



Palma de Mallorca,  
February 18-20th 2008

# DYNAMICS AND EVOLUTION OF BIOLOGICAL AND SOCIAL NETWORKS

## Programme Committee:

- S. C. Manrubia (Astrobiology Center, CSIC-INTA, Madrid)
- A. S. Mikhailov (Fritz Haber Institute of the Max Planck Society, Berlin)
- R. Toral and E. Hernández-García (IFISC, Instituto de Física Interdisciplinar y Sistemas Complejos, UIB-CSIC, Palma de Mallorca)
- M. Vingron (Max Planck Institute for Molecular Genetics, Berlin).

Book of abstracts.

**BIOSOCNETS. Workshop on *Dynamics and evolution of biological and social networks* . February 18-20, 2008. Mallorca, Spain.**

February

Monday 18

Tuesday 19

Wednesday 20

09:30-10:05	<b>Alexander S. Mikhailov</b> , Evolutionary engineering of complex dynamical networks	<b>Stefan Bornholdt</b> , Boolean models of regulatory networks	<b>Federico Vazquez</b> , Absorbing phase transitions in coevolving networks
10:05-10:40	<b>Hiroya Nakao</b> , Turing patterns in random networks	<b>Marc Huett</b> , Network control in gene expression profiles	<b>Santiago Gil</b> , Controlling Chaos in Network Dynamics
10:40-11:10	Coffee break	Coffee break	Coffee break
11:10-11:45	<b>Matteo Marsili</b> , Opportunity and choice in social networks	<b>Bernd Blasius</b> , Epidemic dynamics on an adaptive network	<b>Anirban Banerjee</b> , Graph spectra: A tool for analyzing structure and evolution of a network.
11:45-12:20	<b>Hiroshi Kori</b> , Synchronization Engineering	<b>Miguel A. Fortuna</b> , Spatial networks in ecology	<b>Jacob Bock Axelsen</b> , Heuristic measures for multi-step correlations in molecular networks
12:20-12:55	<b>Raul Toral</b> , Diversity induced effects in the dynamics of social systems	<b>Emilio Hernandez-Garcia</b> , Genetic Similarity Networks in Populations and in Metapopulations	<b>Xavier Castelló</b> , The effects of complex social structure in the dynamics of language competition
12:55-15:00	Lunch	Lunch	Lunch
15:00-15:35	<b>Albert Diaz-Guilera</b> , Dynamical and spectral properties of complex networks	<b>Kim Sneppen</b> , Dynamics of Opinions and Social Structures	
15:35-16:10	<b>Lloyd Demetrius</b> , Boltzman , Darwin and the evolution of Biological networks	<b>M. Angeles Serrano</b> , Structural efficiency of percolation landscapes in flow networks	
16:10-16:45	<b>Victor M. Eguiluz</b> , Scale-free brain functional networks	<b>E. Alejandro Herrada</b> , From genes to species: Universal scaling?	
16:45-17:20	<b>Thomas Manke</b> , An Entropic Characterisation of Biological Networks	<b>Susanna C. Manrubia</b> , Phylogeny and the construction of biological relationships	

## **Evolutionary engineering of complex dynamical networks**

**Alexander S. Mikhailov**

Fritz Haber Institute

Engineering of complex networks is a major challenge. Today, even the best rationally designed networks are inferior to the networks resulting from natural evolution. Modern computers are well behind the information processing capacity of the brain, despite the fact it is based on the elements which are intrinsically very slow. Inside a single biological cell, thousands of different molecular manufacturing and delivery processes proceed in parallel, in a crowded environment in the presence of strong thermal fluctuations, and, nonetheless, characterized by the level of predictability and robust adaptability unprecedented for human designed manufacturing and transportation systems. This suggests that evolutionary optimization approaches may be efficient in the design of artificial networks. In this talk, I provide a review of our recent studies exploring possibilities of evolutionary design of artificial dynamical networks with prescribed functional properties.

