invited Speaker 7

Many complex systems are composed by multi-nets, i.e., multiple networks undergoing change in time series. Understanding the behavior of multi-net systems poses some basic questions:

1) how should we represent and model multiply layered and evolving networks (multi-nets) so as to discover their instabilities and nonlinear dynamics? 2) what are some of the common properties induced by dependence on co-evolution with network topologies? 3) does a generalized Boltzmann-Gibbs entropy, that takes into account network dependencies and hence long-range correlations, have applicability to modeling complexity in social systems? 4) what is the contribution of a combination of multiply layered networks, time series, methods of study for nonlinear dynamic interactions (identifying oscillations and instabilities), simulation, nonextensive BG entropy, and tracking co-evolution of network topology? The examples illustrated are city attributes and networks, industrial networks, agent search behavior, and marriage choice; each includes issues of the co-evolution of network topology and micro-macro linkages. Five sets of results are discussed:

1. A simulation that shows how modeling of results with generalized Boltzmann-Gibbs (q-) entropy takes long range correlations into account in known network dynamics relating to agent search behavior.
http://arxiv.org/abs/cond-mat/0508028

2. A q-entropy worldwide scaling of the 28 historically estimated city-size distributions is investigated for nonlinear instabilities in urban systems.

3. Investigation of a multi-net coding and longitudinal analysis of agrarian civilizations as dynamical networks (Medieval European and Eurasian datasets) showing nonlinear dynamic interactions.

4. Analysis of collaborative multi-nets in the world biotech industry shows an interactive dynamics of recruitment for innovation and organizational consolidation. AJS 210(4): 1132-1205.

5. Multi-net construction of social structure through mate choice and co-evolution of social network topologies. Complexity 8(1):72-81.

The brain seen as a goal-oriented, self-organizing complex system

Wolf Singer
Invited Speaker 8

Our intuition assumes that there is a centre in our brain in which all relevant information converges. This, so our introspection, would be the place where the signals provided by our various sensory systems are bound together into coherent percepts of the surrounding world, where decisions are reached, where plans for future acts are elaborated and where adapted motor responses are programmed. Eventually, this distinguished site would be the place where the intentional self constitutes itself.

The results of neurobiological investigations design a radically different picture. The brain presents itself as a highly distributed system in which a very large number of processes occur simultaneously and in parallel without requiring coordination by a central convergence centre. The connectivity graph of the brain is characterized by a dense network of mainly reciprocal links between the chains of processing nodes that span between the sensory and executive organs. This specific architecture resembles in many respects small world networks and raises the question, how the multiple operations occurring in parallel are bound together in order to give rise to coherent perception and action.

Based on data obtained from investigations of the visual system mechanisms will be discussed that could accomplish the binding of distributed processes into coherent representations. The hypothesis will be forwarded that temporal coherence serves as an important organizing principle and that this coherence is achieved by the synchronization of oscillatory activity in distinct frequency bands.

Design Patterns from Biology for Distributed Computing

Ozalp Babaoglu, Geoffrey Canright, Andreas Deutsch, Gianni Di Caro, Frederick Ducatelle, Luca Gambardella, Niloy Ganguly, Mark Jelasity,, Roberto Montemanni, Alberto Montresor

Bio Inspired Methods 3

Recent developments in information technology have brought about important changes in distributed computing. New environments have emerged such as massively large-scale wide area computer networks and mobile ad hoc networks. These new environments are extremely *dynamic*, *unreliable*and often *large-scale*. Traditional approaches to designing distributed applications based on central control, small scale or strict reliability assumptions are not suitable for exploiting the enormous potential of these environments. Based on the observation that living organisms efficiently organize a large number of unreliable and dynamically changing components(cells, molecules, individuals of a population, etc) it has long been an interesting area of research to try to figure out what are the key ideas that make biological systems work and to apply these ideas in distributed systems engineering. In this paper we propose a conceptual framework that captures a few basic biological processes such as plain diffusion, reaction-diffusion, proliferation, etc.We show through examples how to implement practically relevant functions based on these ideas. Using a common evaluation methodology, we show that these applications have state-of-the-art effectivity and performance while they inherit some nice properties of biological systems, such as adaptivity and robustness to failure.

Elements about the Emergence Issue A survey of emergence definitions

Joris Deguet, Yves Demazeau, Laurent Magnin

Bio Inspired Methods 3

Emergence, a concept that first appeared in philosophy, has been widely explored in the domain of complex systems and is sometimes considered to be the key ingredient that makes "complex systems" "complex". Our goal in this paper is to give a broad survey of emergence definitions, to extract a shared definition structure and to discuss some of the remaining issues. We do not know of any comparable surveys about the emergence concept. For this presentation, we start from a broadly applicable approach and finish with more specific propositions. We first present five selected works with a short analysis of each. We then propose a merged analysis in which we isolate a common structure through all definitions but also what we think needs further research. Finally, we briefly describe some perspectives about the emergence engine idea also referred to as emergent engineering.

Behavior transitions provided by dynamical features of recurrent neural network - a case study of complex phenomena in behavior based robotics

Martin Huelse, Steffen Wischmann, Frank Pasemann

Bio Inspired Methods 3

Complex phenomena like bistability, periodic and quasi-periodic oscillations, and chaos can be already observed in small artificial recurrent neural networks (RNN). We utilize this rich reservoir of dynamical properties for behavior control of autonomous mobile robots. Using a special evolutionary program, the ENS^3 (evolution of neural systems by stochastic synthesis), recurrent neural network structures of general type for robot control are developed. Structure and size of the evolving RNN are open to the evolutionary process, and parameters like synaptic strengths are optimized simultaneously.

The ENS^3 can also be utilized to extend or couple already existing RNNs to achieve additional functionality. In such a way different behavioral (sub)-functionality can be non-linearly integrated in one network solving a global robot task. On the one hand, this strategy allows an incremental evolution of complex control structures solving robot tasks including more and more subtasks and their effective coordination. On the other hand, such incrementally evolved RNNs give us a wide variety of empirical setups to investigate multifunctionality and robust behavior changes in complex systems provided by non-linear coupled neural systems.

As a first simple example of this method we present an incrementally evolved recurrent network generating a motivational driven robot behavior. Following an ALife approach the robot has to maintain the level of its internal energy reservoir. This energy reservoir decrease over time, but can be refilled from energy sources located in the environment. To maintain its energy level the robot has to switch between different behaviors. According to the dynamical features of the underlying network we observed that the transition from one behavior to another bases on the switching from periodic attractors to a domain of bistability and the otherway around. This attractor switching leads to increasing fluctuations on the macroscopic level, i.e. the observable robot-environment interaction. Therefore, we claim that behavior transitions are emergent phenomena generated by the attractor switching of the controller and the boundary conditions given by the robot-environment interaction.

On emergent phenomena in everyday activities taking place in AmI spaces

Ioannis D. Zaharakis, Achilles D. Kameas

Information Tech. Modelling 2

This work aims at a) identifying the forthcoming changes in our everyday life due to the ever-increasing level of complexity that inculcates our interactions with the devices surrounding us, b) introducing a bio-inspired world model (framework) that deals with different perspectives of the interrelations developed in symbiotic ecologies where people and artefacts coexist, and c) proposing a high level architectural scheme of an AmI space reflecting the basic ingredients of the future indoors/outdoors applications based on Swarm Intelligence and Complexity Science.

Improved message passing for inference in densely connected systems

Juan P Neirotti, David Saad

Information Tech. Modelling 2

An improved inference method for densely connected systems is presented. The approach is based on passing condensed messages between variables, representing macroscopic averages of microscopic messages. We extend previous work that showed promising results in cases where the solution space is contiguous to cases where fragmentation occurs, by considering average messages from a large number of replicated systems. We present an application of the problem to the signal detection problem of Code Division Multiple Access(CDMA) for demonstrating its potential. A highly efficient practical algorithm is also derived on the basis of insight gained from the analysis.

Evolutionary Game Theory with Applications to Adaptive Routing

Simon Fischer, Berthold Vöcking

Information Tech. Modelling 2

One of the most important problems in large communication networks like the Internet is the problem of routing traffic through the network. Current Internet technology based on the TCP protocol does not route traffic adaptively to the traffic pattern but uses fixed end-to-end routes and adjusts only the injection rates in order to avoid congestion. A more flexible approach uses load-adaptive rerouting policies that reconsider their routing strategies from time to time depending on the observed latencies. In this manuscript, we survey recent results from [FV04] and [FV05] about the application of methods from evolutionary game theory to such an adaptive traffic management.

Key words: Evolutionary game theory, Wardrop model, adaptive routing, stale information, analysis and dynamics of complex networks

Atomic Selfish Routing in Networks: A Survey

Spyros Kontogiannis, Paul Spirakis

Information Tech. Modelling 2

In this survey we present some recent advances in the atomic congestion games literature. Our main focus is on a special case of congestion games, called network congestion games, which is of particular interest for the networking community. The algorithmic questions that we are interested in have to do with the existence of pure Nash equilibria, the efficiency of their construction when they exist, as well as the gap of the best/worst (mixed in general) Nash equilibria from the social optima in such games, typically called the Price of Anarchy and the Price of Stability respectively.

Measuring preferential Attachment in a Hyper-Textual Dictionary Reference Network: Eksi Sözlük

Amac Herdagdelen, Eser Aygun, Haluk Bingol

Information Tech. Modelling 2

Existing methods used to analyze the relation between preferential attachment and node degree make use of time dependent measures, which result in limited ability to analyze the temporal characteristics of networks. We introduce time independent measures, which allow us to analyze the networks' preferential attachment behavior in a more precise manner. The two different methodologies are compared on a new complex network data: Eksi Sözlük, which spans the whole lifetime (six years) of a complex network with very precise recordings of the node and edge addition events (i.e. one minute). The relation between the likeliness to receive new links and the present degree of a node is found to be linear. Analyses suggest that time independent measures are better in capturing the dynamics of the network and in some cases, provide results that are very hard to obtain by existing methodologies.

Resource allocation on sparse graphs

Michael K.Y. Wong, David Saad, Zhuo Gao

Network Modelling 5

Optimal resource allocation is a well known problem in the area of distributed computing [1][2] to which significant effort has been dedicated within the computer science community. The problem itself is quite general and is applicable to other areas as well where a large number of nodes are required to balance loads/resources, such as reducing internet traffic congestion [3]. The problem has many flavours and usually refers, in the computer science literature, to finding practical algorithmic solutions to the distribution of computational load between computers connected in a predetermined manner. Many of the solutions are heuristic and focus on practical aspects (e.g., communication protocols).

The problem we are addressing is more generic and is represented by nodes of some computational power that should carry out some tasks. Both computational powers and tasks will be chosen at random from some arbitrary distribution. The nodes are located on a randomly chosen sparse graph of some connectivity. The goal is to migrate tasks on the graph such that demands will be satisfied while minimising the migration of (sub-)tasks. Decisions on messages to be passed are carried out locally. We focus here on the satisfiable case where the total computing power is greater than the demand, and where the number of nodes involved is very large.

We have applied the replica method [4] of statistical physics for studying the problem and have used insight gained from the analysis to devise efficient message passing distributed algorithms for solving the problem with a modest computational cost. The approach is based on passing local information between nodes to facilitate decisions about the movement of tasks.

A second algorithm we have devised, on the basis of insight obtained from the statistical physics framework, is linked to quadratic programming; as here one would like to optimise some simple function (total messages) under some hard constraints (carrying out all tasks). The main difference in this case is the typical sparsity of the graphs we study, which is exploited for obtaining efficient distributed algorithms based on *local* computations. This is in contrast to the dense nature of parallel quadratic programming problems, for instance in the area of support vector machines [5], where global computation is required. In many systems, such global approach is not feasible.

To study the efficiency of our method we have carried out a experiments on random graphs of given connectivity and compared the results obtained with those given by the analysis. We see perfect agreement between analysis and theory. Both algorithms show excellent performance.

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Partitioning networks into classes of mutually isolated nodes

J. Diaz, A. Kaporis, L. Kirousis,, X. Perez

Network Modelling 5

Following the work of Newman, we model complex networks with random graphs of a given degree distribution. In particular we study the case where all vertices have exactly the same degree (random regular graphs). We survey some recent results on the problem of partitioning such a graph into the smallest possible number of classes of mutually isolated vertices, known in graph theory as the colorability problem. We also describe the solution of an open problem about 5-regular graphs.

Clustering and robustness in networks

Y Grondin, D J Raine

Network Modelling 5

The robustness of a network is a measure of the integrity of the network subject to the deletion of network nodes and is an important parameter for the design of engineered networks and the evolution of naturally occurring ones. By constructing sequences of networks with the same degree distribution of the nodes, and the same connectivity between nodes of given degrees, but with different clustering of nodes, we show that robustness decreases with an increase in the clustering of the network. The advantage for a network to have a small-world architecture therefore comes at a certain cost.

On the Propagation of Congestion Waves in the Internet

J. Steger, P. Vaderna, G. Vattay

Network Modelling 5

Traffic modeling of communication networks such as the Internet has become a very important field of research. A number of interesting phenomena are found in measurements and traffic simulations. Signatures of long-range correlations, scaling, chaos and phase transitions and pattern formations have been investigated in the literature. Computers connected to a network communicate via data flows consisting of discrete data packets. The flow of these packets along a network path is quite similar to a one-dimensional granular flow of matter through a pipe. Since the slowing down and acceleration of packet flow in computer networks are very similar to those of cellular automaton models of cars in highway traffic, it has been argued that a valid analogy exists between these subjects, which later has been demonstrated quantitatively.

One of the most peculiar features of car traffic and flow of granular media is the propagation of density waves. In car traffic stop-and-go type congestion waves propagate against the direction of the flow. K. Fukuda et al. (Fractals, **7**(1) 23-31; 1999) studied the spatio-temporal correlations of the level of congestion in routers and showed that congestion can propagate from a heavily loaded router to one of its empty neighboring routers.

We focus our studies on finding a simple model that can describe this phenomenon. Computer networks can be studied with the help of network simulators. These tools enable us to assemble any computer network configuration, and to implement the most commonly used packet sending mechanism TCP/IP protocol and to emulate its behavior without building the system from hardware components. In our work we used the popular Berkeley Network Simulator (`ns-2.26`) tool.

We study the network traffic generated in a unidirectional ring of identical routers connected. Routers are connected with given capacity lines with constant forwarding delays. Parameter values in the simulation setup were set to be close to those describing the real Internet. Ring topology was chosen to investigate to have some analogy with other granular flow simulations. The ring geometry mimics periodic boundary conditions. This way we can study the propagation of congestion in an isolated, clean setup, where the effects of inhomogeneity and the complex topology of the real Internet does not interfere with the basic mechanism creating the congestion wave. Computers inject data packets in the network according to the rules of the TCP/IP protocol, which ensures that the data packet-sending rate is decreased whenever congestion occurs and that it is increased when there is an available unused capacity in the system. We show that this system drives itself in a self-organized way into a critical congested state, where the system is overloaded and packets are lost for a long period of time. Both the position of the congested router (where packets are dropped) and the rate of the packet sending activity (packets sent by the router in unit time) at the sites propagate against the direction of the packet flow. The profile of the congestion wave can be reconstructed from the activities of the computers connected to the ring. The velocity of the congestion wave can be measured.

In our study the packet sending activity is large enough so we can neglect its granularity and can treat it as a continuous variable and its dynamics can be well approximated with differential equations. While the continuous equations constitute gross simplification of the original TCP dynamics, the main properties of the traveling wave are recovered from them. Our mathematical model allows several solutions to the system, each solution standing for a congestion wave profile with different slope and speed. We found numerically that only the

slopest possible wave profile is stable against its small random perturbations. A systems started from a smaller slope always shift towards a steeper one. In the network simulator we always observed the realization of the most stable (the steepest possible wave front) solutions of the model.

We showed that congestion waves are formed naturally in the data traffic of computer networks. The mechanism behind the wave formation is that packet losses occur most likely in computers nearest to the site of the actual congestion and other computers sharing the congested link increase their sending rates, moving the site of the congestion one site downstream. This basic mechanism is quite general and can create congestion moving against the direction of the data traffic in more complicated geometries. A formula for the speed of the congestion wave has been derived in a simple ring topology and network simulations have confirmed it. Such formulas can be developed for more complicated geometries, which is our next research goal.

Towards Peer-to-Peer Web Search

Gerhard Weikum, David Hales, Christian Schindelhauer,, Peter Triantafillou

Network Modelling 5

The peer-to-peer computing paradigm is an intriguing alternative to Google-style search engines for querying and ranking Web content. In a network with many thousands or millions of peers the storage and access load requirements per peer are much lighter than for a centralized Google-like server farm; thus more powerful techniques from information retrieval, statistical learning, computational linguistics, and ontological reasoning can be employed on each peer's local search engine for boosting the quality of search results. In addition, peers can dynamically collaborate on advanced and particularly difficult queries. Moroever, a peer-to-peer setting is ideally suited to capture local user behavior, like query logs and click streams, and disseminate and aggregate this information in the network, at the discretion of the corresponding user, in order to incorporate richer cognitive models.

This paper gives an overview of ongoing work in the EU Integrated Project DELIS that aims to develop foundations for a peer-to-peer search engine with Google-or-better scale, functionality, and quality, which will operate in a completely decentralized and self-organizing manner. The paper presents the architecture of such a system and the Minerva prototype testbed,and it discusses various core pieces of the approach: efficient execution of top-k ranking queries,strategies for query routing when a search request needs to be forwarded to other peers, maintaining a self-organizing semantic overlay network,and exploiting and coping with user and community behavior.

Optimization and control of the urban spatial dynamic

Ferdinando Semboloni

Social Modelling 5

The urban planning concerns the assignment of a land use to the land cells. This process coexists and may conflict with the complex spontaneous dynamic of the urban system, which should be constrained by the plan. The purpose of this study is the identification of a method for attaining the established goals trough the utilization of the spontaneous dynamic, and the minimization of the constraints. The paper is organized in three steps. First: the urban plan is defined as a process of optimization. Second: the set of optimum solutions is compared with the configuration resulting by the spontaneous dynamic. Third: a method for the convergence of the spontaneous dynamic with the optimum configuration is proposed. In conclusion the study shows that planning a complex system is an hard even impossible task, while the control and the utilization of the spontaneous dynamic may help in the attainment of a global utility.

Modelling price competition of retail stores under imperfect information

Margaret Edwards, Pablo Jensen, Hernan Larralde

Social Modelling 5

We improve the realism of the economic description of store competition through prices. We use multi-agents simulations to study the Nash equilibrium for prices under imperfect consumer and store information. Stores do not know the profit vs. price curve and have to calculate it "on the fly", as consumers buy. Consumers do not know the actual prices and progressively learn them through information exchange with their social network. We show that under many realistic situations, incomplete dissemination of the information for the consumers distorts the estimation of the profit and prevents convergence of the price to the optimum.

Simulating pedestrians and cars behaviours in a virtual city : an agent-based approach

Arnaud Banos, Abhimanyu Godara, Sylvain Lassarre

Social Modelling 5

Despite the central and fundamental role pedestrian walking plays within the urban transport system, it still remains a badly known transportation mode. Generally speaking, while most of the developed countries have been developing, for the last 40 years, a wide variety of sophisticated methods and tools aimed at studying urban mobility, only a few of them were really designed to deal with pedestrian movement, especially in interaction with the other transportation modes. The key point we will try to defend here, is that pedestrian movement needs not only to be considered as a specific phenomenon. It also needs to be included in a much more global and complex perspective, the urban system as a whole. Pedestrian motion indeed occurs in an ever changing environment, defined by constraints and opportunities, but also nuisances and dangers. The SAMU prototype has been precisely designed to explore the behaviour of pedestrians in interaction with the motorized traffic, in a virtual city where most of the phenomenon can be mastered and studied.

Transition to Coherent Oscillatory Behaviour in a Route Choice Game

Dirk Helbing, Martin Schoenhof, Hans-Ulrich Stark, Janusz A. Holyst

Social Modelling 5

Selfish routing of traffic over alternative routes wastes available street capacities, as individuals tend to generate an equilibrium state (a 'Wardrop' and 'Nash equilibrium') with higher overall travel times than in the optimal state. This system optimum is characterized by coherent oscillatory patterns rather than a stationary behaviour. Here, we study the time-dependent decision behaviour in a day-to-day route choice setting by means of experimental and simulation results. While there is a tendency towards establishing the Nash equilibrium in the beginning, we often find a transition to coherent oscillatory behaviour after a long transient time period. In spite of the complex dynamics leading to co-ordinated oscillations, we have identified mathematical relationships quantifying the observed transition process. Moreover, the main discoveries are reproduced by a reinforcement algorithm, which may help to establish more efficient data traffic on the internet.

Emergent Group-Level Selection in a Peer-to-Peer Network

David Hales
Information Tech. Modelling 3

Many peer-to-peer (P2P) applications benefit from node specialisation. For example, the use of supernodes, the semantic clustering of media files or the distribution of different computing tasks among nodes. We describe simulation experiments with a simple selfish re-wiring protocol (SLAC) that can spontaneously self-organise networks into internally specialized groups (or "tribes"). Peers within the tribes pool their specialisms, sharing tasks and working altruistically as a team – or "tribe" even though their individual behaviour is selfish. This approach is scalable, robust and self-organising. These results have implications and applications in many disciplines and areas beyond P2P systems.

Measuring the Dynamical State of the Internet: Large Scale Network Tomography via the ETOMIC Infrastructure

Gabor Simon, Jozsef Steger, Peter Haga, Istvan Csabai,, Gabor Vattay

Information Tech. Modelling 3

In this paper we show how to go beyond the study of the topological properties of the Internet, by measuring its dynamical state using special active probing techniques and the methods of network tomography. We demonstrate this approach by measuring the key state parameters of Internet paths, the characteristics of queueing delay, in a part of the European Internet. In the paper we describe in detail the ETOMIC measurement platform, that was used to conduct the experiments, and the applied method of queueing delay tomography. The main results of the paper are maps showing various spatial structure in the characteristics of queueing delay corresponding to the resolved part of the European Internet. These maps reveal that the average queueing delay of network segments spans more than two orders of magnitude, and that the distribution of this quantity is very well fitted by the log-normal distribution.

Medusa, a functional model of Internet substructure

Scott Kirkpatrick, Shai Carmi, Eran Shir

Information Tech. Modelling 3

We consider the Internet at the level of its sub-networks (called Autonomous Systems, or ASes). All previous studies have used the connection degree as the indicator variable to decompose the network into what one hopes will be nodes with distinct functions or roles. We consider instead a longer-ranged indicator of connectivity, obtained by k-pruning, which removes all sites with less than k neighbors until no such sites remain. Increasing k from 1 in steps of 1 separates any network into "k-shells," leaving at each stage a k-core, and defining a "k-crust" as the union of the k-shells lying outside of a particular core. The construction is unique, the k-core is maximal, and experiments show that the k-cores are indeed k-connected (a hypothesis which is proven for Erdos-Renyi graphs and plausible for dense scale-free graphs such the Internet IP-level and AS graphs. There are similarities and important differences with the "jellyfish" model introduced for the AS-graph by Faloutsis, hence our title for this model, coming from the Eastern Mediterranean. Its characteristics are a core which is the maximal non-vanishing k-core, a scale free region (the successive k-crusts) in which information flows steadily from the periphery towards the core, but also can propagate laterally for unlimited distances through peer connections, and a community of dependent nodes which project directly from the outside world into the core, without taking advantage of the scale-free region. We are in the process of exploring the extent to which this structure distinguishes different models of the Internet's formation, is a basis for projecting its evolution, and suggests new approaches to routing information in the Internet. This work was stimulated by the availability of Internet maps of unprecedented resolution from the DIMES and EVERGROW projects.

Mining the Inner Structure of the Webgraph

Debora Donato, Stefano Leonardi and Panayiotis Tsaparas

Information Tech. Modelling 3

Despite of being the sum of the decentralized and uncoordinated efforts by heterogeneous groups and individuals, the World Wide Web exhibits a well defined structure, characterized by several interesting properties. This structure was clearly revealed by Broder et al. who presented the evocative bow-tie structure of the Web, with a CORE comprised of a large strongly connected component, and four sets of vertices distinguishable from their relation with the CORE. The bow-tie structure is a relatively clear abstraction of the macroscopic picture of the Web graph, but it is very uninformative with respect to the finer details of the Web graph. In this paper we mine the inner structure of the Web graph. We present a series of measurements on the Web, which offer a better understanding of the individual components of the bow-tie. We also document the algorithmic techniques for performing these measurements. We discover that the scale-free properties permeate all the components of the bow-tie which exhibit the same macroscopic properties as the Web graph itself. However, close inspection reveals that their inner structure is quite distinct. We show that the Web graph does not exhibit self similarity within its components, and we propose a new picture for the Web graph, as it emerges through our experiments.

Towards an Economic Theory of Meaning and Language

Gabor Fath, Miklos Sarvary

Cognition Modelling 1

We present a model in which abstract concepts of a language acquire meaning as the result of competition between heterogeneous interacting agents in a community. We argue that bounded rationality requires individuals to use a reduced number of abstract concepts to represent the rich reality of the world. The meanings of these concepts emerge as a trade-off between two objectives: (i) agents want to use concepts that are best adopted to their idiosyncratic preferences and characteristic distribution of choice alternatives, (ii) agents seek to share concepts to benefit from communication. Agents play a non-cooperative game, whose Nash equilibrium determines the collective meanings of concepts in the population, constituting together the community's language. Analysis of the possible Nash equilibria and the evolutionary game dynamics shed light on interesting theoretical questions such as the origins of meaning, the coherence of language, the language-culture relationship, and Whorf's hypothesis on linguistic relativism.

Stability conditions in the evolution of compositional languages: issues in scaling population sizes

Paul Vogt
Cognition Modelling 1

In the past decade an increasing number of models on the evolution of language have been studied. Most of these model are based on the assumption that language is a complex dynamical adaptive system [2]. The idea of this assumption is roughly that language itself adapts culturally to its users as if it is a complex dynamical system, which contrasts the nativist approach in which language users adapt to use and acquire language.

One important area of research has focused on the emergence and evolution of compositional languages, i.e. languages in which parts of its expressions map onto parts of its meanings. The models that take language as a complex dynamical adaptive system can – with respect to population dynamics – be divided into two classes: those with and those without a population turnover.

Most of these models work with very small populations, typically of size 2 or with somewhat larger populations (up to 50 agents), but where each agent only communicates with a smaller subset of the population. New Ties (see http://www.new-ties.org) is a recently started FP6/IST/FET Open STREP project in which we aim at evolving language in very large populations.

This paper reports a pilot study for New Ties using a recently developed model on the emergence and evolution of compositional languages [3] that incorporates a population turnover in relatively large populations. Although we expect that the agents in the New Ties project do not all communicate with each other (since that may make the simulations intractable, or at least very unstable), we would like to investigate the scalability of the model. The study reports experiments in which the population size is increased to 100 agents. The results show that when the population size increases, after an initial decline in the results, the level of compositionality substantially increases and mostly outperform the levels achieved for lower population sizes. This result is explained by a hypothesised trade off for increasing population sizes between an increasing difficulty in achieving a shared communication system and an increased likelihood of finding co-variations among expressions and meanings that emerge by chance. The increased performance suggest that language evolves easier in a large(r) population.

