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Communications



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Letter from the President

Dear Colleagues,

This issue of the Communications appears at a busy moment in the life of our Society. The year 2018 has been declared by ESMTB, EMS and ICIAM as the Year of Mathematical Biology: in keeping with this engagement to expand the visibility of our discipline, a number of initiatives are taking place this year all over Europe (see more on page 14). Prominent among these events is our main meeting, ECMTB2018 in Lisbon, where more than 700 researchers will present results on diverse topics and where a Mentoring Program and prizes for excellent contributions will help foster an interactive growth environment.

The Board of the Society has been recently renewed: thanks are due to our predecessors who have freely given of their own time, resources and ingenuity. Still, there are a number of issues on the table and the present Board has taken it upon itself to tackle them systematically. Besides doing what we do (and hopefully improving) as a Scientific Society, it is crucial that we showcase what we do for the outside world: academia, EU and national administrators, general public. Susanne Ditlevsen and Sílvia Cuadrado will therefore act for the next three years as the Society's Communication Officers, with a view to improve and/or restructure our webpage, printed matter and social media, as well as to implement ideas about where and how to fruitfully describe our contribution to the World. In connection with that, Torbjörn Lundh has been the main promoter of the Year of Mathematical Biology and is now helping reorganize the Reinhart-Heinrich Doctoral Thesis Award and the other Prizes with which the Society recognizes excellent work by the younger colleagues. The administrative situation of the Society has been in need of a major rehaul for many years now and Ellen Baake and Bob Planqué, in their roles as Secretary and Treasurer, have already done a lot in the past few months (and will have to do even more in the future): updated Official Registered Address,

new bank account and banking procedures, new internal member management system. All of this is not yet completed, it IS complicated, but we'll get there. As we restructure, the Society's scientific life continues: Maíra Aguiar is now handling the organization of ECMTB Lisbon 2018, reaching frantical intensity as the event approaches; Anna Marciniak-Czochra, besides managing our eNewsLetter, is already organizing the next ECMTB, which we are pleased to announce will be in Heidelberg in the summer of 2020; Luděk Berec has taken it upon himself to propel educational initiatives targeted at doctoral students and post-doctoral fellows, among which is the next ESMTB Summer School on ecological modelling, to be held in Sicily in 2019. Lots of work to do, as you see, and more is in the pipeline: we would be very happy for any suggestions, ideas or (possibly constructive) criticism you can give. In Lisbon, Thursday July 26th at 5 P.M. after the Plenary Talk, the Society's General Assembly will be held, with a wine-tasting experience to follow: we hope to see many ESMTB members there for an enjoyable, animated discussion.

During the past thirty years, BioMathematics has transitioned from being an obscure, niche playground for eccentric professors to being a substantial part of the new frontier of applications of mathematics to the 'soft' sciences. Our discipline promises, among many other things, tailored patient therapy, understanding of molecular physiology, control of endocrine processes, interpretation and quantification of interactions of cells in tissues and of individuals in populations. Little surprise then to see that a lot of the contemporary scientific world does one form or other of biomathematics.

In this ebullient, fast-marching and news-oriented climate, it is not always easy to have the time to reflect on problems and make sure that the solutions offered to decision-makers and societal stakeholders are consistent, robust, anchored on sound methodology and established experimental results. This is where our Society has something unique to say and can make a difference, this is where background,

tradition and preparation offer a clear advantage.

We build on a tradition of pioneers, often uninformed about the latest computing resources, but deeply in love with the beauty of the theory and the concepts that they saw how to apply to problems relevant for all of us, be it in disease, nutrition or natural resources. Most of us have spent many years studying, the Research Institutions and Universities we come from are the backbone of the intellectual strength for which Europeans are known in the rest of the world.

In our specific domain, we have much to offer to our extra-European colleagues, with a spirit of cordial collaboration, but also with the quiet pride that comes from the honest realization of our competence. We have much to offer to our people as well, even if it is not always easy to make the public appreciate our contribution. We should be happy to live and work in this privileged environment. Sure, there are practical problems: insufficient funding, competition, suboptimal political guidance. But which generation had no problems? And worse problems at that...

The next few years will see a renewed engagement of ESMTB in fostering collaboration among European theoretical biologists, offer educational opportunities to younger researchers, open avenues of financing and networking, increase the impact of our knowledge on societal issues. It is an exciting time to be a European biomathematician, I am happy to be one.

Andrea De Gaetano
President of ESMTB



The Reinhart-Heinrich Doctoral Thesis Award 2017

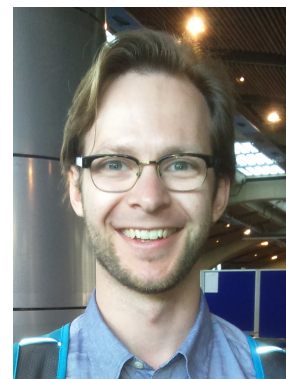
The winner of the ESMTB Reinhart-Heinrich Doctoral Thesis Award for 2017 is Jochen Kursawe, for his thesis “Quantitative Approaches to investigating epithelial morphogenesis”. We congratulate him for his excellent and exciting work! First, he presents himself, and then follows an extended abstract of the thesis.

Jochen Kursawe Personal statement

I moved into mathematical biology from previously working in biophysics. I received my masters degree in physics at the Technical University in Munich and my doctoral degree in Mathematical Biology at the University of Oxford. I am now a postdoc at the University of Manchester, where I work as a mathematical biologist in a wetlab.

My research in biophysics comprised studying fractional diffusion processes with Ralf Metzler in Munich. For my PhD I had developed plans with Ruth Baker to incorporate such fractional diffusion processes into reaction-diffusion systems. However, these plans changed once I arrived in Oxford. Ruth Baker and Alex Fletcher had just started a new collaboration with a developmental biologist, Jeremiah Zartmann at the University of Notre Dame, and they were looking for a student to work on applying vertex models to study tissue size control. I was immediately fascinated by the beauty and complexity of developmental biology, and by how it lends itself to mathematical modelling. It was surprising to me how much remains unknown about the mechanisms governing embryonic development. My doctoral thesis developed into multiple projects in which we developed mathematical tools that can help us understand embryonic development better.

One reason why I find working in mathematical biology fascinating is that it enables me to develop mathematical models that lead to explicit experimental predictions, and to develop tools that can be used to directly facilitate experimental investigation. The aim to closely integrate my work with ongoing experimental research has been the basis for developing research ideas for my PhD, and for my decision to work with Nancy Papalopulu at the University of Manchester after my PhD. Nancy’s lab focusses on dynamic gene expression during embryonic neurogenesis. In this field it is crucial to combine experimental investigation with theoretical tools in order gain quantitative understanding. I find it exciting and fulfilling to be able to develop mathematical models that can be directly compared to data collected by my colleagues conducting experiments in the lab.



Thesis summary: ‘Quantitative Approaches to investigating epithelial morphogenesis’ by Jochen Kursawe

Studying morphogenesis is fascinating and promises to provide cures for a wide range of diseases, for example through the artificial growth of organs. Recently, the study of developmental processes has thrived due to a rise in quantitative experimental data. This advance in quantitative data requires us to rethink the scientific method. We need to design quantitative hypotheses through computational or mathematical models, make quantita-

tive experimental predictions, devise methods for quantitative data analysis, and design methods for quantitative inference between models and data. Jochen’s thesis aims to enable this transition of the scientific method for the cell-based study of epithelia, one of the major tissue types in animals. The thesis is structured in four main chapters that individually address this transition at different stages of the scientific method (Figure 1). In Chapter 3 of his thesis,

Jochen analyses a common cell-based computational model of epithelia, a vertex model, and estimates to what extent quantitative model predictions may be influenced by implementation parameters, such as the simulation time step. In Chapter 4, Jochen applies this model to a key question in developmental biology by designing a theory for tissue size control in the embryonic epidermis of the fruit fly *Drosophila*. He uses the model to predict the outcomes of future experiments. In Chapter 5, Jochen further devises a method for measuring mechanical parameters of vertex models from imaging data and estimates the parameter uncertainty associated with such an inference. Finally, in Chapter 6, Jochen proposes a novel algorithm for cell tracking in live-imaging microscopy videos of epithelial tissues that illustrates how mathematical concepts may be used to overcome challenges in quantitative data analysis. In the following we give a brief overview of each of these four individual thesis projects.