## **Controlling Chaos in Network Dynamics**

**Santiago Gil**, Alexander S. Mikhailov  
Physical Chemistry Department, Fritz Haber Institut

A network of coupled phase oscillators is considered. Interactions between the oscillators are characterized by phase shifts, effectively taking into account interaction delays. We show that in this simple model coherent collective dynamics can emerge. Alternatively, chaos can develop when interaction phase shifts are large enough. Introducing a global feedback, chaotic behavior can be suppressed, giving rise to localized structures in the network with complex dynamical behavior. This transition scenario is analyzed, and special attention is paid to the dynamical properties of self-organized structures.

## **Opportunity and choice in social networks**

**Matteo Marsili(1)**, Paolo Pin(1), Silvio Franz(2)

(1) Abdus Salam ICTP, Trieste Italy

(2) LPTMS, Orsay, Paris, France

The human tendency to establish relations with individuals of the same type -- called inbreeding homophily -- has been related either to a biased choice behavior or to a bias in opportunities. We propose an indicator to distinguish between these effects for minority groups and test it on data on US marriages and friendships in US schools. We find that: for what concerns education i) opportunity--based homophily is much stronger than choice--based homophily and ii) they are both remarkably stationary in time; concerning race iii) school friendships do not exhibit opportunity-based homophily, while marriages do, iv) choice-based homophily is much stronger for marriages than for friendships and v) these effects vary widely across race.

We also discuss how, within the Schelling model of residential segregation, choices influence opportunities. Segregation in this model takes place via a coarsening process which can be characterized quantitatively using tools of statistical physics.

## **Synchronization Engineering**

**H. Kori**

Hokkaido university.

Populations of interacting rhythmic components can produce complex behavior in biology, communications, population dynamics, and chemistry. In biology, synchronization can be beneficial, such as in orchestrating the circadian rhythms in mammals, or pathological, such as in the occurrence of Parkinsons disease. We consider here the engineering of desirable states through the introduction of mild feedback, mild such that the behavior of the individual components is not substantially changed by the introduction of the external signal. Our proposed theoretical framework, which is based on phase models, allows a nonlinear time delayed feedback signal to be constructed which produces an interaction function corresponding to the desired global behavior of the system. It is shown theoretically and confirmed in numerical simulations and in electrochemical experiments that a polynomial, delayed feedback is a versatile tool to tune synchronization patterns. The connection between our results and the formation of society will also be discussed in the talk.

[1] I.Z. Kiss, C.G. Rusin, H. Kori, and J.L. Hudson, "Engineering Complex Dynamical Structures: Sequential Patterns and Desynchronization", Science 316, 1886, 2007.

[2] H. Kori, C.G. Rusin, I.Z. Kiss, and J.L. Hudson. "Synchronization Engineering: Theoretical Framework and Application to Dynamical Clustering", submitted.

## **Diversity induced effects in the dynamics of social systems**

**Raul Toral**

IFISC (CSIC-UIB).

In this communication, we present an example of diversity-induced resonance in a simple opinion formation model. The model incorporates two basic ingredients for the evolution of the opinion held by an individual: social pressure and the effect of advertising. The heterogeneity in the model appears in that every individual has an intrinsic preference for a particular option. We also consider that the network of interactions has a non-uniform distribution of links. In both cases, there is a resonance effect (optimal synchronisation of the average opinion with respect to the external signal) as a function of parameters measuring the diversity in the distribution of the preferred opinions or the rewiring probability of links.

## **Dynamical and spectral properties of complex networks**

**Albert Diaz-Guilera**

Universitat de Barcelona.

We will review some results about the relation between dynamical and spectral properties of complex networks. From the dynamical point of view we will focus on the time the whole population needs to be completely synchronized and how partial synchronization of more tightly connected clusters (communities or modules) appears. This properties can be related with the eigenvalues of the the Laplacian matrix of the network.

## **Boltzman , Darwin and the evolution of Biological networks**

**Lloyd Demetrius**

Max Planck Institute for Molecular Genetics.