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Self-Organizing Communication in Language Games

A. Baronchelli, M. Felici,, E. Caglioti,, V. Loreto, L. Steels

Cognition Modelling 1

Keywords: Language games, Communication, Self-organization, Negotiation dynamics, Shared conventions, Social bookmarkings.

From the point of view of semiotic dynamics language is an evolving complex dynamical system. In this perspective, unrevealing the mechanisms that allow for the birth of shared conventions is a major issue. Here we describe a very simple model in which agents negotiate conventions and reach a global agreement without any intervention from the outside. In particular we focus on the possibility of predicting on which of the several competing conventions the agreement is reached. We find from simulations that early created conventions are favored in the competition process and this advantage can be quantified. Beyond the specific results presented here, we think that this paper provides an example of a new way of investigating language features where simple models allow for the investigation of precise problems and, possibly, for analytical approaches.

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The self-organization of combinatorial vocalization systems

Pierre-Yves Oudeyer

Cognition Modelling 1

Human vocalizations have a complex organization. They are digital and combinatorial: they are built through the combination of units, and these units are systematically re-used from one vocalization to the other. These units appear at multiple levels (e.g.the gestures, the coordination of gestures, the phonemes, the morphemes). While for example the articulatory space that defines the physically possible gestures is continuous, each language only uses a discrete set of gestures. While there is a wide diversity of the repertoires of these units in the world languages, there are also very strong regularities (for example, the high frequency of the 5 vowel system /e,i,o,a,u/). The way the units are combined is also very particular : 1) not all sequences of phonemes are allowed in a given language (this is its phonotactics), 2) the set of allowed phoneme combinations is organized into patterns. This organization into patterns means that for example,one can summarize the allowed phonemes of Japanese by the pattern 'CV(N)': a syllable must be composed of three slots, and in the first slot only the phonemes belonging to a group that we call 'consonant' are allowed, while in the second slot, only the phonemes belonging to the group that we call 'vowels' are allowed, and there is possibly a third slot in which only certain kinds of consonants, which are called 'nasals', are allowed.

It is then obvious to ask where this organization comes from. There are two complementary kinds of answers that must be given (Oudeyer, 2003). The first kind is a functional answer stating which is the function of systems of speech sounds, and then showing that systems having the organization that we described are efficient for achieving this function. This has for example been proposed by (Lindblom, 1992) who showed that digitality and statistical regularities can be predicted by searching for the most efficient vocalization systems. This kind of answer is necessary, but not sufficient : it does not say how evolution (genetic or cultural) might have found this optimal structure. In particular, naive darwinian search with random mutations (i.e. plain natural selection) might not be sufficient to explain the formation of this kind of complex structures : the search space is just too large (Ball, 2003). This is why there needs a second kind of answer stating how evolution might have found these structures. In particular, this amounts to show how self-organization might have constrained the search space and helped natural selection. This can be done by showing that a much simpler system spontaneously self-organizes into the more complex structure that we want to explain.

(Oudeyer, 2005) has shown how a system of this kind, based on the coupling of generic neural devices which were innately randomly wired and implanted in the head of artificial agents, could self-organize so that the agents develop a shared vocalization system with digitality, combinatoriality and statistical regularities. We present here an extension of this system which gives an account of the formation of phonotactics and of the formation of patterns in the allowed phoneme combinations. The extension is based on the addition of a map of neurons with temporal receptive fields. These are initially randomly pre-wired, and control the sequential programming of vocalizations. They evolve with local adaptive synaptic dynamics.

The system provides a necessary complement to the functionalist explanation. Interestingly, it does not require the presence of a functional pressure for efficient communication. It does not require any social pressure and agents have no social skills at all in fact. While

modern speech codes are obviously influenced by the function of communication, the simplicity of the system allows to put forward a new hypothesis for the initial invention of shared organized vocalization systems: they might be a self-organized side effect of certain brain structures evolved for other functions than communication. We will develop this hypothesis by explaining which are these brain structures and what was their initial function.

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When language breaks into pices. A conflict between communication through isolated signals and language.

Ramon Ferrer i Cancho

Cognition Modelling 1

Here we study a communication model where signals associate to stimuli. The model assumes that signals follow Zipf's law and the exponent of the law depends on a balance between maximizing the information transfer and saving cost the cost of communication. We study the effect of tuning that balance on the structure of signal-stimulus associations. The model starts from two recent results. First, the exponent grows as the weight of information transfer increases. Second, a rudimentary form of language is obtained when the network of signal-stimulus associations is almost connected. Here we show the existence of a sudden destruction of language once a critical balance is crossed. The model shows that maximizing the information transfer through isolated signals and language are in conflict. The model proposes a strong reason for not finding large exponents in complex communication systems: language is in danger. Besides, the findings suggests that human words may need to be ambiguous to keep language alive. Interestingly, the model predicts that large exponents should be associated to decreased synaptic density. It is not surprising that the largest exponents correspond to schizophrenic patients since, according to the spirit of Feinberg's hypothesis, decreased synaptic density leads to schizophrenia. Our findings suggests that the exponent of Zipf's law is intimately related to language and that it could be used to detect anomalous structure and organization of the brain.

A Multi-Level Model for Spatial Dynamics of Systems of Cities through Innovation Processes

Denise Pumain

Social Modelling 6

We develop here an evolutionary theory of urban systems as complex systems characterised by a hierarchical structure (following a Zipf's distribution of city sizes and a more or less regular geographical pattern), a functional diversity and various scaling laws according to different urban functions. These properties are summarised in a multi-agents systems called SIMPOP2, that is a generic model for simulating the dynamics of a variety of settlement systems while they emulate and adopt innovations. The basic conception is that a hierarchic urban system emerges from the spatial interactions between settlements over a long time period. Interactions are driven by competition for promoting and capturing the benefits of innovations (territories, market zones or networks according to each type of urban function). They are submitted to different social and political contexts or functional rules, evolving through time. Most of interactions are defined at the meso level of the urban agglomerations but some of them, as urban governance or innovation, may be acted by agents of a lower level or institutions at higher levels. The model helps identifying which key parameters (at micro, meso or macro level) can lead to the emergence of the three major types of observed settlement systems: regular and dense, but more or less concentrated (European or Asiatic countries) ; dual and primate (developing countries); strongly hierarchised and sparse (countries of the "New world"). More detailed versions of SIMPOP2 can be adapted for calibrating observed evolutions (cf. EUROSIM).

Modelling urban networks dynamics with multi-agent systems

Lena Sanders

Social Modelling 6

The paper concerns the geography of system of cities in a dynamic perspective. Already in 1964 Berry wrote a paper called "Cities as systems within system of cities", and obviously the evocated systems were complex, their form and their evolution resulting from sets of interactions operating at different scales. The EUROSIM model (a specific version of SIMPOP2 model), built up within a multi-agent framework, integrates accumulated knowledge about urban systems. The purpose is to simulate the evolution of the European system of cities during the past 50 years, and to explore its future dynamics during next half century according to different scenarios.

The hypothesis is that the properties of the urban system at a macro-geographical level emerge from the interactions between entities of lower geographical levels. The choice of the lower level to be formalized is first discussed. In social sciences, the individuals, the households, or the firms are often considered as the elementary entities for modeling a social system. In the Eurosim model, the cities themselves, as collective entities, are represented by agents, and their ontological state has then to be precised.

The functioning of the model is then presented. The cities larger than 200 000 inhabitants constitute the driving layer of the urban system. Depending on its specialization each city is connected to a set of cities through associated networks which are evolving through time. The mechanisms of supply, demand and exchanges which determine the interactions between the cities are formalized using the protocol of communication of the multi-agent system. The dynamics of each city depend on its ability to gain wealth through successful exchanges, while the global growth is driven by innovation. Multiscalar tools for analyzing the outputs of the model are presented and the question of calibration is discussed.

Analysing the resilience of complex resources management systems: a stylised simulation model of human-nature interactions in a river basin

Maja Schlueter, Claudia Pahl-Wostl

Social Modelling 6

The uncertainties of global change and the complexity and unpredictability of the dynamics of social-ecological systems demand for new approaches to ecosystem and resources management. Rather than attempting to predict and control natural variability those approaches focus on strengthening the flexibility of a system to cope with unexpected change. The aim is to enhance system resilience and its capacity to adapt. Resilience is the potential of a system to remain in a particular configuration, to maintain its feedbacks and functions and to reorganise following disturbance driven change. Resilience is seen as an important stability property that determines the system's capacity to adapt to and benefit from change. A variety of mechanisms of resilience specific for different systems have been identified, such as genetic and biological diversity, redundancy and modularity, the capacity to learn and store knowledge and experience, to create flexibility in problem solving and balance power among interest groups. In the context of natural resources management a system's capacity to learn from and adaptively respond to stress emerges from interactions between biophysical and social processes. A sound understanding of mechanisms determining the resilience of coupled social-ecological systems is the basis for adaptive management of natural resources. Simulation models of human-environment interactions are valuable tools to study factors and mechanisms that determine the resilience of a complex resources management system to stresses such as high variability in resources availability, extreme events and long-term changes. We develop a model of a coupled social-ecological system in a river basin to explore the influence of the organisational structure of water management, of cross-scale interactions among actors, information storage and flows, and other factors for the resilience of the coupled system. Special emphasis is put on the role of feedbacks between the human and the environmental system. The aim is to study the interrelationship between system structure and functioning treating the social-ecological system as a complex adaptive system. The model represents a stylized water management system, based on the context of the Amudarya river delta, where water resources are used to sustain agriculture as well as semi-natural fish populations. Besides irrigated agriculture fish is an additional source of income. The model combines a model of a water flows network with an equation-based model of a simplified aquatic ecosystem and an agent-based model of decision making and resources exploitation composed of simple rules. Decision making and information flows are represented at different scales (local, regional, national). The success of individual agents as well as the state of the human-used ecosystem depends on local water availability. Simulation experiments are carried out to test different settings of the agent's ability to obtain information and manage the resource in the face of different levels of variability and uncertainty in water inflow to the region. The resilience (measured as the global and local achievement of production goals, state of the ecosystem, etc.) of the different management regimes is compared. It is expected that the buffer capacities of a water reservoir and the ecosystem are important factors determining the resilience of the system. Access to and transfer of information and learning processes among agents are major factors influencing the capacity of the system to adapt. In the presentation the model concept and first simulation results are presented.

Reflexivity as a constitutive property of a complex urban system

Sylvie Occelli, Luca Staricco

Social Modelling 6

Applying the notion of complex system to cities and territories has the unwarranted advantage to make it possible to establish several conceptual links between the many facets of urban systems, like openness, self-organization, pro-activity and awareness. While the features concerning openness and self-organization have been extensively scrutinized as constitutive determinants of urban complex systems, those concerning pro-activity and awareness have been generally viewed as external. At most, they have been considered as desirable features of a group of agents, i.e. experts, planners and educated people, entitled to steer the evolution of the urban system towards more desirable and sustainable paths of change. Pro-activity and awareness mean that there exists a reflexive property, which is intrinsically constitutive of an urban system,. i.e. a collective agent constituted by an interacting group of social cognizant agents supported by a physical, social, technological environment. In this regard, Maturana's arguments about the drive of the explanatory search for understanding which characterizes a living being can be understood as an internal drive of the urban system. A Reflexive Urban System (RUS), therefore, is one which: * is able to think about of its knowledge own generative determinants (i.e., the agents involved, the process through which knowledge is yielded, and how it is encoded and decoded in the urban system); * permanently seeks to adapt (improve) those determinants in the course of its evolution. A major challenge for a complexity approach to urban systems, therefore, is that a methodology for a RUS should be viewed as an embedded dimension of the system itself, i.e. it should be an internal endeavour steering the system's own evolution. In order to fully account for the pro-active feature characterizing a RUS, therefore, one cannot be satisfied with an evaluation of the system behavioural performances but has to constructively engage in the knowledge process of building the RUS's own methodology. In addition, as a RUS is a collective entity, the methodological framework cannot help resulting from a collectively determined process. According to this line of reasoning, a claim is made that one major function of applying a complexity approach would be to sustain the systemic coherence necessary to the RUS line of enquire, i.e. to stir its drives in the explanatory search for understanding and help avoiding the constraints and prejudices. Finally it is suggested that underlying a complexity approach for a RUS three major dimensions might be regarded as principal leverages: * recognition, the identification of knowledge needs in order to sustain a pro-active endeavour; * guidance, how to make effective the recognized knowledge needs, in order to get involved in a purposeful line of enquiry ; * capability, the achievements of social valued outcome for somebody who cares.

Complex-city: the shift of urban science from classic to an evolutionary approach

Giovanni A. Rabino
Social Modelling 6

In an effort of interdisciplinary comparison, the aim of this short paper is to illustrate how the new concepts (and methods) of complexity are applied in the science of territory (i.e. cities and towns systems). Being territorial science at the same time a theoretical (e.g. urban geography) and an applied science (e.g. city planning), the presentation is organised in two parts: complexity in urban system analysis and complexity in town planning and design. Note that in the paper all points below are argued referring to real case-studies or experimental applications. Moving from first principles, we describe how urban analysis, namely mathematical models of urban system, leaving from a static functionalist approach (Lowry, 1964), through dynamic modelling, got to a co-evolutionary description of a set of territorial processes (see, for instance, Pumain, 2004). In this framework, it is shown that many classical principles of spatial organisation, such as cities rank-size law or Christaller rule, are better re-interpreted or refined in term of complex phenomena (scale invariance, emergence of order ...). As to the methods of complexity used in urban analysis, we focus on two aspects: - fractal morphology, to describe and explain new trends in urbanisation: sprawl and smart growth; - multi-agent modelling, as a powerful tool for catching many non-linear interactions among the various stakeholders in the city. Going to consider urban planning, first of all it is argued that the traditional net divide between urban analysis and planning no more holds. In the light of complexity, analysis and planning, like many other learning - creativity phenomena, are strictly joined in a (individual and social) evolutionary (conscious and intentional) decision process. In this context, we present: -at a general level, the complexification of planning practices (public participation, governance, e-planning, etc.) in relation to a more complex society and innovative technologies; - at a more specific level, some new planning methods and tools (strategic planning, "best practices" methodology, etc.) directly derived from the new evolutionary approach to the science of the city.

The problem of design in complexity research

Theodore Zamenopoulos, Katerina Alexiou

Social Modelling 6

This paper discusses the contribution of design research problems and abstractions in the formation of a complexity research agenda. Design is a capacity associated with systems that are often characterized as complex - but does design imply a general capacity and class of research problem that is inextricably linked with the complexity of a system? This is a rather uncommon enquiry even though the relation between design and complexity has been explored under two themes: the complexity of design, that is the identification and measurement of the complexity of design objects, processes and problems; and the design of complexity, that is the construction and management of complex (artificial) systems. However, these are mainly applications of complexity concepts and measurements in design research and practice rather an investigation of the meaning of complexity based on the design capacity of systems. The purpose of this paper is to discuss the mathematical basis and problems of a design theory of complexity and demonstrate the uniqueness of design as a distinct problem in the context of a complexity research agenda.

Complexity research is too versatile to be described by an indisputable research agenda. However there are a number of traditions and problems that can characterize the meaning of complexity and the scope of complexity research. For instance, complexity has been identified with the combinatorial capacity of systems; scaling; the capacity to exhibit certain types of critical behaviour or attracted to critical states; the evolutionary capacity of systems, associated with problems of cooperation, competition and reduction of variety; and finally the organizational capacity of systems. For developing the argument of the paper the focus will be on the latter aspect of complexity research.

In this investigation, complexity is associated with the capacity of a system to exhibit a certain type of organization. The motivation for this is that certain types of organized systems, such as the brain, organisms or societies, can exhibit complex functions such as intelligence, life, or governance. The main question is two-fold: first, to identify the organizational conditions that enable such capacities to emerge; and second, to identify the capacity that explains how these organizational conditions are produced and maintained. The production and maintenance of the organizational conditions of a system generally alludes to the capacity of the system to change the structure, behaviour or function of its environment (or its perception of this environment) and through this change to transform itself. Typical examples of such capacities are distinction and intentionality, autonomy and control, creativity and learning, anticipation and - as we claim in this paper - design. Design in particular alludes to the capacity of producing organizational changes in the environment of a system that increase the complexity of the system relative to its environment. Irrespective of where one chooses to embody or allocate this capacity, the special characteristic of design problems -in distinction to other abstractions such as machine, control or evolution- is that the complementary nature of the relation between system-environment is not a given but it is the problem itself.

Goguen and Varela ([1], [2], [3]) have explicitly associated the complementary relation between system and environment with the category-theoretic concept of adjunction. The same adjoint relation can be implicitly found between allonomy and control, machine and language but also to other organizational concepts such as coordination and subordination, or scaling and variety ([4]). Changes in the system and its environment always preserve the system-environment complementarity. Now the question is whether it is possible to

perceive changes where the adjoint relation between levels of organization is not preserved. This class of problems will be generally called design problems. The idea would be to 'push' the system 'far for the adjoint relation' and explore abstractions that underline these capacities and organizations.

In order to fix these ideas, the complementary relation between sets and monoids is analyzed. In particular, a monoid structure is represented in a type of one dimensional cellular automata space. The objects of the structure are realized by natural numbers, whereas the morphisms are realized by mappings between natural numbers. By enabling the state of a cell to play both the role of an object and a morphism between neighbour cells, the operation of composition and coupling is introduced. The paper demonstrates the formation of cells that work as boundaries between inner and outer areas by means of composition and coupling that are not structural preserving. Based on this model, a definition of the design capacity of systems is discussed.

To sum up, the paper identifies the concept of design as a distinct research question in complexity research. It explicitly links general problems of complexity with the specific concept of design and discusses the unique characteristics of design problems. It is hoped that this can be of benefit for both complexity research and design science.

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Understanding fractal analysis? The case of fractal linguistics

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Complex Systems Methods 3

Field: CS questions Key words: Fractal analysis, nonlinear science, communication, linguistics

Terms such as 'self-similarity', 'space filling' 'fractal dimension', and associated concepts have different meanings to different people depending on their background. We examine how methodology in fractal analysis is influenced by diverse definitions of fundamental concepts that lead to difficulties in understanding fundamental issues. The meaning of terms associated with fractal analysis need to be clarified if this method is to be useful in diverse disciplines. It is our premise that communications that are result focused constitute a danger in perpetuating misconceptions of terms due to the concise nature of the writing and the reliance on references to fill in the procedural and conceptual gaps. Communicating effectively requires a sound understanding of the terminology and a clear and meaningful presentation. We address here communication and the nature of scientific discourse, 'fractal linguistics'

Ambiguity in Art

Igor Yevin

Complex Systems Methods 3

Abstract. Non-linear theory proposed different models perception of ambiguous patterns, describing different aspects multi-stable behavior of the brain. This paper aims to review the phenomenon of ambiguity in art and to show that the mathematical models of the perception of ambiguous patterns should regard as one of the basis models of artistic perception. The following type of ambiguity in art will be considered. Visual ambiguity in painting, semantic (meaning) ambiguity in literature (for instance, ambiguity which V.B.Shklovsky called as "the man who is out of his proper place"), ambiguity in puns, jokes, anecdotes, mixed (visual and semantic) ambiguity in acting and sculpture. Synergetics of the brain revealed that the human brain as a complex system is operating close to the point of instability and ambiguity in art must be regarded as important tool for supporting the brain near this critical point that gives human being possibilities for better adaptation.

Hierarchical Organization in Smooth Dynamical Systems

Martin Nilsson Jacobi

Complex Systems Methods 3

We define and characterize hierarchical structures in smooth dynamical systems. Smooth projective maps from the original phase space to a phase space with lower dimensionality define transitions between levels in a dynamical hierarchy. It is required that each level describes a self-contained deterministic dynamical system. We show that a necessary and sufficient condition for a projective map to be a transition between levels in the hierarchy is that the kernel of the differential of the map is tangent to an invariant manifold with respect to the flow. The implications of this condition are discussed in detail. We also show how the projections can be defined using a quotient manifold construction with a Lie group invariant under the flow of the dynamical system. The relation to symmetries of the dynamics is demonstrated. Finally these results are used to define functional components on different levels, interaction networks, and dynamical hierarchies.

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Toward a multi-scale approach for spatial modelling and simulation of complex systems

Thi Minh Luan NGUYEN, Christophe LECERF, Ivan LAVALLEE

Complex Systems Methods 3

Complex systems are composed of many heterogeneous elements organized in a hierarchical way, whose mutual interactions make emergent collective behaviors to appear at the highest levels of observation. In some kind of complex systems, especially in biology as shown by the integrative physiology theory (Chauvet96), space and geometry have a significant role in the simulation results. In this paper we expose a formalized method for modelling and simulation of complex system, going from structural modelling to dynamic simulation while integrating geometrical information in behavior study. Our solution relies on three kind of concepts and techniques: hierarchical graphs for modelling the system structure and organization, Zeigler's formalisms for the specification of agents (Zeigler00) and a space aware Multi Agent System for agent-based simulation. It is shown how complex system simulation benefits from the combination of agent-based simulation and DEVS.

Creativity Patterns in Art Perception

R Adam, J Goldenberg, E Adi-Japh, D Mazursky, S Solomon

Poster

Goldenberg J., Mazursky D. and Solomon S. searched for regularities in creative ideas and creative thinking. They studied those subjects mainly in the field of marketing: advertisements and new products innovations. They found creativity templates, meaning well-defined, objectively verifiable, and generalizable abstract patterns. From those templates, creativity emerges. The templates describe the relations between the components or the attributes of a product. Creativity templates appear in most creative advertisements and new products. For instance, 89Our aim was to check whether creativity templates exist and can achieve similar results in other fields. We chose the most creative and subjective field: art, and to be more specific, creativity perception in photography. What makes a photograph creative? In this study we used 23 photographs that were regarded on the web as "the best pictures of 2003". Fifteen subjects from various countries chose the five most creative photographs from the set of photographs, and explained why, in their opinion, those pictures were creative. We were interested only in the components referred to by viewers when judging art, and not in the whole photograph or all of its objects. Thus,we searched for patterns in subjects' explanations. In total, we had 72 explanations. Only 35 referred to the elements in the photographs. Only these 35 explanations could be translated to the formal way which is essential for detecting creativity templates. The other explanations were unclear or described the subjects' feelings while seeing the photographs. From the 35 explanations, 43Diagonal Link (DL) pattern is a transitive connection: a connection between two components generated by the connection of every one of them to intermediate component. Twenty percent of the 35 explanations contained DL. It is embedded in one frequently seen creativity template known as the Replacement Template. We will demonstrate the DL by a photograph showing a ship sailing in icy water at sunrise. One of the subjects who chose this photograph as creative explained his choice in the following sentence: "The back light is illuminating the fog in a very intense manner so that it almost appears as fire". In this explanation the back light affects the fog, the back light is red, and the transitive result is a 'fire-like' red fog. Properties Tension (PT) appears when the main components in a photograph have contrasting properties. This pattern appeared in twenty percent of the explanations. In one of the photographs one could see the head of a black cat with yellow eyes in a golden wheat field. One subject's explanation was: "...the eyes of the cat look bad and the field of grain looks kind". The main components in this photograph (the cat's eyes and the field) had the same color, but contrasting properties (bad versus kind). Unification pattern appears when two unrelated objects joined to form one hybrid object, which looks like the first object but functions as the second. It was found in 11.4Three fixed formulations of the elements in a photograph were found to cause creativity perception. Those are primary results and our patterns need to be further validated to be called creativity templates. However, those results show that art perception is not as arbitrary as might be imagined.

Agent Based Modeling of Consumer Behavior

Iqbal Adjali, Ben Dias, Robert Hurling

Poster

Understanding the drivers for consumer behavior and the underlying mechanisms of market dynamics is of key importance to marketing practitioners, market strategists and competition and regulatory bodies. Furthermore the cross-disciplinary nature of this area has attracted the interest of researchers in diverse fields such as economists, social scientists, psychologists and computational scientists. Marketers usually ask questions like "What are the chances for success when a new product is launched (e.g. brand extension)?" or "How does word-of-mouth affect sales and the long-term prospects of a brand?" To answer these questions, traditional marketing models, based on equilibrium statistics and macro variables such as market share and price elasticity, have usually been employed with limited success. As a powerful computational method, agent based modeling has the potential to address many of the shortcomings of traditional techniques. Specifically, ABM (i) allows the dynamic nature of markets to be modeled, (ii) treats consumers as individuals therefore retaining the richness of information at the micro level and (iii) allows consumer interactions and social networks to be explicitly modeled. Here we describe the architecture for an agent based consumer behavior model drawing from the marketing and the behavioral sciences literature. We present some simulation results exploring and comparing different consumer behavior models using real, individual-based market data.

Analytic Visualizations and their Applications for the Autonomous System Graph

Vinay Aggarwal, Anja Feldmann, Marco Gaertler, Robert Görke, Yuval Shavitt, Eran Shir, Dorothea Wagner, Arne Wichmann, ,

Poster

The graph of the Autonomous Systems, i.e., collection of computer devices under the same administrative authority that establish global connection in the Internet, is an instance of a small complex system. Out of the vast range of issues that have been addressed in the context of this network, we focus on revealing structural information via visualization. In the following, we present several examples in the context of temporal evolution between 2001 and now, overlay networks, i.e., comparing Gnutella communication and AS peering relations and the comparison of data samples from different sources.

Are epidemics on scale-free networks predictable?

Fabián Alvarez, Pascal Crépey, Marc Barthélemy

Poster

The scale-free topology has been widely described in many artificial and natural networks. It is characterized by a broad distribution of individual connectivities which can take values over several orders of magnitude.

In this work, we study how these large connectivity fluctuations affect the sensitivity to the noise of an epidemic scenario and consequently its predictability. We investigate this problem by inspecting thoroughly the time evolution of the number of infected at the beginning of the outbreak. We study numerically the variability of epidemic outbreaks spreading on scale-free networks and compare these results with simulations on random homogeneous networks, in which connectivities are normally distributed around their average value <k>. Propagation on random networks corresponds to the usual assumption of homogeneous mixing in classical epidemiology and provides a useful reference model to assess the effect of degree fluctuations.

We consider the usual compartmentalization of individuals into three categories: susceptible (S), infected (I) and removed (R). The time evolution of the individuals is described by the usual epidemiological schemes SI, SIS or SIR, and we focus on the temporal evolution of the prevalence (number of infected in the population). For a fixed set of the parameters of the model (infection scheme, infection rate, number of index cases), we simulate numerically a large number of outbreaks (up to 100 000), and we analyze different averages: average over a number e of outbreaks on the same network, average over a single outbreak on r different networks, and average over e outbreaks on r networks. We study quantities such as the coefficient of variation of the prevalence (CV_i), the time to peak of CV_i, and the distribution of the prevalence doubling time. In the light of the numerical results for these quantities, we discuss the influence of the different sources of noise on the variability of the epidemic scenario.

