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Letter from the President

Dear Colleagues and Members,

Near the end of 2013 and 2014 we are arriving (with some delay) at our yearly issue of the European Communications in Mathematical and Theoretical Biology, issue sent to all members. The change of the year seems a moment then to think of past and future. As for the past, 2013 has been proclaimed as a special year for the **Mathematics of Planet Earth** and many of its themes (ecology, biodiversity, evolution, sustainable development, epidemics; invasive species) sound familiar to us mathematical biologists. The year for the Mathematics of Planet Earth has seen many conferences around the world, also in the areas of mathematical biology. I wish particularly to recall the Conference « Biological invasions and evolutionary biology, stochastic and deterministic model », held in Lyon during the special program on "Mathematical Biology" going from March 4th to June 14th. The special program has also hosted the 4th edition of the **ESMTB-EMS Summer School,** this year on "Multiscale modeling in the life sciences**".** Many other conferences and schools were held during this year, a short report on some of which is on this issue. ESMTB supports these activities by hosting the announcements on the web site (http://www.esmtb.org), by supporting student participation through a (limited) travel fund, by publishing reports on the Communications. Please, help us in making these actions more effective.

The **Reinhart Heinrich Doctoral Thesis Award** 2012 was awarded to Christoforos C. Hadjichrysanthou, who received his PhD from the City University London. You will find an extensive summary of his noteworthy thesis "Evolutionary models in structured populations" later in this issue.

Moving to the future, Göteborg (Gothenburg in English) will host from June 15 to June 19 2014 the **9th ESMTB Conference**, for the first time in the Nordic countries. Don't forget of the deadline of February 14th for submitting an abstract. All the information can be found at http://ecmtb2014.org; after all the exciting scientific activities, the conference will conclude on Friday June 20th with Midsummer Eve, announced as the most important holiday in the North, something to which I am definitely looking forward. Moving more into the future, the **10th ESMTB Conference** will take place, as a joint Conference with SMB, in 2016 at the University Park Campus of Nottingham. More news will be forthcoming; for the moment we have already another conference to head for. 2014 will also be the first year of Horizon 2020, the EU Programme for Research and Innovation. Although the phrase "mathematical biology" never occurs, as far as I can tell, in the documents, the drafts centre on "global systems science", call for "multidisciplinary expertise" for "systems (bio) medicine approaches". Analysing complex problems with interdisciplinary efforts is what mathematical biology is (or should be) about, so I hope and wish that good research in mathematical biology will be able to progress towards these aims, and also find its share of funding, despite the difficulties in handling European rules and formats.

Going back to our journal and society, in this issue you will find also a nice essay on "Cancer as evolutionary process". I hope this will be found interesting, and I wish to stress that the Communications is open to such contributions, where one (or a group of) scientist wishes to describe a research area in a free (or even visionary) manner, without being constrained by the rules of scientific journals. Please send suggestions for next year.

Many people have contributed to this issue, and helped in running the society and conferences, by devoting some of their spare time to these activities. I wish especially to thank Vitaly Volpert, who is the main responsible as editor of this issue; Barbara Boldin, secretary of the Society; Andreas Deutsch, treasurer of the society, and in charge of memberships and web site, who has been the main force behind the society; Torbjorn Lundh, the main organizer of ECMTB-2014; Markus Owen, who has volunteered to organize ECMTB-2016, and I apologise to all the other ones that have not been named.

I conclude by inviting you to renew the membership for 2014 (you can check your payments at the web site www.esmtb.org), and to invite your colleagues to join the Society. Beyond the practical advantages to members (free access to JMB, discounts on Springer books, limited travel support for young researchers), we believe that the Society has still a role in promoting exchanges of ideas, in forging collaborations at all levels, and somehow also in giving visibility to new research paths.

Andrea Pugliese
Trento, Dec. 2013

Minutes of the ESMTB Board Meeting

Amsterdam, the Netherlands
10th November 2012

Meeting starts at 10am.

Present: Barbara Boldin (BB; minutes), Reinhard Bürger (RB), Andreas Deutsch (AD), Peter Jagers (PJ), Roeland Merks (RM), Andrea Pugliese (AP; chair), Ryszard Rudnicki (RR), Vitaly Volpert (VV)
Guest: Eva Hiripi (EH; Springer)
Absent with apology: Miguel Herrero, Daphne Manoussaki

1. Springer and JMB

Eva Hiripi introduces herself as a Springer representative and the new associate editor for Biomathematics and Statistics.
The 2011 Publisher's report for the Journal of Mathematical Biology:

- The number of manuscripts submitted to the Journal of Mathematical Biology is increasing. The acceptance ratio remains roughly constant and is around 26%. In order to handle the increased number of accepted manuscripts, issues of JMB now contain more pages. Moreover, two additional issues will be published in 2012, bringing the total number of 2012 JMB issues to 14. EH highlights decreasing the backlog as the most important task in the next years.
- EH presents the distribution of submitted and accepted manuscripts according to authors' country of origin as well the production in the different months of 2010 and 2011. Different subscription types are presented and data concerning manuscript downloads is shown. Covering and abstracting of JMB is discussed.
- The author satisfaction survey that included 1300 journals and had begun in 2008 concluded in December 2011. The results for the Journal of Mathematical Biology show that the authors consider the journal's reputation, the quality of peer review and readership as the three most important factors when deciding to submit a manuscript to JMB.

Comments on the Publisher's report. AD remarks that a report on long-term trends would be useful, in particular to observe the impact of journal's connection to ESMTB. PJ adds that comparison to other Springer journals, for instance journals in Statistics and Probability theory would be useful. It is discussed how much the Board of ESMTB is represented in editorial board of JMB.
JMB Perspectives. RM describes the recent developments. Several invitations for Perspectives articles were sent out. To increase the visibility of Perspectives, a section on JMB and ESMTB websites could be devoted to the Perspectives articles.
JMB website. Suggestions are made as to how to make the JMB website more user friendly and attracting more visitors: editorials could be introduced as well as a short introduction of journal's editors, with links to their personal websites. In addition, "editor's picks" could be introduced to highlight particularly interesting papers.
Special issues. In April 2013, the Journal of Mathematical Biology will publish a special issue to honour Odo Diekmann. Further suggestions for special issues are needed. BB suggests making these special issues more visible by including a link to special issues on the JMB website.

Popular science. AD suggests a popular science journal in mathematical biology. JP adds that such a journal already exists for mathematics (Mathematics Intelligencer), EH mentions Springer Briefs.

2. ESMTB Communications

VV describes the making of the latest issue of ESMTB Communications. AD, who took care of the printing and the distribution of the Communications, reports the costs involved in the production of the Communications. VV suggests making the Communications an official and perhaps a more scientific publication (by including review articles). The latter idea is not embraced as no clear advantage is seen in publishing review articles in the Communications. The majority of the Board is in favour of keeping the Communications as they are. AD suggests that some professional formatting would be welcome to make the style of the Communications more homogeneous. In addition, the Communications should highlight the fact that ESMTB supports workshops. EH introduces some options for publishing Communications.

3. ECMTB 2014

PJ introduces plans for ECMTB 2014. The conference will take place from 15th June – 19th June in Gothenburg, Sweden. Highlights:

- The initial plans for the venue have changed – the new venue is Chalmers University. PJ introduces the preliminary budget of the conference. It is estimated that the registration fee will be around 250 euros. RR adds that the conference in Krakow had similar fees and students were eligible for lower fees. RB suggests that several types of fees should be available in Gothenburg as well. In addition, the possibility to opt in/out lunches and the banquet would be welcome. PJ adds that 719 people can attend the banquet. Subsidized banquet would be welcome; the registration fees can be used for this purpose.
- The conference starts of Sunday but satellite meetings are planned already for Saturday. Introductory lectures for students prior to the conference were well received in Krakow. All Board members agree that it would be a good idea to organise such introductory lectures in Sweden as well.
- It is planned that poster sessions are combined with a social event and one free drink is offered to the participants.
- RR asks how many participants will have a chance to give a talk at the conference. PJ replies that 20 parallel sessions could be hosted, each having about 12 talks. AP suggests that no more than ten parallel sessions are organized.
- Immediately after the conference, Midsummer festivities begin in Sweden, offering participants a chance for a unique experience

Themes of ECMTB 2014: the main themes of the conference in Gothenburg are to be mentioned on the official website of the conference, www.ecmtb2014.org. The main topics include:

- Evolution and populations genetics
- Ecology
- Developmental Biology,
- Cancer
- Population Dynamics and Conservation Biology
- Phylogeny

- Epidemics
- Immunology
- Physiology
- Neuroscience
- Cell and Tissue Biology
- Bio-imaging
- Education in mathematics, biology and biomathematics
- Collective motion
- Systems biology

Scientific committee. A preliminary list is made to cover all the main topics of the conference.