Boltzmann,s statistical thermodynamics rests on the the empirical observation that macroscopic physical and chemical systems have the tendency to change so that the total energy becomes dispersed . Boltzmann showed that this tendency can be explained in terms of a statistical measure , thermodynamic entropy , a measure of the diversity of energy distribution in a network of interacting molecules . Darwin,s theory of evolution by natural selection is a mechanistic explanation of the empirical fact that Biological complexity as measured by various morphological indices increases over geological time . Darwin,s argument is based on the concept Fitness , a mesure of the diversity of Energy flow in a network of interacting organisms . I will discuss the connection between these two theories and show how the ideas they invoke can be extended to analyse the evolution of various classes of biological networks at the molecular , cellular and population levels

## **Scale-free brain functional networks**

**V.M. Eguíluz (1)**, D.R. Chialvo (2), G.A. Cecchi (3), M. Baliki (2), A.V. Apkarian (2)

(1) IFISC (CSIC-UIB).

(2) Department of Physiology, Northwestern University, Chicago, Illinois, 60611, USA;

(3) IBM T.J. Watson Research Center, 1101 Kitchawan Rd., Yorktown Heights, New York 10598, USA

Functional magnetic resonance imaging is used to extract functional networks connecting correlated human brain sites. Analysis of the resulting networks in different tasks shows that (a) the distribution of functional connections, and the probability of finding a link versus distance are both scale-free, (b) the characteristic path length is small and comparable with those of equivalent random networks, and (c) the clustering coefficient is orders of magnitude larger than those of equivalent random networks. All these properties, typical of scale-free small-world networks, reflect important functional information about brain states.

## **An Entropic Characterisation of Biological Networks**

**Thomas Manke**, Lloyd Demetrius and Martin Vingron  
Max Planck Institute for Molecular Genetics, Berlin,  
Germany

The structure of biological networks is often believed to determine important aspects of their functional and dynamic behaviour, such as their resilience against fluctuations in the operational parameters. One of us (LD) has recently introduced a quantity, called network entropy, as a measure to characterize the diversity of pathways and parameters in a network. The importance of this measure rests on a fluctuation theorem which states that changes in network entropy are positively correlated with changes in network robustness.

Here I present numerical studies to explore the relationship of network entropy with several other measures of network resilience. The entropic formalism also suggests a novel method to rank network elements according to their relative contribution to network entropy and their perceived importance for robust network function. I will present studies on real biological networks which suggest that entropy-based measures provide a better descriptor of biological importance than other heuristic measures, such as node degree.

## **Boolean models of regulatory networks**

**Stefan Bornholdt**

University of Bremen

Boolean models of cellular regulation have long been an anecdotal concept for how regulation in complex networks might function. Recently, however, several such models have been proposed that predict dynamics of regulatory modules in real cell from simple discrete dynamical network models. I here review these recent developments and discuss prospects and limitations of Boolean models for biological regulation.

## **Network control in gene expression profiles**

**Marc Huett**

Jacobs University Bremen.

The set of regulatory interactions between genes, mediated by transcription factors (TFs) forms a complex transcriptional regulatory network (TRN). For the bacterium *E. coli* we mapped microarray expression data onto the TRN to study the correspondence between a gene's expression level and its TRN characteristics at different levels of network organization.

In particular we look at the properties of effective networks derived from significant gene expression changes under variation of the two forms of control and find that upon limitations of one type of control (caused e.g. by mutation of a global DNA architectural factor) the other type can compensate for compromised regulation. Mutations of global regulators significantly enhance the digital control; in the presence of global DNA architectural proteins regulation is mostly of the analog type, coupling spatially neighboring genomic loci; together our data suggest that two logically distinct - digital and analog - types of control are balancing each other. By revealing two distinct logical types of control, our approach provides basic insights into both the organizational principles of transcriptional regulation and the mechanisms buffering genetic flexibility. We believe that the general concept of distinguishing logical types of control will apply to many complex biological networks.

## **Epidemic dynamics on an adaptive network**

**Bernd Blasius**

ICBM, University of Oldenburg.