In particular, our results show that on scale-free networks, a peak of the CV_i is reached in the very first stages of the epidemic outbreaks, before its exponential growth. At this peak, the CV_i is of order 2-3 in contrast with a CV_i of order 1 (1.0 to 1.5) obtained for random homogeneous networks. These value are calculated when "dying" outbreaks are discarded (SIS and SIR models), and then may be larger if all outbreaks are considered. We also verified that the results are robust for large ranges of the models' parameters.

Our results suggest that in the situation of an emerging disease spreading on a scale-free network, the epidemic scenario is very sensitive to the topology of the network. Furthermore, these large fluctuations make the prediction of the disease time evolution -based solely on the topology of the network and on the first infected cases- almost impossible.

Amino acid evolution: an alternative hypothesis

Peter Andras, Alina Andras, Csaba D. Andras

Poster

The understanding of the evolution of amino acid usage in proteins of living organisms is a fundamental issue in the context of theories about the origins of life. The commonly accepted view is that life started with a few amino acids and newer ones were added to the amino acid library of organisms during evolution. Here we propose an alternative hypothesis, suggesting that life might have started with an initial expansion of amino acids followed by gradual decrease of the number of amino acids used in proteins.

Environmental uncertainty and language complexity

P Andras, J Lazarus, J G Roberts

Poster

We examine how the complexity of language is influenced by the level of uncertainty (= risk) in the environment (Andras, Roberts and Lazarus 2005), when language is used to communicate cooperative intentions between interacting agents. Since cooperation increases with risk (measured as both environmental adversity and uncertainty) in a number of biological contexts (Andras and Lazarus 2005), and cooperation requires communication between interacting agents, the question arises of whether language complexity might vary adaptively as a function of risk. An example is the evolution of human language in the small cooperative groups of early hunter-gatherers.

We model a world of simple agents that own resources that are used for survival and to produce new resources, environmental risk being expressed as the variance in the reproduction of these resources (Andras, Roberts and Lazarus 2003). Agents produce offspring and the number of offspring depends on the amount of resources owned by the agent. New agents inherit the language of their parent with some random mutations.

Agents communicate with each other about their intention to cooperate by sharing resources. The language contains the following semantic elements: no interest in communicating; start of communication; intend to communicate further; want to engage in sharing; lost interest; share action; not share action. Agents remember previous encounters and if they meet again an agent with whom they have previously cooperated then communication symbols likely to lead to cooperation increase in probability in the current encounter (and vice versa).

As risk increased in the simulations cooperation increased, and cheating and non-cooperation decreased, as found in nature (Andras and Lazarus 2005). Overall, there was no clear relationship between language complexity (i.e. the length of communication sequences between agents) and environmental risk, although communication sequences were shortest in the most risky environments.

The lack of a clear relationship between language complexity and environmental risk may have been because the model language was too simple, varying between only 4 and 6 elements at the outset. For a richer language – which we plan to investigate - we predict that communications will be shorter as risk increases (as the data for our highest risk level suggested) since: (1) there was a positive correlation between cooperation level and risk, and (2) there was a negative correlation between cooperation level and language complexity. Those who cooperated had shorter communication strings than those who cheated or failed to cooperate. This is because if a cooperator meets an agent for whom it has a memory biased towards cooperation then it has a higher probability of producing positive communication symbols (those encouraging cooperation) and therefore moves with fewer communication steps into an interaction that is likely to be cooperative. Thus cooperative agents, by positive feedback, build an increasingly cooperative relationship with each other. Cooperation thus saves on communication effort.

The results have implications for the design and use of communication systems under conditions of uncertainty, and for the role of environmental uncertainty – for example, in foraging - in shaping the evolution of human communication patterns.

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Keywords

multi-agent systems, communication, language, cooperation, environmental uncertainty

Fault tolerance and network integrity measures: the case of computer-based systems

Peter Andras, Olusola Dowu, Panayiotis Periorelis

Poster

Fault tolerance is a key aspect of the dependability of complex computer-based systems. Fault tolerance may be difficult to measure directly in complex real world systems, and we propose here to measure it in terms of integrity preservation of the system under the assumption of a particular fault occurrence distribution. We measure the integrity preservation ability of the system by measuring the change of structural integrity of the graph representing the system while it is exposed to random node removal according to the assumed fault distribution. We show how to use such measures to measure the integrity reservation of computer-based systems and in this way indirectly their fault tolerance. We discuss the application of the proposed method in the context of a real world example, the Linux operating system. The results indicate that integrity preservation metrics can serve as an appropriate measure of fault tolerance of complex computer-based systems.

Towards adaptive self-aware software

Peter Andras, Bruce Charlton

Poster

Self-aware adaptive software is a saint Grail of computer science. Recent advances are very promising, and software systems have several features required for being self-aware and adaptive (e.g., introspection and self-modification). However no truly self-aware adaptive software system exists currently. We analyse biological and social systems as abstract communication systems, building an analogy with software systems (i.e., systems of communicating objects). We highlight three critical features of natural systems: the asymmetry of true/false, the growth by correctness checks, and error-induced adaptation based on self-monitoring. Based on the established analogy we propose to build software systems with non-terminating proofs of correctness, to achieve self-aware adaptive software.

How complexity theory may explain influence of music

Svetlana Apjonova, Igor Yevin

Poster

Recent researches revealed that music reduces the degree of chaos in brain waves. A.Loskutov, A.Hubler, and others carried out a series of studies concerning control of deterministic chaotic systems. It turned out, that carefully chosen tiny perturbation could stabilize any of unstable periodic orbits making up a strange attractor. V.Bondarenko shown in computer experiments a possibility to control a chaotic behavior in neural network by external periodic pulsed force or sinusoidal force. Low-dimensional outputs are observed when the frequency of the external force is close to delta-, theta-, alpha-, and beta frequencies. We suggest that music acts on the brain near these eigenfrequencies of self-excited oscillations in the neural network to suppress chaos. We explain the structure of music tonalities using concept of attractor network model. Three stable steps of tonality: tonic, median, and dominant are keynotes or attractors of neural network model. There are many reasons to believe that among four types of instinctive behaviors and four frequencies of the brain exists one-to one correspondence: delta rhythm – food behavior, theta – fear, alpha – sex, and beta – aggression. This hypothesis does not contradict with available empirical date. Delta rhythm is the main rhythm for all newborns both animals and humans (infants up to one years of age). Undoubtedly, the food instinct is the main instinctive behavior for all newborns. Therefore, delta rhythm may be connected with the pleasure taken from food. Theta rhythm one usually connects with waking behavior in different species which are pivotal to the animal's survival. For instance, it is predation for cats, exploration for rats, and apprehension for rabbits. Undoubtedly, the basic for all such kinds of pivotal behaviors is food behavior. There is never-ending conflict and tension between food searching and avoiding predators which is the strongest natural stressor that wild animals experience. Theta rhythm is also dominant rhythm for human infants by 13 years old. We may suggest that all such kinds pivotal behaviors are accompanied by fear because namely during food searching and during childhood animals and humans are the least defended and protected from different threats outside. The source of theta oscillations is the hippocampus which has strong reciprocal connections with amygdala - the centre of fear emotion. Therefore the fear is the next in importance and the next in order instinctive behavior and it may be connected with alarm, threat, and fear feelings. Completion of the alpha rhythm occurs at the puberty period. Children before 12-13 years old have rather weak alpha waves. Adult humans have maximal alpha rhythm when he or she is relaxing with close eyes. But relaxing state with closed eyes usually accompanies sexual enjoyment. Beta rhythm is associated with focused attention toward external stimuli, alert mental activity with increasing muscle tension and raising blood pressure. We suppose that beta rhythm is connected with aggression. This assumption is supported by A.Blood and R.Zatorre experiment that music involves the brain regions such as ventral stratum, midbrain, amygdala that are connected with such biologically relevant stimuli as food, sex and others.

Stochastic Processes in Complex Systems: exactly solvable models

V.E. Arkhincheev

Poster

The different models of random walks with anomalous diffusion such as Comb model, Continuous time random walks and Levy flight diffusion are considered. The first part of report is devoted to the problem of obtaining of the generalized diffusion equations for anomalous random walks. It is shown that these equations have form of the fractional integro-differential equations. There are three types of generalized equations are possible: fractional temporal equations, fractional spatial equations and mixed fractional temporal-spatial ones. The solutions of these equations in the non-gaussian form are constructed and the physical sense of these generalized fractional equations and of the solutions are discussed. In the second part the problem of anomalous transport in an electric field is studied. The relation between diffusion and conductivity is studied and the well-known Einstein relation is generalized for the anomalous diffusion case. It is shown that for Levy flight diffusion the Ohm's law is not applied and the current depends on electric field in a nonlinear way due to the anomalous character of Levy flights. It is more clear if one consider the case when there are Levy flight diffusion and usual diffusion. In correspondence with two types of diffusion behavior the response of the system have two asymptotic: linear and nonlinear. At the scales , when the diffusion has usual character mainly, the Ohm's law exists. At the scales, corresponding Levy flight diffusion, the nonlinear response appears. The results of independent numerical simulations of Levy flight diffusion in an electric field confirm this conclusion about nonlinear law and also are discussed in the report.

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Bayesian Reconstruction of Particle Size Dynamic Distributions of Particulate Polydisperse Systems from in vitro Drug Dissolution Data

Ana Barat, Heather Ruskin, Martin Crane

Poster

The direct deterministic modelling of in vitro drug dissolution is not a trivial problem, because of the complexity of the various physical phenomena involved in the dissolution process, which should be accounted for when setting models. The most typical experimental data of the in vitro dissolution are obtained in practice by dissolution testing in the USP (United States Pharmacopoeia) Apparatus II. The hydrodynamic conditions in the USP Apparatus are time-dependent and very heterogeneous in space, which result in a quite undesirable feature: high variability of the dissolution profiles. Some kinds of drug delivery systems like disintegrating or particulate polydisperse systems have an extremely complex behaviour in the USP because of the variable distribution of the solid particle sizes combined with heterogeneous flow conditions in the apparatus, thus many aspects of their dissolution are subject to uncertainty. In this work, we create a range of models based on Inverse Monte Carlo simulations in a Bayesian context, that are capable to extract knowledge from experimental data (time series of dissolved quantities). At different time-steps of the dissolution, we consider the parameters of the particle size distribution as random variables. A deterministic function based on classical equations for drug dissolution (or based on less classical particle-tracking techniques in the apparatus) is used to assess the relation between the particle size distribution and then the amount of dissolved drug in the solution. The inaccuracy in the dynamics of the model is considered stochastic and represented by some noise factors. In reporting simulated results to the experimental dissolution results, we re-update the unknown size distributions in order to obtain their reconstruction at the end of the simulation, within a previously specified error range. This method is at experimental stage, but can prove to be very useful in the field of drug dissolution: the time series of reconstructed particle size distribution can be used for solving the direct dissolution problem for different sets of parameters in optimisation research.

A Novel Medical Diagnosis System

Iantovics Barna Laszlo

Poster

The purpose of the study consists in the development of an open, large-scale heterogeneous medical diagnosis system, which is able to solve a large variety of difficult medical diagnosis problems. We propose the endowment of the expert systems specialized in medical diagnosis with the agents capabilities. We call these agents expert system agents. The expert system agents can solve cooperatively difficult diagnosis problems in a more flexible way than the expert systems. In this paper, we propose a cooperative heterogeneous medical diagnosis system. The proposed system is composed from expert system agents and doctors with different specializations in medical domains. The main advantage of the proposed medical diagnosis problem solving is the flexible and precise solving of a large variety of medical diagnosis problems, which's solving require knowledge from different medical diagnosis domains. The necessary knowledge to the diagnosis problems solving are not specified in advance, the diagnosis system members must discover cooperatively the problems solving.

The effects of topology on the dynamics of Naming Games

Andrea Baronchelli, Luca Dall'Asta, Alain Barrat, Vittorio Loreto

Poster

The study of language as the result of a complex adaptive system allows to understand how a population of agents can develop a coherent set of linguistic conventions on the basis of simple interactions and negotiating processes. Among the language games used to study the evolution of language, Naming games (Steels, 1996) are conceived as simple models reproducing the dynamics by which a word or a minimal set of words are selected as a commonly shared vocabulary to identify one or more objects. We consider a minimal model of naming game in which all interactions among pairs of individuals, one selected as speaker and the other as hearer, are focused to communicate the name of a single object. At each step of dynamics two agents discuss on the name of the objects, updating their inventory of words on the basis of the result of the game. A two-agents game has a success if the hearer understands the word pronounced by the speaker, i.e. if they both possess it in their words inventories. The type of dynamics favors the spreading of a word having high rate of success, with a final state in which all individuals share a single common word to identify the object. We study the effects of topological constraints on the dynamics embedding the system in graphs, where the agents can interact only with their neighbors. The emergence of a common linguistic convention for the object's name seems to be solid with respect to different topological structures: regular (1D and 2D lattices), homogeneous random graphs and heterogeneous scale-free graphs. However, the temporal scale of the dynamical process as well as the evolution of spatial structures (groups of agents sharing a words) show a variety of interesting different behaviors, that are analyzed using both analytical and numerical techniques. In particular, the dynamics on low dimensional lattices is characterized by diffusive phenomena that are explained using a simple master equation's approach.

The structure of large social networks

Dominik Batorski

Poster

The last few years have seen a burst of interest in the properties of large networked systems such as the Internet, the WWW, and social and biological networks. The main goal of our research was to identify structural patterns of relations in a large social network. We examined the networks of acquaintanceship and communication between the users of Gadu-Gadu – the most popular Instant Messenger in Poland. This kind of computer-mediated communication is used mainly to communicate with people known from off-line world. For that reason the research in question, although carried out on the Internet, was aimed at identifying the patterns of relations typical also for the social networks outside the Internet. At the moment Gadu-Gadu has 3.4 million users. The number of registered relations exceeds 75 millions.

Using the whole network data on relations from Gadu-Gadu buddy lists and communication between users we focus on main statistical properties of complex networks that have received attention recently. We report that social networks show the characteristics of small-world networks – most pairs of vertices in network are connected by a short path through the network, and scale-free networks – highly skewed degree distributions. We consider also degree correlations; it has been observed that the degrees of adjacent vertices in social networks are positively correlated.

In the last part of the paper we describe the possible consequences of measured structural properties of network for social processes that take place in social networks.

Managing as Designing : how designers can help managers in designing their organization as complex environments ?

Brigitte Borja de Mozota

Poster

Keywords: design ,complexity, design management ,design thinking , organizational design,strategy

Jim Hackett president & CEO Steelcase Inc Organizations tend to drive for simplicity when attempting to solve complex,systemic problems. These practices are sweeping the rich opportunities of complexity under the carpet. Jim contends that successful organizations will embrace systems thinking,approaching their system of business as a design to be tested against the fitness of other businesses Source Institute of Design Strategy Conference May 2005

Summary : -organizations as complex systems -design as system thinking -rethinking design thinking with complexity theory -beyond the representations the importance of 'sense making' -design as organizational design

1. Organizations as complex systems Managers are facing complexity at three stages : 1.the complexity by itself :They see the real world as complex . Their perceived reality always remains incomplete and unfinished.The 'all' and the 'parts' are linked in inextricable and entangled interactions .The product is producing what organization is produces it in a spiral of cause and effect. Different logics co-exist in dialogical manner. Reality considered as complex is difficult to understand and to control .

2.the level of representation. Managers as observers who perceive the reality as complex build their representation of the phenomenon observed. But this is the major difficulty since how can they represent something that basically they dont understand? For this issue, they have to go back to the methods of representation and to understand their representation systems. A representation system is a set of elements including the past,the present and the future.

Our representations are not the image of the reality but a construction of our minds. In this universe of complexity, managers have to practice 'an ecology of mind' which means to adapt their way of thinking the environment and to consider themselves as a part of the complexity they have to control.

3.The level of the finality Since our representations are the source of our actions,it is urgent to understand and to control the paradigm of the system and to broaden its scope. This systemic modelisation is an intellectual tool , a mental construction , a method to construct a finality. It is the model that provides the finality and 'makes sense' to the whole system.

2. Design as system thinking

But managers are trained to think analytically in order to decide and control. Designers on the contrary are encouraged to adopt a holistic approach to any situation, to adopt a system thinking.(fig1)

Descartes System thinking Evidence is what makes a thing real. A representation is not true in itself; its pertinence comes from the intention of the person that formulates the representation Analysis :difficulties should be divided in as many parts necessary in order to understand them separately Global approach of interactions recommends to link together the elements of a system in order to be able to understand them in the globality of their interactions Hierarchical structure: you have to conduct your thinking by startign from

the things simple to the more compses by orderign them together the concept of teleology that places the finality of the system is the essence of its dynamic.a system does not find its meaning in a preexisting structure but in a project that induces its behavior Number: one has to number the whole in order to be sure not to forget something. Representation is always 'limited rationality'; it consists of a non exhaustive selection of aggregates that are thought pertinent to the situation one wants to shed light on Fig 1 : 'Discours de la méthode' versus systems thinking (adapted from Genelot 2001)

The process of constructive thought and action called 'Design thinking' belongs to the center of basic design education today because -design thinking is multidisciplinary and applicable to any subject, -design thinking integrates imagination and analytical thinking -design thinking emphasizes constructive thinking over factual retention -design thinking requires ongoing definition, representation and assessement: it is a continuous learning experience. -design thinking links information to experience and reasonable action . -design thinking encourages objective assessment (source Charles Burnette www.Idesignthinking.com 2005) Systems perception of design recognize its universal role as a core human activity. Design as a systemic activity is well summarized by Herbert Simon definition: 'Everyones designs who devises courses of action aimed at changing existing situations into preferred ones'.

This view typically integrates design into dynamic systems and in so doing recognizes the highly complex multi faceted nature of designing. It requires that hard systems methodologies of the reducionist perspective be augmented with soft system methodologies (Broadbent 2005 for a list of definitions)

Designers are creating systems in organizations whether brand identity systems or global systems of customer experience relationship. Design creates also value in a systemic way .Design creates value to the global value chain: substantial value as well as financial value . (Borja de Mozota 2003)

But this design thinking is targeted towards an end, a project. In summary , design thinking is sipmple system thinking.

3. Rethinking design with complexity theory Complexity science explores non linear dynamic systems which balance both order and chaos have emergent properties and are adaptive in nature (Sardar and Adams 2003).

But there is a dsitinction between simple systems and complex systems.Complex systems are exploring the principles of complexity such as richness, interconnections, iteration, emergence, holism and fluctuations.

For David Thomson (2005) ,the application of complexity theory in organizations is providing new insight into strategic organisatioanl management. Stacey (2000) believes that where a system shows traits of complexity strategic management takes on a new meaning.It becomes a domain of adaptive responses rather than control.

But much design is about successive design projects and design management literature is about control . However if you are truly holistic in your design thinking then you have to let go of control. And rethink design as a complex system

Many tools exist to help organizations pilot a course of action and communicate a plan however these tools are often prescriptive and do not account for the reality of the complex responsive processes at work.

A key skill of the designer is the ability to visualise in a form such that others can comprehend its meaning.With product, graphic, web design, design dsicipline project based - we can show people a physical model, a rough, a representation.

With strategy and strategic design , designers have to present a conceptual model. Conceptual mapping is one technique that holds promise for modelling design strategy in complex organisational systems. A new field of research opens for information designers

:dealing with conceptual models invention for improving strategic decisions in a dynamic emergent way . This complexity theory background is another way to explain the cognitive shift the design profession has to face from an 'activity based' profession to a 'knowledge based' profession . Developing 'global design' thinking as a sense making' decision environment on top of each design discipline - product, packaging, graphic, web,interface - with new specific conceptual tools.

4. Behind the representations 'sense making' "La pensée n'est pas faite pour servir la logique ; elle se sert de la logique" Edgar Morin

Hence the major responsibility in the governance of complex organizations is the search for and the expression of 'sense making'. For this issue , information and communication and knowledge are fundamental keys to pilot complex systems .

This responsiblity demands vigilance because the proliferation of signs in our present world intensified by NTIC have lead to a loss of meaning. So how to manage information and communication in order to make sense in complex situations ?

Give a shared meaning , put the communication media into a coherent framework of shared finality this is the objective . Designers have created graphic signs that are giving sense to corporate strategy values. But what complexity tells us is the importance of sense making for all the parts of the systems .Which means probably adapt the sign and design outputs to the level of logics of the different actors. The designer as transmitter has to refer to the mind of the users at different logics level.And to learn more on Karl Weick theory and research on representations and 'sense making'.

'User Oriented Design' or human centered design is a new trend of design model (Veryzer & Borja de Mozota 2005). But it is rather focused on understanding users externally. The systems should be broadened to internal users. This is already taking place in brand management where the objective of brand equity building has emphasized the neccessity of managing brand value both externally and internally.

Another level of design responsibility in building representations that make sense is innovation. Because innovation is by essence a complex process uncertain,it does not go very well with traditional management tools .Innovation requires approaches that come from complex thinking.The challenge is to conduct a process which results are not predetermined.One can create the conditions to innovate but not ex ante the contents of innovation. The exercise of mental mobility proposed by complex thinking is one of the best openings for innovation . Design thinking is pertinent here because innovation means transgressing existing models , cross fertilization of ideas , cognitive process for piloting organizational learning rather than rationalizing .

The change in strategic thinking from a planification view to a managerial view of does not deny complexity .Practices change in order to be able to take into account complexity. There is a progressive evloution of the concept of strategy towards the integration of complexity explains why more and more MBAs are partnering with design schools or why design education is more and more research and PhD based

5. Rethinking organizational design The organization is weaving together different logics of invention not of conformity.It has to invent practices for self-organization .Any organization learns , memorizes and builds the intelligence of its evolution ,

Students in management seem to be developing the topic of organizational design in an unwieldy direction.As the variables multiply ,they tend to simplify the reality and say less and less about more and more. If you look into the definition of organizational design you begin to see the obstacles that management has put in its own path . Consider a definition of organizational design : 'the choosing of structures and associated managerial processes to enable an organization to operate effectively'.

On one hand organizational design creates nothing but one the other hand organizational design creates everything since organizational design will have a fundamental framing effect on people's expectations and perceptions . If designing the organization is both nothing and everything ,one needs to dig deeper into the process.

When people try to make sense of the world around them, they follow a progression towards abstraction ,from perception to form naming .And at this stage the reification of things dictate behavior .Labels are seen as intrinsic and imposed rather than emergent and discovered.

At each step in the sequence of compounded abstraction details get lost; the concrete is replaced by the abstract and design options gets foreclosed. Managing as designing means in part the monitoring ,containing and reversing of compounded abstraction .

The necessity to act this way becomes clearer when we connect the image of compounded abstraction more directly to the complexities of organizational life. If managers keep imposing machine metaphors and mechanistic assumptions onto events in a effort to stabilize them,predict them,and control them ,then categories, stereotypes,schemas,routines seem like useful tools.This is a pervasive scenario in organizational design where management expertise has become the creation and control of constants ,uniformity and efficiency .

The problem is that version of managerial expertise is no longer what we need. Instead the need has become the understanding and coordination of variability, complexity and effectiveness.(Weick 2004)

This means that managers need to create designs that mix together perceptual and conceptual modes of action .Design can be seen as a mental concept of human relationships in a world of exploding complexity and diversity .

Conclusion : The reality of the firms may be only the reality of the models its various actors have been building .There is probably not a good ,a better or a true model by itself but on the contrary multiple and lively projects by which everyone represents the firm he or she contributes to build by its action .And these rich ,intelligible ,communicative and dynamic respresentations are in permanent transformations :they have sense and they are sense making.

It is not because eveyone is active at every level that a firm builds sense . Sense making emerges when people are able at their level of responsibility to understand and interpret the level of logics superior to them. This progression in the sense making elaboration supposes an improvement in the richness of the contexts of interpretation . This asks the question of the cultural openess of the firm and of the richness of the profound intentions whether individual and collective , nourishing themselves reciprocically .

Firms are not to produce 'de l'organise' mais de l'organisant' organized routines but rather organizing schemes. Firms are active actors of a building that does not pre-exist. Managing in complexity might be enriching our representations of the firm and enriching our reasoning on the models of the firm .

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Measuring graph symmetry: discussion and applications

Carlos Bousoño-Calzón

Poster

Apart form its aestetical appeal, symmetry is considered as an essential tool for understanding complex systems[1]: It has been traditionaly used in the realm of theoretical physics, to study differential equations or dynamical properties [2], to name just a few. Recently, since network and graph theoretic tools grow as unifying concepts for complexity and universal properties studies [5], it seems natural to ask for the symmetry of networks and its implications.

In order to address this target, a reference to algebraic graph theory is deserved [6,7]. Nevertheless, there is an additional need of effective computational tools to tackle real applications. In this line of research, two measures for graph symmetry have been proposed recently which have rendered useful in order to predict dynamical behaviour [3] or robustness of a network in the face of attack [4].

This short paper elaborates on this kind of measure. Although the both aformentioned measures are essentially equivalent for a subset of graphs, their application to graph spectra (for Erdos or scale free random models [5]) raises some validity questions which are empirically explored in this proposal in order to propose a better symmetry measure. Some applications so as to illustrate its potential utility are developed in toy problems.

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A generic model simulating two temporalities of evolution in the European system of cities

Anne Bretagnolle, Jean-Marc Favaro

Poster

SIMPOP2 and EUROSIM are two versions of a same generic multi-agent systems model. The model is built in cooperation between geographers (UMR Geographie-cités) and computer scientists (LIP6). The model simulates the evolution of a network of interacting cities. The main interaction is the competition for resources (population, goods, information, innovation). The cities produce and invent new resources and exchange them on a spatialised market. Cities are heterogeneous agents that differ according to their functional specialisation (central market places, territorial capitals and production of non central manufacturing goods or services). They are also different according to their strategy, as defined by an agent called "governance". Two applications are presented here: - the first one (model SIMPOP2) is theoretical and aims at simulating the emergence and the evolution of the European system of cities, from the end of the Middle Ages to nowadays. Two main features are to be reproduced by the model: 1) the persistency of a hierarchical configuration both at macrogeographic level of the system as a whole and in the individual trajectories of cities; 2) the dramatic increase of contrasts in city sizes since the first industrial revolution. The key parameters that will be experimented are: i) the succession of innovation cycles of different temporal scales and their more or less rapid diffusion within the system of cities; ii) the increasing spatial range of exchanges due to the progress in communication technologies. - the second application (model EUROSIM) refers to the European urban system during the last 50 years. Urban functions and parameters are described more precisely, in order to reproduce as accurately as possible the operating and evolution of the system during the last decades. In that case, simulations are used for testing scenarios and making predictions at a 50 years horizon, according to migration policies, demographic expectations from different sources, and the evolution of the international boundaries barrier effects as a function of enlargement of European Union.