4. EMS Summer School 2013

VV introduces plans for the EMS Summer School in 2013. The summer school entitled *Multiscale modeling in biology* will take place in Lion from 27th - 31st May 2013 during the Trimester of biomathematics. The School will include seven three-hour lectures and several short presentations covering the topics Individual based modelling, Stochastic modelling, Mechanics of cytoplasm, Cancer, Neuroscience, Networks and genes, Particles and interaction.

5. ECMTB 2016

Two suggestions are put forward for ECMTB in 2016. AP suggests gathering more information about the two options before the next Board meeting.

6. ESMTB Website

AD discusses ways to improve the Society's website and invites all Board members to send their own ideas to improve the website.

7. Report of the Treasurer

AD hands out printed reports on ESMTB financial and membership data.

- *Membership development*. AD presents the data on ESMTB memberships in the years 2003-2012. The number of memberships peaked in 2005 (in the year of ECMTB in Dresden). Despite the conference in Krakow, the number of members dropped in 2011. In 2012, the number of members again decreased. The idea of sending personalized payment reminders is put forward again. AD presents figures describing the different membership and payment types and adds that, in 2012, a new category "life membership" was introduced.
- *ESMTB Support*. Two inquiries were received for ESMTB support of conferences in 2013. AD suggests supporting both and the Board concurs. In 2011, no requests for ESMTB support of schools/conferences were received. In 2012, four requests for ESMTB Travel Support were received, all four were granted. In 2011, ESMTB granted 30 out of 47 travel supports.

- *ESMTB accounts and audits.* AD informs the Board that the Dresden account will now be closed. A. Czirok and C. Braumann approved the Society's account data for 2010 and 2011.
- AD concludes by presenting the current ESMTB balance.

The end of AD's term as the Society's Treasurer is approaching and a new, perhaps more permanent, solution should be found. AD suggests to step down at the end of 2013 so as to allow for a transitional year. JP suggests two options for the next financial centre of ESMTB.

8. The Reinhart Heinrich award

AD reports on the latest Reinhart Heinrich prize competition. Six applications were received. Four out of six were pre-selected and the authors were invited to submit the full thesis for consideration. Stefan Höhme from the University of Leipzig was chosen as the 2011 Reinhart Heinrich prize winner.
The 30th November 2012 is the deadline for the 2012 Reinhart Heinrich prize nominations. AD adds that more promotion of the award is needed.

9. Diverse

AP and RM discuss ways to promote the Society via new media. RM volunteers to set up a Twitter account where information about activities could be posted.

The meeting ends at 18.05. The next Board meeting is planned for May 2013 in Lyon.

Remarks:
- ESMTB Twitter account is @ESMTBio.
- The Board meeting has been postponed until autumn 2013.

Reinhart Heinrich Doctoral Thesis Award 2012

For 2012 the awarding committee obtained applications by six young scientists. The theses represent a broad and interesting range of research topics in the growing field of mathematical and theoretical biology.

The awarding committee nominated as winner of the Reinhart- Heinrich Doctoral Thesis Award 2012 **Christoforos C. Hadjichrysanthou**.

Christoforos C. Hadjichrysanthou received his PhD from the City University London in 2012. The topic of his thesis “EVOLUTIONARY MODELS IN STRUCTURED POPULATIONS” is an impressive mathematical work elucidating evolutionary dynamics in several types of finite populations with structure. In particular, Dr Hadjichrysanthou derived several novel results using and extending the mathematical theory of evolutionary game theory and evolutionary graph theory. Specifically, he developed an analytical expression for the mean time to absorption and fixation on the star graph – the first general formula of this type for irregular graphs; he proposed an approximation scheme for general structured populations when invaded by mutants; and, finally, he constructed and explored a new game-theoretical model for food sharing behaviour of animals in kleptoparasitic populations. His work is characterized by asking biologically interesting and very relevant questions and by answering these questions using innovative and mathematically sound approaches. Moreover, his significant and non-trivial extensions of a very well studied problem have led to several papers in leading journals.

Andreas Deutsch
(head of awarding committee)
Dresden, Dec. 2013

Extended abstract of the awarded thesis

Evolutionary Models in Structured Populations

Doctoral Thesis by Christoforos Hadjichrysanthou
Supervisor: Professor Mark Broom

Thesis Summary

The evolution of populations has been an issue of great concern in the last centuries. According to Darwin's theory of evolution, populations evolve by natural selection. Individuals occasionally mutate. Those that have a survival and reproductive advantage in their environment reproduce at higher rates passing on their characteristics to their offspring.

Evolutionary game theory has been proved to be a powerful mathematical tool for the description and study of the evolution of biological and other populations consisting of interacting individuals. Evolutionary game dynamics have been traditionally studied in infinitely large homogeneous populations, where each individual is equally likely to interact with every other individual. However, real populations are finite and characterised by complex interactions among individuals. Such populations can be represented by graphs, where each individual occupies a vertex and the edges of the graph represent interactive relationships between individuals. Building on the work of Lieberman *et al*. (2005), this work explores the influence of the population contact structure on the outcome of various biological evolutionary processes.

Another component of this research work involves the use of game theory for the modelling of a very common phenomenon in the natural world. The models developed examine the evolution of kleptoparasitic populations, foraging populations in which animals can steal prey from other animals for their survival. Through a game-theoretical approach, the features of the population structure that may favour the appearance of kleptoparasitic behaviour among animals are addressed. In addition, a model is proposed for the investigation of the ecological conditions that encourage foraging animals to share their prey, behaviour observed in a wide range of animal species.

This thesis is divided into the following main chapters.

Evolutionary dynamics on simple graphs

The analytic investigation of the evolutionary process may be possible when the population can be represented by simple graphs with a lot of symmetry and lack of complexity. We study analytically the evolution on three simple graphs; the complete, the circle and the star graph.

The most commonly considered stochastic evolutionary process in structured populations represented by graphs is the *invasion process* (IP) (or the birth-death process with selection on the birth), an adaptation of the famous Moran process (see Figure 1). Initially, a number of mutant individuals X invade a population of resident individuals Y by replacing an equivalent number of Ys at random. Then, at each time-step an individual is randomly selected for

reproduction with probability proportional to its fitness. The offspring of that individual, which is a perfect copy of its parent, replaces a neighbouring connected individual which is chosen at random. Due to the finiteness of the population size and the absence of mutations during the process, inevitably one of the two types of individuals will replace all the individuals of the other type and fixate in the population. So, there are some reasonable questions:

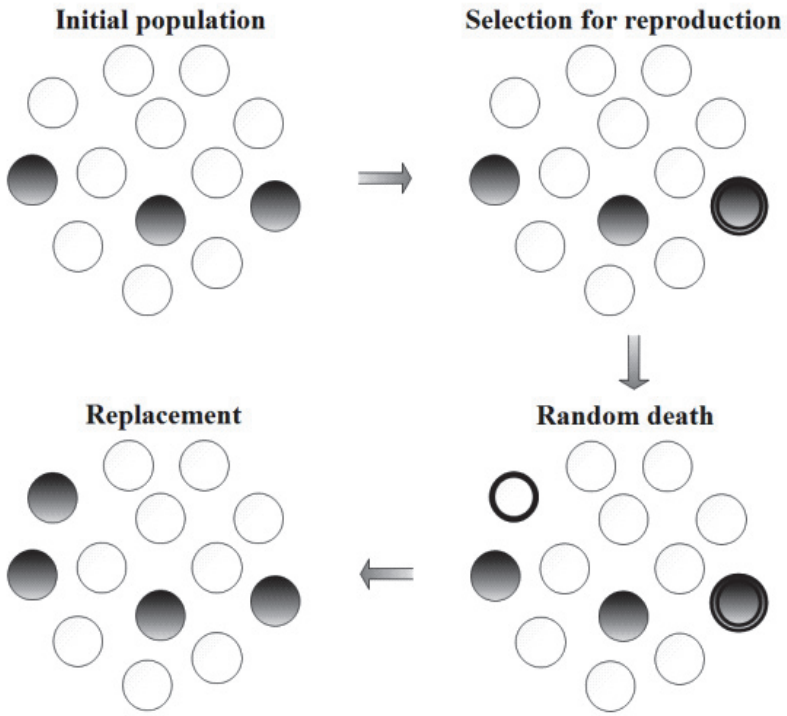

Figure 1: The Moran process with frequency dependent fitness. A finite population consists of two types of individuals, A and B. In each time step, an individual is randomly selected for reproduction with probability proportional to its fitness. Another individual is chosen for death at random. An identical offspring of the individual chosen for reproduction replaces the dead individual.

- What is the probability that a particular type will fixate, i.e. the probability that at the end of the evolutionary process the population will consist only of that type of individuals? We call this probability the *fixation probability*.
- What is the *mean fixation time* of a type of individual, i.e. how long will it take to fixate given that this will happen?
- What is the *mean absorption time*, that is, the mean time needed for one of the two types to fixate?

Another quantity of potential interest that we introduce in this work is the *mean number of transitions* to absorption or fixation, where the number of transitions is the number of times the population changes its state before the process ends. We derive the exact solutions of the above quantities starting from any number of mutant individuals introduced into the three graphs. In particular, the exact formulae of the mean time to absorption and fixation on the star graph are the first general formulae for absorption and fixation times derived on an irregular graph. Using the results derived, we also obtain conditions under which mutants are

favoured over residents. These solutions give the possibility of a systematic and detailed consideration of the evolutionary process on the above graphs in various scenarios.

Numerical examples have shown the significant influence of the structure of a population on its evolution. The extent of this effect depends significantly on the fitness of individuals, as well as on the population size. For example, it is shown that an advantageous mutant always has a higher probability to fixate on the star compared to the complete graph and the circle. Thus, the star graph acts as an amplifier of the fitness and enhances selection. However, the fixation on a star graph takes a very long time. In previous studies emphasis was given to the fixation probability, whereas the study of the speed of the evolutionary process is relatively rare. Moreover, we demonstrated that the fixation probability may not be sufficient to describe the evolutionary dynamics in some systems; a mutant may have a high chance to fixate but the time required to fixate is extremely large.

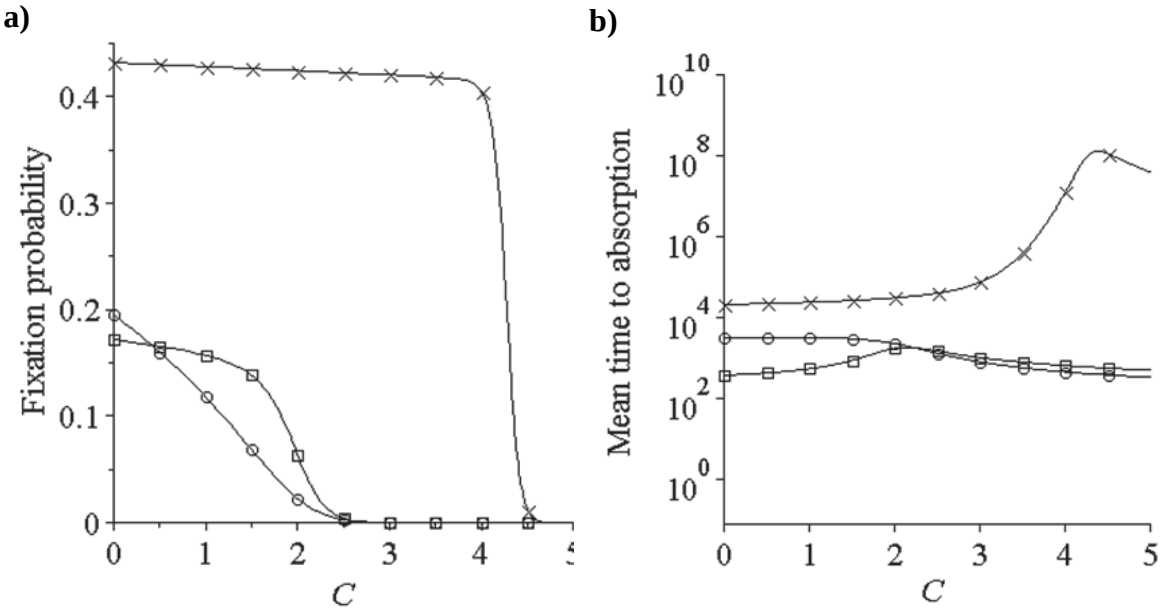

Figure 2: The fixation probability of Hawks, and b) the mean time to absorption, when a single mutant Hawk invades into a resident population of Doves on a star (crosses), a circle (circles) and a complete graph (boxes), in a Hawk-Dove game in the case where the number of vertices is equal to 60 and the fight cost varies.

One of the main examples of our work is the application of the Hawk-Dove game, which has been used widely for the modelling of competition of animals over food, mates, territories, and other biological resources. Among interesting observations is that on the complete graph and the star when the value of the resource, and the cost of fighting for the resource, are such that the fixation probability of a single Hawk, , is equal to the fixation probability of a single Dove, then the fixation times are remarkably large, as selection pressure favours the mixture of the two strategies. For such values of and there is also a step change in the fixation probability of a single Hawk, with a significant non-zero probability for , and a near zero value otherwise (see Figure 2, also Broom *et al*. (2010a, 2010b)).

Evolutionary dynamics on graphs under various update rules

In biological situations, there are a number of strategy update rules that can be followed. The investigation of the evolutionary process under different update rules has not been of great importance historically, since the evolutionary process on homogeneous populations is not significantly affected by the choice of the update rules. This research considers to what extent the change of the strategy update rules of the evolutionary dynamics can affect the evolution of a population having a non-homogeneous contact structure. As an example, the evolutionary game dynamics on the extreme heterogeneous structure of the star graph is studied under three update rules additional to the IP:

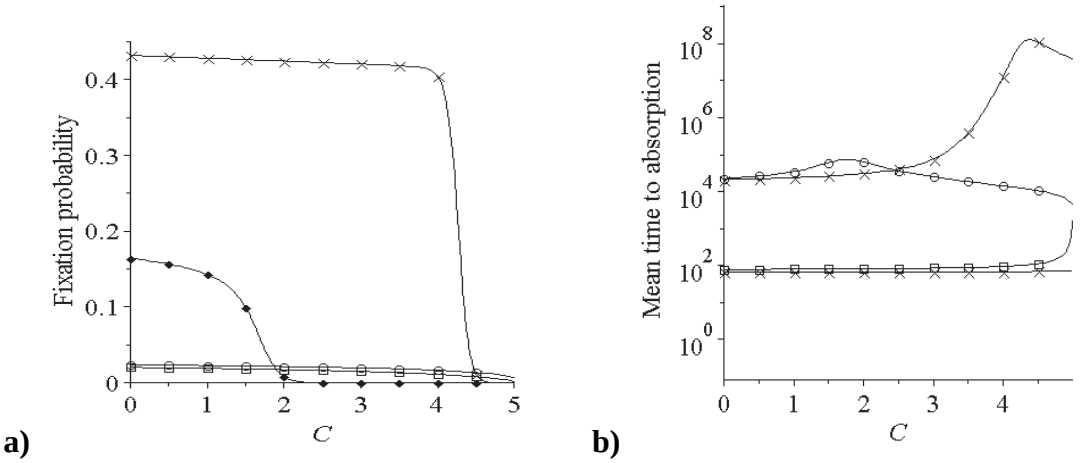

Figure 3: a) The fixation probability of Hawks, and b) the mean time to absorption, when a single mutant Hawk invades into a resident population of Doves on a star graph with 60 vertices under the IP (crosses), the BD-D (diamonds), the VM (circles) and the DB-B (boxes), in a Hawk-Dove game as the fight cost varies.