Numerical analysis of vertex model behaviour

‘Cell-based’ models provide a powerful computational tool for studying the mechanisms underlying the growth and dynamics of biological tissues in health and disease. An increasing amount of quantitative data with cellular resolution has paved the way for the quantitative parameterisation and validation of such models. However, the numerical implementation of cell-based models remains challenging, and little work has been done to understand to what extent implementation choices may influence model predictions. In the thesis chapter “Numerical analysis of vertex model behaviour” Jochen considers the numerical implementation of a popular class of cell-based models called vertex models (Figure 2). In two-dimensional vertex models, a tissue is approximated as a tessellation of polygons and the vertices of these polygons move due to mechanical forces originating from the cells. Such models have been used extensively to study the mechanical regulation of tissue topology in the literature. Here, Jochen analyses how the model

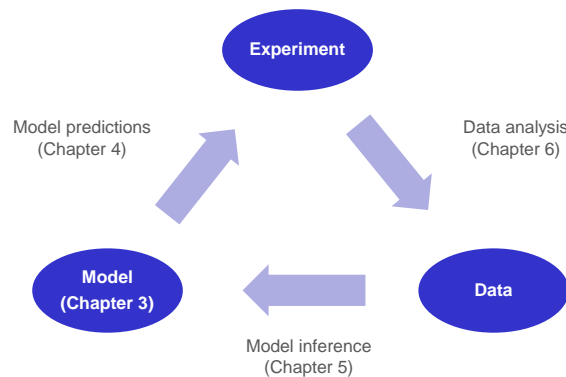


Figure 1: Jochen’s thesis contributes to the quantitative study of epithelia at different stages of the scientific method. *The scientific method comprises a cycle of hypothesis building and experimental analysis that iteratively improves our scientific understanding. When the scientific method is applied quantitatively, the hypothesis constitutes a mathematical or computational model. In Chapter 3 of his thesis, Jochen provides a numerical analysis of the well-established vertex model. In Chapter 4, Jochen applies the vertex model to study embryonic tissue size control and make experimental predictions. In Chapter 5, Jochen designs a inference method to estimate vertex model parameters. In Chapter 6, Jochen employs graph-theoretical concepts to track cells in live-imaging microscopy videos.*

predictions may be affected by numerical parameters, such as the size of the time step, and non-physical model parameters, such as length thresholds for cell rearrangement. Jochen finds that vertex positions and summary statistics are sensitive to several of these implementation parameters. For example, the predicted tissue size decreases with decreasing cell cycle durations, and cell rearrangement may be suppressed by large time steps. These findings are counter-intuitive and illustrate that model predictions need to be thoroughly analysed and implementation details carefully considered when applying cell-based computational models in a quantitative setting. This work has separately been published in the Journal of Computational Physics [1].

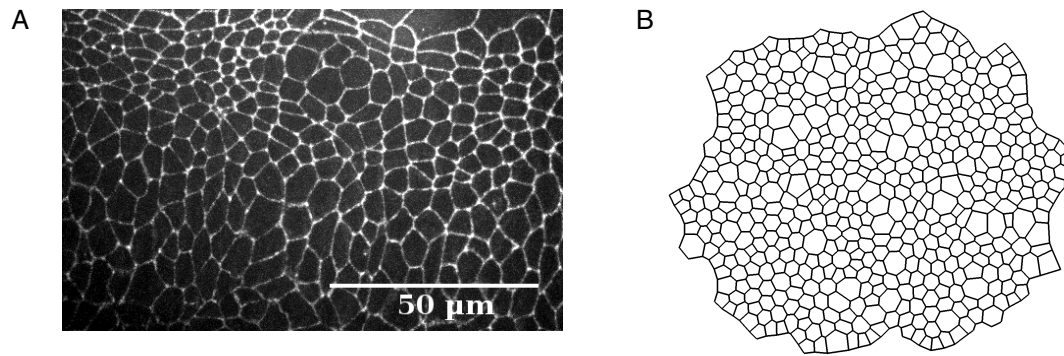


Figure 2: **Two-dimensional vertex models represent cells in an epithelial tissue as polygons.** (A) Example microscopy image of an epithelial tissue, the *Drosophila* embryonic epidermis. Cell shapes are distinctly polygonal. (B) Snapshot of a vertex model simulation of a growing tissue used in Jochen’s thesis. Cell shapes are always polygonal and vertices move due to forces originating from the cells.

Mechanical modelling of tissue size control

Jochen proceeds by applying the vertex model to study tissue size control, a key question in developmental biology. Embryogenesis is an extraordinarily robust process, exhibiting the ability to control tissue size and repair patterning defects in the face of environmental and genetic perturbations. The size and shape of a developing tissue is a function of the number and size of its constituent cells as well as their geometric packing. How these cellular properties are coordinated at the tissue level to ensure developmental robustness remains a mystery; understanding this process requires studying multiple concurrent processes that make up morphogenesis, including the spatial patterning of cell fates and apoptosis, as well as cell intercalations. In this work, Jochen develops a computational model that aims to understand aspects of the robust pattern repair mechanisms of the *Drosophila* embryonic epidermal tissues. Size control in this system has previously been shown to rely on the regulation of apoptosis rather than proliferation; however, to date little work has been done to understand the role of cellular mechanics in this process. Jochen employs a vertex model of an embryonic segment to test hypotheses about the emergence of this size control (Figure 3). Comparing the model to previously published data across wild type and genetic perturbations, Jochen shows

that passive mechanical forces suffice to explain the observed size control in the posterior (P) compartment of a segment. However, observed asymmetries in cell death frequencies across the segment are demonstrated to require patterning of cellular properties in the model. Finally, Jochen shows that distinct forms of mechanical regulation in the model may be distinguished by differences in cell shapes in the P compartment, as quantified through experimentally accessible summary statistics, as well as by the tissue recoil after laser ablation experiments. This work has separately been published in PLoS Computational Biology [2].

Parameter inference on vertex models

Jochen’s work on tissue size control illustrates how computational models can help us understand and interpret observations, and then make predictions for future experiments that can distinguish between hypothesised mechanisms. The experimental predictions of this work are not sensitive to the mechanical parameters of the vertex model. However, in other contexts it may be necessary to measure these parameters from experimental data. It remains unclear to what extent such a parameter estimate is possible, since mechanical parameters in the vertex model reflect properties of single cells or pairwise interactions. To measure the mechanical properties of a single cell it may be necessary to remove it from the surrounding

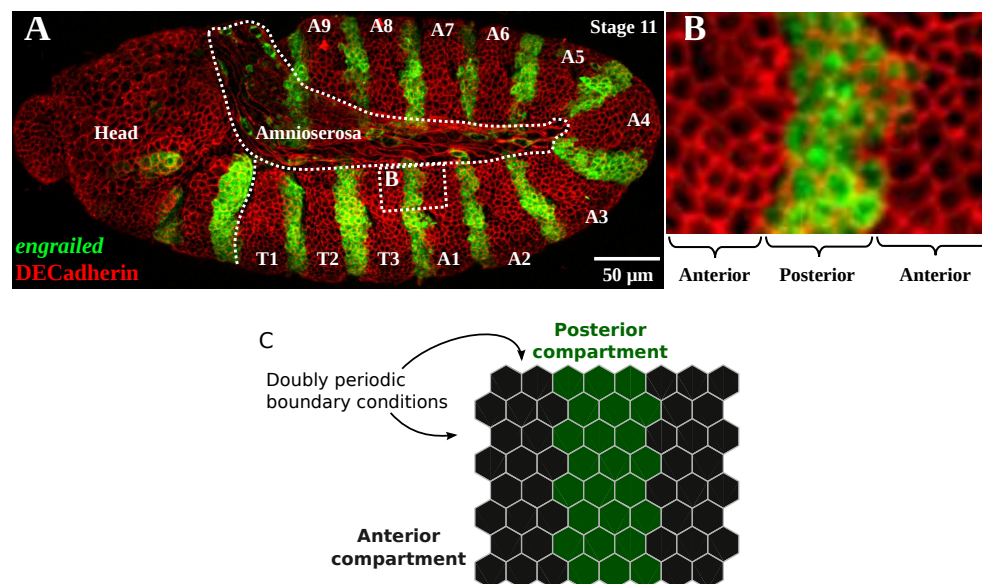


Figure 3: **The vertex model can be applied to simulate tissue sizes in the *Drosophila* embryonic epidermis.** Stage 11 *Drosophila* embryo expressing green fluorescent protein in the posterior compartment (*engrailed*), stained for DE-cadherin to show cell boundaries (A). Jochen models cell interactions in the simulation domain (B) using a vertex model (C) in order to test hypotheses on tissue size control within the posterior compartments.

tissue, which may, in turn, influence its properties. To address this issue, Jochen performs an *in silico* study to investigate whether vertex model parameters can be inferred from imaging data, and explores methods to quantify the uncertainty of such estimates. Jochen's approach requires the use of summary statistics to estimate parameters. He focusses on summary statistics of cellular packing and of laser ablation experiments, as are commonly reported from imaging studies. Jochen finds that including data from repeated experiments is necessary to generate reliable parameter estimates that can facilitate quantitative model predictions. This work has separately been published in the Journal of Theoretical Biology [3].