Many real world networks are characterized by adaptive changes in their topology depending on the state of their nodes. Here we study epidemic dynamics on an adaptive network, where the susceptibles are able to avoid contact with infected by rewiring their network connections. As we show, this gives rise to assortative degree correlation, oscillations, hysteresis and 1st order transitions. We propose a low-dimensional model, based on a pair-approximation, to describe the system and present a full local bifurcation analysis. Our results indicate that the interplay between dynamics and topology can have important consequences for the spreading of infectious diseases and related applications.

## **Spatial networks in ecology**

**Miguel A. Fortuna**, Integrative Ecology Group  
Estación Biológica de Doñana, CSIC

Space is the last frontier in ecological research. Lots of important questions such as species extinction in fragmented landscapes or the efficacy of marine reserves depend on a spatial representation of ecological processes. In this talk I will show how the network approach can be useful as a tool for the conservation and management of endangered species. Specifically, I will consider three case studies, namely the persistence of amphibians in stochastic ponds, the mating network of an insect-pollinated tree, and the network of roosting sites used by a bat species. Using these case studies, I will illustrate how the network approach can shed light into problems as diverse as species persistence in fluctuating environments, gene flow, and information exchange among individuals in an animal society.

## **Genetic Similarity Networks in Populations and in Metapopulations**

**Emilio Hernandez-Garcia(1)**, A. F. Rozenfeld(2), S. Arnaud-Haond(3,4), V.M. Eguíluz(1), E. Serrão(3) and C. M. Duarte(2)

(1) IFISC, Instituto de Física Interdisciplinar y Sistemas Complejos (CSIC-UIB), Campus Universitat de les Illes Balears, E-07122 Palma de Mallorca, Spain.

(2) IMEDEA (CSIC-UIB), Instituto Mediterráneo de Estudios Avanzados, C/ Miquel Marqués 21, 07190 Esporles, Mallorca, Spain.

(3) CCMAR, CIMAR-Laboratório Associado, Universidade do Algarve, Gambelas, 8005-139, Faro, Portugal

(4) IFREMER, Centre de Brest, BP70, 29280 Plouzané, France

The development of evolutionary theory in the framework of population genetics has undergone major progress with the arrival of molecular biology and molecular markers. Some major gaps have been identified between natural populations and theoretical models based on assumptions, such as panmixia, that are seldom realized in nature. Novel tools of analysis, free of most of the traditional theoretical assumptions, are needed for taking full advantage of the huge amount of information available in modern genetic data sets.

Here we use recently introduced networks of genetic similarity (A.F. Rozenfeld et al., J. Roy. Soc. Interface 4, 1093, 2007) to analyze the hierarchy and organization of the genetic diversity of a marine plant *Posidonia oceanica*, across its entire geographical range. On the one hand, we characterize population substructure by constructing networks in which nodes are genotypes. The networks are of the small-world type, and clustering measures indicate strong correlations not easily detectable by other means.

On the other hand, we characterize the pattern of genetic relationships among populations by constructing networks of genetic similarity in which the nodes are plant populations. Betweenness-centrality and degree-distribution calculations allowed to identify some geographical regions acting as major hubs relaying gene flow in the metapopulation system.



## **Dynamics of Opinions and Social Structures**

**Kim Sneppen**, Martin Rosvall  
Niels Bohr Institute.

Social groups with widely different music tastes, political convictions, and religious beliefs emerge and disappear on scales from extreme subcultures to mainstream mass-cultures. Both the underlying social structure and the formation of opinions are dynamic and changes in one affect the other. Several positive feedback mechanisms have been proposed to drive the diversity in social and economic systems. We analyze this phenomenon in terms of a social network-model that explicitly simulates the feedback between information assembly and emergence of social structures: changing beliefs are coupled to changing relationships because agents self-organize a dynamic network to facilitate their hunter-gatherer behavior in information space. Our analysis demonstrates that tribal organizations and modular social networks can emerge as a result of contact-seeking agents that reinforce their beliefs among like-minded.