- The *birth-death process with selection on the death* (BD-D)
- The *biased voter model* (VM) (or the death-birth process with selection on the death)
- The death-birth *process with selection on the birth* (DB-B).

Through an analytic approach it is demonstrated that the change of the update rules of the evolutionary process may be crucial in a non-homogeneous population (see also Hadjichrysanthou *et al*. (2011)). Two quantitatively and qualitatively different behaviours, one for birth-death processes and another for death-birth processes, are observed. In most of the cases, birth-death processes yield higher (lower) fixation probabilities of advantageous (disadvantageous) mutants than the death-birth processes. However, these processes usually require exceedingly long times to fixation, which are much larger than the fixation times in the death-birth processes (see for example Figure 3).

Evolutionary dynamics on complex graphs

An analytic approach of the evolutionary dynamics is possible when individuals of the population occupy the vertices of simple graphs, such as the complete, the circle and the star

graph. However, real populations have more complex structures, and an analytic investigation of the dynamics on such structures is usually infeasible. In such cases the use of various assumptions and approximation techniques is essential. Stochastic simulation algorithms have been used extensively for the investigation of the effect of the structure on populations' evolution, as well as of numerous other complex systems. However, stochastic simulations can lack generality and are usually computationally very expensive. In this work we propose an effective model, the *Neighbourhood Configuration model*, which can describe very well the stochastic evolutionary dynamics and offer a flexible way to do a systematic analysis of evolutionary game dynamics on structured populations.

We consider a two-strategy game played on complex graphs when individuals update their strategies following the update rules of the biased voter model (VM). VM type dynamics is one of the classical interacting particle systems, which has been applied to many evolutionary processes from opinion and culture dynamics to processes in population genetics and kinetics of catalytic reactions. The idea of the suggested approximation method is to divide the population into classes. Each individual on the graph is classified according to its strategy and the number of its connected individuals playing each of the strategies. An individual may move from one class to another either because of the change of its strategy or due to a change of a neighbour's strategy. We find approximations of the probabilities of moving from one class to another. Finding the transition probabilities, we then construct a differential equation based compartmental model describing the dynamics of the different classes of the population.

Numerical examples indicate that the predictions of the Neighbourhood Configuration model agree very well with the outcome of stochastic simulations on a range of graphs (see Figure 4 for an example on a random graph). Investigations on a number of graphs when a Hawk-Dove game is played among individuals suggest that heterogeneous graphs facilitate the spread of Hawks. In particular, the existence of highly connected vertices promotes the Hawk strategy and scale-free networks appear to be a very hospitable environment for Hawks. However, the most important feature of a graph that affects the evolutionary process seems to be average connectivity, at least for graphs that can be described by their degree distribution. The results of our examples indicate that a decrease in the average number of neighbours of each individual tends to deviate the equilibrium frequency of Hawks from the equilibrium frequency in a homogeneous well-mixed population, in the direction of the nearest absorption state (see also Hadjichrysanthou *et al*. (2012)).

Models of kleptoparasitism on graphs

Game theory has facilitated the mathematical modelling of systems emanated from natural and social sciences. Based on the modelling framework provided by game theory, we model and study a very common foraging behaviour of animals, kleptoparasitism. *Kleptoparasitism* is a form of feeding, where animals attempt to steal food already discovered by others for their survival. Different forms of kleptoparasitic behaviour are observed in many species in the animal kingdom.

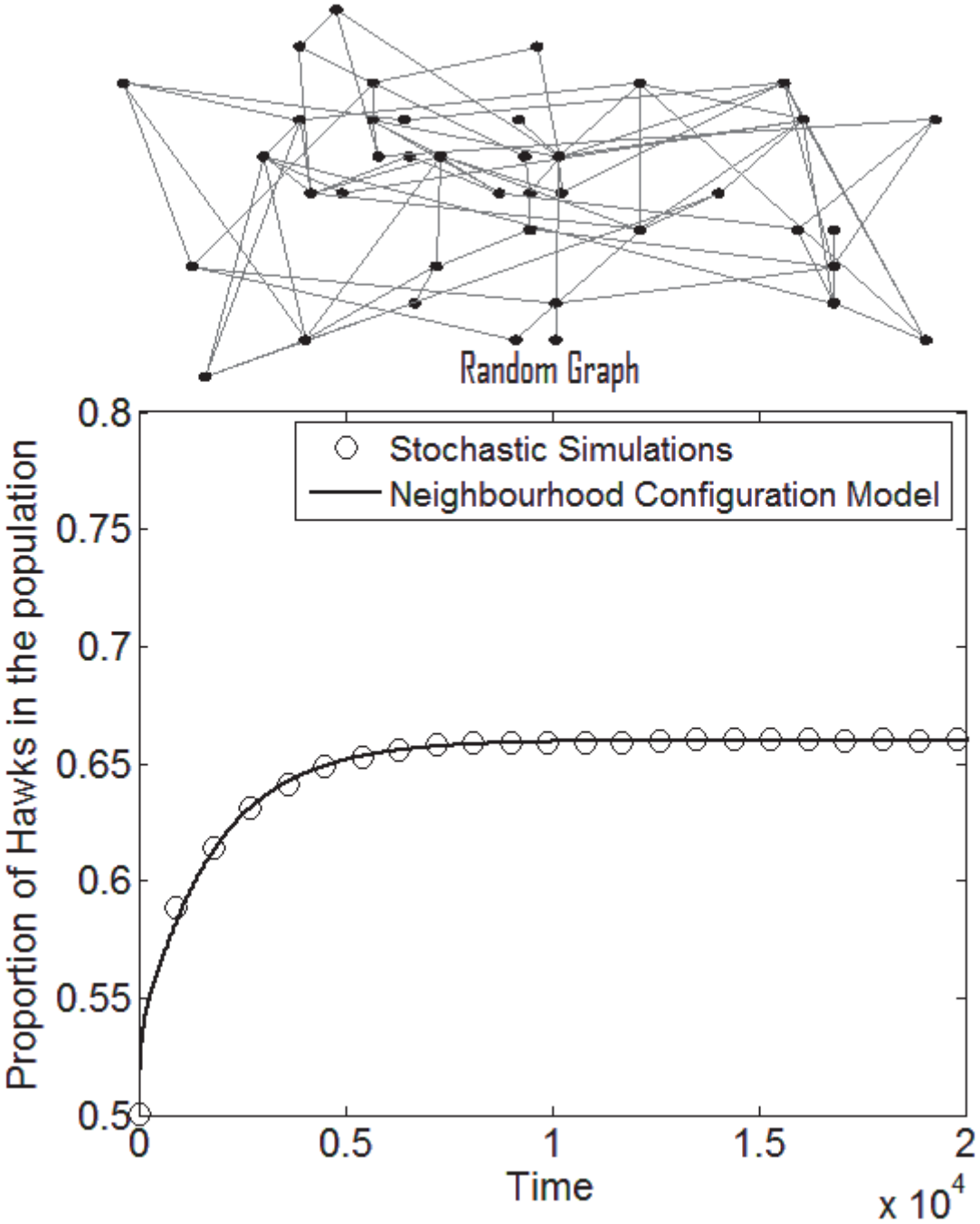

Figure 4: Change over time in the proportion of individuals playing the Hawk strategy in a Hawk-Dove game played on a random graph of 100 vertices with average degree equal to 4 and maximum degree of a vertex equal to 8. The solid lines represent the solution of the Neighborhood Configuration model and the circles represent the average of 100000 stochastic simulations.