Complexity in living organisms : mosaic structures

Georges Chapouthier, Chapouthier,

Poster

The present thesis (Chapouthier, G., 2001, L'homme, ce singe en mosaïque, Odile Jacob, Paris), which is compatible with Darwinian theory and arguments, endeavours to provide original answers to the question of why the evolution of species leads to beings more complex than those existing before. It is based on the repetition of two main principles alleged to play a role in evolution towards complexity, i.e. "juxtaposition" and "integration". Juxtaposition is the addition of identical entities. Integration is the modification, or specialisation, of these entities, leading to entities on a higher level which use the previous entities as units. Several concrete examples of the process will be given. At the genetic level there is silent duplication and integration of introns, which explains the origin of complex organs. At the anatomical level, the application of the two principles can be found in unicellular organisms (that develop into "juxtaposed organisms", e.g. Gonium, and then into "integrated organisms", e.g. Volvox). In more complex didermic species, juxtaposition produces colonies of polyps and the integration of these polyps produces intagrated siphonophores. In tridermic organisms, the juxtaposition of metamers produces the earthworm, whereas integration leads to the bee, the octopus or the chimpanzee. At higher levels, juxtaposition and integration become social, with the grouping of identical individuals (crowds) or the specialisation (or integration) of their roles (colonies of bees or societies of primates). For these structures, where integration at one level leaves the units at a lower level in a state of relative autonomy, the metaphor of the "mosaic" could be used. In complex living beings, as in a mosaic, the properties of a given level, taken as a whole, leave the autonomy of the component parts intact. Several examples will be given, specifically in the human brain and the functioning of thought, where essential functions such as language or memory have a mosaic structure.

Complex biological memory conceptualized as an abstract communication system - human long term memories grow in complexity during sleep and undergo selection while awake

Bruce G Charlton, Peter Andras

Poster

We propose a description of memory from the perspective of complex systems. The long term memory system consists of networks of self-reproducing communications between the neurons. Memory systems spontaneously grow by recruitment of neurons to participate in expanding networks of communications. Growth of memories occurs mainly during sleep. Memories are subject to selection mainly while the organism is awake. The 'memory function' of a complex biological memory system represents a small proportion of the possessing of the memory system, while much greater amounts of internal processing are intrinsic to the existence of biological memory. The primary function of sleep is to maintain and increase the complexity of the long term memory system. In a paradoxical sense, the LTM system exists mainly to sleep, and its memory function is merely the 'rent' that the LTM system pays in order that the organism will allow the LTM system's continued existence.

Peer-to-peer data management: the SP2+SP6 perspective

Giovanni Cortese,, Stefano Leonardi, Friedhelm Meyer auf der Heide, Christian Schindelhauer

Poster

The goal of this workshop is to enlight the contribution of complex systems research towards the goal of a new generation of information architectures built on a self-organizing P2P architectures.

The Web bears the potential of being the world's largest encyclopedia and knowledge base, but we are very far from being able to exploit this potential. Search-engine technologies provide support for organizing and querying information. Yet, the current systems mainly support the simple mass-user queries. While advanced information queries too often require excessive manual pre- and postprocessing.

Approaches based on Collaborative Web information search in an Internet-scale peer-to-peer (P2P) system bear the potential of overcoming the shortcomings of today's Google-style search engine technology. In the approach proposed within the DELIS project every user (peer) has a full-fledged search engine that indexes a small portion of the Web, according to the interest profile of the user. Thus the requirements to the peer-to-peer overlay network are higher than in the usual key lookup or file sharing scenario. Consistent Hashing, aka. Distributed Hash Tables (DHT), is the state of the art data structure for such peer-to-peer networks. Because of the more involved task of evaluating documents and various locality issues new designs are necessary. Therefore work on the design of peer-to-peer networks is an important part of the scope of this workshop.

From a different perspective, Delis is studying large-scale IT infrastructures which, in order to be managed or used, pose challenging data management requirements. Such infrastructures include GRIDs, large networks, peer-to-peer applications etc. Their management requires (at least) the ability of building and querying large resource directories, of collecting and processing (summarising) lots of usage and performance data, also mining such data (in real time or near-real time) for detection of significant episodes (e.g. routing failures, denial of service attacks etc).

Access to management data should be decentralised, thus allowing many components in the system to efficiently query or subscribe to information. Also, management information should be organized and indexed to allow users (or applications) to issue queries at a higher level than supported by current frameworks (e.g. SNMP, HTML/XML), using query languages that support taxonomical reasoning and eventually the full power of ontology languages such as Owl. Again, the peer-to-peer approach based on DHTs with its promises for load balancing is a starting point for our research, to be explored for building large-scale, self-managing data repositories, however requiring a number of extensions.

Emphasis in the workshop will be given to understanding the dynamics and behavior of such a network requires analyses at different levels and scales of the overall network.

The Inter-disciplinary Analysis of Multidimensionality of Complex Systems' Evolution and the Method of its Topological Estimation

Victor F. Dailyudenko

Poster

The inter-disciplinary analysis of complex systems (CS) is implemented from standpoint of enlarging their degrees of freedom that is shown to be the intrinsic feature of their functionating. The method of nonlinear analysis of data describing evolution of CS is developed. Using temporal localization along phase trajectories of the attractor, we achieve the essential reduction of computation time and required experimental data at computational analysis of the attractor's topological dynamics that allows the algorithm to be realized even for higher-dimensional cases (much more than a hundred degrees of freedom). The numerical simulations confirm reliability of the developed algorithm and its high efficiency. So, the algorithm is applicable for the sake of statistical characterization of CS under investigation. In particular, within tasks of modeling of turbulent flows the method can be applied for the automatic detection of appearance of turbulence in technical devices. Time series (TS) obtained from CS are essentially nonlinear [1,2] and often lead to a multidimensional attractor in a relevant phase space [2]. Namely, it occurs at investigation of highly-developed turbulence where applying three-dimensional models (as in the model of Lorenz) is not enough for description of complex processes and higher-order modes become important for increasing reliability [1]. Multidimensional attractor also arises at modeling of nonlinear delayed feedback described by delay differential equations [2], those are widely applied for modeling of nonlinear processes in optics and laser physics, medicine and population dynamics, nonlinear vibrating systems and various self-sustained oscillations, in tasks of automatic control. But it is worthy to note that the main problem of numerical analysis of TS in such high-dimensional cases is that the computation complexity of fractal-topological algorithms essentially increases with enlarging a dimension m, as well as a quantity of required experimental data N. Namely, the computation complexity increases exponentially for the box-count algorithm and almost linearly for the Grassberger - Procaccia algorithm (GPA) with growth of m at expense of growing a number of computation operations. Again, additional increase of computation complexity results from respective growth of N (N increases exponentially for the GPA with enlarging m). For this reason, implementation of such algorithms for multidimensional attractors is cumbersome and even impossible for high m. So, with comprehensive inter-disciplinary analysis of multidimensional systems, the main purpose of this work is to develop a method allowing reduction of N and computation time as well as being insensible to growing m on these characteristics. This is attained by elaborating a topological method based on temporal localization in relation to points of the attractor. The most conventional methods of fractal-topological analysis imply just the spatial localization, i.e. investigation of distribution of points on the attractor basin based on estimating the quantity of hits into the m-dimensional cell with a size l. In particular, for the GPA this cell can be considered as a ball with a center in an attractor point. Similar approach of spatial localization (but with fixed number of nearest points) is used in a "nearest neighbor" method. In contrast to these methods, we show that temporal localization provides more convenient realization of topological analysis with essential reduction of required experimental data and computation time and makes these characteristics practically independent on dimensionality within some restricted range of changing m, that is the development of the approach couched in [3].

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Centrality and vulnerability in weighted complex networks with spatialconstraints

Luca Dall'Asta, Alain Barrat,, Marc Barthelemy, Alessandro Vespignani

Poster

Structure and functionality of real weighted networks are results of a complex interplay between topological and weights properties. The present work is devoted to understand the influence that topology and weights have on the vulnerability of weighted networks under intentional damage. In particular, weighted networks with spatial constraints are considered, the world-wide air-transportation network being a typical example.

Since different attacking strategies can lead to very different conclusions on the vulnerability of a network, we first characterize some relevant topological and weighted centrality measures. These quantities are then used as selection criteria for the removal of vertices, in order to find which measure of centrality is the most effective.

We also apply the same analysis on a recent model of growing weighted network with spatial constraints, that has been shown to reproduce some particular characteristics observed in air-transportation networks. By comparing the results, we gain useful information for a better understanding of the properties of growing weighted networks with spatial constraints.

Fractal Analysis of Eastern and Western Musical Instruments

Atin Das, Pritha Das

Poster

In this paper, we attempt musical analysis by measuring fractal dimension (D) of musical pieces played by several musical instruments. We collected solo performances of popular instruments of Western and Easter origin as samples. We attempted usual spectral analysis of the selected clips to observe peaks of fundamental and harmonics in frequency regime. After appropriate processing, we converted them into time series data sets and computed their fractal dimension. Based on our results we conclude musical sounds may have higher Ds.

Random versus Chaotic data: Identification using surrogate method

Pritha Das, Atin Das

Poster

Distinguishing between chaotic and random data are quite difficult. Many chaotic processes generate outcomes, which are random while random processes may generate data that satisfy tests for chaos. Here, we show with example of both random and chaotic data sets that they can be characterized by applying surrogate data method and then comparing values of correlation dimension calculated from the original data set and its surrogate counter-part. Obviously, we comment on the data generated by the process- not about the process as a whole.

R&D networks as complex system: the case of european networks

J. C. Fdez. de Arroyabe, N. Arranz

Poster

The aim of this paper is to study the management of technological networks. It works from the basic axiom that networks are a complex reality presenting multiple aspects that need to be tackled from different theoretical approaches. The network, considered as a complex system, will be studied through the different subsystems making it up (structural, technological and management subsystem) analysing the different variables that underlie and delimit the management thereof. An empirical study will then be made of the networks set up for the development of technological projects in the framework of the European RTD programmes. The sample comprises 185 institutions taking an active part in said programmes, enabling a description to be made of the main features of the networks and the main challenges posed in the management of technological projects in the network.

Complex Systems and Cognition: the incoherent dynamics implementation using multi-agents systems

Leonardo Lana de Carvalho, Salima Hassas

Poster

This paper presents an approach of addressing cognition from the perspective of complex systems by using the multi-agents paradigm. Whitaker's notion of cognition is based on Maturana and Varela's theory and stipulates that cognitive systems are a consequence of complex systems capable of self-adaptation (Whitaker, 1997). Rocha and Hordijk (2004) suggest representation or incoherent dynamics as "inert" structures: « organisms employ "inert" structures to store initial conditions used to construct appropriate dynamical (active bio-chemical) components as well as reproduce other organisms such as themselves ». For a given dynamics, « ... we can treat certain components as incoherent, if their dynamics are irrelevant for those time scales. We can further treat them as memory, if such dynamically incoherent components are used as information to specify sets of initial conditions for the original dynamics. » (p-11). According to authors it would be enough to stop the reactivity of the system. Evolving Cellular Automate and Genetic Algorithm, however « the information they store is still not separated from the dynamics »; « CA were able to create static memory stores, [but] these are still reactive with the embedding dynamics » (Rocha and Hordijk, 2004, p-25). Agent-based models demonstrated their effectiveness on several computation problems. "The variation of the population size provides the swarm with mechanisms that improves its self-adaptability and causes the emergence of a more robust self-organized behavior, resulting in a higher efficiency on searching peaks and valleys over dynamic search landscapes..." (Fernandes et all, 2004). To go further than the Rocha and Hordijk's work, we make the hypothesis that Incoherent Dynamics (ID) is what makes the emergence of representations possible in complex systems, by making cognitive the computational system. This emergence of representations takes place like an opposition of the system to its environment, breaking its reactivity while being embodied. To illustrate this idea, a metaphor of natural ants collective sorting was implemented. Agents were designed like simple automatas which obey linear functions to move randomly in the environment by leaving a central point. As expected, after the agent-environment interactions the behavior of agents is no more linear, but exhibits emergent complexity. We observe that small modifications in automated functions of moving causes a greater or minor dispersion of the amount of f̈ood. Ahead this emergent property, dispersion-centralization, characterizes a new system, called here Order. A dispersed order is got with agents who cover small distances before verifying the food existence. A centralized order is got with agents who make it after covering long distances. Thus we have implemented different orders on one same environment and an order after the emergence and stabilization of another. It is instructive to recognize which relationship exists between the two emergent orders. We stress that relationship between orders are not reducible to agent-environment level. With the studies of the relationships between orders, it was possible to observe an opposing emergent system, that is, completely not programmed. We had observed that a dispersed order can always be isolated in a certain environmental site where was embodied a previous order. The emergence of opposition is obtained by heterogeneity of agents. It is necessary that the implementation of heterogeneity takes place after the stabilization of the first observed order which corresponds to the centralization phenomenon. Indeed the emergence of opposition opens a new way in approaching Incoherent Dynamics. Isolated orders are incoherent systems because they are essential for maintaining the global pattern.

They have their own dynamics, they can be controlled by the global pattern itself and they could be used as an internal representation of an external system able to promote heterogeneity effects into agents. Thus, it seems that we have a bridge between the computability and the cognitivity. However, the heterogeneity of agents is still directly programmed. To generate ID based systems able of solving problems representatively and non reactively, it will be essential to have more profound levels of heterogeneity in the agents behaviors. We have two ways. Ascend multiples levels of emergence changing agent more insignificant or conceiving not only situated agents but embodied agents.

Percolation for Power Control

Emilio De Santis, Fabrizio Grandoni, Alessandro Panconesi

Poster

We give an efficient distributed algorithm for power control that uses local information alone. When N devices are distributed uniformly at random, the protocol generates with very high probability a connected network in which every device is connected on average to constantly many neighbours and moreover no device has more than O(log N) neighbours. The number of communication rounds is poly-logarithmic. This is an exponential improvment over previous results. Our solution is obtained by making use of techniques from percolation theory.

Science and Engineering of Business Systems

Kemal A. Delic

Poster

We are surrounded by the systems involving people, technologies and processes better known as the "business systems". They function well despite all deficiencies, imperfections and lack of coordination while creating the wealth and moving the world's economy forward. However, it seems that the practice of business systems is well ahead of the science of business systems.

Thinking about world's economy as the business ecosystem, implies dealing with large-scale systems, saturated with complexity, high uncertainty and rapid dynamics. As such, the large-scale business systems should represent an excellent playing field for the multiple, multi-faceted scientific disciplines and scientists, while, for the various reasons and causes, they are or disregarded or sometimes even carefully avoided.

Analysis of the complex system

J Deschatrette, C Wolfrom

Poster

Despite the difficulty for analyzing the physiopathological mechanisms which are involved, the practical importance of biological oscillations justifies the development of their study because they condition the response to an external stimulation depending on the time when it is applied to the system. The Te-TA-P network includes 3 oscillating parameters : - length of telomeres (chromosome endings) - telomerase activity (telomere repair)- cell proliferation rate. The Te-TA-P system is paradigmatic among oscillatory biological systems, because it is a key both for normal tissular development (characterized by progressive cell senescence due to definitive telomere erosion), and for long-term survival of stem cells and tumor cells (characterized by telomere repair which allows unlimited proliferative capacity). The maintenance of the system TE-TA-P at equilibrium is linked to the cancerous character of the cells. One can foresee that pushing the cells out of this equilibrium by light impulsions on a component of the system will durably change the proliferation dynamics. Our hypothesis is that such bifurcation of the dynamics, incompatible with persistent high proliferation, will induce the slow-down of mitoses and/or increase apoptosis, resulting in a negative balance of tumor cell growth. The purpose of our experimental work on tumor cultured cells is 1) to analyse the interactions of the 3 variables in the Te-TA-P network by simultaneous quantification in long time series, 2) to modelize the metabolic loops that link them in order to predict the fluctuations, and finally 3) to control the activity of this system by external forcing. This approach of the cell proliferation dynamics already brought us important results. It bears important applications on practical problems such as tumor regression and intermittent resistance to anticancer drugs.

Criteria for coalition formation

Jean-Louis Dessalles

Poster

Like many other species, Human beings establish stable social bonds that are not necessarily based on kin. This ability is an essential component of sociality, and may be a crucial factor for the evolutionary emergence of the human species (Dunbar 1996). However, the criteria used by individuals to choose their social partners is poorly understood. In particular, no general law has been proposed to delineate what would count as a valid preference criterion in a strict Darwinian framework.

Social groupings based on mutual partner choice are sometimes said to be political. A typical example is the formation of political coalitions among chimps to take or keep control over the group (de Waal 1982). Another example is offered by babblers, those little birds living in the desert, which form coalitions to defend sheltering bushes against other babbler coalitions (Zahavi & Zahavi 1997). The human species could be characterised by the complexity of political bonds: friendship networks, alliances, supporters, partisans, leaders, factions, all emerge in a political context in which individuals are prone to choose each other. These social phenomena have often been described as resulting from psychological factors such as esteem, feeling of security, dominance. They have also been considered as cultural constructs emerging from a general willingness to cooperate, in which case the partner choice chiefly relies on reliability (Axelrod 1984).

We want to explore an alternative account of coalition formation, which is that individuals choose their partners according to their potential usefulness for the fate of the coalition. This approach departs from studies based on cooperation in several aspects. - social bonds do not depend on some utilitarian trade of goods or services. - the criteria for partner choice are expected to be in part biologically determined, and not based on pure rational choice. - potential partners are expected to display qualities corresponding to those criteria, even if the display is costly (Dessalles 1999; Gintis, Smith & Bowles 2001). - criteria for social bonding are required to be positively correlated with the success of the coalition.

The latter requirement is the main result we arrived at, both theoretically and through computer simulation (Dessalles 1999). In a political settings, isolated individuals have little chance of success, and they must choose their partners with discernment to resist coalitions formed by others.

In the present paper, we will explore the coexistence of several criteria. It may be in the interest of individuals to choose partners who have qualities different from their own. The result may be seen as a marketplace on which individuals advertise various competences and gauge each other's corresponding qualities. The marketplace metaphor is somewhat misleading, though, as no exchange of goods or services is necessary. The goods are the individuals themselves that may join to form or maintain coalitions.

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Coarse-graining and continuum physics

Antonio DiCarlo

Poster

I claim that an adequate continuum treatment of gross physics should be able to interact with the models of atomistic physics at small scales, and have a word to say on collective multiscale phenomena, which are of paramount interest in, say, materials physics and biophysics. Continuum physics as it stands today, however, is unfit for this task, being hampered by deeply rooted misconceptions, which make it blind to key scale issues.

In any physical theory, matter forms patterns in space that evolve in time. In an atomistic theory, molecules do not exist as matter: they are "mere" patterns. However, they are often the interesting objects, to be recognized among a terrible host of more ephemeral patterns on smaller space-time scales. A finer theory would deprive atoms of their material status, making them patterns of quarks, etc. The same conceptual scheme holds at supra-molecular levels including all of continuum physics: selected patterns of micro-matter appear as macro-matter in coarser grained theories. In continuum physics, matter is represented by spacetime averaged densities of molecular quantities, taken on a suitable meso-scale; fields of substantial markers are contrived according to rules in the candidate model of the system at the same scale, and the patterns that they form on larger scales are the objects one is interested in observing.

In complex systems, it is of the essence to relate phenomena happening at widely scattered scales, both in time and space, converting information from finer to coarser levels of description (and vice versa). A special difficulty resides in mechanics, which filters off more and more phenomena under up-scaling: only a tiny portion of the information contained in a detailed, microscopic knowledge of motions and interactions is subsumed by the corresponding macroscopic mechanical quantities, the rest being (partly) summarized in other macroscopic theories. While, in principle, all of chemistry is contained in quantum mechanics, macroscopic mechanics ignores all of it, and the coupling between mechanical and chemical phenomena (which can be of paramount importance: think of molecular motors in our own muscles) has to be rebuilt by the modeller.

Conventional continuum mechanics - supposedly representing the phenomena of interest at the macroscale - has too few sockets where to plug in the vast amount of macro-useful information surfacing from the depths of microscales. Too much of what comes from the bottom gets lost, or is bluntly lumped into constitutive black boxes. In the standard model of continuum thermomechanics, the body-points labeled by meso-markers possess as their only attributes position and temperature. Such a model is by far insufficient when dealing with complex systems, and has to be extended and generalized in two different directions. First, position is to be supplemented by extra order parameters, providing meso-averaged information on the presence of different molecular species and their conformations. Second - and more innovative - a mesoaverage of the stress-free, chemically determined, molecular conformation is to be tracked: in fact, the key for developing a comprehensive theory is in the ability to compare the actual conformation (stressed in general) with the corresponding stress-free prototype, which is also evolving in time because of the changing chemical conditions.

The format I call material remodelling comprises new balances, which govern the time evolution of material properties, such as the relaxed (i.e., stress-free) metric of body elements, or their elastic stiffness. Therefore, it is able to capture the gross mechanical effects of phenomena such as conformational changes and structural rearrangements. I advocate

its potential usefulness in bridging the gap between continuum physics and the physics of the invisible worlds underlying the continuum model.

What are Complex Systems? - What is DELIS?

Debora Donato, Marco Gaertler, Robert Görke, Stefano Leonardi, Dorothea Wagner

Poster

"What are Complex Systems?" - Commonly, the quest for information is accomplished by various search engines adapted to specific tasks such as Google or Yahoo! for web search and Citeseer for publication lookup. The results of these tools are usually lists that are sorted according to a relevance concept for the items. Nowadays, search queries become more complex and ambiguous. Therefore a simple evaluation of a query may not produce satisfactory results. User-defined exploration of the information space provides a flexible means to incorporate implicit knowledge and requirements of the users. To accomplish this, a readable and customizable visualization of the search space is needed.

In the following, we present several visualizations of web graphs, coauthor and cocitation networks that emphasize structural and relevant information.

Connectivity and Routing in Poisson Small-World Networks

Moez Draief, Ayalvadi Ganesh

Poster

In recent work, Jon Kleinberg considered a small-world network model consisting of a d-dimensional lattice augmented with shortcuts.The probability of a shortcut being present between two points decays as a power, $r^{-\alpha}$ of the distance r between them. Kleinberg showed that greedy routing is efficient if $\alpha = d$ and that there is no efficient decentralized routing algorithm if $\alpha \neq d$. The results were extended to a continuum model by Franceschetti and Meester. In our work, we extend the result to more realistic models constructed from a Poisson point process, wherein each point is connected to all its neighbours within some fixed radius, as well as possessing random shortcuts to more distant nodes as described above.

The New Ties project: 3 dimensions of adaptivity and 3 dimensions of complexity scale-up

A.E. Eiben,, N. Gilbert,, A. Lörincz, B. Paechter, P. Vogt

Poster

New Ties is an FP6/IST/FET open STREP project (started in fall 2004) seeking New and Emergent World Models Through Individual, Evolutionary, and Social Learning.

The project is concerned with emergence and complexity in socially-inspired artificial systems. It investigates large systems consisting of an environment and an inhabitant population. The main goal of the project is to realize an evolving artificial society capable of exploring the environment and developing its own image of this environment and the society through cooperation and interaction. The "physical" environment is based on virtual grid worlds that are sufficiently complex and demanding so that communication and cooperation are necessary to adapt to the given tasks. The populationś "toolkitẗo develop advanced skills bottom-up consists of 1. individual learning, 2. evolutionary learning, and 3. social learning. One of the main innovations of this project is social learning interpreted as passing knowledge explicitly via a language, which is evolved in the simulation, to others in the same generation. This has a synergetic effect on the learning processes and enables the society to rapidly develop an ünderstandingöf the world collectively. If the learning process stabilises, the collective must have formed an appropriate world map. Then the collective mind can be investigated to learn how the agents perceive the environment, including themselves, and what skills and procedures they have developed to adapt successfully. This could yield new knowledge and surprising perspectives about the environment and the survival task. The project represents a significant scale-up beyond the state-of-the-art in three dimensions: 1. the inner complexity of inhabitants, 2. the size of the population, and 3. the total processing power for duration of the simulations. To achieve and explore highly complex organisms and behaviours, very large populations will be studied. This will make the system at the macro level complex enough to allow significant behaviours (cultures etc) to emerge in separate parts of the system and to interact. To enable this, a large distributed computing infrastructure is being set up, together with a shared platform to allow very large scale experiments in a p2p fashion.

The short presentation will outline the vision behind the project, the main objectives, the approach to be followed, and the expected outcomes. By the time of the conference we will have technical results that will be also briefly summarized (and given in more details by other presentations).

Monotonicity and Almost-Monotoniciy in Biological Systems

G.A. Enciso, E.D. Sontag

Poster

A dynamical system is a type of continuous mathematical model which is frequently used to describe the behavior of physical systems over time. Dynamical systems are powerful modeling tools, and they have been succesfully used for many applications, but they are conspicuously hard to study, especially when there is a high number of variables involved. One increasingly important application of dynamical systems modeling is the description of molecular biological processes at the cell level. It allows the modeler to incorporate a large amount of information about the process, such as what proteins influence which genes and at what rates these influences take place. A drawback for the modeler is precisely the fact that often there is a very large number of variables (proteins, genes, etc) involved. On the other hand, and for all the apparent complexity of the models, the behavior of the solutions over time is often relatively simple: the convergence of all solutions towards one or two points, or a stable oscillatory behavior, seem the rule rather than the exception. Moreover, the direct influence of one variable on another is often consistent: if a protein influences the production of a given gene, say, it often does so in order to consistently inhibit it or to consistently promote it.

A concept that allows to exploit these characteristics is that of a monotone dynamical system. In its simplest form, a monotone system is one in which all the influences among the variables are promoting, and no inhibitory influences are observed. But many systems with inhibitory reactions can also be monotone, as long as the indirect effect from any given variable to another is consistent along any path in the network. A necessary condition for a system to be monotone is for it to have consistent direct influences, which is commonly satisfied for molecular biological systems as described above. Also, monotone systems have a very stable behavior over time. By considering monotone systems with inputs and outputs and introducing a negative feedback, we were able to describe the behavior of systems that are not monotone ('almost-monotone') in terms of that of monotone systems, and to give sufficient conditions for such a system to converge globally towards an equilibrium. This approach can potentially be used for a formal study of complex, non-monotone, large scale dynamical systems using techniques from monotone systems theory. We give a simple example of a testosterone dynamics model with delay, and show even in the presence of arbitrary delays all the solutions of the system converge.

RNA secondary structure prediction

Stefan Engelen, Fariza Tahi

Poster

One approach to predict the secondary structure of RNA is to search covarying residues which maintain the Watson-Crick pairings. This approach is called the comparative approach and consists to retrieve mutation informations from homologous sequence alignments. We present an algorithm, called P-DCFold, based on the comparative approach, for the prediction of RNA secondary structures including all kinds of pseudoknots. The helices are searched recursively using the "Divide and Conquer" approach, searching the helices from the "most significant" to the "less significant". The main problem of the comparative approach is that not all sequences of the alignment contain interesting information. So, one must select combinations of interesting sequences which give good structure predictions. We expound a second algorithm, called $SSCA$, which measures the interest of sequences for the comparative approach. The measurement is based on evolutionary model in helices regions. The two algorithms have been combined to test their efficiently on known RNA secondary structure.