## **Structural efficiency of percolation landscapes in flow networks**

**M. Angeles Serrano**, Paolo De Los Rios

Institute of Theoretical Physics, LBS, SB, EPFL, 1015  
Lausanne, Switzerland

The large-scale structure of complex systems is intimately related to their functionality and evolution. In particular, global transport processes associated to complex networks rely on the presence of directed paths from input to output nodes and edges, which organize in network-spanning linked components. However, the precise relation between such structures and functional or evolutionary aspects remains to be understood. Here, we define quantitatively the structural efficiency of these percolation landscapes in relation to global transport and discuss the key role of edges in the interfaces between core and peripheral components. Furthermore, we assess that optimal topologies should look like "hairy balls" so to minimize bottleneck effects and the sensitivity to failures. Our results on two real networks shaped by very different dynamics and time-scales, the Internet customer-provider set of relationships and the nervous system of the worm *Caenorhabditis elegans*, suggest that whereas biological evolution has selected a structure close to the optimal layout, competition does not necessarily tend toward the most efficient global architecture.

## **From genes to species: Universal scaling?**

**E. Alejandro Herrada**(1), Claudio Juan Tessone(2),  
Konstantin Klemm (3), Víctor M. Eguíluz (1), Emilio  
Hernández-García (1), Carlos M. Duarte (4)

(1) IFISC (CSIC-UIB)

(2) ETH Zurich

(3) University of Leipzig

(4) IMEDEA

Many biological processes, from cellular metabolism to population dynamics, are characterized by allometric scaling (power-law) relationships between size and rate. During the last years different research groups have developed statistical analysis tools, based on allometric scaling concepts, for the study of tree-like transportation networks (for example to characterize how branching properties change with network size). Among the biological processes naturally described in terms of a tree-like topology, the expansion of both the protein families phylogenies and the species phylogenies happening during the evolution of the organisms are conveniently represented as phylogenetic trees. Here we compare the allometric scaling approaches for the statistical analysis of both protein families phylogenies and species phylogenies.

Considering the phylogenies as a group of tips and nodes linked by branches, a node ultimately represents a diversification event. For each node  $i$ , a subtree  $S_i$  is made up of a root at node  $i$  and all the descendant nodes bellow  $i$ . That point of view allows us to understand how much the (sub)tree members diversify from  $i$ , through the subtree size  $A_i$ , and how is this diversity arranged, through several topological measures characterizing the shape of the subtree  $S_i$ . Universal scaling relationships between shape and size of protein and species phylogenies are revealed and discussed.

## **Phylogeny and the construction of biological relationships**

**Susanna C. Manrubia**

Centro de Astrobiología, INTA-CSIC.

Biological systems, as we see them today, are the result of a long process where new variants have been fixed or discarded depending on their suitability to enhance survival in fluctuating environments. Evolution and selection act at different levels, from the molecular organization of genomes to the stable association of species in ecosystems. In all cases, the network of relationships among molecules or species, e.g., is the result of a very long period of construction where, likely, many proposals were unsuccessful. The topology of phylogenetic trees and the structure of networks in biological systems are two sides of the same coin, and the latter could in principle retain a sort of (evolutionary) memory of the former process. Advances in our understanding of the universal features of natural systems might benefit from the simultaneous analysis of trees (which carry a time signal) and networks (displaying the relationships at a fixed time). As an example, we will discuss the relevance that ecological networks constructed through the slow addition of new species to the global ecosystem could have in explaining large-scale evolutionary patterns. On-going studies on the phylogenetic patterns displayed by evolving molecular quasispecies might shed light on the mechanisms that confer generic topological properties to phylogenetic trees.