We extend a fundamental game-theoretical model of kleptoparasitism, the model of Broom and Ruxton (1998), to structured populations represented by different graphs and explore the role of the population structure in the appearance of kleptoparasitic behaviour among animals. This relaxes some of the strong implicit assumptions of some classic models, such as the

homogeneously mixing of animals and the infiniteness of the population size. Applying the pair approximation method, we first consider the evolution of populations that can be represented by a random regular graph. Then, using numerical simulations, we examine evolution when animals form more complex structures. We show that, in general, the population structure does not greatly affect the evolution of the population in the models considered, mainly due to the fact that animals can discover food independently of their position on the graph. A considerable influence of the population structure on the evolution of kleptoparasitic populations is observed on degree-heterogeneous structures, where the chance of an animal being engaged in a fight, either as a searcher or a handler, is not the same for every animal in the population, due to the different degree of connectivity of animals. Especially in scale-free networks, where the variance in the degree distribution is high, the effect of the structure is more pronounced.

Food sharing in kleptoparasitic populations

Animals adopt varied foraging tactics to survive. One of these is food sharing, a commonly observed behaviour occurring in many animal species. Many mathematical models have been developed in order to explore the reasons why animals share their food. However, many of these models were not sufficient to explain why in various situations animals present this behaviour. Our work gives some important answers and raises some key questions for further study on understanding this interesting animal behaviour.

A game-theoretical model is proposed for the investigation of the ecological conditions that encourage foraging animals to share their food in kleptoparasitic populations. According to the model, a foraging animal encountering an animal handling a food item has the possibility to either attack attempting to steal or share the food (with probability), or just ignore it and continue foraging. On the other hand, an attacked animal which owns a food item has the possibility to share its food (with probability), to defend it (with probability) or to retreat leaving all the food to the attacking animal. We are interested in finding Evolutionarily Stable Strategies (ESS), under different conditions. We show that there are only pure ESSs. Strategies (0,0,0) and (0,1,0) can never resist all of the possible invading strategies and there are thus four possible ESSs; Retaliator (0,0,1), Marauder (1,0,0), Attacking Sharer (1,1,0) and Hawk (1,0,1).

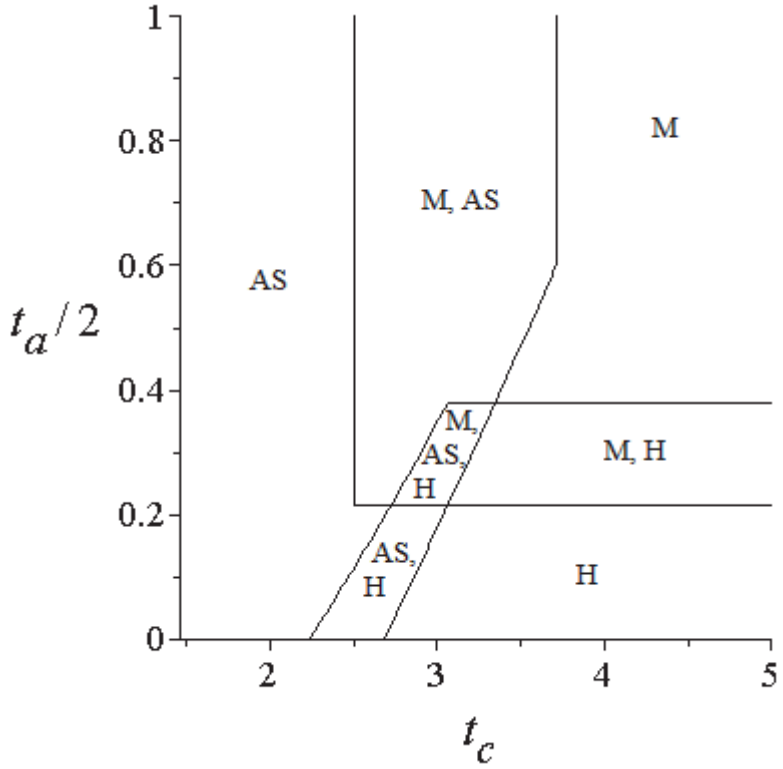

Figure 5: A graph showing the region where each of the 4 possible ESSs (Retaliator [R], Marauder [M], Attacking Sharer [AS], and Hawk [H]) is an ESS as the duration of a content, , and the time cost of sharing, , vary under specific ecological conditions. In each region, a single letter 'X' indicates that the strategy X is the unique ESS, 'X, Y' indicates that the strategies X and Y are simultaneous ESSs, and 'X, Y, Z' that the 3 strategies X, Y and Z are simultaneous ESSs.

The model predicts that there is a wide range of ecological conditions in which attempting to share the food at every opportunity and sharing the food when attacked is the optimal strategy that should be used by animals (see for example Figure 5). Different ecological factors may influence the strategic choice of food sharing. Food availability is one of the crucial factors. In conditions of limited food availability the use of the sharing strategy is enhanced, whereas at high food densities food sharing becomes a less profitable strategy. A high time cost of food defence, a small probability of a successful food defence, a high rate at which searchers encounter handlers, a high population density and a low time cost of food sharing are also conditions which favour animals sharing their food (see also Hadjichrysanthou and Broom (2012)).

Acknowledgements

I would like to express my deepest gratitude to the supervisor of this work Professor Mark Broom. My sincerest thanks and appreciation goes to the awarding committee for awarding my thesis the Reinhart Heinrich Doctoral Thesis Award 2012. I would also like to extend my thanks to ESMTB for giving me the opportunity to present my thesis.

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Cancer as evolutionary process

The theory of evolution, a major scientific advance of the last two centuries, has naturally been applied to the evolution of species, by its founder Charles Darwin and also by his contemporary Alfred Wallace. This has seldom been the case of evolution in cell populations, which is however a viewpoint that should shed light on the question of cancer. In recent years, scientists from different fields of knowledge (evolutionary biology, oncology, applied mathematics) have begun to unite their efforts, aiming at understanding cancer as an evolutionary disease, in particular under the impulsion of Robert Gatenby and Carlo Maley. These efforts, that are partly reported in a review paper [1], have led to two international conferences in 2011 and 2013 (http://cancer.ucsf.edu/evolution/conference-2011, resp.-2013). This emergent field of research offers challenging questions to mathematicians.

Cancer cells present modifications of their DNA, inducing phenotypic heterogeneity in the cell populations they constitute, that can be of genetic or epigenetic origin. Random mutations and other modifications of the genome result in a high variety of cell genotypes and phenotypes. Cell competition for resources in changing environments leads to selection of clones best adapted to the environmental configuration at the moment. From this point of view, the development of cancer can be considered as a sequence of events in which cells acquire new properties, some of which can be advantageous for their survival and proliferation. The concept of cancer considered as an evolutionary system was suggested by Nowell in 1976 [2] (see also [3, 4] and references therein). Presently there is growing experimental and clinical evidence in favour of this concept of *Darwinian evolution of cancer*. It can be used to develop new strategies of cancer treatment. However this point of view can be argued and other concepts about the emergence of cancer may be debated. We discuss some of them below.

Darwinian evolution of cancer cells

The growth of tumours, which occurs due to proliferation of somatic cells, is accompanied by numerous mutations. A tumour of 1 cm in diameter contains about a billion of cells and up to a thousand billions of mutations in the process of its development [5, 6]. These mutations result either from some exogenous factors due to chemicals, ionising radiations and so on, or from endogenous factors related to genomic instability. An essential part of them is neutral from the point of view of a selective advantage while the others can reinforce adaptation of the tumour cells to their microenvironment.