Cell tracking in epithelia

In the chapters described so far Jochen has focussed on the design of quantitative cell-based models for epithelia, on how to apply these models to make experimental predictions, and on how to compare cell-based models to experiments. In his final content chapter Jochen turns to the most crucial step of scientific inves-

tigation, the collection and analysis of experimental data. Mathematical tools can significantly enhance the processing of quantitative data. For epithelia, data analysis often comprises two steps, image segmentation and cell tracking (Figure 4). Tracking of cells in live-imaging microscopy videos of epithelial sheets is a powerful tool for investigating fundamental processes in embryonic development. Characterizing cell growth, proliferation, intercalation and apoptosis in epithelia helps us to understand how morphogenetic processes such as tissue invagination and extension are locally regulated and controlled. Accurate cell tracking requires correctly resolving cells entering or leaving the field of view between frames, cell neighbour exchanges, cell removals and cell divisions. However, current tracking methods for epithelial sheets are not robust to large morphogenetic deformations and require significant manual interventions. Here, Jochen presents a novel algorithm for epithelial cell tracking, exploiting the graph-theoretic concept of a maximum common subgraph to track cells between frames of a video. The algorithm does not require the

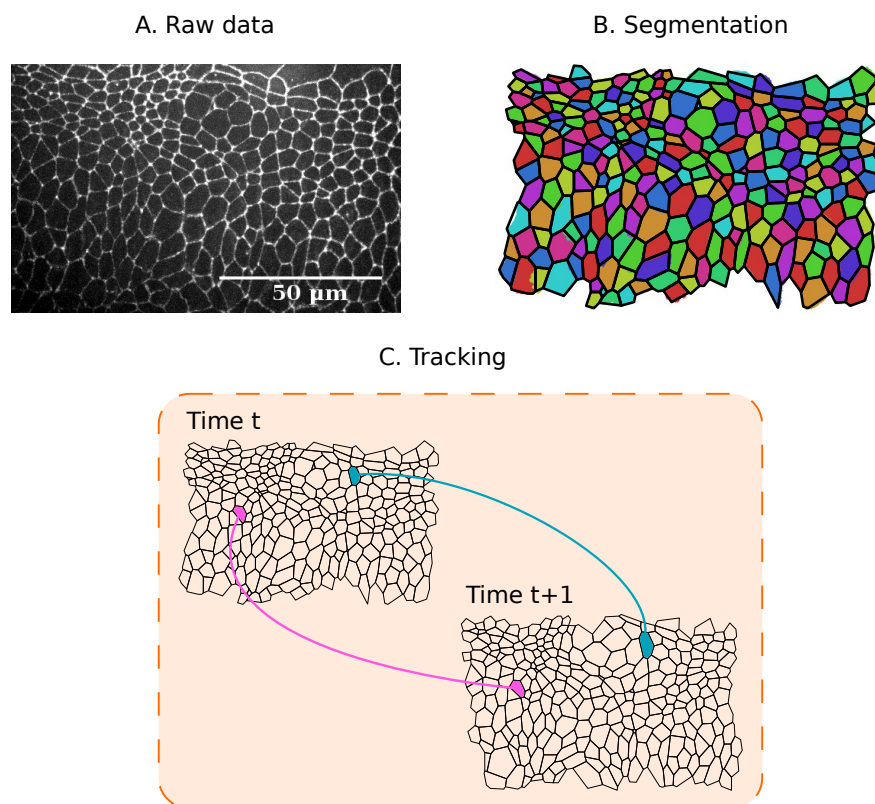


Figure 4: **Pipeline for analysing epithelial tissues.** (A) Example raw data of an epithelial tissue. Frame of a live-imaging microscopy video of the lateral epidermis of a stage-11 *Drosophila* embryo, expressing DE-Cadherin::GFP to highlight cell-outliers. (B) Segmentation of this image, showing cell shapes (coloured regions) and polygonal approximation based on three-cell junctions (black lines). (C) Cell tracking involves registering individual cells across consecutive segmented images.

adjustment of tissue-specific parameters, and scales in sub-quadratic time with tissue size. It does not rely on precise positional information, permitting large cell movements between frames and enabling tracking in datasets acquired at low temporal resolution due to experimental constraints such as phototoxicity. To demonstrate the method, Jochen performs tracking on the *Drosophila* embryonic epidermis and compares cell-cell rearrangements to previous studies in other tissues. The implementation is open source and generally applicable to epithelial tissues. This work has separately been published in the Journal of the Royal Society Interface [4].

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[1] Kursawe, J., Baker, R. E., and Fletcher, A. G. Impact of implementation choices on quanti-

tative predictions of cell-based computational models. *J Comput Phys*, 345:752–767, 2017.

[2] Kursawe, J., Brodskiy, P. A., Zartman, J. J., Baker, R. E., and Fletcher, A. G. Capabilities and limitations of tissue size control through passive mechanical forces. *PLoS Comput Biol*, 11(12):e1004679, 2015.

[3] Kursawe, J., Baker, R. E., and Fletcher, A. G. Approximate Bayesian computation reveals the importance of repeated measurements for parameterising cell-based models of growing tissues. *J Theor Biol*, 443:66–81, 2018.

[4] Kursawe, J., Bardenet, R., Zartman, J. J., Baker, R. E., and Fletcher, A. G. Robust cell tracking in epithelial tissues through identification of maximum common subgraphs. *J R Soc Interface*, 13(124):20160725, 2016.

A biomathematical tale of two cities

After several, progressively more intense contacts throughout years before the actual event (*a detailed history can be found on the Communications issue No. 13, June 2011*), such champions of mathematical biology as Jim Murray, Willi Jaeger, Lee Segel, Jacques Demongeot, Odo Diekmann, Johan Metz, Albert Goldbeter and Niels Keiding, together with Simon Levin and Vincenzo Capasso, organized at L'Alpe d'Huez, Grenoble, the first European Conference on Mathematics applied to Biology and Medicine, during which ESMTB was born.

A ski resort of some renown, situated in the French department of Isère not too far from the border with northern Italy, this location was chosen because of its proximity with Grenoble, where Prof. Demongeot was Director of the Department of Medical Information and of the Pole of Public Health. While being nowadays one of the most technology-centered cities in Europe (about one fifth of the inhabitants are connected with the research industry), Grenoble in fact started out as a modest Allobrogian village, elevated to Roman Municipium dignity by Emperor Gratian (hence Gratianopolis then Graignovol and finally Grenoble), who was traveling through the neighborhood on business.

In those days (approximately 370-380 A.D.), Gratian had a rather rough time handling the Western Roman Empire, but, being a diligent, dutiful fellow, he had established his area of action in turbulent Gaul, leaving the quieter Italy and Africa to be administered by his mother and his brother, who established their capital in Milan. It was a good choice because they could count, in those days of crumbling Roman Imperial organization, on the collaborating forces of the newly established religion, Christianity. A very able Milanese governmental administrator, Ambrose, was so appreciated both for his humanity and for his organizing abilities, that, notwithstanding the mere facts that he was neither baptized nor trained in theology, the citizenry demanded that he be simultaneously ordained priest and made bishop of the city, all this against his own expressly stated wishes.

Well, Ambrose was duly made Bishop of Milan, was an example of piety, became one of the Fathers of the Church, was made Saint, converted the debaucher Augustine (later to be made Saint himself) and in the meantime ruled the Country on behalf of the Emperor, very possibly not always interpreting the Emperor's wishes to the letter.

The relationship between Milan and the Empire was in fact always troubled. In later years, after a bunch of "barbaric" states succeeded one another in Northern Italy, and after the reunification of Germany and Northern Italy into the Holy Roman Empire (from the days of Charles the Great), Milan and the Emperor typically disagreed. This led to alternating punishing expeditions by the Germany-based monarch against the unruly metropolis beyond the Alps, and successful rebellions by the City against the Imperial troops. One such rebellion was crowned by the victorious Battle of Legnano, where the City soldiers, fighting in the field from positions around an ox-pulled cart on which Mass was being said continuously, defeated Frederick Barbarossa. What appears of interest in this case is that several lesser Lombard towns (Pavia and Como first and foremost) had actually allied themselves with the Emperor against Milan: evidently, however efficient, the Milanese were not very much liked by their immediate neighbors. The conflict between pro-Imperial and anti-Imperial feelings in Milan itself was well captured by the French writer Stendahl (born in Grenoble) in the novel "The Charterhouse of Parma", portraying the



rift between a pro-Austrian Milanese father and his pro-Napoleon son, embodying two antithetical conceptions of life's values.

While the wind of revolutionary freedom carried by Napoleonic troops throughout Europe is possibly easier to sympathize with, the industry, perseverance and practicality of the inhabitants of what was once the southernmost metropolis of the Augsburg Empire contributed materially to its economic development. Milan was thus the focus of much immigration from southern Italy in the post-WWII period, attracting simple labourers and technically gifted individuals at any level. Several years later, a Professor from Bari, in the Italian deep South, moved to Milan to a University chair in Probability and Mathematical Statistics. Together with colleagues from all over Europe, he started the grass-roots movement that would have eventually determined the birth of ESMTB: when Vincenzo Capasso from Milan and his colleagues had to situate the first European Conference in Biomathematics, the choice fell, fatefully, on Grenoble.