## **Turing patterns in random networks**

**Hiroya Nakao (1,2)**, Alexander S. Mikhailov (1)

(1) Fritz-Haber-Institut der MPG

(2) Kyoto Univ

We analyze diffusion-induced instability of reaction-diffusion systems on random networks. As in the ordinary Turing instability in continuous media, a homogeneous state loses its stability and gives way to inhomogeneous states when the diffusion of the inhibitor is sufficiently faster than that of the activator. We formulate linear stability of the homogeneous state using the Laplacian eigenvectors of the network, and then present numerical results of the Brusselator and Mimura-Murray models on the Erdos-Renyi and Barabasi-Albert networks. We show that the final stationary patterns are considerably different from the unstable linear modes even in the vicinity of the bifurcation point, and that those patterns can, to a certain extent, be explained based on a simple mean-field approximation of the random networks.

## Absorbing phase transitions in coevolving networks

**Federico Vazquez**, Victor M. Eguiluz and Maxi San Miguel  
IFISC (CSIC-UIB).

I will talk about a particular type of absorbing transitions that has recently been observed in models of adaptive networks. In these models, a node can change its state by interacting with its neighbors, and at the same time, links can be rewired depending on the state of the nodes at their ends. In this way, the dynamics of nodes and links are not independent, but they coevolve. It is found that when the rewiring is fast enough compare to the rate at which nodes update their states, the network breaks into disconnected components, each composed by nodes holding the same state. In order to understand the mechanism of this fragmentation transition I will introduce a simple model, that possesses all the ingredients of related models, and has the advantage of being analytically tractable. A mean-field approximation reveals an absorbing transition from an active to a frozen phase at a critical value of the rewiring probability  $p_c = \frac{\mu-2}{\mu-1}$ , that only depends on the

average degree  $\mu$  of the network. In finite-size systems, the active and frozen phases correspond to a connected and a fragmented network respectively. The transition can be seen as the sudden change in the trajectory of an equivalent random walk at the critical point, resulting in an approach to the final frozen state whose time scale diverges as  $\tau \approx |p_c - p|^{-1}$  near  $p_c$ .

## **Graph spectra: A tool for analyzing structure and evolution of a network.**

**Anirban Banerjee**

Max Planck Institute for Molecular Genetics.

The existing graph invariants are not sufficient to capture all qualitative aspects of a graph. One of the aim of graph theory to identify on one hand the unique and special feature for the network from a particular class and on the other hand the universal qualities that are shared by other network structures. It is a challenge to specify the domain of a given a network structure, on the basis of certain unique qualitative features. We develop theoretical scheme and apply the general method, based on the spectral plot of the normalized graph Laplacian, that is easily visually analyzed and can be considered as excellent diagnostic to categorize the networks from different sources. We show how useful plausible hypothesis about evolutionary process can be made by investigating the spectra of a graph constructed from actual data. Based on this idea we have reconstructed protein-protein interaction network which is structurally more close to real protein-protein interaction networks than the networks constructed by other models. We also introduced a tentative classification scheme for empirical networks based on global qualitative properties detected through the spectrum of the Laplacian of the graph

## **Heuristic measures for multi-step correlations in molecular networks**

**Jacob Bock Axelsen**

Centro de Astrobiologia.

We have studied the full protein reaction network of *E.coli* and the regulatory network of *S.cerevisiae*. In the case of *E.coli* we define signalling as a property of given paths. By counting the number of protein species involved in a given reaction path we find that signals rarely escape their local neighborhood. We detect modules by condensing the network into strong components, thus showing that the real network is subcritical. In *S.cerevisiae* we study the regulatory network by the use of annotations, sequence similarities and expression dynamics. We find that the signalling is dictated by dynamical processes centered on hubs which in turn are largely independent.

## **The effects of complex social structure in the dynamics of language competition**

**Xavier Castelló**, Víctor Eguíluz, Maxi San Miguel  
IFISC (CSIC-UIB).

In the general context of dynamics of social consensus, we study an agent based model for the competition between two socially equivalent languages, addressing the role of bilingualism and social structure. In a regular network, we study the formation of linguistic domains and their interaction across the boundaries. We analyze also the dynamics on a small world network and on a network with community structure. In all cases, a final scenario of dominance of one language and extinction of the other is obtained. In comparison with the regular network, smaller times for extinction are found in the small world network. In the network with communities instead, the average time for extinction is not defined and metastable states are observed at all time scales.