An important characteristic of these mutations is their randomness. The role of random mutations is to produce a high variety of cell phenotypes which will be submitted to the process of natural selection in a changing environment. Darwinian selection will ‘choose for survival’ the most adapted cell subpopulations, i.e., those with the highest survival and proliferation rates. This does not mean that some Lamarckian phenomenon is involved at the level of single cells, but rather that at the level of cell populations, a process of selection of the phenotypically fittest - already existing, not created *ex nihilo* – subpopulations of cells with randomly expressed phenotype [7] has occurred. Emergence and development of cancer is thus a multi-stage process determined by Darwinian evolution of cell populations.

The genotype of tumour cells is expressed by means of metabolic networks, involving transcription (from DNA to RNA) and translation (from RNA to proteins) and other intracellular mechanisms such as RNA splicing or nuclear transport. The huge amount of mutations involved in cancer as a matter of fact act on a limited number of transduction pathways. The number of main signal transduction pathways influenced by cancer has been evaluated to be around twenty [8]. Hence many different mutations can be associated with the same phenotype advantageous for cell survival and multiplication.

Cancer cells can promote genetic instability producing proteins that help cells escape normal genome maintenance. However, if genetic instability is too large, it can decrease survival of cancer cells, whereas if it is too small, the evolution and adaptation of cancer cells may not be sufficient. Hence some intermediate values of genetic instability should be optimal for cancer cells. Driving cancer cells out of such optimum, in either sense, might thus inspire new therapeutic tracks [9].

Cancer cell populations thus possess high plasticity determined by random mutations or epimutations of their constituent cells, and also by the process of natural selection which chooses cell clones that are best adapted for survival and proliferation. Such plasticity makes this disease so difficult to understand and to cure. On the other hand, this force of cancer can be used against it. For instance, development of drugs which increase genetic instability to the level, where normal cells survive but cancer cells die because they have already a higher level of instability, can open new ways in the treatment of cancer [3]. These strategies can also aim at reduction of repair of radiation-induced damage in cancer cells in the process on radiotherapy [9, 10].

The formation of metastases is a hallmark of cancer that implies transition from the epithelial to mesenchymal phenotype in the cancer cells which are at their origin, and this is another important instance of evolution in cancer cells. As regards resistance to treatment in cancer cell populations, one of the main pitfalls encountered in clinical oncology, they can result from two different mechanisms, i.e., either from evolution or from mere adaptation to the environment set by newly imposed drug pressure. As in the previous case (evolution towards a metastatic phenotype), it can occur through different mechanisms, either epigenetic or genetic, likely both and in this order, resulting in the selection of subclones in the population of cells under treatment, because treatment has given a selective advantage (in terms of proliferation) to these resistant clones already existing in the tumour. It seems highly probable indeed that the selection mechanism due to drug pressure results firstly in epigenetic mutations (a.k.a. ‘epimutations’, that are in principle reversible) and that it is only when the pressure is maintained that can mutations be genetically constituted [11]. Early use of *combinations* of anticancer drugs can thus be crucial, at a stage when mutations are still reversible and the probability of appearance of *multi*drug-resistant mutated cells is small.

Assessing and modelling evolution versus adaptation in cancer cell populations

We have stressed above that Darwinian evolution, due to selection pressure that may be manifest (e.g., drugs affecting proliferation) or hidden (uncontrolled environmental changes), is a process that applies to cell *populations*, resulting in changes of their observed phenotypes, rather than to individual cells. The right level of description is indeed the cell population if one wants to follow such phenotype changes, obviously because a new phenotype appearing in a single cell without progeny will not induce any observable evolution.

Even with an important progeny, it is not always clear whether a phenotypically homogeneous cell clone results from actual - irreversible, permanently acquired - evolution in the Darwinian sense, or from a reversible adaptive process. This is in particular a question that is raised about emergence of drug-resistant cell clones in cancer cell populations [11]. As mentioned above, drug resistance can result from genetic mutations or from epigenetic modifications silencing genes in a reversible or irreversible manner at the level of the genome of a single cell.

At the level of the cell population, it is important to know whether such modifications endow the resulting clones, constituted of such phenotypically modified cells, with irreversible mutations that require their eradication, or at least their containment, or whether on the contrary these modifications (e.g., methylation of tumour suppressor genes) can be eliminated without unduly - and at a high biological cost - harming cells that are still not intrinsically malignant. Such hoped-for 'harmless therapies' (or less harmful than the only cytotoxic ones) might rely on cell environment-changing therapies (e.g., metabolism modifiers [11]), or on the action of epigenetic drugs, presently the object of active research in various pharmaceutical companies [13, chap. 11].

Now, how about mathematical modelling to represent evolution of cancer cell populations, in particular under drug pressure? One can consider at least two different theoretical frames within the same central one, *adaptive population dynamics*: the first one, adapted to describing speciation through branching [14, 16], to represent irreversible mutations, and the second one [16] to represent reversible epimutations occurring in drug resistance adaptive phenomena in cancer cell populations. From a very close viewpoint, *evolutionary game theory* has also very naturally been called to tackle this question [17]. Optimisation of combined drug delivery with the aim of containing (rather than eradicating) tumour growth is then the following question, sketched in [16] and more consistently developed in [17].

Cancer reveals mechanisms developed in evolution of multicellular organisms

The concept of Darwinian evolution of cancer cells is based on their random mutations and subsequent selection of the most adapted cell lines. However tumour growth is not only based on excessive proliferation of individual cells. It has a complex organisation which implies particular properties of cancer cells, their interactions between them and with their environment. So that the question of whether all these properties can be achieved by random mutations during a relatively short period of time is far from being obvious. Therefore another understanding of cancer, as a process revealing pre-existing mechanisms "written" in the genome and initiated by mutations, can also be debated [17].

A fully developed cancer possesses a high variety of adaptive mechanisms that concern their survival, proliferation, motility and resistance to various control mechanisms. "Hallmarks of cancer" include silencing tumour suppressor genes, switching off apoptosis and anoikis, switching off senescence by manufacturing enzymes to repair eroding telomeres, evading control by the immune system achieved by removing surface receptors, dramatically changing the viscoelastic properties of cells to facilitate motility, invasion and colonisation secreting corrosive enzymes to dissolve through organ membranes, thriving in hypoxic conditions by switching off the normal oxydation-phosphorylation metabolism, manufacturing their own "mitogenic signals" [18] and other properties.

Is it possible that random mutations make all these numerous properties emerge in a certain order, and natural selection preserves them, even if not all of them give an immediate selective advantage? With the benefit of the doubt, another concept of cancer development is discussed in literature [18]. The main hypothesis here is that cancer is deeply evolutionarily rooted in the process of transition from unicellular to multicellular organisms. It is an "atavistic state" kept in the silent genes. If for some reasons normal functioning of the multicellular organism is damaged, it can return to the "safe mode" option. So that, according to this conception, random mutations do not create cancer, they just switch it on.

If this hypothesis is true, then emergence of cancer cell properties can follow the path laid by evolution when it made multicellular organisms [18]. This would mean that development of cancer obeys particular rules established by evolution, which could thus be elicited and taken into account in new treatment strategies.

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Past and Future Activities

EMS-ESMTB summer schools: The Helsinki Summer School on Mathematical Ecology and Evolution 2012 on the Theory of Speciation

The EMS-ESMTB summer school series continued with a thematic school on the theory of speciation, held in Turku during the last week of August 2012. Five courses formed the core of the program, featuring some of the best-known experts of the field. Sergey Gavrilets (University of Tennessee) lectured on the population genetics of speciation, Nick Barton (IST Austria) on multilocus models of speciation, Sander van Doorn (University of Bern) on the role of sexual selection in speciation, whereas Eva Kisdi (one of the organizers) addressed some topics in mathematical ecology relevant to the origin of species. To keep up with the fast developments in empirical speciation research, we were very glad to have Dan Bolnick (University of Texas) lecture about the interface between theory and empirical research in speciation. In addition, Mats Gyllenberg, the director of the school, gave a lecture on limiting similarity, and we invited Anneli Hoikkala to talk about speciation research in her group based in Jyväskylä, Finland.