Studying decentralized collective change of behaviours : the example of phase transitions in elementary cellular automata

Nazim Fates

Poster

Complex systems are usually defined using the well-known formula that the ẅhole is more than the sum of its parts.̈ This informal idea expresses the possibility for a system defined as a collection of simple components in interaction to exhibit a c̈omplexb̈ehaviour even when each component behaviour is very-well understood.

Cellular automata (CA) are a well-known model for defining such systems : they are constituted by a collection of finite state automata that are regularly located alond a line (1D) or a grid (2D). These automata, or cells, interact with their neighbours and change their state according to a transition function. In this work, we shall only consider elementary cellular automata (ECA), i.e., two-state one-dimensional CA that change their state according to their own state and the state of their two immediate neighbours. Classically, CA are updateed sycnrhonously : the transition function is applied to all cells simultaneously. The model we here investigate does not use this hypothesis of perfect synchrony : instead each cell has propability α, called the synchrony rate, to be updated and if it is not updated it stays in the same state.

The question we here investigate is to know whether it is possible that the CA (collective) behaviour undergoes a brutal change while the synchrony rate is continuously increased. In a previous work [1] we showed that some ECA had indeed the striking property of displaying two different behaviours when the synchrony rate was lower or higher than a critical value α_c. This article aims at finding an explanation for such a phenomenon.

Using a methodolgy very close to the one used in Grassbergerś work [2], we conducted two sets of experiments to determine if the change of behaviour was was a directed percolation phenomenon (i;e., a particular king of second order phase transition). The first set of experiments aimed at determining α_c for which the transition occurs and teh second set aimed at calculating the critical exponents.

Analysis of the results allowed us to deduce good agreement with the values predicted for directed percolation. Moreover, observation of space-time diagrams also show similarities of patterns observed with other experiments that involved directed percolation (e.g., in hydrodynamics see work of Pomeau).

To conclude, we will discuss why such phase transitions are important. Indeed,they provide an striking example where the synchronization of elements is a key feature to understand the collective behaviour of *complex system*. Such mechanisms could provide a way to explain some phenomena in the biological domain : it is for example striking to see how the amiboe *Dictyostelium Discoidum* brutally change their behviour form an individual one to a collective one when the yare submitted to a stress. Modelling such organisms with cellular automata may thus help us understand some of their most interesting features.

refs: [1] An Experimental Study of Robustness to Asynchronism for Elementary Cellular Automata, Nazim Fatès, Michel Morvan To appear in Complex Systems

[2] Sycnhronization of coupled systems with spatiotemporal chaos Peter Grassberger Physical Review E vol. 59 Number 3

Traffic distribution in scale-free networks

A Fekete, G Vattay, L Kocarev

Poster

In this paper we study one of the most relevant example of scale-free networks with embedded flow dynamics: the Internet. The dominant algorithm which controls the data traffic in the Internet is the Transmission Control Protocol (TCP). We will present a simple model, which considers both the scale-free structure of the Internet and the adaptive nature of the underlying dynamics. Since links mean real physical boundaries for the traffic flow in the Internet, bottlenecks are formed at links. It follows that edge betweenness should be investigated. An exact analytic solution is presented for its distribution, which apply for even finite networks. Finally, the performance of the TCP model is compared in different network scenarios using simulation methods.

Thresholds for the emergence of cooperation between signals

Ramon Ferrer i Cancho, Vittorio Loreto

Poster

Little is known from the mathematical point of view about the reasons why signals start to cooperate spontaneously for communicating. Human words combine to form phrases and sentences. Often, the meaning of a single word is incomplete or too vague. A combination of two or more words is needed in many cases. Recent mathematical models have studied the conditions turning combinatorial communication advantageous over isolated signals in the context of biological evolution (Nowak et Krakauer, 1999; Nowak et al., 2000). Some of the models indicate that the presence of noise in the communication channel may eventually turn signal combinations advantageous over isolated signals (Nowak et Krakauer, 1999), which is not surprising from the point of view of Shannon's noisy coding theorem (Shannon, 1948; Plotkin et Nowak,2000). Besides, those models make little use of information theory and use a particular pay-off function for defining the reliability of a communication system.

Here we start from the communication framework developed in (Ferrer i Cancho, 2005b-d) on a noiseless channel. We assume that biological evolution cannot choose cooperation between signals unless the information transferred by a combinatorial system is larger than the amount transmitted by isolated signals. Thus, we study the topological properties of the network of signal-object associations under which cooperation is advantageous and under which it is not using an information theory approach. We find the existence of domains where cooperation does not have any advantage and domains where it has. We identify some wide mathematical conditions for belonging to one or the other domain. Previous models (Nowak & Krakauer, 1999; Nowak et al., 2000) have shown the existence of thresholds in the number of signals or stimuli for the emergence of cooperation. Our model indicates that the topology of the network of signal-stimulus associations (e.g. the network density) cannot be neglected for the emergence of cooperation. The presence of phases and thresholds between them suggests that cooperation may be not accessible to any species.

We show that maximizing the information transferred by individual signals, decreases the chances of advantageous cooperation. Our results support the hypothesis that cooperation has higher chances of being advantageous in degenerated communication systems, which confirms a possible track for the origins of human language language(Ferrer i Cancho, et al. 2005). Being a bad communicator with individual signals should not be seen as a very negative feature since it translates into higher chances of developing advantageous cooperation.

Clusters of computations for a linear transition system

Vladimir Filatov, Rostislav Yavorskiy, Nikolay Zemtsov

Poster

In our work we consider definitions of equivalence relations on the set of all computations. The main tasks here are the following. First, to find a reasonable definition of equivalence with rather small number of the equivalence classes. Second, to get a representative for every equivalence class or to prove that the class is empty.

A note on fixed points of generalized ice pile models

E. Formenti, B. Masson

Poster

Ice Pile Models (IPM) were introduced to study the lattice of integers partitions. They are also a perused model for studying the behavior of systems governed by self-organised criticality (SOC systems). These systems, starting from any initial configuration, evolve to a "critical state"; any perturbation of this critical state, no matter how small, originates a deep and uncontrollable reorganisation of the whole system. Then, they start evolving towards another critical state and so on. SOC systems are commonly used for simulating natural phenomena like snow avalanches,dunes formation, but also wood fires and even stock exchange crashes. IPM can be seen as an extension of Sand Pile Models (SPM). SPM are a simple model based on a single local rule (vertical rule): a sand grain falls on its right if the difference its sandpile and the one on its right is bigger than a certain amount of grains. In the case of IPM, one more rule is added (horizontal rule): a grain slides to the right when there is a plateau.

Remark that the horizontal rule is not a local one. For this reason, they have introduced a variant for bounding the radius of the horizontal rule. They denote IPM(k), an IPM system in which a grain can slide to the right of at most k grains. This is the variant that we are going to discuss in the present abstract.

Both SPM and IPM have been mathematically characterized.In particular, it has been proved that both systems have fixed point behavior and explicit formulas for the fixed points have been found. The issue is that these results are given only for a special initial configuration:all grains are concentrated in a single pile (column).

The authors exhibited a fast algorithm for computing fixed points of SPM under general initial conditions. They also claimed that it could be easily adapted to IPM. The present paper aims at giving a formal proof to that claim.

Clustering Data Streams - A Survey

Gereon Frahling, Christian Sohler

Poster

In modern computer society huge data sets occur in the form of data streams. The data traffic at an internet backbone router, the measurement of data (e.g. from satellite systems), and financial stock data are prominent examples of data streams. However, data stream algorithms are important as well in scenarios where random access to a huge data set is possible, but in fact too expensive. All huge data sets stored on hard disks or archive tapes can be accessed much faster sequentially.

The theoretical model of data streaming algorithms addresses problems of huge data sets consisting of n items which arrive in a sequential order. The computer has very limited local memory (the memory usage is bounded by a polynomial in $\log n$) and computation time for each element seen in the stream is limited (the computation time is again bounded by a polynomial in $\log n$). Since a data streaming algorithm is not able to store the whole data set, it must maintain statistics about the data seen so far. To analyse huge data sets it is often a good idea to group the vast number of items into a small set of clusters. In a second step an algorithm can analyse the clusters in local memory. The method of clustering can furthermore be a good tool to reduce the complexity of a data set and make it ascertainable for human beings.

In this survey we will recapitulate several theoretical results for clustering data streams. To cluster data one first has to provide a distance function between the items within the data stream. All clustering algorithms in this paper assume that this distance function is a metric. Some algorithms furthermore assume that the items are assigned to a point within a Euclidean space, and the distance between items is measured by the distance within this Euclidean space.

Having a distance function we have to decide which properties the clustering should have. The k-Median problem asks for k centers and an assignment of each item to a center, such that the sum of distances of each item to it's nearest center is minimized. In the k-Means problem the sum of the squares of these distances is minimized. The k-Center problem asks for a similar assignment to k centers, but the goal is to minimize the largest assignment distance. The Facility Location Problem is a relaxation to the k-Median problem, where the number of centers is unrestricted, but there is an additional constant cost for each center.

We will summarize recent theoretic results on how to obtain approximate clusterings, when the items are given in a data stream.

A model for the genetic code

L Frappat, A Sciarrino, Paul Sorba

Poster

Among the numerous and important questions offered to the physicist by the sciences of life, the ones relative to the genetic code present a particular interest. An attempt for modelizing the genetic code can be seen as a step further in the understanding of the complexity of the genetic code processes.

The heart of the genetic code machinery is the double helix shaped DNA macromolecule, constituted by two linear chains of four types of nucleotides characterized by their bases: adenine (A) and guanine (G) deriving from purine, and cytosine (C) and thymine (T) coming from pyrimidine. The genetic information is transmitted via the messenger ribonucleic acid or mRNA through the transcription in which the A, G, C, T bases in the DNA are associated respectively to the U, C, G, A bases, U denoting the uracile base. The translation process then associates to an ordered triplet of nucleotides (or codon) an amino-acid. Following the universal eukariotic code, 61 of such codons can be connected in an unambiguous way to the twenty amino-acids (except the three codons UAA, UAG and UGA, the role of which is to stop the biosynthesis), showing a degeneracy of the genetic code, the codons being arranged into sextets, quadruplets, triplets, doublets and singlets, each multiplet corresponding to a specific amino-acid (note that degeneracy is primarily found in the third position of the codon). Such a picture suggests to look for an underlying symmetry able to describe the observed structure.

The starting point of the mathematical framework we have developed is to consider the four nucleotides as basic states of a certain representation of some algebra, and to construct a codon as a state in the tensor product of three such representations. The complementarity rule in the DNA–mRNA transcription may suggest to assign a "quantum number" with opposite values to the couples (A,T/U) and (C,G). The distinction between the purine bases (A,G) and the pyrimidine ones (C,T/U) can be algebraically represented in an analogous way. Morevover, the fact that a codon is an ordered triplet of nucleotides imposes to construct the composite states as pure states (i.e. that cannot be linear combinations of other states). Such a structure is provided by using quantum enveloping algebras $\mathcal{U}\_q(\mathcal{G})$, in the limit $q \to 0$, called crystal basis. One is then naturally led to consider the fundamental representation $(1/2, 1/2)$ of the quantum enveloping algebra $\mathcal{U}\_q \to 0(sl(2) \oplus sl(2))$. Note that we do not deal anymore with a Lie algebra (which are the structure usually emerging in physics).

A "charge" Q of a dinucleotide state can be defined: the dinucleotide states are split into two octets with respect to the charge Q: the eight strong dinucleotides associated to the quadruplet or sextets of codons satisfy $Q > 0$, while the eight weak dinucleotides associated to the doublets or singlets of codons satisfy $Q < 0$. The model does not gather codons associated to one particular amino-acid in the same irreducible multiplet. However, it is possible to construct an operator $\mathcal{R}$ out of the algebra, acting on the codons, that will describe the various genetic codes: two codons have the same eigenvalue under $\mathcal{R}$ if and only if they are associated to the same amino-acid. Remarkably, the various genetic codes share the same basic structure.

It is a nearly universal phenomenon that alternative synonymous codons inside a multiplet are generally not used with equal frequency (codon usage). Considering branching ratios of probabilities of usage (i.e. frequencies of usage in the limit of very large number of codons) for codons differing only by their third nucleotide (XYZ and XYZ′, Z $\neq$

Z′), correlations has been remarked for biological species belonging to the vertebrate class when the dinucleotides XY correspond to quartets. One may wonder why the model is able to explain the observed correlations. A possible answer is that the model incorporates information which is typical of the organisation of the code, and that such information is in itself relevant to determine the correlations. One can also deduce, in the crystal basis model, that the sum of usage probabilities of the codons with C and A in the third position for the quartets and/or sextets is independent of the biological species for the vertebrate class ("sum rules"). A comparison between the theoretical predictions and the experimental data shows a satisfactory agreement.

Finally, a set of relations between the physical-chemical properties of the amino-acids, based on the content of the irreducible representations of the dinucleotides and of the codons coding for the amino-acids, can be derived and compared with the experimental data (of course, not all the physical-chemical properties are supposed to follow the scheme above; some of them are essentially given by the specific chemical structure of the amino acid itself).

Genetic Self-Assembly: Many Simple or a Few Complex?

Rudolf M. Füchslin, Thomas Maeke, Uwe Tangen, John S. McCaskill

Poster

Keywords: Self-assembly, inductive generalization, evolvable logic, circuit design, genetic algorithm, evolution, multiplier

In a recent paper, we investigated a genetically encoded system of a small number of different types of self-assembling components and showed that, if these components were equipped with type-dependent logical functions, scalable circuitry for several problems can be evolved. The evolution of scalable circuitry requires inductive generalization, which means in this context the inductive derivation of a solution to a problem with a potentially infinite number of instances from a limited set of test examples. To effectuate this by the mechanisms of evolution is known to be difficult; one of the investigated problems, digital multiplication, has been intensively studied in recent years, where, until employing self-assembling components, only the evolutionary design of specific small multipliers has been achieved.

This work investigates the relation between the evolutionary efficiency and the number of different types of self-assembling components and the complexity of the logic they carry respectively. We address the question for the optimal size and complexity for an evolving self-assembling system with respect to different problems. This sheds light on the evolutionary role of self-assembly in biology and is of relevance for the design of complex systems in nano- and bionanotechnology.

A way to characterize complex cellular automata and those able to perform density classification

Anna Rosa Gabriele, Stefania Gervasi

Poster

In this work we consider particular mathematical models useful in studying complexity: the cellular automata (CA). The genetic algorithms have been used for exploring the rulesśpace of elementary CA and multi-states CA with the aim to characterize, by different fitness functions, the rules that show complex behaviors and the rules able to perform density classification. Rules have been evolved using GA. The input entropy, able to select complex rules, was used as fitness function in some experiments. In other experiments, another fitness function was specifically chosen in order to select rules which perform density classification. The evolved rules have been subsequently evaluated by computing, for each rule, some parameters taken from the literature, by broadening their applicability to multi-state CA. Finally, some considerations have been drawn about the relationships between the values of the parameters described above and the specific characteristics of the analyzed rules.

Keywords: Complex cellular automata, density classification, genetic algorithms.

Markov chain analysis of an agent based growth model

B. Gaujal, E. Thierry

Poster

In this paper we investigate the asymptotic behavior of a discrete and probabilistic dynamical system which can be described as a growth model where autonomous agents aggregates.

The aim of this paper is to give a mathematical analysis of the dynamics. The analysis uses face homogeneous Markov chains and thanks to this study we validate a conjecture set by Laszlo Gulyas concerning a growth model for cities where simulations had shown that the sizes of the cities asymptotically distribute as a Zipf's law. In light of our analysis, we discuss how the emergence of such a Zipf's law could be expected in Gulyas' model and in its variants.

Keywords: discrete probabilistic dynamics, face homogeneous Markov chains, Zipf's law.

A General Methodology for Designing Self-Organizing Systems

Carlos Gershenson

Poster

Our technologies complexify our environments. Thus, new technologies need to deal with more and more complexity. Several attempts have been made to deal with this complexity using the concept of self-organization. However, we must first have a pragmatic understanding of complexity and self-organization. This paper presents a conceptual framework for speaking about self-organizing systems. The aim is to provide a methodology useful for designing and controlling systems developed to solve complex problems. First, practical notions of complexity and self-organization are given. Then, starting from the agent metaphor, the conceptual framework is presented. This provides formal ways of speaking about "satisfaction" of elements and systems. The main premise of the methodology claims that reducing the "friction" or "interference" of interactions between elements of a system will result in a higher "satisfaction" of the system, i.e. better performance. The methodology discusses different ways in which this can be achieved. A case study on self-organizing traffic lights illustrates the ideas presented in the paper.

[Full paper at http://uk.arxiv.org/abs/nlin.AO/0505009

Probing the robustness of the clustering

David Gfeller, Jean-Cédric Chappelier, Paolo De Los Rios

Poster

Keywords: analysis of complex networks, clustering.

We present a new method to probe the robustness of the cluster structure of complex networks. The idea is to add noise over the edges weight and to compare the clusters obtained with different noisy realization of the network.

This method allows to identify nodes lying between clusters, whose classification is very arguable. Furthemore we introduce a general measure, defined as the clustering entropy, to estimate the robustness of the clusters and to discriminate networks with well-defined cluster structure from networks without significant clusters.

We present several applications of the method on real-world complex networks.

Robust Cooperation in Multi-Agent Systems

Robert Ghanea-Hercock

Poster

In large-scale heterogeneous multi-agent systems (MAS) the ability of such agents to form coalitions of trusted partners and reputation networks is vital to autonomous operation. This paper investigates the dynamic formation of cooperative communities within a simulated MAS. In particular this work considers the requirements for stable high-trust coalitions to self-organise and survive, while some percentage of agents in the population is defecting. A model of dynamic group formation is presented which enables the rapid formation of a self-organising cooperative agent community. The results presented indicate that by utilizing a self-reinforcing cooperative trust model, a very high degree of resilience to perturbation and defection can be achieved. A number of critical parameters are investigated which indicate a phase transition in the formation and resilience of the cooperative structures that emerge.

What Models for Complex Systems?

Sica Giandomenico

Poster

Following Bar-Yam ["Overview: The Dynamics of Complex Systems"], one approach to the study of complex systems begins from an understanding of the relationship of systems to their descriptions. In this context, our enquiry focuses on the construction of rigorous easy-to-use models to describe complex systems. In particular, we consider a model as defined by a mathematical structure, where the expression "mathematical structure" aims to indicate a combination of different kinds of sets through an arbitrary order. The concept of "set" and the modalities to construct sets are defined through the following axioms and corollary ("Elementary Set Theory"): Axiom I (extensionality): A set is completely determined by its elements and by the composition relations among the same elements. Element of a set is always a set. The composition relations are not commutative. Axiom II (construction): It is possible to construct a set through the execution of the algorithm $<$ Df1, Df2, Df3$>$, where Df1 represents the operation of elements definition, Df2 represents the operation of composition relations definition, Df3 represents the operation defining the membership relation among elements and set. Corollary: Given two sets A and B between which there exists a composition relation r, it's always possible to determine a set C, having A and B as elements, ordered through the composition relation r. Having defined the mathematical structure, in order to complete our task, we have to call the different sets and composition relations (namely, create a label for the variety of sets and composition relations): as result, we obtain a model, mathematically exact and linguistically precise. Our goal is to introduce this technique in order to construct models able to describe the different typologies of systems (e.g. biological, physical, economical, social ones) keeping intact, in the complexity, the precision degree.

Complexity Measures in Manufacturing Systems

Zanutto Gianluca,, Alberto F De Toni, Fabio, Nonino, Alessio Nardini

Poster

This study analyzes the most widewpread methodologies available in literature used to measure complexity. The research moves from a theoretical physic perspective, through the Complexity Theory, to a manufacturing system. On these subjects, two classification frameworks are proposed in order to categorize the most widespread measures. In particular, the second classification framework regards entropic measures widely used to measure complexity in manufacturing systems. With reference to this second framework, two indexes were selected (static and dynamic complexity index) and a Business Dynamic model was developed. This model was used with empirical data collected in a job shop manufacturing system in order to test the usefulness and validity of the dynamic complex index. The Business Dynamic model analyzed the trend of the index in function of different inputs in a selected work center. The results showed that the maximum value of the dynamic complexity index represents the so called "edge of chaos", where the amount of information needed to manage the system is maximum and where there is the trade off between flexibility and efficiency of the production system. In conclusion, the main result reached in this study regards the "edge of chaos" that is the target configuration for a company, in a particular system and under the same external conditions.

What Proteins Are Made From? Informational Way To Protein Alphabet

A.N Gorban, M Kudryashev, T Popova

Poster

Keywords. Amino acid, protein, classification, relative entropy, alphabet reduction

What proteins are made from, as the working parts of the living cells protein machines? To answer this question, we need a technology to disassemble proteins onto elementary functional details and to prepare lumped description of such details. Our hypothesis is that informational approach to this problem is possible. We propose a way of hierarchical classification of amino acids that makes the primary structure of protein maximally non-random. In order to formalize this idea we follow [1,2] and analyse frequency dictionaries of short protein fragments, and relative entropies of such frequency dictionaries. The entropic optimality principle is formulated and applied for amino acids classifications for various databases of primary protein sequences. In contrary to the widespread MaxEnt approach (that is, of maximal disorder), we deal with the principle of maximal order. The following properties of amino acids binary informational classifications are studied 1) the existence and uniqueness of optimal classification for given frequency dictionary, 2) structure of the set of highly informative classifications in the vicinity of the optimal one, 3) stability/instability of the optimal classification with respect to variations of the frequency dictionary, 4) similarity between classifications constructed on the basis of 2-letter words frequencies and those constructed on the basis 3, 4 and 5-letter words frequencies. We compared informational binary classifications of amino acids with classifications obtained by other methods. Amino acids groupings mentioned in most of reviewed papers do have moderate similarity with two types of Hydrophobic/Polar classification while informational classifications is shifted to Charged/Uncharged property. Classification of [3] is the only one to be rather close to informational classifications. Detailed statistic data are published in preprint [2]. The binary informational classification gives us "the first letter of protein alphabet". Algorithms of hierarchical information classification are developed in order to find the following "letters". On each level of hierarchy we find the optimal classification that is independent (with given accuracy) of classifications obtained on the previous levels. The second level is surprisingly independent of all known "usual" amino acids classifications. Below the example of the first and the second classifications is presented for E-coli proteome (number of proteins is 5797 [4]): 1st classification: 1st class: A,C,D,E,F,G,I,K,L,M,N,P,S,T,V; 2nd class: H,Q,R,W,Y. 2nd classification 1st class: A,E,K,L,M,P,Q,R,T,V,W; 2nd class: C,D,F,G,H,I,N,S,Y. Binary classification tree: Zero level (one class) A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y First level (two classes) A,C,D,E,F,G,I,K,L,M,N,P,S,T,V, H,Q,R,W,Y Third level (four classes) A,E,K,L,M,P,T,V, C,D,F,G,I,N,S, Q,R,W, H,Y. The next step of the research program should be the informational classifications analysis of 2 and 3-symbol elements of primary structures presented as a sequence of 2 and 3-letters elements and so on.

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Investigating Complexity with the New Ties Agent

A.R. Griffioen, Á. Bontovics, A.E Eiben, Gy Hévízi, A. Lorincz

Poster

It has been widely acknowledged that there are different levels of complexity and it increases if one starts from atoms and progresses towards societies [**?**, **?**]. There are still many unresolved questions about how this increase takes place in different systems. One way to investigate this is by constructing systems that have this property of complexity increase. This is why agent based research seems to be a very good way of studying complexity. The New Ties project aims at setting up a large scale multi-agent simulation in which the population is to learn and evolve a social culture and individual capabilities that enables them to (co-) operate viable in their environment [**?**]. [1] The New Ties agent seems particularly suited to investigate complexity for the following reasons:

- the agents are complex,
- the agents are tools to analyse complexity,
- the agents have to form complex structures.

This abstract places emphasis on the first subject, since it gives an insight into how complexity is engineered. The subsequent two subjects are important from the point of view of the detection of complexity increase.

The New Ties agents are equipped with standard capabilities to perceive and act in their (virtual) world. They can recognize the objects of the world including messages sent by other agents. They can perform different actions like moving, picking up objects, and communicating with body language and auditory messages such as talking and shouting (for a complete description of the New Ties agent see the Technical Report [**?**]). Most of the complexity of the New Ties agent, however, resides in its capability to adapt.

In the New Ties agent we distinguish three types of adaptation or learning algorithms, namely individual, evolutionary and social learning. Each learning type is defined with respect to the direction of knowledge transfer from the perspective of an agent. In individual learning the knowledge transfer goes from the agent via the environment to itself. The learning agent is a sink. Individually learned knowledge remains with the agent that has acquired it, it is not passed to its offspring and in the absence of social learning it is not transferred to fellow agents either. In evolutionary learning the knowledge transfer is vertical, along the line of successive generations. Learning takes place at the population level. Good genomes are contained in well-performing individuals that obtain more offspring thus changing the allele distribution. In social learning the knowledge transfer is horizontal as the knowledge that inhabitants learn individually is shared by explicitly "telling" it to each other, thereby collectively developing knowledge that covers different situations they encounter. To be able to tell 'something' there should be mutual understanding about the meaning of 'something'. We do not hardwire the meaning of words in agents: agents should develop language on their own. They have to find common words for objects in their world (for more details see [**?**]). Language evolution is thus an important aspect of social learning.

The agent controller, the decision making mechanism of the agent, will undergo all three types of learning. To integrate the different learning types in the controller we have

[1] see also http://www.newties.org

developed the Decision Q -Tree, where a decision is made by tree traversal. A DQT consists of test, bias, and action nodes. In test nodes the decision determines whether the yes or no edge is taken. Every test node uses a model of the world, build by genetic and life time experience, that is used to make a decision. A bias node can have more edges. Each edge is labeled by a bias or a probability of choosing the given edge. An action node is almost similar to a bias node except that each edge leads to an action, while the edges of bias and test nodes can lead to any type of nodes. Individual learning, based on reinforcement learning [**?**], changes the preferences and decision making process in test nodes on the basis of rewards given to the action and propagates these rewards through the tree. Evolutionary learning uses the Genetic Programming paradigm [**?**] to recombine trees and evolves them further by means of specific mutation operators. Note that both operate on the initial tree templates of the parents to avoid Lamarkian evolution. Social learning changes the world model in the test nodes used for decision making.

With the statement "the agents are tools to analyse complexity" we mean that agents themselves can be used to analyse their environment, where the environment includes the other agents, as well. We can learn something from the environment and (other) agents by studying the agent. For example, information about (un-)successful behavior in a given environment can be extracted from the agent controller. Agents thus comprise knowledge bits of the world.

In the New Ties project one of the objectives is the formation of complex agent structures, or in other words the generation of complex patterns, which can be interpreted as social patterns. We expect the agents to start using tokens for trade, to learn to plan future actions, to remember their previous locations, and also to develop memory to span larger distances for going from one location to another. If the agents manage to learn and achieve some of the previously mentioned aims, it can result in a behaviour similar to the so-called Kula ring, which is an intricate social trading system practised by islanders to exchange necklaces in a non-competitive way to establish alliances with locals of the neighboring islands.(For a more detailed description see Gilbert et al. [**?**]). Another objective is the aforementioned language evolution, in particular the evolution of a grounded common language. These two objectives, considered as two major transitions in evolution [**?**], may contribute significantly to complexity research.