Andrea De Gaetano



ESMTB Travel Support

The ESMTB provides travel support to mathematical/theoretical biology events such as meetings, conferences, workshops or schools. Support is provided only to ESMTB members, so that an applicant needs to be an ESMTB member in good standing, that is, at the moment of submitting her/his application. The maximum amount of travel support provided by the ESMTB per single application is currently set to 350 euro. However, funding will in most cases be only partial, in order to support a greater number of applicants. In general, preference will be given to:

- applicants who have been members of the ESMTB for a longer time,
- doctoral students and post-docs, but graduate students and senior scientists may also apply,
- applicants who present a paper or poster at the attended event,
- applicants who did not receive travel support from the ESMTB before,
- applicants in conditions of economic hardship.

Several calls for travel support are made each year. Responses can be expected within 15 days after a respective deadline. The application form (when a call is made) can be approached from the link <https://www.esmtb.org/travel-support>

Applicants awarded by ESMTB Travel Support are expected to send the ESMTB a brief report about the attended event. The report (500 to 1000 words) must be sent to info@esmtb.org within 15 days after the event has taken place and will be published in the Society's "Communications".

In 2017, ESMTB granted six people travel support, for 350 euro each. The grants covered different kinds of events such as ECMTB 2018, EMS-ESMTB summer schools, different modelling workshops and schools, and the 2017 MMEE conference.

Report from Luisa Fernanda Rodriguez Carrillo, participant at the 5th Helsinki Summer School on Mathematical Ecology and Evolution, 21 – 28 August 2016, supported by an ESMTB travel grant

I attended to the 5th Helsinki Summer School on Mathematical Ecology and Evolution, held in the city of Turku, Finland by the University of Helsinki. This school consisted of a series of lectures in the topics of Structured populations, and workgroup sessions whose purpose was to understand a proposed topic by studying a series of given working papers that accompany the lectures, with the aim to prepare a 20 minutes presentation to be exhibited at the end of the meeting. The project in which I worked along with four students was about Adaptive dynamics in structured populations, we worked under the professor Hans Metz supervision. We discussed a model for evolutionary dynamics of seed size when there exists a trade-off between the seed size and seed number, and seedlings from large seeds are better competitors and have a higher precompetitive survival than seedlings from small seeds [1]. The main discussion was that different parameter combinations may lead to different singularities, but at the same time, the mathematical model exhibits model-independent general results for the field of bifurcation theory. The conferences that were presented were: *The Delay formulation of Physiologically Structured Populations* by Mats Gyllenberg, *Evolutionary Dynamics of Seed Size and Seedling Competitive Ability* by Hans Metz (IIASA), *Physiologically structured population models: from numerical techniques to ecological insight* by Andr M. de Roos (University of Amsterdam), *Infectious Disease in Structured Populations* by Hisashi Inaba (University of Tokio) and, *Population Genetics of Spatially Structured Populations* by Reinhard Bürger (Universität Wien).

The take-home messages from my point of view were (a) the opportunity to learn new theory from experts, (b) to have a clear knowledge about the state of the art in the structured populations research area, and (c) as a master student from Latin America, for me was very inter-

esting and rewarding to share experiences with students and professors from around the world.

Thanks to this event I was able to consider new aspects for my master thesis, and this summer school gave me insights into future research interests by proportionating me high-quality theoretical foundations to move forward in my professional career. In particular, I found interesting the professor Bürger conference about Dispersal in continuous space and PDE models, he discussed the theoretical framework of a model with spatially heterogeneous selection and clines (nonconstant stationary equilibrium solution), also was interesting the professor Gyllenberg conference, he proportionated an introduction to structured populations, extending the concept of the analysis of the basic reproductive number inside the classical epidemiological models. Finally, I would like to say that to visit a country as Finland for me was very pleasant since was my first time visiting a country from Europe. I learned from their work culture, and their high ethical values.

Luisa Fernanda Rodriguez Carrillo

[1] A.H. Geritz, E. van der Meijden, and J. Metz. Evolutionary Dynamics of Seed Size and Seedling Competitive Ability. *Theoretical Population Biology* 55, 324-343 (1999).



ECMTB 2018 (www.ecmtb2018.org)

The **European Conference on Mathematical and Theoretical Biology (ECMTB)** is organized regularly by the **European Society for Mathematical and Theoretical Biology (ESMTB)** and is a major worldwide scientific event in this field, attracting researchers from all over the world.

The 11th ECMTB is taking place in the exciting city of Lisbon, Portugal, from 23 to 27 July, 2018, and it is the main event of the **Year of Mathematical Biology**, set up by ESMTB and by the European Mathematical Society (EMS). For that reason, ECMTB 2018 will, for the first time, be a joint ESMTB-EMS conference and will be co-organized by SPM (Portuguese Mathematical Society). The venue is the Faculty of Sciences of the University of Lisbon and its research centre CMAF-CIO will host the event.

The ECMTB 2018 invited speakers are:

- Helen Byrne (Oxford University, UK)
- Antonio DeSimone (Scuola Internazionale Superiore di Studi Avanzati, Italy)
- Eva Kisdi (Helsinki University, Finland)
- Samuel Kou - BS-EMS Joint Lecture (Harvard University, USA)
- Mirjam Kretzschmar (University Medical Centre Utrecht, The Netherlands)
- Eva Löcherbach (Cergy-Pontoise University, France)
- Andrea Pugliese (Trento University, Italy)
- Eörs Szathmáry (Eötvös Loránd University, Hungary)
- Kees Weijer (Dundee University, UK).

Besides the invited talks by these remarkable scientists, we are happy to announce that this ECMTB 2018 will have an exciting programme, from cutting-edge minisymposia to the many contributed talks and posters on recent research developments in all areas of Mathematical Biology, as well as lectures from the recent winners of the Reinhart-Heinrich Doctoral Theses Award. We are also happy to inform that, thanks to the support of several scientific publishers, there will be four poster prizes.

This Conference is a great opportunity for fruitful interactions among members of our scientific community, taking advantage of the coffee and lunch breaks and of the poster parties, as well as of the Mentorship Program designed to help young researchers establishing contacts with more senior members. Of course, participants are also able to enjoy the nice optional excursions and the Conference Dinner (please visit the Conference website for more information).

ESMTB will held its General Assembly meeting during the Conference. Conference participants that are not yet members are also invited to attend this meeting and to join our scientific community, benefiting from the following special invitation offer:

Special invitation: The ESMTB, to celebrate the Year of Mathematical Biology 2018 and wishing to extend its membership to other researchers in the area, invites **every participant registered for the ECMTB 2018, that is not yet an ESMTB member**, to become a member and welcomes those accepting such invitation by exempting them of the first year membership fee. NOTE: If you accept this invitation, **it only takes effect after you becoming a Conference participant**, that is, after payment of the ECMTB 2018 registration fee, so the Conference fee should be according to your current status (prior to becoming an ESMTB member).

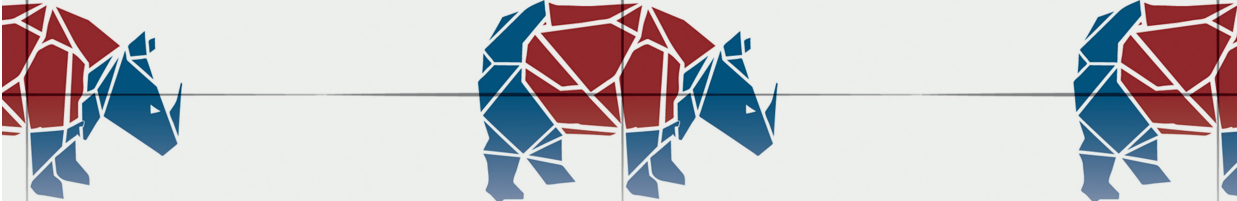
To know more about ESMTB, visit the Society webpage <http://www.esmtb.org>

To stay updated on the latest news on the ECMTB 2018, follow us at <https://www.facebook.com/ecmtb2018/>.






In case of any need, please do not hesitate in contacting us by email (info@ecmtb2018.org).

We wish all participants a nice stay in Lisbon and a fruitful conference. Enjoy ECMTB 2018!