The school included discussion groups based on literature the participants studied ahead of the school. The discussion groups were a great success of intense activity, leading up to group presentations that reported back to the entire school on the last day.

The school had a wonderfully productive and relaxed atmosphere, thanks to the lecturers, who put much effort into the program and were very easy to approach by the students, and thanks to the 32 participants selected from 94 applicants, who brought their enthusiasm, commitment, and hard work. As for the earlier schools of our series, the Linnasmäki Congress Centre in Turku provided every service to our full satisfaction. It was a great week that ended with our group finally relaxing in the nearby seaside town of Naantali, looking for sticklebacks at the shore (an important study species of Bolnick) and enjoying some bigger fish as part of traditional Finnish cuisine. We are grateful to the Research Networking Programme FroSpects of the European Science Foundation and to the Finnish Doctoral Programme in Computational Sciences for financial support, and we are looking forward to the next Helsinki Summer School on Mathematical Ecology and Evolution in 2014!

Eva Kisdi (University of Helsinki), organizer
visit the homepage of the school at http://wiki.helsinki.fi/display/huippu/mathbio2012

UT Austin|Portugal Workshop on Modeling and Simulation of Physiological Systems December 6-8, 2012, IST, Lisbon, Portugal

Scientific research has long scrutinized with much interest phenomena occurring in nature. What has been observed and learnt is a constant and rich source of wonder throughout a number of scientific disciplines. A critical field of research intimately linked to natural phenomena is that of understanding human physiology, since comprehending the underlying processes and systems are paramount in providing ever improving healthcare and medical

assistance. Research in human physiology poses significant challenges, not only due to the intricate and coupled complexity of each physiological system, but also due to the fact that each individual is unique with considerable variability within a population.

Within the UT Austin|Portugal collaboration program (CoLab) in the area of Advanced Computing, a Workshop on Modelling and Simulation of Physiological Systems (MSPS2012) was run during the period of December 6-8, 2012, at the Instituto Superior Técnico, Lisbon, Portugal http://cemat.ist.utl.pt/MSPS2012/. The workshop was scheduled to coincide with the closing of project UTAustin/CA/0047/2008 - "Cardiovascular Imaging, Modelling and Simulation: SIMCARD". The SIMCARD project was focused on developing approaches to query and observe human physiological systems through numerical simulations. Modelling issues and analysis of results was carried out with close support from Portuguese medical teams at different hospitals and institutions. This interaction allowed for a greater awareness from the mathematicians and engineers to the current medical concerns, and conversely how modelling and simulation can provide to support for clinical teams. Ultimately this collaboration and exchange will allow for greater progress and breakthroughs in the understanding of human physiology and also advances in current medical treatments and technologies.

State of the art in a wide range of research topics regarding physiological systems was addressed at MSPS2012, principally in the fields of Advanced Computing and Mathematics. Numerical models and simulations for varied topics including: arterial hemodynamics, blood rheology, micro-fluidics, mathematical and computational modelling, programming architecture, clinical intervention and observables, computational fluid mechanics, thrombosis and inflammation, fluid-structure interaction, heart mechanics, electro-mechanical coupling, cerebral aneurysm development, continuous and discrete mathematical models, experimental studies, medical imaging and processing, patient specific studies, cell behaviour, prognosis and diagnosis practices, optimal control, cancer therapy, medical devices.

Participants of different countries attended the workshop, including peer academic professors, undergraduate and postgraduate students, as well as medical doctors and clinicians. A national interest to the event meant that around half the participants were from Portuguese institutions, giving them the possibility of meeting and discussing with eminent researchers and peers with relative ease. The total number of participants was around sixty, with over thirty speakers. The workshop promoted collaboration among engineers, mathematicians, computer scientists and medical researchers, providing a moment of discussing their latest results, share their expertise and expose difficulties in order to overcome these through exchanging ideas.

The large set of topics covered was discussed between peers and students, with the input and feedback from medical doctors, giving a vital contribution and resource to accurate modeling and simulation issues. The clinical doctors participating were in turn enthusiastic of the potential resources that modeling and simulation can provide to the medical community. The set of topics covered allowed participants to learn about the state of the art in physiological systems beyond their solid ground of expertise, and often permitted or gave novel insight and solutions to problems to be provided. The presentations were from all levels, from undergraduate students to established professors, and medical doctors, giving an open field for exchange throughout the participants. The concurrence of the workshop with the closing of the SIMCARD project provided a greater wealth of discussion and setting up of new collaborations.

The CoLab framework will run for a further five years. Moreover, a new project, entitled "Mathematical an Computational Modeling of Human Physiology - PHSIOMATH" (EXCL/MAT-NAN/0114/2012), funded by the Portuguese Foundation for Science and Technology (FCT) just started. Future scientific events, including topics of HPC applied to physiological systems, are expected in the near future.

The organizers are grateful and would like to thank the UT Austin|Portugal Program, the Portuguese Foundation for Science and Technology and CEMAT/IST for support and funding. A final thanks goes to all the attendees and speakers to the workshop, who made the meeting lively and exciting.

Adélia Sequeira
Alberto Massimo Gambaruto

Interdisciplinary Workshop "Stem Cells and Regeneration-Mathematical Formalization", June 24-29, Paris, France

The workshop was organized in Marilyn & James Simons Conference Centre of IHES on June 24 to 29 2013 by Vincenzo Capasso (University of Milano), Mikhail Gromov (IHÉS), Annick Harel-Bellan (CNRS) and Nadya Morozova (CNRS).This Workshop was the next event in the series of Pattern Formation in Morphogenesis Workshops, organized in IHES and aiming to generate an interdisciplinary space in which embryologists, geneticists and molecular biologists interacted with mathematicians for the discussion of one of the most intriguing and unsolved problem-the regulation of the formation of the geometrical shape of the living organism and its parts (tissues and organs).

For this end, the Workshop structure has special framework, designed for the improvement of intercommunication between leading scientists from different disciplines. For example, the Invited Participants of the Workshop were invited not only as speakers but also as invited discussants, with the main aim to contribute to the discussions.

The «conference part» of the Workshop had 20 Plenary talks during which the leading biologists in the field of stem cells biology, regeneration and pattern formation showed the biological problems together with the necessary biological background and raised unsolved questions. Some of Plenary talks were delivered by mathematicians, working on mathematical modeling of Pattern Formation.The « discussion part » allowed several modes of possible communications:

-10 scheduled "Discussion sessions" devoted to the hot problems in stem cells and regenerative biology, with the possibility to be continued during all other days of the workshop in the case of interest;
-a work within small "working groups" generated according to specific questions raised by biologists or mathematicians;
-a poster session;

Some of the key topics explored included: mechanisms of regeneration and determination of pattern formation; mathematical models of cancer and normal stem cells; the comparison of totipotency and regeneration ability in plants versus animals, the problem of

mathematical formalization of the phenomena of cell differentiation; models of gene regulatory networks; the role of stem cells in aging; chaos and stochasticity in cell behavior and fate decision; models of stem cell defects in neurodevelopment; the role of epigenetic factors in stem cell fate decision.

The list of invited speakers biologists included:
D.S. Adams, J. Baguñà, P. Beachy, I. Efroni, E. Davidson, A. Fleming, S. Fre, P.B. Gupta, E. Heard, T. Holstein, T.D. Palmer, M. Ros.
The list of invited speakers mathematicians included: V. Capasso, A. Friedman,T. Hillen, H. Meinhardt, P. Prusinkiewicz, V. Volpert

The less number of speakers mathematicians was compensated by grater number of mathematicians-discussunts, participating in working groups and discussion sessions with the intend to suggest the possible ways of mathematical formalization and next solution of the problems of pattern formation presented by biologists.