In the New Ties agents most of the complexity will be in the adaptive capability of decision making. This adaptive capability may allow for a second order emergence system as was described by Steels [**?**]; a system which is able to detect, amplify, and build upon emergent behavior. Learning mechanisms may cause a repeating loop of knowledge transfer with which new knowledge structures can be build that can be exchanged again. This may not only affect the knowledge structures, but also the way in which they are built. For example, evolution may find the controller structure best fitted for individual learning, which is known as the Baldwin effect [**?**]. This research may not only show that major transitions as societies and language development are possible, but it will also give us insight in how they *can* occur.

Our approach of studying complexity is thus by constructing large scale agent simulations. The project just started in autumn 2004. For now, we only have a vision, approach and design. We will gladly present them along with the first technical results by November 2005.

Modeling tumor growth as the evolution of a biological complex system with variable fractal dimensions

Caterina Guiot,, Pier Paolo Delsanto, Nicola Pugno, Thomas S. Deisboeck

Poster

Universal growth laws, as proposed by West and collaborators for all living organisms (West et al, Nature 413: 628-631,2001), may be extended to describe the growth of tumors in vivo, provided the scaling exponent p (assumed by West et al. to be equal to 3/4) varies according to the tumor and its vascular network evolution (Guiot et al, J. Theor. Biol. 225: 147-283, 2003, Delsanto et al, Appl Phys Lett. 85: 4225-4227,2004). In fact, the idea of a fractal topology of the tumor vasculature has already been proposed by Baish (Microvasc. Res. 51: 327-346,1996) and Baish & Jain (Cancer Res. 60:3683-3688, 2000), and in-vivo estimates of the fractal dimensions of planar vascular networks based on the box-counting method were performed. The evolution of cancer topology during the growth of tumors implanted in mice has been studied by Gazit et al. (Microcirculation 4:395-402,1997) ,in the chick embryo by Vico et al (J. Theor. Biol. 195:525-532,1998) and after delivering docetaxel to cultured HUVEC cells in Matrigel by Guidolin et al (Microvasc. Res., 67: 117-124, 2003) . In a completely different context, Carpinteri and Pugno (J. Appl. Mech. 69: 854-856, 2002) have developed universal scaling laws for energy dissipation during the fragmentation of solids, by assuming a self-similar size distribution of fragments. It is interesting to note that, according to an interpretation based on their analysis, the exponent p should be strongly related to the fractal nature of cancer topology and thus susceptible of independent measurements. It could possibly also be applied for diagnostic purposes to mark the emergence of a functionally effective neo-angiogenetic structure.

Generation of robust networks: a bottom-up model with optimization under budget constraints

Laszlo Gulyas

Poster

This paper addresses the problem of generating networks that are robust against random failures (i.e., against the random removal of nodes). We construct an agent-based model in which agents represent the nodes of the network that connect to one another aiming to maximize their connectivity. Each agent can build a fixed number of links. However, information about the existing network is costly, so the agents must optimize under budget constraints, i.e., only having information about a limited number of existing nodes. Numerical simulation shows that this scheme generates robust networks under a wide range of conditions. A key observation is that the pattern of information access, determined by the scheme used for pricing information about the existing network, is pivotal for the desired system-level property.

Vasomotion in arteriolar networks

Martin H. Kroll

Poster

The microvasculature forms an interconnecting network of vessels that supplies nutrients to the tissues in a timely manner and removes waste products. It serves as a conduit for blood and provides peripheral vascular resistance (necessary to maintain adequate blood pressure). The arterioles react to the accumulation of waste products from the tissues, dilating and constricting, resulting in rhythmic patterns of blood flow known as vasomotion. The intricate geometric structure, biochemical negative feedback, flexible adaptation to changing demands, and distribution of multiple units demonstrating synchronization characterize the microvasculature as a complex system. Alteration of structure induces dynamic changes, which may become altered by disease. We studied the inherent rhythm in blood flow in the microvasculature using spectral analysis. Blood flow was measured in the skin of the forehead using the Periflux PF3 Laser Doppler flow meter (Perimed, Sweden) in male and female subjects between the ages of 20 and 60. The data was collected at 8 Hz. Spectral analysis was performed by means of fast Fourier transforms using Matlab v. 6.5. The raw data (blood flow vs. time) demonstrated rare sinusoidal behavior. Spectral analysis (power spectra) revealed multiple frequencies. Distinct peaks occurred between 0 and 0.2 Hz, with no peaks above 0.4 Hz. All studies showed a fundamental frequency of 0.000977 Hz (a period of 17 minutes). Each subject demonstrated numerous frequencies between the fundamental frequency and 0.16 Hz. Division of the higher frequencies by the fundamental frequency resulted in unique series of integers, such as 1,3,6,12,15,18,22,...101; 1,6,11,13,18,23,26,28,...101; 1,5,9,15,18,21,23,28,30,...101; 1,4,8,13,16,18,22,28,31,...101. The original data set could be reconstructed by the summation of a series of sine waves, indicating a highly ordered deterministic system. Spectra from subjects with diabetes or hypertension demonstrate a decreased number of frequencies below 0.1 Hz and an increased power of those between 0.11 and 0.17 Hz. Combining architectural structure, nonlinear response, time-delay and the dissipative use of energy with the presence of a complex periodic system (the frequencies are commensurate with the fundamental frequency) demonstrated by the spectra analysis defines the microvasculature as a nonlinear, dissipative system with limit cycles providing the source for the periodic behavior. Only a few elements in the series of frequencies represent a harmonic series. The non-harmonic components offer a means to study highly complex systems.

Analysis of the vasomotion spectra reveals that each person produces distinct sharp frequencies. Disease causes distinctive alteration in pattern with a decrease in the number of dominant frequencies and a preponderance of frequencies between 0.11 and 0.17 Hz. Such a change in pattern may be the result of a simplification of the relationships among the component variables of the system. Spectral analysis of blood flow in the microvasculature offers a unique tool in understanding the complex behavior of blood delivery at the tissue level and may be useful in assessing the impact of disease prior to end-organ tissue damage.
keywords: analysis of complex networks, microvasulature, multiple limit cycle behavior

Adaptive rational modelling of complex systems

Wouter Hendrickx, Tom Dhaene

Poster

Complex computer simulations take a very long time to compute. In many engineering applications such simulations depend on several tuning parameters. Abstractly we therefore see a simulator as an unknown system

$$H : R^d \rightarrow R^p$$

which maps the tuning parameters onto certain output values of the simulation. Frequently one wants to have an overview of the outputs of the simulator as a function of the inputs. To run the simulator at a huge number of input points would be too expensive. Therefore, we try to use adaptive rational modelling techniques in order to minimise the number of simulations needed to get an accurate approximation of the system's global output behaviour.

We have developed a MATLAB framework for adaptively building rational models for systems which depend on 1 to 4 input parameters. The framework starts with an initial set of simulation outputs for several random inputs. Based on these input/output pairs (*samples*) we try to approximate the system's global behaviour by constructing several interpolants through the samples. To assess the quality of the models, we calculate the difference between each pair of models. Models which are most similar to each other are considered more accurate than those that deviate from the others. In an adaptive loop, new simulations are run at the inputs where the most accurate models differ the most. Afterwards, the sample set is augmented with these newly found input/output pairs and the process starts all over again.

In the sequel we present the results of tests on both artificial and real-life examples. We will demonstrate how the framework succeeds in improving accuracy by adding more and more samples.

A Collaborative Open Architecture for Data Collecting and Interpretation on Complex Artificial Systems

Silviu Ionita, Ionel Bostan, Petre Anghelescu, Alin Mazare

Poster

A tremendous effort to manage the complex systems in a very dynamic society is currently made. Understanding the complex systems and the investigation of the related processes requires a large amount of knowledge and the appropriate techniques for their representation and reasoning. The key issue in the knowledge-based model building on complex systems is the capability of acquisition and interpretation of high quantity and multi-resolution data. In this paper is proposed an architecture for data collecting and fusion on the large scale heterogeneous distributed systems in order to make useful analysis for decision making. The real time data availability and the high capability of their processing are essential for the efficient and robust control of complex systems. The main steps of our research are reported in the following. First, we identify the systems and subsystems and investigate the available and prospective communication infrastructure. We also provide an analysis of the major communication standards and candidate technologies for data acquisition and preprocessing. Second, an original classification of data is given according with criteria of level of resolution, real time availability, relevancy, degree of uncertainty, etc. These aspects are very important for data processing and interpretation. Third, with the development of network-based enabling technologies the novel concept of web-Centric society was introduced to coin a novel organizational paradigm that is information-exchange driven and knowledge empowered. Recent developments in distributed artificial intelligence and network technologies have enabled technological paradigms such as holonic and global organizations to become a reality. A worthwhile approach is based on dynamical systems theory and their relation to Multi-Agent Systems (MAS) whose objective is to support a so-called "going concern". Under these circumstances, the proposed collaborative open architecture is designed as a multi-agent monitoring heterarchy with a large capability in gathering, grabbing and processing the data with the goal of their interpreting in benefit of the large scale distributed systems. From an evolutionary perspective, these are powerful communication systems that receive data from their environments; find regularities in the data extract the information and then identify internal models that process this information in an optimal manner with respect to goal achievement. These distributed systems exhibit self-organization at higher aggregate system levels via information exchange through interactions between the individual agents. Communication between the distributed entities results in knowledge distribution across the overall system in a manner that optimizes goal achievement. This results in emergent and adaptive properties of the overall distributed system that are not exhibited by the individual component entities. All in all, some very suggestive examples and simulation results are presented from the relevant study cases focused on the complex systems like the urban traffic road, power distributed networks, communication networks. A special attention is dedicated of the data interpretation in order to evaluate the interdependency in terms of so called "side-effects" of different sub systems.

Conceptual analysis of the complexity of socio-technical systems

Bjørn Jespersen, Maarten Ottens, Maarten Franssen

Poster

Keywords: infrastructure, socio-technical system, modal constraints.

Infrastructure typically divides into transportation, energy supply and telecommunications. We wish to make two claims. First, it is both conceptually enlightening and of pragmatic import to construe infrastructural objects as socio-technical systems. Second, socio-technical systems are irreducible either to purely social or purely technical systems. Nor can they be factored out into either of them in the final analysis. Thus, we are going to introduce a conceptual category of inherently hybrid systems sui generis. This conception of system is somewhat more inclusive than other approaches to large-scale technical systems by incorporating not only technology and agents (whether individuals or groups) but also legislation and social conventions into the system. The two fundamental questions of our research are: · What is the character and degree of the complexity of a socio-technical system? · How, if possible, are the boundaries of a socio-technical system to be delineated? We suggest calibrating the complexity of a socio-technical system by means of the formal distinction between operations and factors or elements amenable to the operations. Our thesis is that a system boasting two operations is more complex than a system boasting only one, regardless of the quantity of elements the operation applies to. These operations are subject to various modal constraints, namely what is possible or necessary legally, conventionally, technologically, nomologically and logically speaking. Socio-technical systems are bound to contain various operations that are subject to various kinds of constraints, thereby increasing the complexity of the sytem. By exceeding the boundaries of what normally passes for a technical system, it becomes less than obvious exactly how to redraw them. A socio-technical system is one that contains several subystems and is at the same time itself a subsystem of larger systems. Our research is directed toward rigorously defining the notion of socio-technical system and demarcating, in a principled manner, any given such system. It is crucial to do so, not least because engineers are participate in designing, constructing, controlling, maintaining, mending and improving such systems and need to know what falls within the system, and what factors impact the functioning of the system in what ways. We will use air transportation as a paradigmatic example of a socio-technical system. Air transportation is an input/output system that transforms a highly diversified pool of resources into the facilitation of the switchover between air and ground transportation and transfer between any two airports considered as nodes of the air transportation network. This system could not possibly perform this kind of transformation and transfer without a multitude of technological, societal, social and legal parameters being operational.

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Robotics in the science of complex systems

Jeffrey Johnson

Poster

Multi-robot systems may provide an important step towards a general science of complex systems. When classified according to experimental replicability, teams of interacting robots form an intermediate class of systems, more complex than many systems in traditional physical science but less complex than most human systems. It is difficult for humans to study human systems from the inside; and often impossible to perform repeatable experiments on complex human systems. Team robotics does not have these problems, while still exhibiting many of the characteristics of complex systems. It thus provides an ideal laboratory to investigate some of the most fundamental questions in the evolving science of complex systems.

A Generative Complexity Theory of Minds Evolving in Peer Interaction

Ton Jörg

Poster

The focus is on formulating a complexity theory of minds evolving in the generative process of development through human interaction among peers. This interaction between two persons and their minds are taken as the unit of study. This unit will be regarded as a complex system, with their different parameters. A system, consisting of generative reciprocal influences within complex relationships of mutual, simultaneous reciprocal causal relations. The complexity of it still lacks an adequate vocabulary. What is needed, is a link between thinking in complexity, an adequate theory of personal development through human interaction, and the conceptual thinking of evolution theory as a methodological tool. The processes involved are both auto- and cross-catalytic of nature, leading to self-enhanced causal loop effects. The unexpected effects of human interaction may be described and explained as non-linear effects of 'bootstrapping' each other as a result of the causal dynamics of human interaction within peer relations.

Fractal Analysis of Microglial Morphology

A Karperien, C. Lucas, C. Depardieu, G Aurel, H.F Jelinek

Poster

Field: Particular complex systems Keywords: fractal analysis, nonlinear systems, fractal dimension, microglia classification, pathology

Microglial morphology is an important clue to microglial activity and thus may be an important indicator in several pathologies, including dementia and schizophrenia, but is rather difficult to quantify. Structural complexity has been assessed using fractal analysis, offering a way to quantitatively describe otherwise difficult to characterize forms and may be useful in the study of the role of microglia in human disease. We used box-counting dimension to ascertain the utility of fractal analysis in the classification of microglia cells and have found statistically significant differences between subpopulations of these cells ($P < 0.05$).

Introduction Microglial form depends on context and is a continuum in a changing context. Not only is form different for subpopulations of microglia; microglia change form over minutes to hours; microglia move; they change complexity with age; they become activated in many different ways; and they are influenced by the local and overall physiological environments. Nevertheless, perhaps form can be assessed during an interval as manifested by their morphology and divided into ramified, bushy or reactive. While much about microglial function can be inferred from staining and morphological features, several studies argue that nearly imperceptibly altered microglia may underlie chronic, subtle pathology in schizophrenia and other brain diseases not always detectable by histological methods. If this is the case, detecting problems prior to overt damage will be a priority. Yet it is currently difficult to detect subtle abnormalities in microglia. Fractal analysis may be of use here to identify these subtle changes in morphology associated with functional states.

Method Three exclusive operational definitions for microglia structure were applied: ramified=having usually many processes; bushy=having usually shorter, thicker processes; and reactive=having few relatively very short, thick extensions with large round to amorphous cell body. Cells were randomly selected from within 15 image areas from a random sample of the set of microglia images, unsorted with respect to species, staining and gender. Cells were then classified into one of the above categories, then blindly and randomly matched as pairs from within each area. This gave 29 ramified and bushy pairs and 7 bushy and reactive pairs. Contours of cells were analysed using FracLac as a plug in for ImageJ, with a maximum box size set at 47

Results For the ramified (mean=1.42; standard deviation=0.004) and bushy (mean=1.40; standard deviation=0.086) pairs, the mean difference was 0.015 (standard deviation of the differences=0.152). Using a two-tailed t-test, a p value of 0.5 and r=0. 0.3950 was obtained. For the bushy (mean=1.43; standard deviation=0.0901) and reactive (mean=1.27; standard deviation= 0.1394) pairs, at $p = 0.0143$; r=0.51 for these pairs. There is also significant difference between ramified and reactive, $p < 0.05$ (mean=1.42; standard deviation=0.004 & mean=1.27; standard deviation= 0.1394).

Discussion This investigation looked at how well the Db differentiates individual microglia in a general sense, looking not at absolute values of the Db but at differences in differently classified cells within one environment. The major finding was that the Db differentiated cells classified as bushy from cells classified as reactive, and ramified from reactive but did not clearly differentiate those classified as bushy from those classified as

ramified when multiple paradigms were considered together and a consistent relative difference between categories was looked for. The Db proved useful for measuring differences between different functional states and thus may provide novel insights into understanding the complex development of pathology associated with schizophrenia or dementias, which have been reported to have microglia involvement.

Visualising Interactions in Complex Design

Rene Keller, Claudia M. Eckert, P. John Clarkson

Poster

Designing a product is complex in many ways. Four layers, which can be sources of complexity in design, can be identified. First, the product itself can be complex as it might have many components that are highly interrelated and linked in various ways. Second, the process of designing the product can consist of many interlinked tasks with probabilistic outcomes that can cause costly iteration. Third, the organisation that designs the product can be considered complex, as it consists of a large number of multidisciplinary teams. Fourth, the relation of the product to its environment can be complex. In addition representations used to interact with the product can also be highly complex. We concentrate on how to visualise the first two aspects of complexity, the complexity of the product architecture and the complexity of the corresponding design process. Both, products and processes can be modelled as networks, consisting of items (components and tasks) and interactions and dependencies between them. Networks that show an appropriate level of detail can easily become very huge, consisting of hundreds or thousands of items connected in various ways. The key for successful design is to have appropriate interfaces and visualisations of this information so that the designer can effectively make use of the models. Two main representations for network data exist: Adjacency matrices and node edge diagrams. Both representations have advantages and disadvantages when showing such data. While matrices are very compact representations that let users easily extract information about direct linkages between items, networks proved superior behaviour when indirect interactions between items are to be visualised. However, for very large and complex models, further advanced information visualisation techniques such as filtering and fisheye techniques are necessary in order not to overwhelm the user with the amount of available information. We will introduce network and matrix representations that make use of advanced information visualisation techniques and are used in two methods developed at the Engineering Design Centre Cambridge to support the design of complex products. The signposting methodology allows a dynamic approach to planning and analysing the design process used to design complex products. The basic idea is to dynamically update the state of the design and present the designer at each state of the design using a signpost of how to proceed with the design process. Simulations of such design processes allow further analyses in order to detect bottlenecks and to find optimal task execution orders. The other method that makes extensive use of network visualisations is the CPM (Change Prediction Method) to predict direct and indirect design changes. When a component of a complex product has to be changed (e.g. because of a customer request), this change can have knock-on effects on other components that then equally affect further components. Using the CPM method allows designers to predict the impacts of changes to directly and not directly connected components. In both examples it is important for the designer to get detailed information about a particular case as well as a global overview over the entire information space. In this paper we will introduce displays that visualise complex process and product data taking advantage of enhanced information visualisation techniques and that have shown to be highly beneficial to the design process.

Evolutionary influence of the protein network topology on gene organisation in artificial organisms

Carole Knibbe, Guillaume Beslon, Jean-Michel Fayard

Poster

Although molecular biology provided us with a huge amount of data about individual genes, their roles cannot be fully understood unless we put them into the broader context of their interactions. Indeed, multiple links exist between genes: they can share the same ancestral sequence, they can be neighbours on a chromosome, they can be coregulated or regulate each other's expression level, the proteins they encode can interact physically or be involved in the same metabolic pathway. Those various points of view lead to different biological networks - different but not independent, notably because they are involved in a common evolutionary story. Therefore, understanding these structures requires to understand how they build up and interact at the evolutionary time scale.

In particular, are genes randomly distributed on the chromosomes, or does their organisation depend on their functional interactions? It is difficult to answer this question directly for living cells, notably because the notion of gene function is subjective in this context. We therefore chose an artificial life approach, using the fuzzy logic formalism as a generic framework for the functional level.

In our model, called aevol, each organism is able to perform abstract biological processes with various degrees of efficiency, depending on the set of interacting functional elements ("proteins") its genome encodes. The genome is a binary string that contains coding sequences (genes) separated by non-coding sequences. Each gene is translated into a protein able to either realize or inhibit a fuzzy set of processes. Two proteins can have the same process in their fuzzy sets, implying that for the organism, the degree of efficiency of the process depends on their interaction. Thus, the organism's phenotype is the logic combination of the sets of its proteins. Like in the genetic algorithms used in computer science, selection and variation mechanisms allow the phenotypes to become closer and closer to an arbitrary optimal fuzzy set. When the fittest organisms reproduce, their genomes are replicated with random errors, affecting a few positions (punctual mutations, small insertions, small deletions) or large genomic segments (duplications, translocations, large deletions, inversions).

Since the fitness computation does not include genomic criteria like genome length or gene order, the genome is free to self-organise. Similarly, the functional network is not predefined, and the number of proteins can evolve, as well as the strengths of their interactions. We can however set the maximal interaction potential of the proteins - that is to say the maximal number of processes they can be involved in -, thereby limiting the average connectivity of the network. This feature is expected to have evolutionary consequences, since deleting a highly connected gene, for instance, may have much more deleterious effects than deleting an "independent" gene.

One can assume that the lineages that survive are those where large-scale mutations produce some effects on the phenotype, but only moderately, so as to enable the discovery of better solutions (evolvability) while not destroying the current one (robustness). When genes are highly connected, deleting or duplicating several genes at once is likely to have too drastic effects. Therefore, the genome should adapt itself by changing its length, gene number and gene organisation: the average number of genes affected by a large-scale mutation should adapt to the connectivity of the interaction network.

To test this hypothesis, we carried out experiments with five different maximal interaction potentials, letting in each case 1,000 individuals evolve during 30,000 generations. Statistical analysis of the spatial distribution of genes along the chromosome reveals that in most cases, the gene organisation alternates shuffling phases with steady states throughout the evolution. Two steady states are possible: genes can either form clusters or be regularly distributed (overdispersed pattern). While both states are observed when the interaction network is loosely connected, allowing for highly connected protein networks seems to lead the gene organisation towards the overdispersed pattern. This reduces the probability of affecting many genes with a single large-scale event.

These preliminary results tend to support the hypothesis that when many proteins interact, the need for robustness can be strong enough to make links emerge between the functional and the genomic level in our artificial system. Additional experiments and further analysis of the impact of the mutational events should help us test this hypothesis.

Morphometrica

Romulo Krafta

Poster

Agents and Space in a Urban Model

Key words: spatial dynamics simulation, urban morphology; urban growth

It is reported efforts towards the construction of a model for urban spatial dynamics simulation, based on multi-agents and space. The underlying idea is to have urban space producers and consumers operating in a two-layer, two-circuit model. The first one holds urban space and its successive transformations; one second layer contains agents related to space; one first circuit simulates space production, and a second one simulates space consumption. Relationship between layers is represented as objective spatial features that agents are submitted to and subjective meanings agents attach to each spatial feature. While space works always in the same way, meanings vary according to each agent's background and context. Relationship between circuits are represented by means of a market game in which producers try to maximize their profits by gambling with their risks, whereas consumers try to foresee the spatial distribution of local externalities that maximizes their utilities and investments.

Reliable Broadcasting in an Automotive Scenario

Jaroslaw Kutylowski, Filip Zagorski

Poster

We propose a dynamic, ad-hoc communication network consisting of mobile units that can warn about traffic jams on highways.

Our goal is to provide a practical, low cost so- lution. Therefore we consider very simple wire- less communication hardware, without collision detection, with very small bandwidth and a prob- abilistic model of link failure.

We provide a complete system architecture, consisting of three fine-tuned algorithms which allow the stations to self-organize and transmit traffic jam warnings.

Peanuts: A Top-Down Peer-to-Peer Network

Peter Mahlmann, Christian Schindelhauer

Poster

We introduce Peanuts – a top-down Peer-to-Peer network combining the benefits of reliable random graphs and semantic search trees. The main goal of Peanuts is to overcome the restricted query languages of almost all current peer-to-peer networks. These restrictions are a consequence of the use of distributed hash tables where any semantic relationship of the data is lost. In a top-down approach such semantic relationship is preserved since the peers are assigned to the data and not vice versa.

Peanuts allows nontrivial lookups, like range queries, neighborhood search, and estimation of the popularity of prefixes. Furthermore, the maintenance of the network structure is kept local so that periodic handshake operations suffice to maintain the network structure. Simplifying, Peanuts supports three kinds of locality what results in the possibility to support non-trivial queries:

Network Locality: Lookup operations can be performed with small latency.

Information Locality: Closely related data elements are stored on network-wise close peers.

Interest Locality: Peers can choose on providing lookup service and data storage for certain data. If peers choose to provide certain data, the network structure will improve their lookup of related data.

Random graphs are Peanuts main component to build arbitrary search trees supporting these kinds of locality. There is a *Reliable Backbone* which is a random graph consisting of all participating peers. This Backbone represents the root of the semantic search tree. The backbone network should be simple and reliable under churn. Therefore, the backbone is realized by a random network. A random network has several advantages compared to deterministic structured networks. For example the maintenance costs in highly dynamic networks are minimal, since there is no predetermined neighborhood. In [**?**] we introduce a simple scheme to maintain such random networks. The main component of this scheme is a simple periodically performed local link exchange, guaranteeing connectivity and establishing expander graphs with high probability.

The peers of the backbone are recursively assigned into sub-sets, each representing one child node of the current tree node. Instead of the usual approach of hashing data onto peers, we hash peers onto data. The assignment of peers to tree nodes is done using weighted consistent hashing [**?**], an extension of consistent hashing to support non-uniform load distributions. In Peanuts, the number of peers assigned to a tree node depends on its load, i.e. the amount respectively popularity of data stored on this nodes subtree. This way unbalanced trees can be handled efficiently.

Peanuts is currently implemented in cooperation within the EU-project DELIS to provide an efficient peer-to-peer based data structure for the implementation of a distributed Web search engine.

[1]Peter Mahlmann, Christian Schindelhauer, Peer-to-Peer Networks based on Random Transformations of Connected Regular Undirected Graphs, 17th ACM Symposium on Parallelism in Algorithms and Architectures, (SPAA 2005), Las Vegas, NV, USA, July 17-20, 2005

[2]Christian Schindelhauer, Gunnar Schomaker, Weighted Consistent Hashing, 17th ACM Symposium on Parallelism in Algorithms and Architectures 2005, (SPAA 2005), Las Vegas, NV, USA, July 17-20, 2005

Tubes

Alexandre Makarovitsch

Poster

This is a journey in complex systems. Starting with a tube made of a "virtual material", and applying a set of couples of operators - cut/paste, fold/unfold, pierce/patch - at each clock tic, systems more and more complex appear at each generation. The research has the ambition to model such innovative shapes generation and try to provide a new look into the complex systems generation from simpler shapes, using simple operators. The research is pursued within the Institute of Applied Mathematics of the Université Catholique de l'Ouest, the POLIS initiative.

One single molecule to access another scale? PAI-1, Microenvironment and Cancer cell migration.

M. Malo, F. Delaplace, G . Barlovatz Meimon

Poster

The cancer pathology is a complex process caused by a cellular dysfunction leading to a whole organ or even organism vital perturbation. To better understand this process we need to understand each of the levels involved and what allows the change of scales.