Maira Aguiar, Carlos Braumann,
Nico Stollenwerk (Conference Chairs)



11th European Conference *on* Mathematical *and* Theoretical Biology

www.ecmtb2018.org

Lisbon July 23-27

Celebrating the *Year*
of *Mathematical Biology!*

PLENARY SPEAKERS:

Helen Byrne

University of Oxford, UK

Samuel Kou

Harvard University, USA

Andrea Pugliese

University of Trento, Italy

Antonio DeSimone

Scuola Internazionale Superiore
di Studi Avanzati, Italy

Mirjam Kretzschmar

UMC Utrecht, The Netherlands

Eörs Szathmáry

Eötvös Loránd University, Hungary

Eva Kisdi

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University of Dundee, UK

Supported by



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Year of Mathematical Biology 2018



The Year of Mathematical Biology 2018 is a joint venture of the European Mathematical Society (EMS) and the European Society for Mathematical and Theoretical Biology (ESMTB). The main objectives are to celebrate the huge increase and importance of applications of mathematics to biology and life sciences in the last years and to foster the feedback loop between life sciences and mathematics for years to come. Applications of mathematics in Biology are opening completely new pathways of interactions and they are a huge source of new mathematical problems. The activities already scheduled during this event are summarized in three large programs in different aspects of Mathematical Biology at three ERCOM institutes:

- Simons Semester on Mathematical Biology, December 2017-March 2018, Banach Center, Warsaw, Poland.
- Intensive Research Program in Mathematical Biology, April-June 2018, Centre de Recerca Matemàtica, Spain.
- Thematic Program in Mathematical Biology, September-December 2018, Institut Mittag-Leffler, Sweden.

and many other activities across Europe spanning a wide range of nowadays aspects of interest in Mathematical Biology. The Year of Mathematical Biology will kick off with an event sponsored by the EMS and ESMTB: EMS-Finnish Mathematical Society-ESMTB joint Mathematical Weekend, A kick-off event for the Year of Mathematical Biology, 4-5 January 2018, Joensuu, Finland. Later in the year, the

largest European Mathematical Biology conference series, ECMTB, will be organized jointly by the EMS and the ESMTB: The 11th European Conference on Mathematical and Theoretical Biology (ECMTB 2018), a joint conference of the European Society for Mathematical and Theoretical Biology and the European Mathematical Society, 23-27 July 2018, Lisbon, Portugal. We encourage all our fellow society members with interests in Mathematical Biology to get involved in this transversal event and participate actively. Other activities include the following events and more are being planned:

- Understanding Cancer Through Evolutionary Game Theory, January 29th - February 2nd, 2018, Lorentz Centre, Leiden, The Netherlands.
- Statistics applied to biology and health sciences, Journée de rencontres scientifiques autour de la statistique pour la biologie et la médecine, 1 févr. 2018 Technople du FUTUROSCOPE, Poitiers, France.
- Dynamical Systems Applied to Biology and Natural Sciences (DSABNS2018), February 7-9, 2018, Torino, Italy.
- Think tank: Host-microbiome research, March 12-13, 2018, Amsterdam, The Netherlands.
- Stochastic Models in Ecology and Evolutionary Biology, April 5-7, 2018, Venice, Italy.
- Annual Meeting of the Netherlands Society for Theoretical Biology (NVTB), April 5-6, 2018, Schoorl, The Netherlands.
- Models in Population Dynamics, Ecology, and Evolution (MPDEE'18), April 9-13, 2018, University of Leicester, UK.
- UK Conference on Multiscale Biology, April 16-18, University of Nottingham, UK.
- Collective dynamics and self-organization in biological sciences, Apr 30, 2018 - May 04, 2018, ICMS, Edinburgh, UK.
- Mathematical Modelling in Biology, Modelling Seminar, Summer term, Wuppertal, Germany.



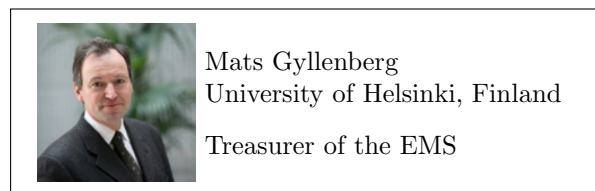
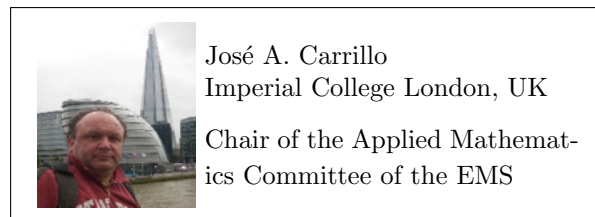
- Mathematical Biology Modelling Days of Besançon, 19-22 June 2018, Besançon, France.
- Probability and biological evolution, CIRM, 25-29 June 2018, Marseille, France.
- International Conference on Mathematical Methods and Models (BIOMATH 2018), 24-29 June, Sofia, Bulgaria.
- Mathematical perspectives in the biology and therapeutics of cancer, 9-13 July 2018, CIRM, France.
- CEMRACS 2018, Numerical and mathematical modeling for biological and medical applications: deterministic, probabilistic and statistical descriptions, 16 July - 24 August 2018, CIRM, Marseille, France.
- The Helsinki Summer School on Mathematical Ecology and Evolution, August 2018, Helsinki, Finland.
- Erice MathCompEpi 2 - Mathematical and Computational Epidemiology of Infectious diseases, 28 August - 5 September 2018, International Centre "Ettore Majorana", Erice, Italy.
- Populations: Interactions and evolution, Institut Henri Poincaré, 10-14 September 2018, Paris, France.
- GreifOlution: 1st Greifswald Summer School on Mathematics of Evolution, 16-22 September, 2018, Greifswald, Germany.
- Differential Equations arising from Organising Principles in Biology, 23-29 September 2018, Mathematisches Forschungsinstitut Oberwolfach, Germany.
- Workshop on Mathematical Biology, 8-12 October 2018, Institut Mittag-Leffler, Sweden.
- Mathematics for BioMedicine, 8-11 October 2018, Accademia dei Lincei-CNR, Rome.
- Workshop on Mathematical Challenges in the Analysis of Continuum Models for Cancer Growth, Evolution and Therapy, 25-30 November 2018, BIRS-CMS, Oaxaca, Mexico.

An organization committee for the Year of Mathematical Biology has been set up through the Applied Mathematics Committee of the EMS:

- Jose A. Carrillo, Imperial College London, UK. (Chair)
- Mathisca de Gunst, University of Amsterdam, The Netherlands.
- Mats Gyllenberg, University of Helsinki, Finland.

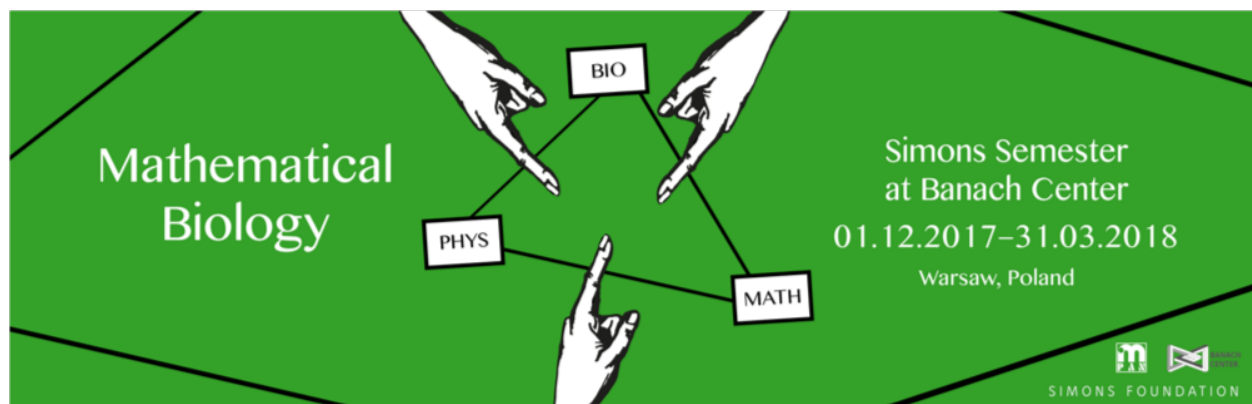
- Torbjörn Lundh, Chalmers University, Sweden.
- Anna Marciniak-Czochra, Heidelberg Universität, Germany.
- Roeland Merks, CWI, The Netherlands.
- Marek Niezgodka, ICM, Poland.
- Gael Raoul, École Polytechnique, France.

If you have any suggestions or ideas that you want to share with us, activities to be done, activities to be included or any queries, please contact any member of the committee. We want to thank everybody involved in the organization, scientific committees, and speakers of each of the events above for the effort put into this endeavour. It is a pleasure to see how this idea has developed over the years from a very small-scale project with origins in 2014 to celebrate collaborations between mathematics and biology to a full year of mathematical biology events. This could not be done without the generous effort of a large community believing in the fantastic outcome that this cross-pollination between disciplines can bring to Mathematics as a whole.



Simons Semester on Mathematical Biology, Banach Center, Warsaw, Poland.

The Banach Center of the Institute of Mathematics of Polish Academy of Sciences (IMPAN) hosted (from 01.12.2017 to 31.03.2018) Simons Semester on Mathematical Biology, organized by Odo Diekmann



(Utrecht University), Piotr Gwiazda (IMPAN and MIMUW), Jacek Miękiś (IMPAN and MIMUW), Benoît Perthame (Sorbonne Université, Paris), Joanna Renclawowicz (IMPAN), Ryszard Rudnicki (IMPAN), see <https://www.mimuw.edu.pl/~miekisz/index.php>

It was one of many semesters which are organized at the Banach Center within the framework of a 5-year research and training program in IMPAN, financed by the grant received from the Simons Foundation.

The general goal of the Simons Semester on Mathematical Biology was to attract young people to a broadly defined mathematical biology and to foster international interdisciplinary collaborations between mathematicians, physicists, and biologists. We brought to Warsaw, as Simons professors, top mathematicians and theoretical physicists working in qualitative biology who presented state-of-the-art in their fields, and PhD students to work in the frontier of science under the supervision of Simons mentors.