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Attendants list:

1. Axelsen, Jacob Bock  
Centro de Astrobiologia  
bochaj@inta.es
2. Banerjee, Anirban  
Max Planck Institute for Molecular Genetics  
banerjee@molgen.mpg.de
3. Blasius, Bernd  
ICBM, University of Oldenburg  
blasius@icbm.de
4. Bornholdt, Stefan  
University of Bremen  
bornholdt@itp.uni-bremen.de
5. Castelló, Xavier  
IFISC (CSIC-UIB)  
xavi@ifisc.uib.es
6. Cornelles Soriano, Miguel  
IFISC  
miguel@ifisc.uib.es
7. Demetrius, Lloyd  
Max Planck Institute for Molecular Genetics  
lloyd.demetrius@molgen.mpg.de
8. Diaz-Guilera, Albert  
Universitat de Barcelona  
albert.diaz@ub.edu
9. Eguíluz, Víctor M.  
IFISC (CSIC-UIB)  
victor@ifisc.uib.es
10. Flechsig, Holger  
Fritz Haber Institute  
flechsig@fhi-berlin.mpg.de
11. Fortuna, Miguel A.  
Estación Biológica de Doñana  
fortuna@ebd.csic.es
12. Gil, Santiago  
Fritz Haber Institute  
gil@fhi-berlin.mpg.de
13. Gollo, Leonardo  
IFISC, CSIC-UIB  
leonardo@ifisc.uib.es

14. Gomez-Marin, Alex  
Universitat de Barcelona  
agomezmarin@gmail.com
15. Hernandez-Garcia, Emilio  
IFISC (CSIC-UIB)  
emilio@ifisc.uib.es
16. Herrada, E. Alejandro  
IFISC (CSIC-UIB)  
alejandro@ifisc.uib.es
17. Huett, Marc  
Jacobs University Bremen  
m.huett@jacobs-university.de
18. Kori, Hiroshi  
Hokkaido university  
kori@nsc.es.hokudai.ac.jp
19. Manke, Thomas  
Max Planck Institute for Molecular Genetics  
manke@molgen.mpg.de
20. Manrubia, Susanna C.  
Centro de Astrobiología, INTA-CSIC  
cuevasms@inta.es
21. Marsili, Matteo  
Abdus Salam ICTP  
marsili@ictp.it
22. Mikhailov, Alexander  
Fritz Haber Institute  
mikhailov@fhi-berlin.mpg.de
23. Nakao, Hiroya  
Fritz-Haber-Institut der MPG / Kyoto Univ.  
nakao@ton.scphys.kyoto-u.ac.jp
24. Pérez, Toni  
IFISC (CSIC-UIB)  
toni@ifisc.uib.es
25. Rozenfeld, Alejandro F.  
IMEDEA (CSIC-UIB)  
alex@ifisc.uib.es
26. San Miguel, Maxi  
IFISC (CSIC-UIB)  
maxi@ifisc.uib.es
27. Serrano, M. Angeles  
Institute of Theoretical Physics, EPFL  
mariangeles.serrano@epfl.ch
28. Sintés, Tomas

- IFISC (CSIC-UIB)  
tomas@ifisc.uib.es
29. Sneppen, Kim  
Niels Bohr Institute  
sneppen@nbi.dk
30. Souza Bacelar, Flora  
IFISC (CSIC-UIB)  
florabacelar@ifisc.uib.es
31. Toral, Raul  
IFISC (CSIC-UIB)  
raul@ifisc.uib.es
32. Tronciu, Vasile  
IFISC (CSIC-UIB)  
vasile@ifisc.uib.es
33. Tugrul, Murat  
IFISC (CSIC-UIB)  
mtugrul@ifisc.uib.es
34. Vazquez, Federico  
IFISC (CSIC-UIB)  
federico@ifisc.uib.es
35. Vingron, Martin  
Max Planck Institute for Molecular Genetics  
vingron@molgen.mpg.de