One of the main results of this Workshop, so as of the previous one of the same subject and style, is the next continuation of the discussions initiated by/during the workshop in a frame of small interdisciplinary international working groups, each devoted to a specific problem concerning the biology of stem cells and pattern formation.

Nadya Morozova

Trimester on "Mathematical Biology", Lyon (France) from March - June, 2013

Organizing committee:

M. Adimy (INRIA), J. Bérard (Univ. Lyon 1), S. Bernard (Univ. Lyon 1) H. Berry (INRIA), V. Calvez (ENS de Lyon), F. Crauste (Univ. Lyon 1), O. Gandrillon (Univ. Lyon 1), E. Grenier (ENS de Lyon), Th. Lepoutre (INRIA), L. Pujo-Menjouet (Univ. Lyon 1), G. Raoul (CNRS, CEFE), B. Ribba (INRIA), V. Volpert (Univ. Lyon 1).

http://mathbio2013.sciencesconf.org/

Main events:

1- Conference « Biological invasions and evolutionary biology, stochastic and deterministic model », March 11-15, 2013. Organizing committee : Jean Bérard (Univ. Lyon 1), Vincent Calvez (ENS de Lyon) et Gaël Raoul (CEFE, Montpellier)

2- Conference « Cell biology », March 25-29, 2013. Organizing committee : Hugues Berry (INRIA) et Vincent Calvez (ENS de Lyon)

3- Conference « Systems Biology Approach to Infectious Processes », May 13-15, 2013 Organizing committee : Hubert Charles (BioSyL)- François Loïc Cosset (Ecofect)- Fabien Crauste (Milyon)- Eric Fleury (BioSyL)- Olivier Gandrillon (BioSyL)- Daniel Kahn (BioSyL)- Jacqueline Marvel (BioSyL)- Dominique Pontier (Ecofect) and Sylvie Ricard-Blum (BioSyL)

4- Spring school « Multiscale modeling in the life sciences », May 27-31, 2013. Organizing committee : Vincent Calvez (ENS de Lyon), Thomas Lepoutre (INRIA), Vitaly Volpert (Univ. Lyon 1)

5- Conference in honour of Michael Mackey's 70th birthday, June 3-7, 2013. Organizing committee : Samuel Bernard (Univ. Lyon 1), Fabien Crauste (Univ. Lyon 1), Moises Santillan (IPN, Mexico), Laurent Pujo-Menjouet (Univ. Lyon 1)

MPDE'13 – Models in Population Dynamics and Ecology 2013, Institute of Environmental Systems Research School of Mathematics / Computer Science, Osnabruck University, Germany

Since 2007, the series of MPDE conferences attracted more and more attention of the international community. In 2013, after UK and Brazil, it was the first of these meetings in Germany and one of the few topical conferences in Europe that year.

The MPDE conferences aim at the enlightenment of ecosystem dynamics on all scales via various mathematical, computational and interdisciplinary methods. The 2013 meeting focused on the mathematical aspect of population dynamics and ecosystem functioning and explored the corresponding processes and mechanisms from the micro-scale of individual growth and evolutionary dynamics to the macro-scale of population interactions and dispersal, with applications to metapopulations, regional dynamics and geographical invasions. The meeting also explored similarities between modelling techniques traditionally applied in ecology and those used in physics, systems biology and other life sciences with the purpose to enhance interdisciplinary approaches and to stimulate further advances in mathematical ecology and population dynamics.

Specific issues that had been presented and discussed include bioinvasions and epidemic spread, biological and ecological networks,biological flows, dynamic energy budget modelling, pattern formation, epidemiology and ecoepidemiology, evolutionary dynamics, individual and collective dynamics, noise in bio-and ecodynamics as well as scaling and aggregation.

The meeting was generously funded by the German Science Foundation (DFG) and the Lower Saxony Ministry for Science and Culture (MWK). ESMTB and SMB had supported the travel of a couple of young members.

Almost 200 scientists, graduate and PhD students from all continents (except Antarctica) attended the conference. Nanako Shigesada (Kyoto, JPN) and Masayasu Mimura (Tokyo, JPN) were honorary speakers. Both are pioneers of the mathematical theory of ecological pattern formation and biological invasions. Their acceptance was a great pleasure and honour. SMB and JSMB have announced that the 2013 Akira Okubo Prize will be awarded to Nanako Shigesada.

Further invited plenary speakers were Ulrike Feudel (Oldenburg, GER), Volker Grimm (Potsdam/ Leipzig, GER), Mats Gyllenberg (Helsinki, FIN), Alan Hastings (Davis, USA), Emilio Hern´andezGarc´ıa (Palma d. M., ESP), Jean-Christophe Poggiale (Marseille, FRA), Bas Kooijman (Amsterdam, NED), Michel Langlais (Bordeaux, FRA), Ran Nathan (Jerusalem, ISR), Roger Nisbet (Santa Barbara, USA) and Sergei V. Petrovskii (Leicester, GBR). The programme, abstracts of talks, posters and other informations can be found at http://www.mathebios.net/Conferences/mpde13.

Selected contributions will be published after peer review in a special issues of Ecological Complexity and Movement Ecology.

Also the offered social programme was well accepted. We had wonderful summer weather and could enjoy long evenings outside. The conference dinner was in a typical German brewpub in the historical center of Osnabr¨uck. Furthermore, night-watchman tours through old Osnabruck and a visit of the Jewish Art Museum Felix Nussbaum Haus were arranged.

The 2014 conference will be organized by Ezio Venturino at the University of Torino, Italy.

The Living, discrete and continuous. modes of representation in theoretical biology

Nicolas Glade & Angélique Stéphanou (Editors)

Editions Matériologiques

http://www.materiologiques.com/Le-vivant-discret-et-continu-Modes

Authors: Hugues Berry, S. Randall Thomas, Jacques Demongeot, Samuel Bernard, Vitaly Volpert, Nikolai Bessonov, Nathalie Eymard, Alen Tosenberger, Arnaud Chauvière, Haralampos Hatzikirou, Marco Tektonidis, Andreas Deutsch, Emmanuel Promayon, Julien Berro, Stéphanie Portet, Patrick Amar, Pierre Baconnier, Eric Fanchon, Sylvain Lespinats, Pascal Ballet, Anne Jeannin-Girardon, Alain Pothet, Gradimir Misevic, Alexandra Fronville, Vincent Rodin, Angélique Stéphanou, Nicolas Glade

« Le vivant discret et continu » can be translated by ***« The living, discrete and continuous »*** is a book that assembles fourteen courses given on the occasion of the spring school 2012 of the French-Speaking Society for Theoretical Biology ». The school aimed to discuss and inform on numerical experimentation and hybrid systems as efficient alternatives to more classical mathematical approaches for the understanding of living systems.

The theme of the school was motivated by the observation of the increasing diversity of *in silico* or computational approaches in biology. The intrinsic multi-scale nature of the biological systems, both in space and time, makes it exceedingly difficult to model them uniformly. There is no denying that theoretical biology cannot be restricted any more to a mathematical approach based on continuous equations only. The models now inevitably result from the fusion of macro and microscopic representations, some based on a continuous (global) formalism, classically expressed with partial differential equations, the others, constrained by the necessity of describing rare or isolated events, favour discrete or agent-based approaches, which bring the required level of “finesse”.

Hybrid approaches, which associate the power of mathematics to the exploratory capacity of automata, allow us to apprehend the all wealth of behaviours that characterizes the natural systems. This requires to make compromises such as to accept to lose the control that differential equations were providing in particular. However, this defect is largely overcome by the descriptive and explanatory gains brought by these new methods.

This book is in french, but addresses a wide scientific audience of students or researchers in biology, medicine, physics, mathematics or computing as well as all individuals wondering about the methodologies to employ for solving the complex issues raised by the living. One important feature of this book is to show the impact, the diversity and the fecundity of the approaches, methods and ideas gathered under the name of “theoretical biology”.

http://www.materiologiques.com/Le-vivant-discret-et-continu-Modes

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ECMTB November 2013, No. 16 : CONTENTS