Main topics of the semester included structured population models, information transmission in biological systems, infectious diseases, and chemotaxis.

The BioPhysMath kickoff meeting of the semester was held in Warsaw in December 2017 and it was sort of a prelude to the 2018 Year in Mathematical Biology. One day of the meeting was devoted to lectures given by the members of the Board of the European Society for Mathematical and Theoretical Biology (the Board of ESMTB had its meeting in Warsaw on Decem-

ber 8). In the remaining two days of the workshop we had review talks given by some Simons Semester professors and by other lecturers presenting main themes of the semester.

The title of this workshop, BioPhysMath, indicates the interdisciplinary character of the workshop and the semester. It was a special edition of the two-day BioPhysMath workshops organized twice a year at the Banach Center in Warsaw by Jacek Miękiś and Ryszard Rudnicki.

It was followed by a two-month intensive course *Stochastic processes and inference in biology* given by physicists Thierry Mora and Aleksandra Walczak from École Normale Supérieure, Paris. Several students attended lectures, worked in groups on projects, presented their results, and then submitted a report.

Then followed technical workshops concentrated on specific models of mathematical biology: *Transport phenomena in mathematical biology*, *Infectious disease epidemiology: from theoretical models to inference*, and *Mathematical aspects of chemotaxis, cross-diffusion effects and concentration phenomena*.

The semester ended with two schools organized in the Banach Center in Będlewo: *Information transmission in biological systems* and *From individual based models to structured population level description*. Participants of both schools consisted of roughly 15 lecturers and 30 students (bachelor, master, PhD students, and post-docs). Some of them are now working on projects proposed by lecturers.



CRM
INTENSIVE RESEARCH PROGRAMMES

IRP on Recent Progress in Mathematical Biology

AGENDA:

- ✓ Advanced Course: School on Mathematical Modelling of Tumour Growth and Therapy April 3 to 6, 2018
- ✓ Conference New Trends in Mathematical Biology June 4 to 6, 2018

Further information on the Research Programme and activities in www.crm.cat/2018/irp-MathBio

Biology and biomedicine are experiencing a revolution driven by new high-throughput technologies (OMICS, new imaging methodologies, etc.). These new technologies are producing a wealth of high-quality, high-resolution data that, perhaps for the first time, allow for quantitative characterisation of biological phenomena. However, there is also the danger that biologists and biomedical researchers are overwhelmed by the amount of data they are generating, unless new methods for data-management and quantitative bioinformatics that allow them to interpret and contextualise their observations. Driven by this need, new developments in Mathematical Biology have emerged. The aim of this programme is to bring together experts from different areas of Mathematical Biology (neuroscience, tumour modelling, population dynamics, ...) which have developed different methods trying to address the new challenges in their associated areas of biological and biomedical research.

This activity will be included among the scientific activities organized in the framework of the "Year of Mathematical Biology" organized by the European Mathematical Society (EMS) and the European Society of Mathematical and Theoretical Biology (ESMTB) in 2018. Therefore, it will be a way to increase the international impact of the CRM and the groups in mathematical biology of the Barcelona area. José Antonio Carrillo is the chairman of the Applied Mathematics Committee of the EMS and it will be acting as the main coordinator of this activity in 2018.

Scientific organizers:
Tomás Alarcón (ICREA- CRM)
Toni Guillamon (UPC)
Sílvia Cuadrado (UAB)
José Antonio Carrillo (Imperial College London)

CRM
Centre de Recerca Matemàtica • Campus UAB, Bellaterra [Barcelona]
Tel.: +34 935868192 • email: IRP@crm.cat • www.crm.cat

The semester has ended but we hope that it will result in many fruitful collaborations, new insights into old problems, new directions of research, and many new ideas and results in mathematical and quantitative biology.

Ryszard Rudnicki

Intensive Research Program in Mathematical Biology, Centre de Recerca Matemàtica, Spain.

During the months of April, May and June of 2018 the Centre de Recerca Matemàtica (CRM) in Barcelona hosted the Intensive Research Program Recent progress in Mathematical Biology. This program, organized by Tomás Alarcón (ICREA-CRM), José Antonio Carrillo (Imperial College London), Sílvia Cuadrado (Universitat Autònoma de Barcelona) and Toni Guillamon (Universitat Politècnica de Catalunya) was one of the scientific activities organized in the

framework of the "Year of Mathematical Biology".

The aim of the programme was to bring together experts from different areas of Mathematical Biology (neuroscience, tumour modelling, population dynamics, ...) which have developed different methods trying to address the new challenges in their associated areas of biological and biomedical research.

The program was structured around three main activities: *The Advanced course: School on Mathematical Modelling of Tumour Growth and Therapy*, the conference *New Trends in Mathematical Biology* and the seminar where visitors of the program gave lectures about different topics along the semester.

The Advanced course: School on Mathematical Modelling of Tumour Growth and Therapy took place from 3-6 April and consisted of four very enlightening courses by Helen Byrne (University of Oxford), Vincent Calvez (École Normale Supérieure de Lyon), Jean Clairambaut

(INRIA Paris-Rocquencourt Research Centre) and Anna Marciniak-Czochra (Heidelberg University).

The conference *New Trends in Mathematical Biology* took place from 4-8 June and consisted in a series of lectures in the fields of Angiogenesis, Mathematical Neuroscience and Population and Evolutionary Dynamics given by the following invited speakers: Oscar Angulo, Odo Diekmann, Laurent Desvillettes, Jozsef Farkas, Mats Gyllenberg, Andrea Pugliese, Gaël Raoul, Zuzanna Szymanska, Horst R. Thieme, Dumitru Trucu, Mathieu Desroches, Susanne Ditlevsen, Serafim Rodrigues, Horacio Rotstein, Helmut Schmidt, Katie Bentley, Miguel Bernabeu, Roeland Merks and Rui D.M. Travasso.

Altogether, the program activities produced many interactions that will hopefully lead to fruitful collaborations that will start new directions of research and advances in the field in the years to come.

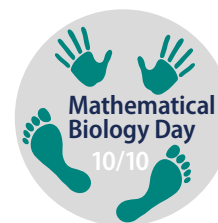
Sílvia Cuadrado

Thematic Program in Mathematical Biology, Institut Mittag-Leffler, Sweden.

For the first time in its 102 year's long history, Institute Mittag-Leffler will have a theme semester (www.mittag-leffler.se/langa-program/mathematical-biology) on mathematical biology. The different sub-themes will be mathematical models on morphology (Sep), collective behaviour (Oct), population dynamics (Nov) and cancer (Dec).

Other highlights will be two Simon's workshops; one around the first Mathematical Biology Day 10/10 (and yes, the date works on both sides of the Atlantic Ocean) with celebration with some popularisation talks at the Royal Swedish Academy of Sciences, and one workshop on cancer treatment in mid December and the official farewell party on December 11 when the mathematical jazz quartet "da Möbius Band" will perform.

We have ten fingers and ten toes and these are the direct interface between our anatomy and mathematics and the reason for base 10, furthermore 10 in base 2 is written 1010.



Let's make October 10 a day to celebrate both for biology and for mathematics.



A selfie with our benefactor Gösta Mittag-Leffler himself on his 172 year birthday March 16. The statue in a corner of the library was created by the celebrated Carl Milles.



The institute was created on Gösta Mittag-Leffler's 70th birthday.

Torbjörn Lundh

European teams in mathematical biology

In each issue we present some of the European groups working in the field of mathematical biology. We try to cover different subjects and geography. If you think some group should be portrayed in the next issue, please let us know. Enjoy!

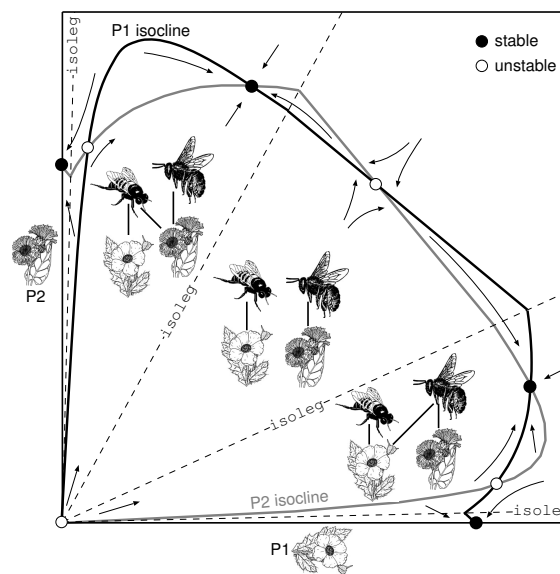
Centre for Mathematical Biology, České Budějovice, Czech Republic

Mathematical and theoretical ecology in České Budějovice (Czech Republic) started in early 80s in the newly established Biology Centre of the Czech Academy of Sciences. When Faculty of Science of the University of South Bohemia was opened, members of the mathematical biology group became faculties there. To further promote mathematical biology by teaching specialized courses and supervising students and to foster collaboration between mathematicians and biologists, both locally and internationally, a new Centre for Mathematical Biology was recently established. Current faculties are Vlastimil Křivan, Luděk Berec and Tomáš Revilla.