A matricellular protein, called PAI-1* has been identified as able to induce cell adhesion, reorganization of actin cytoskeleton and morphological changes, and to promote cell migration. PAI-1 participates in a regulation network linking the extracellular matrix and the cell. The molecular bridge formed by this protein and others is able to transduce biochemical and biomechanical signals to the cell. The cell response can be evaluated in terms of mRNA rate constants. It can further be assessed by the evaluation of migration speed. We are using the game theory and the game network theory to model this dynamic at the cell scale.

PAI-1, found closely around the most invasive tumors represents an independent factor of bad prognosis. Cancer cells, having undergone the epithelial-mesenchymal transition (EMT), can use PAI-1 for their migration. However, if the environnement is very rich in PAI-1, the cells undergo a second transition, the so-called mesenchymal-amaeboid transition (MAT). Then their migration becomes "amaeboid" very different from the previous one by the independence towards integrins and proteases activity. This amaeboid state is characterized by a complete reorganisation of actin (with actin rings) and by the activation of the Rho GTPases transduction pathways. Furthermore, in the presence of this particular (i.e. PAI-1 enriched) environment, the cells down-regulate their PAI-1 mRNAs rate constants.

From the cellular level to the tissue level. Here the regulation network occurs at the cellular/microenvironmental level and includes a PAI-1 concentration threshold. However, the consequences of a unique cell MAT can be its escape from the initial tumour, i.e. metastatic migration. If this occurs, the moving cancer cell will meet a microenvironment in which PAI-1 progressively decreases, and the cell could return to the mesenchymal condition through an inverse transition (form amaeboid to mesenchymal behaviour). As it is a cancer cell, it will proliferate, produce more PAI-1 (a characteristic of the most invasive cells) and perhaps again undergo MAT. The PAI-1 negative feed-back in terms of RNAs, described earlier, could help this regulation to occur. We have perhaps identified one of the conditions for a cell to undergo MAT and return.

A "grain of sand" The regulation of a cancer cell behaviour by its PAI-1 microenvironment could then be considered as a cause leading to consequences at the organ or the organism level. And its critical transition point is that one single molecule of PAI-1 could do the job! In avalanches, it is known that at the critical state the output is not proportional to the input, that is, the system is highly nonlinear and gives rise to "non-obvious" effects. Could one molecule of PAI-1 play the role of a "grain of sand" in the "biological avalanche" of cancer? Is the suggestion of self-organised criticality useful to explain such scale changes?

*Plasminogen Activator Inhibitor type 1

Games networks and elementary modules

M Manceny, F Delaplace

Poster

In this paper we propose an original modular extension of game theory named games network. The objective of games networks is to provide a theoretical framework which suits to modular dynamics resulting from different local interactions between various agents and which enables us to describe complex system in a modular way. Games networks describes situations where an agent can be involved in several different games, with several different other agents at the same time. However, several games networks can represent the same dynamics. We focus on the determination of a global equilibria, resulting from the composition of local Nash equilibria, which allows us to compute a games network normal form. This normal form emphasizes the elementary modules which compose the games network.

Modeling Reflective, Anticipatory, Complex Adaptive Systems

Peter McBurney

Poster

KEYWORDS: Anticipatory systems, Economic systems, Multiagent systems, Performatives, Rational expectations, Reflexivity.

Robert Rosen [1985] defined "anticipatory systems" as those where some or all entities have models of the system itself, which they use to predict system properties. Most living and human social systems are anticipatory in this sense. I define "reflective systems" to be those where some or all entities exchange predictions of system properties with other entities. The challenge in modeling such systems is that reflective messages passed between the entities in the system may modify not only each others' predictions of system properties, but also their current behaviours, and thus modify the system itself and its properties.

Modern economies are reflective, with considerable discussion by participants on the future developments of the economy, and thedirect exchange of predictions and forecasts. The theory of rational expectations (Muth 1961) is an attempt within economics to model the impact of such discussion on the revision of agents' beliefs and actions. However, economic theory itself may have a reflective impact on economic phemonena, as is shown by the progress of the Black-Scholes equation in financial markets (MacKenzie 2003). These performative aspects of utterances makes control of such systems difficult if not impossible, because the impacts of utterances and interventions (on participants and on the system) need to be taken into account when intervening. An example is shown, in the setting of interest rates by central banks, such as the US Federal Reserve System or the Bank of England. Central bankers need to allow not only for the real economic impact that increases or decreases in interest rates will have on underlying economic activity, but also for their impacts on the expectations of economic actors, such as investors and stock analysts. In order to manage these expectations, central banks in some countries (eg, the UK, the USA) have recently begun to make public the minutes of their deliberations, so as to better inform other economic actors as to the Banks' reasoning processes (Kohn 2005). It is not obvious that better-informed actors are less susceptible to major fluctuations in expectations, but this is certainly the view of central bankers.

How should reflective, anticipatory complex adaptive systems be modeled? Current multi-agent models of complex human systems have typically used only cognitively-simple agents, such as those playing the minority game in simulations of financial markets, e.g. Johnson et al. [2001]. These agents are usually not equipped to undertake sophisticated anticipatory reasoning or engage in much joint reflective activity. However, within the computer science agent technology community, considerable efforts have been devoted to the design and implementation of intelligent software agents and to the design of sophisticated, human-like, communications languages for their interactions (Luck et al. 2003). The computational technologies therefore now exist to enable effective modeling of large-scale anticipatory, reflective systems.

In this paper, I present a layered multi-agent architecture for modeling such systems. The architecture comprises intelligent software agents who communicate using sophisticated agent interaction protocols, with the layers being (in ascending order):

- Layer 1: The underlying socio-economic phenomena

- Layer 2: The anticipatory phenomena (ie, the ability of some agents to engage in prediction of system properties)

- Layer 3: The reflective phenomena (ie, the ability of some agents to engage in discussion about system properties).

Activities of each layer may impact those above and below it, in defined ways. Agents are connected to other agents at each layer, with possibly different connections at different layers. Not all agents may be active at all layers. In this paper, I present this architecture in detail and describe an implementation of it in the domain of malaria epidemiology.

Developing a domain independent model of Emergence

Diane M. McDonald, George R.S. Weir

Poster

The complex and rapidly changing demands of the Information Society and the recognition of the power of community learning has led to the observation that learning communities could be a pivotal tool for achieving more complex aims and objectives than learning alone. For example, the use of learning communities to stimulate learning, creativity and economic capacity is emerging as a potential tool to increase economic success. These Complex Learning Communities (CLC) are radically heterogeneous and non-linear with multiple drivers and desired 'products' (McDonald 2005a). This complex nature means that emergence may occur; new properties - be it behaviour or characteristics, at the individual 'actor' level or collective properties of the system as a whole - may emerge from the interactions within the CLCs. For example, relevant emergence may include social capital (Daniel et al 2003), eLiteracy (McDonald & McGill 2005) and creativity (Cavalletti 2003). The intrinsic unpredictability of Complex Systems and hence CLCs means, however, that specific emergence is not guaranteed; it is dependent on the dynamics of interaction and initial conditions. Indeed other unwanted emergence may occur – for example, spamming or digital exclusion. If successful CLCs are to be 'seeded' and their effectiveness maximised, the factors which may contribute to the desired emergence need to be identified and the dynamics of their interaction understood. Emergence itself is however not yet fully understood in all its many forms (Kubik 2003). While one of the principle drivers of Complexity Science is the vision of seeking out generalisations based on the well-researched instances of emergence and using those understandings to make sense of less researched complex phenomena, current conceptual models of emergence are either too simplistic to be useful when examining real life social systems (Funtowicz and Ravetz 1994) or do not encompass the full range of possibilities (Gross and Jeffries 2001). The identification of emergence, its potential range, the generation of desired emergence and the effect of intervention, in contexts such as CLCs, are still difficult to achieve. Improved domain independent conceptual understanding of emergence and its dynamics at a 'meta level' is required before the pivotal role of emergence can be incorporated into understanding, seeding and intervention of complex social systems such as CLCs. This paper reports on the development of a domain independent 'meta classification' of emergence from examination of well-researched domain specific emergence, which is then used to develop instruments to examine emergence in a specific domain – CLCs – and the issues encountered. The methodology employed consists of traditional literature review and synthesis combined with focus groups and peer review to assess the validity of the new conceptual model and inform instrumentation requirements analysis. This forms part of a general research strategy being developed which applies the instrumentation developed from the 'meta classification' to investigate emergence in real CLCs, through a case study approach. This latter investigation is reported elsewhere (McDonald 2005b). The ultimate research goal is to develop a framework for understanding, seeding and 'managing' CLCs. The results reported in this paper support the need for new tools and instruments to analyse and seed emergence in social systems such as CLCs and lend credence to the hypothesis that a domain independent 'meta' classification of emergence comprising seven factors will enable appropriate investigatory and seeding frameworks to be developed in domains such as CLCs. Thus, it offers a promising way forward to improve detection and understanding of emergence in complex social systems, capitalising on existing research

in other domains. Its novelty is two-fold: (i) it introduces an improved conceptual model of emergence which addresses the fundamental problem of extracting, at a 'meta' level, generalisations of emergence and applying them to gain insight in a different domain and (ii) it develops instrumentation for investigation of emergence in complex social systems. Future work includes further refinement of instrumentation and its application to other complex systems with the aim of developing understanding of how the various forms of emergence arise, thus ultimately developing an ontology of emergence in complex social systems.

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Modeling of the Exocytotic Process by Chemical Kinetic Formalism

Aviv Mezer, Esther Nachliel, Menachem Gutman, Uri Ashery

Poster

The exocytotic process in neurons and neuroendocrine cells consists of a consecutive reactions between well-defined proteins. Even that the partial reactions had been investigated by variety of methods, a comprehensive description, based on chemical kinetics had not been attempted. In the present study, we have, created, a comprehensive kinetic model that reconstructs the physiological process using a standard chemical kinetic formalism. the reactions between the synaptic proteins were transformed into a set of coupled, non-linear ordinary differential equations where the rate constants and some of the reactants concentrations are adjustable parameters. Upon integration over time the reactions equations, reconstructed the experimental signal. The model can perfectly reconstruct the kinetics of exocytosis, the calcium-dependent priming and fusion processes and the effects of genetic manipulation of synaptic proteins. The model suggests that fusion occurs from two parallel pathways and assigns precise, non-identical synaptic protein complexes to the two pathways. In addition, it provides a unique opportunity to study the dynamics of intermediate protein complexes during the fusion process, a possibility that is hidden in most experimental systems. We have used the Genetic Algorithm analysis to achieve high level of accuracy and to find a single global minimum, over a multi dimensional parameter space. Our study demonstrates that complex biological processes can be mathematically modeled and gain high predictive power, up to the level of serving as research tools. It is our intention to expand the model from the level of a comprehensive description of the whole exocytotic process, to the level of cell physiology.

Towards evaluation methodology of p2p systems for complex network management scenarios

Federico Morabito, Giovanni Cortese, Fabrizio Davide

Poster

Network Management In the management domain, we support a vision where information will no longer be exchanged only along a manager-agent hierarchy, (as it is today based on the SNMP and Policy architectures defined by IETF), which represent the standards for monitoring and configuration of networks, respectively. Instead, we build on communicating in a peer-2-peer fashion among nodes. A new monitoring architecture should then support a scalable, data centric communication model, allowing efficient many-to-many information exchange. Also, the information model should be much more flexible than today, allowing peers to communicate even when data schemas have not been agreed in advance as in the currently used standard-based approach. System Model In order to support a flexible management infrastructure, we are working on a distributed system model for data management, built on a peer to peer overlay infrastructure. Current system architecture is based on DHT, and we are designing/ evaluating technologies for Storage/ query – including a) algorithms for efficient multi-dimensional range query processing b) algorithms for distributed storage and query of information using richer data models based on ontologies.

Classic approach for p2p system evaluation The performance evaluation is a relevant issue to be integrated in the design and deployment phase of the functional prototype. Proper evaluation mechanisms of non-functional qualities of different designs are needed. The classical approaches for evaluation of p2p system try to measure traditional network parameters, for example link capacity of nodes, physical distance of nodes, packet loss, cost of maintaining the respective overlay structure. The main limitation of the current approach is that they do not show the complex aspects of the system model, but they try to monitor the efficiency from a communications and network point of view. In this sense, some examples of used metrics are average bandwidth overhead (induced for maintain the overlay structure), the latency (dued to the physical topology) and the bandwidth stretch. Furthermore, these metrics do not consider the application scenarios in which the p2p approaches are used. For example, in a network management scenario, an important issue to be measured and monitored is the ability to propagate the information despite of changing pattern of the overlay topology (robustness against dynamics).

Innovative approaches for complex systems Recent works have criticized the intrinsically property of uniform randomness for large complex networks, revealing the hyperlinked structure of the WWW and complex topology of the Internet Over the complex networks, also the applications built using overlay mechanisms, can be treated as a dynamic systems: for example a network management infrastructure over Internet should take in account the dynamics of nodes, data and resources over a complex, wide-area topology and should maintain a statistics overall view of the system behaviour. As result of the integration between complex networks and applications with fast dynamics (for example, a data management application will require data replication mechanisms, data migration techniques), we need innovative approaches and metrics for evaluation, deeply dependent on the applications dynamics and deployment scenarios. For this purpose, we define an evaluation framework composed by a testbed, a prototype for advanced network management and a measurement methodology. The evaluation framework will permit the monitor and measurement of dynamic parameters for investigating robustness property and reliability, using a graph

theoretical approach. Some examples of parameters that can be used in the evaluation of the robustness property for a prototype for network management are degree distribution, average path length, clustering coefficient. The proposed methodology will aim at evaluating some critical parameters, using a statistical load characterization that models the application scenarios. The approach will permit the real-time evaluation of critical parameters for the management applications, bringing together the complex aspects of the underlying network and the dynamics of the specific applications. The testbed will permit the emulation of a distributed, large scale environment and the final deployment in an experimental setup.

A structured approach for modelling of integrated systems in biology

Nicolas Parisey, Marie Beurton-Aimar, Randall S. Thomas

Poster

Data and information-flow processes applied to the description of living systems present a new challenge to computational biology. The level of complexity attained by biological knowledge and the development of ever more sophisticated informatics tools for the modelling and simulation of biological processes have revealed the need for methods to structure the manipulated data (where "data" is taken in its most general sense) in a more formal way. Structured approaches like Object Oriented Methods (OOM) allow the definition of data types and relations among these types in order to qualify them semantically. Thus structured, it becomes possible to design computer programs that can automatically interpret the information.

Data types and relations between them can be mapped to arborescences described by a structuration language. Following the emergence of XML (eXtended Markup Language), which is such a language, two XML-languages for biology, SBML (Systems Biology Markup Language) and CellML have attracted a growing community of users in the bioinformatics/ bio-modelling/ systems biology community.

XML provides a means to supplement a text file with any relevant information describing its contents, its origin, its intended use,etc. That is, an XML file is a self-describing ascii file. XML is a structured language with marks (called tags) which wrap thefile's contents with defining concepts or object classes. SBML and CellML are augmented versions of XML that specify tags for descriptions of mathematical models of biological processes and specifically for metabolic networks, kineticequations, and so on.

The principle of XML is to define a *schema* which specifies the nested tags and their hierarchical tree structure. Users are free to define the tags as they see fit. However, when a community of users wishes to share files with a common purpose and with a minimum of ambiguity, they agree on a standardized tag structure, fixing its definition in a shared formal description, of which there are two standard types: Data Type Definition (DTD) files, and XML Schema. Many thousands of such specifications have been developed for a myriad of applications, of which SBML and CellML are two typical examples. They both have specific DTD and XML Schema definitions, which have gone through several revisions, the latest being available on the respective websites. It is the standardization of these publically available definitions that makes it possible for anyone to design a software program taking one or both of these description formats as input (or producing them as an output file).

As with any standardized language, new situations arise that are not well captured by the current schemas, which leads to continual pressure to extend them to the new situations. Such extensions are a natural part of the evolving use of such systems, but they bring with them the inevitable problem of backward compatibility with previous versions.

Our particular concern is with the modelling of integrated biological systems at not only the cellular and sub-cellular levels (which are essentially the focus of present versions of SBML and CellML) but also of multi-cellular systems, tissues, and even organs. We acutely feel the need to standardize the model-descriptions of such systems using a markup language, but the current versions of SBML and CellML are inadequate to this task. We have thus formed a French Working Group on Markup Languages for Integrated Systems Modelling to characterize these shortcomings and to suggest relevant extensions and im-

provements to the developers of these two existing MLs (with whom we have established a dialogue).

We present two specific but simple examples drawn from our work (in very different fields) which typify the features we most miss in SBML and CellML: 1) epithelial transport, with transcellular and paracellular transport of water and several solutes; and 2) mitochondrial metabolism modelling. Extension of SBML and CellML to cover these two cases would in fact render them adequate for a much larger class of models which are currently outside their scope.

Why Does BitTorrent Work So Well?

Simon Patarin, David Hales

Poster

Keywords: Cooperation, Emergence, Engineering with Complexity

BitTorrent (BT) is currently "king" of the popular file-sharing peer-to-peer (P2P) clients [1]. Some reports have claimed that it accounts for the majority of peer-to-peer traffic on the Internet and others that Hollywood is doomed. Bram Cohen, the inventor of BT, is now in high demand on the invited talks circuit. However, leaving the media attention aside for one moment, we ask the question: Why does BT work so well?

BT attempts to build robustness to freeloading (i.e. downloading without uploading) by implementing a tit-for-tat-like strategy (TFT) within its protocol. It is often believed that this strategy alone is responsible for the high-levels of cooperation found. The TFT strategy was championed in Axelrod's, now classic, 1980's book "the evolution of cooperation" [5]. He held computer tournaments in which programs, submitted by different researchers, repeatedly played the canonical game of cooperation - the Prisoner's Dilemma (PD). He found that in a round-robin tournament the TFT strategy did best on average against the other submitted strategies. The TFT strategy is relatively simple. It starts by selecting a cooperative move and then for subsequent moves copies the last move made by its opponent. This strategy is encapsulated in the BT tagline: Give and ye shall receive.

BitTorrent works by groups of peers (called swarms) with an interest in downloading a specific file coordinating and cooperating to speed-up the process. Cohen describes how this works in some detail in his paper [3]. Essentially each swarm is supported by a "tracker" node which stores a list of peers in the swarm thus allowing new peers to join the swarm. Each peer in the swarm stores pieces of the file. Cooperating peers download and upload required pieces. If a peer stops uploading it will tend to be "choked" by other peers, meaning they stop uploading to it. This implements the TFT-like process.

So-called "seeder" peers that store the whole file are very important to the functioning of a swarm. If a swarm contains no seeders, it may lead to a situation in which pieces of the file are missing from the swarm as a whole. Since seeders have nothing left to gain the system requires some altruistic behavior from peers. This requirement is evidence by the mantra often repeated on BT web-sites: leave your download running for a little while after you've got the entire file.

We argue that the TFT strategy is not an adequate explanation of the high-levels of cooperation found within BT because:

(*) The TFT strategy can be bettered by other less cooperative strategies (*) Identity can be faked by modifying the client thus circumventing TFT (*) Unconditional altruism is required for BT to operate in any case

Given that such loopholes exist: Why is the system not dominated by freeloaders?

HYPOTHESIS: GROUP SELECTION

We hypothesize that BT may resist freeloaders and support altruism, at least in part, in a way that has not been previously fully comprehended. Ironically, this process relies on what is commonly believed to be a weakness of BT - the lack of integrated meta-data search. One consequence of this is to partition the BT network into numerous isolated swarms - often with several independent swarms for an identical file - which is one of the necessary conditions for a kind of novel group selective process that has been recently identified in similar simulated systems both in the context of computational sociology and simulated P2P file sharing.

Essentially, if users move between swarms (leave one swarm and enter another) based on the quality of the service they receive then this process means that swarms containing many freeloaders will tend to "die" as peers leave the swarm for better swarms. Swarms that contain altruists will tend to grow since they support a quality service. Similar models have been advanced in computational sociology [4,5,6].

A further implication of the hypothesis is that, given the choice, users may choose unconditional altruism rather than the more restrictive reciprocal approach [7] because of the same group selective process has been shown to select for pure altruism – peers acting for the benefit of the group to their own individual cost.

CONCLUSIONS

We hope to have shown that an awareness of some results from social scientific work, particularly the emerging area of computational sociology, can help to inform the analysis of existing working systems "in the wild". This is valuable because such systems currently demonstrate some of the desirable features required of future software systems. We are proposing an empirical approach in contrast to, but supporting, traditional engineering approaches – such as formal methods or "simulating from scratch". The specific example we considered involves a novel hypothesis concerning how altruism may be supported in the BitTorrent (BT) system. Following the empirical line, one way to test our hypothesis would be to implement and distribute a modified BT client that allows users to select pure altruism over the more restrictive reciprocal protocol currently implemented. This may be the subject of future work.

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Scaling laws in urban systems (France, South Africa, United States of America)

Fabien Paulus, Céline Vacchiani-Marcuzzo

Poster

The aim of this poster is to bring evidence about scaling laws in urban systems. Scaling laws are providing a theoretical framework for understanding the dynamics in complex systems. They are used as a methodological device for investigating the location process of activities in the cities. The relationship between urban activities and the sizes of cities where they are located give insights about the interactions between economic activities and dynamics of urban systems.

Contrary to Christaller's central place theory explaining the urban hierarchy by population oriented services, we take into account the whole set of urban activities, including specialisation in national or global networks, to build an evolutionary theory on cities. A representation, more suggestive and more precise than rank-size plots, consists to examine the direct statistic relation between the urban activities and the population of each city. Empirical results are obtained from data sets on employment figures in France and USA and number of foreign firms in South Africa. The slope of the adjustment gives a scaling measurement of the dependence of the location of activities to the size of the cities: if the coefficient is equal to 1, it reveals a simple proportionality compared to the population, if it is larger than 1, the relation is superlinear, i.e. there is an effect of selection of the cities, in favour of the largest ones; if the coefficient is lower than 1, the relation, sublinear, indicates on the contrary a selection of the smallest towns. We can still interpret the slope as a measurement of the elasticity of the presence of one kind of activities according to the size of the cities. It is an indicator of the power of the centrality for a function or a given activity, whose significance would approach the concept of economy of agglomeration, or of increasing returns with the size. We prefer an evolutionary interpretation that links the value of the scaling parameter and the stage of specific activities within innovation cycles. Data about evolution of employment on a rather long period (France, 1962-99) confirm the validity of such hypothesis.

Analysis of large set of elementary flux modes : application to energetic mitochondrial metabolism

Sabine Pérès, Marie Beurton-Aimar, Jean-Pierre Mazat

Poster

The concept of elementary flux mode is a promising approach for pathway-oriented perspective of metabolic networks. This concept defines a unique set of pathways, which represents a set of generating vectors of the solution space of feasible steady states. This set can be determined from the stoichiometric matrix of the network only. However, in large networks the combinatorial explosion of their number prevent to derive simple conclusions from their analysis. We applied a clustering method to describe the decomposition in elementary flux modes of the bioenergetic mitochondrial metabolism (Krebs cycle,beta-oxidation of fatty-acids, oxidative phosphorylation, etc.). This network involves 41 enzymatic reactions, 31 metabolites. 7,250 elementary flux modes are derived from the stoichiometry matrix of the network. We clustered them by similarity and described physiological properties of most of the groups, which could in some instances be attached to specific types of mitochondria.

The importance of parallel and anti-parallel alignment in the collective motion of self-propelled particles

F. Peruani,, M. Baer, A. Deutsch

Poster

Collective motion constitutes a challenging example of self-organization. Applications range from robotics to biology. In particular, emergent large-scale patterns mediated by merely local interactions of individual system components are observed in an amazingly huge number of biological systems of different complexity (e.g. herds, fish schools, bird flocks, swarms of social insects, amoebae and bacteria). Despite the fact that in each case the interactions between individuals are of a different nature, it is possible to determine common requirements for self-organization. Here, we focus on the implications of alignment and analyze 'ferromagnetic' (1, 2) and 'liquid crystal'-like (3) alignment mechanisms. The latter allows parallel and anti-parallel alignment, while the former only admits parallel alignment. For the two types of alignment mechanisms, we observe phase-transitions related to the noise introduced into the system. In the case of parallel and anti-parallel alignment, we also observe spontaneous symmetry breaking of the rotation symmetry. We present numerical evidence of this phase transition. In addition, we show that the effect of attractive and repulsive forces lead to different responses depending upon the type of alignment mechanism.

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Keyword: particular complex systems

Strong emergence in a population of agents

Denis Phan, Jean-Louis Dessalles

Poster

Characterising emerging properties is a crucial challenge when studying complex systems. The problem is especially challenging in case of "strong emergence" (Müller 2002), when the agents involved in the emerging phenomenon are able to detect it and are influenced by it. Strong emergence is often observed in populations of human agents. The identification of emerging phenomena by the agents themselves induces a feedback from the observation to the process. As there is a coupling between the process level (the system) and the observation level due to the agents themselves, emergence is immanent in the system. In order to simulate cases of strong emergence, the simulated agents must be given means to detect the collective phenomena of which they are part. Our claim is that algorithmic complexity may provide such means.

Various characterisations of emergence have been proposed (see Bonabeau et al., 1995 for a review). One definition seems to capture the common intuition underlying most accounts: emerging phenomena correspond to a sudden decrease of relative algorithmic complexity (RAC) (Bonabeau & Dessalles 1997). If S is the current state of the system and Di is a set of available detection tools, then emergence occurs whenever the RAC, i.e. the shortest description of S using a subset of Di, paradoxically decreases when the subset is augmented.

Ct+dt(S | D1, ..., ,Dk-1, Dk) < Ct(S | D1, ...,Dk-1)

Taking an additional description tool Dk into account should normally increase the complexity, as Dk must be computed on S. However, when some Di are redundant with Dk, the complexity of the minimal description may drop by an amount that characterises the quality of the emergence.

To simulate strong emergence, agents must be given ways to assess RAC. In this paper, we explore such a possibility in an experiment about the emergence of classes (Axtell, Epstein, Young 2001). In that experiment, agents play an iterative Nash bargaining tournament, where they may make high, low or medium claims. When agents are assigned arbitrary tags such as green and red, the system may evolve in such a way that a dominant high-claiming class, the red, say, emerges together with a submissive low-claiming class, the green. This is not a case of strong emergence, though, as agents have no way to shift to a binary class-based decision when choosing a claim.

We designed an extension of Axtell et al. experiment, where individuals display a combination of T tags and may include the tags observed on the opponent in their decision to play high, low or medium. Agents are biased to favour simplicity, i.e. they base their decision on tags whenever some simple tag combination offers a more concise description of the behaviours hold in memory. Not only is the emergence of classes preserved, as in Axtell et al. experiment, but also the decision by individual agents to shift to a class-based decision offers a genuine case of strong emergence.