Our primary research interests include mathematical modelling in ecology, epidemiology and evolutionary biology. Our research focus in ecology is on integrating individual-level behaviour with population and community dynamics, covering especially Allee effects, predator-prey dynamics and mutualistic interactions. We combine methods of evolutionary game theory, differential equations as well as stochastic, individual-based simulation modelling. Our models in epidemiology are actually eco-epidemiological models aimed at exploring how various kinds of infectious diseases affect and are affected by population dynamics.

At the Faculty of Science, we teach courses that cover various topics in ecology, epidemiology and evolutionary biology. These courses are mandatory in the bachelor programme in Applied Mathematics and facultative in the bachelor and master programmes in Teaching Mathematics. Apart from the theory, small modelling

projects are offered to students, as well as leadership of theses with a variety of topics from mathematical biology. Recent these topics include modelling predator-prey dynamics with structurally variable functional responses and modelling various cellular-level processes.



Link: mathbio.prf.jcu.cz

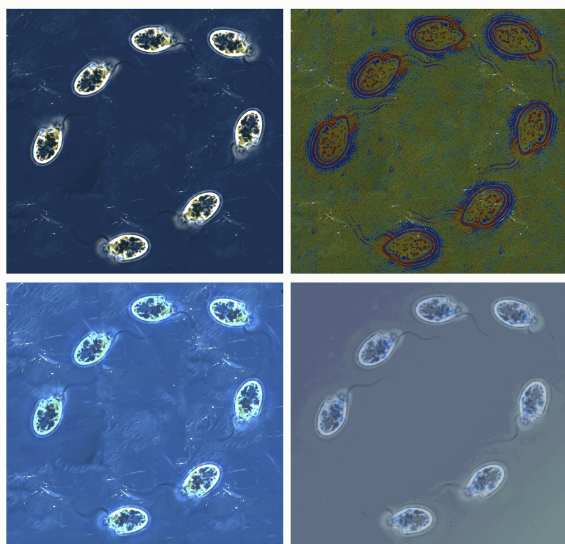
Biomathematics in Gothenburg, Sweden

The Biomathematics Group at the Department of Mathematical Sciences, Chalmers University of Technology and the University of Gothenburg, is part of the larger research area Biomathematics and biostatistics <http://www.chalmers.se/en/departments/math/research/research-groups/biomathematics-and-biostatistics/Pages/default.aspx>.

Group members in the photo are (from the left) Niek Welkenhuysen, Serik Sagitov, Johannes Borgqvist, Felix Held, Julie Rowlett, Marija Cvijovic, Philip Gerlee, Linnea Österberg, Adam Malik, Henrik Imberg, Olle Nerman, Peter Jagers, Yvonne Krumbeck, Jose Esteban Pérez Hidalgo, Anton Johansson, Marina Axelson-Fisk, Erik Kristiansson, and Torbjörn Lundh.

Some research examples:

Marija Cvijovic is leading an interdisciplinary research group of biologists, biotechnologists, physicists and mathematicians engaged in a broad range of activities in the area of systems biology. Their primary focus is on studying the complexity of cellular ageing using experimental (postdoc Niek Welkenhuysen) and computational methods (PhD students Johannes Borgqvist and Barbara Schnitzer). They are focusing on the ageing at the single-cell level using yeast as model systems and they are developing and integrating kinetic, multi-scale and non-linear mixed effect models to gain a systems view of ageing. There are also working on the dynamic regulation of central metabolism and cell signaling (PhD student Linnea Österberg) and pharmacokinetics and pharmacodynamics modelling (PhD students Felix Held and Jacob Leander).



Visualisation of age induced protein aggregates in the cell through fluorescent microscopy. Left hand side is an image of the yeast cells, right hand side is the fluorescent image of the protein aggregates. Size of a yeast cell is around 5-7 μm .

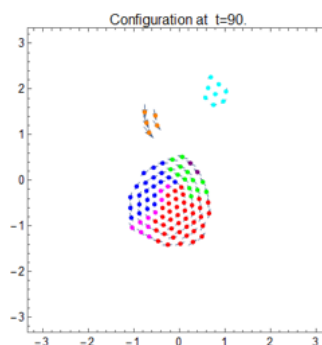
*Susanne Menden-Deuer, plankton of the species *Oxyrrhis marina*, for the cover of the Journal of the Royal Society Interface*

Philip Gerlee works mostly in cancer modelling and tries to understand the macroscopic effects of microscopic mechanisms such as cell

division, migration and cell-cell interactions. Together with cancer biologists he is working in a project with the aim of measuring patient-specific cell parameters that can be used for predicting the rate of disease progression. His PhD-student Adam Malik is working on a mechanical model of cell migration which accounts for the mechanical properties of both the cell and the substrate, and can make predictions about cell diffusion and drift.

Julie Rowlett work together with Susanne Menden-Deuer, Professor of Oceanography at the University of Rhode Island, to investigate long-standing problems in microbe ecology. She uses the mathematical tools of non-cooperative game theory, geometric and microlocal analysis, and dynamical systems, while Susanne provides biological insights from field & laboratory observations. The biological insights guide the theoretical mathematics, which they subsequently test against observations by creating model simulations based on the mathematics. It is an iterative and truly interdisciplinary research process.

Serik Sagitov and Peter Jagers develop and study stochastic population models addressing various issues in demography, phylogenetics, and population genetics, as well as conceptual questions from population biology, like those of extinction, stabilization or growth. Their current collaboration effort is with Anders Ståhlberg's group at Sahlgrenska, which proposes a probabilistic model for the multi-stage PCR protocol aimed at detecting cancer cells in blood samples.



A simulation by Bernt Wennberg of flocking behaviour using a model with anticipation.

Bernt Wennberg, Philip Gerlee and Torbjörn Lundh work together in a project on hierar-

chical mixed-effects models and they are also engaged in studies regarding modeling of collective behavior in schools of fish and flocks of birds. Torbjörn Lundh is also involved in medtech inventions using mathematics and smart textile on clinical problems from vascular surgery.



For a broader picture of theoretical biological research in Gothenburg, see also the site mathbio.se.

Barcelona Biomathematics Group UAB-UdG

Topics: structured population dynamics and mathematical models for biological evolution; dynamics on and of complex networks and models for epidemic spreading of infectious diseases.

Our group, originated at the end of the nineties at the Autonomous University of Barcelona is nowadays split into two main locations in the northwestern Mediterranean area: the Mathematics Department of the Autonomous University of Barcelona and the Computer Science, Applied Mathematics and Statistics Department of the University of Girona. The members of the group are Carles Barril, Àngel Calsina, Sílvia Cuadrado, David Juher, Jordi Ripoll and Joan Saldaña. We are part of a larger team of researchers named PDEs and applications, accredited by the Catalan Government.

Since the beginning of the group, our main interest has been population dynamics applied to ecology, epidemiology and evolution theory. Simple population models can be made more capable of better capturing biologically meaningful issues by means of adding continuous and

discrete structure to the population. Within the broad research area of mathematical biology, we feel members of the very active area of structured population dynamics which addresses ecological, epidemiological and evolutionary problems through evolution equations for the densities of individuals with respect to structuring variables such as age, size, genotype, phenotype or, also, physical space for instance. On the other hand, another line of research of the group is the modelling of realistic epidemic models with the formalism of the complex networks (systems of many elements with a non-trivial pattern of connections). The mathematical tools we use are ODE and PDE (transport, reaction-diffusion and integro-differential equations) with special emphasis on qualitative behavior of solutions via semilinear formulation and also stochastic simulations when dealing with models of epidemic spreading.



Both in the UAB as in the UdG, we teach regular mathematics courses to undergraduate students of life and environmental sciences, food science and chemical and industrial engineering; modelling workshop and partial differential equations to undergraduate mathematics and physics students and also partial differential equations and modelling in master courses of mathematical modelling for science and engineering and of mathematical finance.

Website: Grups de recerca GREDPA (UAB-UdG-UPC-CRM) and EDMA (UdG).

Research Centre for Mathematics and Applications, Portugal

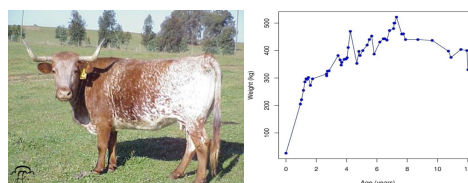
The Research Centre for Mathematics and Applications (CIMA) is based at the University of Évora and the University of Madeira, Portugal. Its aim is to create new mathematical tools, concepts and theories and to contribute to the development of mathematical knowledge and cultural awareness at different levels (local, regional, national, Portuguese-speaking worldwide, international). Our study of mathematical models and structures is mainly motivated by applications coming from life sciences, economics and finance, fluid dynamics, optimal design and other areas of physics and engineering.