Our model may offer a new insight into how abstract entities like "group" or "collective behaviour" should be understood. Individuals are expected to assign behavioural characteristics to collective entities, though such entities may have no central control, as soon as it reduces the algorithmic complexity of their own decision process. Thanks to this hypothesised bias for simplicity, such decisions behave like self-realising anticipations.

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Complexity, Networks and the Modernization of Antitrust

Cristina Poncibo'

Poster

Title: Complexity, Networks and the Modernization of Antitrust

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Key Words: Complexity Science, Antitrust, Networks

Abstract:

One perspective for understanding competition that has garnered increased attention by those in antitrust is the field of science known as complexity science. Incorporating insights and relying on metaphors from population ecology, evolutionary biology, systems theory, chaos and the study of networks, the science of complexity attempts to describe and explain how systems and their occupants, including industries and firms, evolve and compete against one another over time through adaptation, co-evolution and other dynamic processes. Insights from complexity science are also being applied to describe and better understand the evolution and competition taking place in various sectors and industries of the new economy. Although the integration of knowledge gained through the study of the science of complexity to antitrust remains to be more fully developed, initial findings have yielded some provocative insights. For example, networks may be different from antitrust markets, encompassing multiple markets or even industries. This challenges standard neoclassical antitrust economics, whose focus is the relevant market, where the primary test of membership is substitutability. Within some networks, huge market power may be accrued, even when the size of the dominating firm is relatively small within the system, a possibility that cuts against the concentration thesis of neoclassical antitrust economics, which only recognizes market power in the context of very large market shares. The network phenomenon calls attention to the importance to competition of relationships of power and influence that tend to be more familiar to business people and political scientists than to neoclassical economists. The question of whether complexity science can contribute to antitrust has also been brought into sharp focus through the workings of the antitrust modernization in order to explore whether industries involving significant technological innovation should be treated differently under the antitrust laws and, whether there are features of the modern economy that warrant special antitrust treatment - whether harsher or more lenient.

"Complexity in Neuroscience: How to relate the Digital aspects of Brain function with the Analog-driven Mind Processes?"

Walter Riofrio

Poster

If we consider that mind (especially, consciousness and self-reference) is more than a collection of mechanisms (we are not just robots or zombies), this question arise: what more "it is added" at the brain function (the mechanisms) to produce the mental phenomena?The so called "hard problem" in the studies about the consciousness, alert us that always we are confronted with the subjective component of it. But, if we are not so ambitious in the scope of our investigations, the possibility of success it may be more probable.The dynamical development of living forms, with the management of matter and energy from the environment, will generate the basic forms of transmitted information processes.In this respect, the emergence of mental properties and processes from the normal activity of the brain will be a central focus of our presentation. So, with this clarification, we propose an investigation about the most fundamental forms of mental processes.An important issue, it is to ask how the brain structures the data that comes from external and internal to organism. And with these has the possibility or capacity to represent information.In this respect our first question is: Which are the conditions that make it possible the emergence of "meaning" or "semantic" in the information coming from the data received in the brain?In our presentation, we centre in a region of information management that code analogic signals to digital signs: auditive perceptions.With the final purpose to open the debate about if neuron are able to pass the analogic information to digital information and again to analogic information; and incorporate the Â'meaningÂ' capable to be expressed in an integrated spatial-temporal network organizations by neurons (for us, they certainly do continuously).

Evolving cell phone families

José Salgado, Ricardo Gama

Poster

Cell phone networks is usually refered as a good example of a social complex system. Indeed, we are inquiring students, between 12 and 18 years old, and using their cell phone contact numbers and their cell phone contact statistics to meet the following investigation questions: - how does the cell phone network evolve with age? - Is there a peak of frequent contacts? That is, does students contact more people as they become old? - Does the "cell phone family" becomes regional with age? That is, we expect that students first contacts are local (students from the same school) and then with increasing age and social interactions they become more scatered. - Does the networks go beyond the portuguese borders? What are the countries that these networks reach? The scope of this project goes beyond this questions. In fact we would like to study later on the role that time plays in the network of each individual. This study may be crucial to the understanding of the portuguese society structure strenght and the understanding of the youth portuguese place in europe. Although our study is not finished yet, we would like to present our results.

Comparison between parallel and serial dynamical behaviour of boolean networks.

Lilian Salinas, Eric Goles

Poster

In this article we study some aspects about the parallel and serial dynamical behaviour of a boolean network.

We study the relationship between the structure of the associated graph and the attractors of a boolean network. We show that for boolean networks with an arborescent associated graph, the length of the dynamical cycles are a power of two and under certain conditions the attractors are only fixed points.

Furthermore, we study the robustness of the dynamical behaviour of a boolean network with an arborescent associated graph, for serial and parallel updates. We show that, if we choose a good order of update then the dynamical behaviour is the same in both cases, and if the associated graph does not have loops the converse is also true.

On the other hand, we are interested in the robustness of the set of attractors of a boolean network for serial and parallel updates. It is well known that the set of fixed points of a boolean network is the same for both types of update. In this article we prove that a dynamical cycle of a boolean network without loops with parallel update is not a dynamical cycle for the same network with serial update and viceversa.

Simple Concepts for Complex Systems: A Model of Emotions as Energy Management Systems Adapted to Social Life

Jorge Simão

Poster

Complex systems require that new concepts be developed or be used in novel ways if they are to be understood fully. We have been working on a computational theory of human and animal emotions inspired in the concepts of complex systems and the methodology of agent-based modeling [**?**]. We treat organismic agents as indivisible and incompressible entities as is done in particle physics. However, contrary to what is done in particle physics, agents in our model have internal structure and multiple types of forces are exert on them.

The forces exerted on each agent are driven by the emotional mechanisms of the agent's cognitive architecture. These mechanisms respond to external stimuli created by the presence of other agents. Namely, each agent is subject to attraction and repulsion forces created by the presence of all other agents in the arena. The magnitude of these forces is dependent of the internal structure of the agents. For each pair of agents there are several forces involved, one for each emotion considered. This way, each emotional mechanism works as a reactive behavioral module that is used by the organism as a strategic component. Each such strategic component allow the agent to manage effectively the stock of stored energy used to perform survival and reproduction activities.

To model the attractive/repulsive effects of each emotional sub-system we have introduced several new concepts that can be seen as laying at the interception between the physical, the natural, and the social sciences. The concept of *energy distribution* is equated with the amount of energy stored by the organism to be used to perform work. This energy distribution has both an aggregate quantity as well as a quality. Computationally speaking, we model this energy distribution simply as an array of scalar values each for a energetic component. Comparing this concept with more well know concepts used in the psychology we can say that the energy distribution determines individual personality, character, and/or preferences.

The concept of *(energetic) affinity* represent a measure of resonance between the energetic distributions of two agents. We equated affinity with complementarity. This complementarity is measured as the difference in *subjective well-being* that an observed agent creates to the observer when compared to the previous well-being of the observer. Subjective-well being is operationalized as a measure inversely proportional to the variance of the value of the energy components of the agent. Thus, we endorse a holistic perspective, and assume that the well-being of an organism depends an adequate balance of energy values in all its sub-systems [**?**].

The model captures the working of several emotions. The first to be investigated where *seeking*, *fear*, *love*, and *discrimination* [**?**, **?**]. To specify the magnitude of the forces we use a mathematical expression that depends on four elements: 1) the average energy value of the observer (average quality) M_i; 2) the average quality of the agent observed M_j; 3) the (square of the) distance between the observer and the observed agent d_ij^2; 4) the affinity between the observed and the observer AF_ij. The second and third element is used to compute the intensity of the stimulus produce by the observed agent and detected by the observer, i.e. it is a sensation magnitude S_ij (in psychophysical sense of the word). The first and the fourth element are used to compute the response to this stimulus, i.e. it is a gain G_ij. To formalize this, we write the magnitude of the emotional force

generated by the emotional mechanism k in agent i in response to the presence of agent j as: $FE\_ijk = S(M\_j, d\_ij^2) \cdot G(M\_i, AF\_ij)$.

The concrete force magnitude generated by each emotion depends on the form of functions for stim-AFijulus intensity and gain. Our intuition made us consider the following hypotheses:

- *Seek:* This emotion is used for an agent to approach energy sources or conspecifics that can potentially provide energy sources. Therefore, an agent is more motivated to seek individuals of high quality since they are more likely to provide energy. An agent is also more likely to provide energy is there is a high affinity with the recipient. Addi-AFijtionally, an agent is more likely to search for energy sources when its internal energy is low. Formally, we write:

$$FE\_ij, seek \propto \frac{M\_j}{d\_ij^2} \cdot \frac{1}{M\_i} Max(0, AF\_ij)$$

- *Fear:* This emotion is used by an agent to avoid conspecifics that can be hostile to the agent and may induce a loss of energy. We assume that an agent is motivate to run away due to fear from other agent the higher the quality of that other agent and the lower the affinity value between the two agents. Additionally, an agent is more likely to search for energy sources when its internal energy is low. Formally, we write:

$$FE\_ij, fear \propto -\frac{M\_j}{d\_ij^2} \cdot \frac{1}{M\_i} Max(0, -AF\_ij)$$

- *Love:* This emotion is used by an agent to give energy to other agents it cares about. This may include kin or other individuals involved in reciprocity relations with the agent. We assume that agents are motivated to give energy the higher their energy stock and the lower the energy level of the recipient. Moreover, high affinity makes agents more motivated to give energy. Formally, we write:

$$FE\_ij, love \propto \frac{1}{M\_j} \frac{1}{d\_ij^2} \cdot M\_iMax(0, AFij)$$

- *Discrimination:* This emotion is dual to seeking, and is used by an agent to avoid low quality individual who might demand energy from the agent. We assume agents are more likely to avoid others the lower the quality of the other agents, the higher its own quality, and the lower the affinity between the agents. Formally, we write:

$$FE\_ij, descr \propto -\frac{1}{M\_j} \frac{1}{d\_ij^2} \cdot M\_iMax(0, -AF\_ij)$$

Other emotions can be accommodated in our model, but we limited our initial modeling to the above four emotions to simplify analysis. Using our model it is possible to study what agent structures and patterns of interaction lead to stable social structures and why. We consider three types of study: 1) Settings involving only two agents are used to verify model correctness [**?**]; 2) Settings involving three agents are used to observe the common pattern of interaction and study non-linearities; 3) Settings involving N agents are used to study the formation of local spatial clusters (groups) and measuring their stability.

We conclude our paper by advocating that a computational oriented approach inspired in the theory of complex system is a very valuable approach in the study of human and animal emotions. Moreover, this approach can provide considerable more rigor and insight than is possible using verbal theories of emotions.

Tracing experience as a potential support for meaning negotiation between human and computer agents

Arnaud Stuber,, Salima Hassas, Alain Mille

Poster

The paper presents a hybrid system to allow the experience sharing, exchange and co-construction in a community. This system has a fractal architecture with generic principles that are implemented for each subsystem. An operational issue exists to capture, to represent and to manipulate the experience, we propose an formal grammar-based model. A semantic issue then exists to express the meaning of the experience, we detail our approach based on the mechanisms of the emergence of language. A prototype is presented to illustrate our proposal, some experiments are to come.

Complex Systems Perspectives & Inter-Discilinary Curriculum-a real challenge and opportunity for the Romanian Higher Education System

Marta-Christina Suciu

Poster

Keywords organised within a particular complex systems-education: global knowledge-based society;complex systems; interdisciplinary curriculum.

Main Topic :education

The global knowledge-based society and creative economy are very dynamic and increasingly complex systems. Change seems to be the single constant of the universe. Connectivity and networks of interactive entities are more and more relevant for this new type of society called also a network society. Complex systems questions ask for new ways to manage a s̈uper-complexs̈ociety as knowledge-based society is also called.Traditionally ätoms,̈ individuals and tangible things were the key determinants of wealth. Networks involve interactions and connectivity and focus more on intangible assets such as: intellectual capital, knowledge, innovation and creativity considered new sources of wealth in the context of knowledge-based society and creative economy.

Complex and adaptative systems have to learn constantly. Traditionally adaptative systems deal with n̈egative feed-back;̈ complex adaptative systems in a network society seem to ask for p̈ositive feed-backs̈ince the systems might function more effectively in a process of long-life-learning; society itself is considered to be a l̈earning society.̈ The complex systems approach provide a solid foundation for understanding better the complexity of the knowledge-based society. There are multitude of problems that have to be addressed mostly in a country like Romania. It becomes more difficult to manage complexity applying traditional ways of learning seen mostly as convergent ways.

In the highly complex education system there may be various combinations of the different approaches to teach using a mix of convergent and divergent teaching strategies, methods and styles. Traditionally there is a tendency to teach s̈tep by step,̈ p̈iece by piece,̈ b̈it by bitj̈ust partially information related to a particular disciplines. By applying the perspective of complex systems in education there is a strong need to focus more on interdisciplinary and cross-disciplinary approaches. The curriculum can be integrated-mostly in the higher education system-around topics that reflect the patterns, interactions, and interdependencies of different fields. This is a real challenge and a great opportunity for Romanian higher education system!

Competitive Adaptive Lotka-Volterra Systems with Complex Behavior

Claudio Tebaldi

Poster

We study a NxN dimensional Lotka-Volterra system which describes competition among N species and includes behavioral adaptation, i. e. a learning mechanism. The existence of reduced models, where N appears as a parameter, is discussed, depending on the level of symmetry of the system. Such models give full account of equilibria and their stability in the complete system and are effective also in describing the time dependent regimes, even chaotic ones, for a large range of parameter values. Relevant questions, as species survival/exclusion and different kind of coexistence (stable equilibria, periodic oscillations, strange attractors, sincronization) are addressed focusing on the role of adaptation

Functioning-dependent structures

Michel Thellier, Camille Ripoll, Patrick Amar, Guillaume Legent, Vic Norris

Poster

Numerous studies have shown that proteins involved in metabolic or signalling pathways are often distributed non-randomly as multimolecular assemblies. Such assemblies range from quasi-static, multi-enzyme complexes (such as the fatty acid synthase or the (-oxo acid dehydrogenase systems) to transient, dynamic protein associations. Multi-molecular assemblies may comprise proteins but also nucleic acids, lipids, small molecules and inorganic ions. Such assemblies may interact with membranes, skeletal elements and/or cell organelles. They have been termed *metabolons*, *transducons* and *repairosomes* in the case of metabolic pathways, signal transduction and DNA repair, respectively, or, more generally, *hyperstructures*.

Although channelling is sometimes challenged, most authors have assumed that, in many molecular assemblies, intermediates are channelled from each enzyme to the next without diffusion of the intermediates into the surrounding cytoplasm. Potential advantages of channelling are:

1. reduction in the size of the pools of intermediates (a point however contested by some authors),
2. protection of unstable or scarce intermediates by maintaining them in a protein-bound state,
3. avoidance of an "underground" metabolism in which intermediates become the substrates of other enzymes and
4. protection of the cytoplasm from toxic or very reactive intermediates.

In the case of transient, dynamic multi-molecular assemblies, certain only form in an activity-dependent manner due, for example, to an association between enzymes that only occurs when they are engaged in transporting or transforming substrates or transducing a signal. We have proposed to term *functioning-dependent structure* (FDS) any such type of dynamic, multi-molecular structure; in other words, an FDS assembles when functioning and disassembles when no longer functioning and thus is created and maintained by the very fact that it is in the process of accomplishing a task.

The formation of an FDS adds protein-protein interactions to the classical protein-substrate (or protein-signal) interactions and is therefore likely to generate novel kinetic behaviours. Given the extremely diverse mechanisms at work in the variety of biological systems quoted above, it is difficult to devise a single approach that would be appropriate to model them all. Therefore, in the following, we begin by determining whether the metabolite-induced association of two enzymes into an FDS (a so-called metabolite-induced metabolon) may, under steady-state conditions, confer to the overall FDS kinetic features that the individual enzymes do not have; this particular two-enzyme FDS is fairly straightforward to model, which is why we have chosen it. We then discuss how the type of approach used here to analyse the metabolite-induced metabolon may be used to analyse other varied assemblies. Finally, we speculate on the relevance of such concepts to the debate on the nature of life.

An overview of the quest for regulatory pathway in microarray data

Nizar Touleimat, Florence d'Alche-Buc, Marie Dutreix

Biological Modelling 3

An overview of the quest for regulatory pathway in microarray data

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Complex regulatory networks allow living cells to respond and adapt to a large set of stimuli coming from their environment. Understanding these networks is one of the major challenges to modern molecular biology. The recent developments of biotechnological tools that allow to study global transcriptional response (i.e. variation of expression of all the genes of a cell) open a new field of investigation and knowledge building. However, the tremendious amount of data generated requires new methods of data mining, classification, normalization, comparison, crossing ...thinking. Here, we will try, through a concrete exemple, to present the different analysis that can be done starting from a define set of genes and looking for the regulatory pathway that control there expression. The first challenge is to define as precisely as possible the set of genes to study. A potentially regulated gene group may be constructed in two different ways : by ranking differentially expressed genes in a supervised analysis comparing to classes of conditions (i.e with or without stimuli) or by clustering genes by their expression profiles in hierarchical classification or kinetic profile similarity. Once a set of genes determined, many questions arise. Has this cluster of genes any biological signification? Are the genes co-regulated and if so, by what? Are they specific to the studied stimulus? Do they share more biological characteristics (i.e. gene locus, function)? In order to answer these questions, we used a simple method based on the systematic analysis of the set of genes and its comparison to the full set of data. Genes within a set can be compared for shared qualities like conserved sequence patterns, common promoter sequences, common functions or molecular processes. The informations are considered as relevant if the frequency of these qualities within the group studied are significantly different from their distribution in the whole set of genes. In some cases, the respective chromosome gene positions can indicate a correlation between genes within the given set. ChIP-on-chip data analysis and transcriptional factor data indicates transcriptional factors that could control the expression of this set of gene. Analysis of the average behavior of our set of genes in other experimental conditions (with one or more experimental parameter changing) using laboratory data as well as published microarray allow to test the persistence of the gene clustering in different conditions. The integration of all this data enables us to find potential common regulators for genes grouped by their transcriptomic response to a stimulus. This method must respect some limits and precautions. As the gene clustering based on the gene expression profiles and intensities is the first step of our methodology, the coherence of the gene groups and the quality of our analysis are bound to be strongly affected by the quality of the gene clustering. Another limit comes from the crossing of our gene clustering with data from other laboratories. Raw data are not always accessible and different normalization methods are applied. The number of genes data available strongly vary from an experiment to another and from a laboratory to another. We will illustrate the full process of analysis starting from a group of genes clustered according to their expression profiles after irradiation with ?-rays of Saccharomyces cerevisiae.

A Simulation Environment for Emergent Properties

Heather R. Turner, Susan Stepney, Fiona A. C. Polack

Poster

We propose a multi-layer architecture for simulating emergent properties. This is implemented as a form of cellular automaton at the lowest layer, with mobile processes to represent objects at multiple upper layers. This architecture supports multiple levels of emergence.

Studying complex social change: Linking levels and meaning through adult and child personal reflections

David Uprichard, Emma Byrne

Poster

Complex social systems are recognized as multi-level and multi-dimensional entities. However, understanding the ways in which the multiple multi-dimensional levels interact together and produce social change at the local level is methodologically problematic. So far, the dominant mode of representation of social systems as complex systems has been through iconic modelling. Iconic models are founded on algorithms that derive complex emergence from the iterative progression of either non-linear equation sets or 'game' rules in simulations. However, whilst such approaches certainly have their uses, they do not address crucial aspects of the processes of complex causation in social systems. There are three main reasons for this. First, they have a limited capacity for capturing generative dynamics that occur across the multiple hierarchical levels. Most models only account for two or three levels whereas aggregate social form is derived from the multiple nonlinear interactions of multiple levels; the interactions are interdependent across and between levels. If we are to construct representations of the social then somehow, we also need to construct models that acknowledge multiple non-linear multi-level interactions.

Second, whilst many models are based on empirical data, few use this data directly within the model and instead take the form of hypothetical predictive propositions about particular systems rather than working with what is known to be real about the system. We stress the importance of exploring modes or representations in which actual data is directly integrated. Traditionally, data would be understood in this sort of context as the quantitative products of measurement processes. We absolutely agree that social measurements are relevant but we think that measurements alone will not resolve the issue. Third, measured data and the structures of explanation we construct with it are not adequate either as account of the nature of complex systems incorporating human agency or as modes of establishing such accounts. We also need data forms, which can convey meaning and the potential for social action. Narratives have this capacity.

Hence, this paper argues that personal narratives are a way of responding to this methodological challenge because narratives allow access to the multi-level and multi-dimensional meaning that underlies human agency. This argument is illustrated in relation to studying urban change (where cities and urban regions are understood as complex systems) by drawing on first-hand empirical examples from Byrne and Doyle's examination of people's understanding of 'post-industrial transformation' in South Shields (UK) from the past through the present to the future, and Uprichard's work on children's understanding of York (UK) and Dijon (France) in the present and the future. In turn, the paper proposes that the use of adult and child personal narratives must be part of the methodological repertoire of approaches to studying and understanding complex social change.

Analysis of branched-chain amino acid biosynthesis by a Thomas network approach

A. Urbain, P Renault,, S.D. Ehrlich, J-M Batto

Poster

Keywords : Subsystem comparisons, Network design, ILV regulation, Prokaryotes

Cellular growth depends upon the ability of the cell to form new molecules from nutrients available in the environment. In most bacteria, growth involves increase in cell mass, number of ribosomes, duplication of the bacterial chromosome, replication and translation of RNAs. During the phase of exponential growth, cells divide a constant rate depending on disponibility of nutrients and rapidity to form new membrane and proteins. In biosynthesis of amino acids for Bacillus subtilis 120 genes are requested [1]. If we encompass all the interactions within such a large pool of gene with a holistic approach it may be a difficult task. So we prefer to adopt a step-by-step approach and work on a targeted mechanism. We try to predict a biological mechanism in one species, with the objective to achieve a general understanding of the mechanism, holding true for many, and ideally all, species. Thus, we are working on a local/transversal approach with the aim of combining genetic and enzymatic level of regulation. We are developing a subset of Isoleucine Leucine and Valine (ILV) regulation in B.subtilis, L.lactis and E.coli. Our model aims to describe the evolution of ILV during growth of the bacteria. We are attempting to draw a first draft of a common regulation pattern in the absence of the requested wet lab data, using a regulation network modeling. In fact, we can build a topological view of interaction for the studied regulation, but we lack in-vitro view of the metabolite-protein interactions. As the topological model can only support a set of untested hypotheses, we use the formal logic of René Thomas [2-4] for describing the differential equations governing the chemical equilibrium. However, the space of possibilities is huge, as a model with 4 interactants and 12 direct activation and feedback regulations yields a set of 1022 networks. To reduce this space we use a model checker (NuSMV [5]) associated with SMBioNet [6] to represent the global regulatory network as a graph. The reduction of the space is based on a systematic validation of each graph. A selected biological regulatory graph would establish a regulation network as it describes a biological fact. In the prospect of describing the differences between the selected networks, we have designed a protocol allowing to classify the set of networks. We use the length of the graph, the existence of a dead-end and the number of loops for traveling between René Thomas state's. Our next objective is to establish a link between the numerical property of a graph, derived by our protocol, and the biological property of the subset we study. This approach should be relevant to a number of complex systems. As it attempts to mix different levels of regulation, it should be easier for the wet lab biologist to test in silico hypothesis.

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The Uncertainty in Modelling Complex Systems

Steve Whittle, Eshan Rajabally, John Dalton, Simon Snape

Poster

One of the great challenges in complex system development is the control of design properties throughout the lifecycle. Modelling plays a key role in this activity but current approaches do not adequately support an integrated approach. In particular, there is a failure to provide proper traceability of design properties throughout the product breakdown structure. Furthermore, there is inadequate management of the impact of uncertainties in modelling activity throughout the lifecycle. A system model may give accurate results but absolute fidelity cannot be demonstrated for most practical applications due to our incomplete understanding of the world. Typically, certifying that a model is appropriate for a specific purpose is an informal, ad hoc procedure. This paper will explain the benefits of formally capturing this procedure and present the need for the development of a decision support capability to advance the effective modelling of increasingly complex systems. The technical aspects of the developed methodology will be introduced describing the modelling framework representation, which enables model and design decision traceability and the capture of emergent property flow, and a Bayesian Belief Net based methodology to capture the reasoning associated with justifying the dependability of models.

Furthermore, the link to Design Margins and Critical Design Features (A sub-set of top level product attributes / requirements that are agreed as being critical to project success) is explained and an approach to determine and manage both will be introduced.

Coordinated Action of a Large Scale Robotic System through Self-Organizing Processes

Steffen Wischmann, Martin Huelse

Poster

Within the context of Artificial Life and Evolutionary Robotics, we are facing the problem of how to coordinate the behavior of large scale distributed robotic systems (n $>$ 100). Following the ideas of decentralized control and self-organizing processes we present an example of how to implemented such principles in a homogeneous group of robots controlled by artificial recurrent neural networks (RNN). It is important to emphasize that we are aiming at situated and embodied real world robots acting in dynamically changing environments.

The behavior of the described overall system is determined by three kinds of structural coupling. Every agent within the group is controlled by a RNN. By following a modular neurodynamics approach three evolved basic behaviors are encoded within the RNN that (i) have to be coupled in a way to maintain stable behavioral patterns which (ii) have to be robust against dynamically changing environmental conditions. Furthermore, agents are able to interact with each other through acoustic signaling. Hence, due to this local interaction, each agent (iii) is coupled to others in its surrounding in a way that it can influence the behavior of others as well as itself can be influenced by others. Here, we want to focus on the latter aspect. On a macroscopic level we show how a group of robots coordinates individual foraging and homing behavior in order to transfer collected energy to a nest while avoiding obstacles. Within the control architecture of each single robot a neural pattern generator is implemented that is able to generate very low frequent internal rhythms (period lengths up to two million time steps are possible). This pattern generator determines whether the robot displays foraging or homing behavior. Each robot is able to communicate its behavior switching through acoustic signaling that in turn can reset the pattern generator of perceiving robots. To some extend this reset of internal neural oscillators through external stimuli is inspired by biological systems, for example the flashing of fireflies during mating.

We show that it is possible to almost perfectly synchronize the behavior of a population containing up to 150 autonomous robots through simple local interactions, whereby at the beginning their behavioral patterns are completely out of phase. Furthermore we can demonstrate that is also possible to get individual rhythms in-phase even if the period length of individual internal rhythms are different among the population.

Incremental and unifying modelling formalism for biological interaction networks

Anastasia Yartseva, Hanna Klaudel, Francois Kepes

Poster

This article introduces a new unifying incremental formalism for the modelling of biological regulatory networks. The semantics of the model is given through the translation into the multivalued logical formalism. A methodology for constructing such models is presented on a classical benchmark: the lambda phage genetic switch system. The main advantage of the presented approach is to provide an intermediate level of representing the biological data about interaction networks. From one side, this level enables the expression of the knowledge in a form intuitive for a biologist. From the other side, the knowledge is represented as a formal structured model. This formal model can be translated automatically in existing formalisms enabling the complex study of the dynamical properties of the biological system.

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