Although other CIMA research groups are also involved in Mathematical Biology modelling, in this note we will focus on the Research Group in Statistics, Stochastic Processes and Applications (SSPA; <http://www.cima.uevora.pt/nSSPA.htm>), which has effective members (José Luís Silva - Coordinator, Álvaro Silva Ribeiro, Anabela Afonso, Carlos A. Braumann, Clara Carlos, Dulce Gomes, Dulce Pereira, Gonçalo Jacinto, Joaquim Azevedo, João Alves e Sousa, Jorge Santos, Ludwig Streit, Manuela Oliveira, Patrícia Filipe, Paulo Infante, Russell Alpizar-Jara), collaborators and Ph.D. students.

The Mathematical Biology research in SSPA is developed under two main lines, a) Stochastic Processes and Applications and b) Statistical Modeling and Data Analysis. The former focusses on population and individual modelling in random environments, stochastic processes, time series analysis and space-time modelling. Applications include models to monitor epidemics such as dengue, chikungunya and zika, as well as stochastic differential equations to model population growth and fisheries, designing optimal sustainable harvesting policies and examining equilibrium conditions and extinction probabilities. Statistical Modeling and Data Analysis focus on population size and parameter estimation of elusive populations, on multivariate analysis and experimental designs and on quality control and survival analysis,

with applications mainly in wildlife, agriculture and medicine. Applications include the development of wildfire occurrence probability models as well as wildfire damage models that have as independent variables biometric indicators (e.g., stand density, fuel biomass) that may be controlled by forest managers, for the main forest cover types in Portugal. CIMA is involved in several national and international networks and projects to develop and disseminate research in CIMA's core areas. For example, it participates in the project "Models and decision Support tools for integrated Forest policy development under global change and associated Risk and Uncertainty", funded by the Marie Curie International Staff Exchange Scheme (<http://suforum.ctfc.cat>), where it contributes to the development of ecosystem dynamics' models within a multidisciplinary framework. Another example is the participation in GoBov+ (<http://www.bovmais.pt>), an operational group for the improvement of productivity in bovine raising, involving research institutions and producers and funded by the European Union FEADER program PDR2020. The SSPA team (Patrícia Filipe, Gonalo Jacinto, Carlos Braumann) deals with prediction and profit optimization using stochastic differential equation individual bovine growth models and the genetic values of the animal. CIMA is a sponsor of ECMTB 2018 (Lisbon, July 23-27) and participates in its organization (Carlos Braumann is co-chair of the organizing committee and member of the scientific committee and Patrícia Filipe is a member of the organizing committee).

Website: <http://www.cima.uevora.pt>



$$dX_i(t) = \beta X_i(t) (\ln A_i - \ln X_i(t)) dt + \sigma X_i(t) dW(t) \text{ for animal } i$$

$$\alpha_i = \ln A_i \text{ i.i.d. Gaussian}$$

Figure: A typical mertolengo cow and its growth data. The SDE mixed model shown is a baseline model initially used in prediction and profit optimization

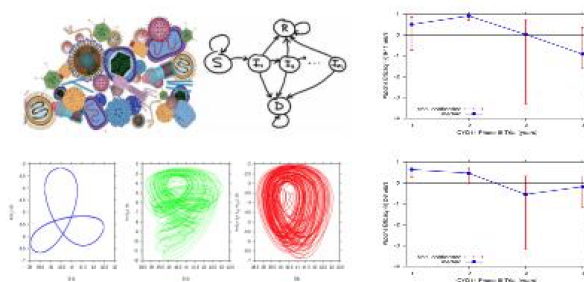
Center for Mathematics, Fundamental Applications and Operations Research, Lisbon University & Centre for Mathematics and Applications, NOVA University of Lisbon, Portugal

The Center for Mathematics, Fundamental Applications and Operations Research (CMAF-CIO) from Faculty of Sciences in Lisbon University is a R&D Unit engaged in research in Mathematical Sciences, covering domains that range from foundations to applications. Its main objectives are to pursue deep studies in areas of mathematics, to train young researchers at several stages of their career, and to foster and develop applications to relevant problems in the Sciences and from Industry. Along with dissemination of scientific results, the unit promotes the communication of mathematics in conferences, schools and for the wider public.

The international visibility of CMAF-CIO can be seen in many aspects, resulting from the active research of its members: i) journal Editorial Boards, ii) membership and leadership in international research groups and scientific organizations, iii) chairing and organization of international conferences and schools, iv) collaborations with many international researchers.

The “Biomathematics and Statistics Group” at CMAF-CIO, now included in the research area of “Nonlinear Analysis and Differential Equations”, works with methods from nonlinear dynamics, bifurcation analysis, stochastic processes, bio-statistics and financial statistics. The research focusses as well on developing theoretical methods as on practical applications, covering research topics in population dynamics, epidemiology of infectious diseases, molecular and antigenic evolution, public health management, economic systems and investigates methodical topics in the natural sciences and mathematics, like large fluctuations and strongly correlated systems. Research members of this group includes Nico Stollenwerk, Maíra Aguiar, Luis Mateus and Raquel Filipe, all participating on the 11th European Conference in Mathematical and Theoretical

Biology (ECMTB 2018) organization, that will take place in Lisbon from 23-27 of July, 2018, the main event of the “Year of Mathematical Biology”.



The Center for Mathematics and Applications (CMA), Universidade Nova de Lisboa, Portugal is also a research unity, funded by the Portuguese Science and Technology Foundation and dedicated to all areas of mathematics. One of the strongest fields of research is biomathematics, involving several members, including, among others, Fabio Chalub, Maíra Aguiar, Paula Rodrigues, Paulo Doutor, which are also involved in the ECMTB 2018 organization.

Topics of research varies from Epidemiology (including vaccination and disease control), Statistical Methods in Medicine and Agriculture, Evolutionary Dynamics, Biology of Conservation and Ecology etc. Most of the research is developed in international partnership. Since 2015, this team is organized in a thematic line, “Mathematical Modelling in Ecology, Evolution and Genetics”, whose goal is to establish CMA as a competent partner for addressing mathematical issues arising in biology and to strengthen further collaborations with the biology community. This team is deeply involved in the organization of the European Conference on Mathematical and Theoretical Biology, to be held in Lisbon, in 2018.

Minutes of the ESMTB Board Meeting

Warsaw, Poland
8th December 2017

Present: Maíra Aguiar (MA), Luděk Berec (LB), Barbara Boldin (BB; Minutes), Reinhard Bürger (RB), Sílvia Cuadrado (SC), Andrea De Gaetano (ADG), Susanne Ditlevsen (SD), Anna Marciniak-Czochra (AMC), Torbjörn Lundh (TL), Roeland Merks (RM; Chair), Ryszard Rudnicki (RR; departs after the welcome address), Bob Planqué (BP), Vitaly Volpert (VV)

Absent: (with apology) Ellen Baake, Frank Hilker

The meeting starts at 9.15 with a welcome address from the host Ryszard Rudnicki and ESMTB president Roeland Merks. RR then departs to host the BioPhysMath meeting, the kick-off meeting of the Simons Semester on Mathematical Biology at the Banach center (<https://www.impan.pl/en/activities/banach-center/conferences/17-ssbiophysmath>).

1. Board elections and constitution of the ESMTB Board for 2018-2020

A brief summary of ESMTB Board elections 2017. The end of 2017 brings about the end of a six-year term for five Board members (Barbara Boldin, Reinhard Bürger, Roeland Merks, Ryszard Rudnicki and Vitaly Volpert). The following nine candidates accepted the Boards invitation to run in the 2017 Board elections:

- Maíra Aguiar (Lisbon, Portugal)
- Alexander Anderson (Tampa, Florida)
- Ellen Baake (Bielefeld, Germany)
- Luděk Berec (České Budějovice, Czech Republic)
- Vincent Calvez (Lyon, France)
- Sílvia Cuadrado (Barcelona, Spain)
- Julia Gog (Cambridge, UK)
- Bob Planqué (Amsterdam, The Netherlands)
- Sander van Doorn (Groningen, The Netherlands)

In July 2017, ESMTB members were invited to cast their votes in an electronic ballot. The results of the elections were as follows:

- Luděk Berec: 36 votes
- Ellen Baake: 35 votes

- Sílvia Cuadrado: 35 votes
- Bob Planqué: 34 votes
- Maíra Aguiar: 33 votes
- the remaining candidates received less than 30 votes.

So the five new ESMTB Board members for the term 2018-2023 are Luděk Berec, Ellen Baake, Sílvia Cuadrado, Bob Planqué and Maíra Aguiar.

The constitution of the ESMTB Board for the term 2018-2020. Following a round of introductions, the first task of the new Board is to elect the President, Vice president, Treasurer and Secretary of ESMTB for the term 2018-2020. The outcome is as follows:

- Ellen Baake (who sadly could not attend the meeting, but has kindly offered herself as a candidate) is elected Secretary of ESMTB
- Bob Planqué is elected ESMTB Treasurer
- Maíra Aguiar is elected ESMTB Vice president
- Elections of the new ESMTB President provide a bit of an excitement as Andrea De Gaetano and Torbjörn Lundh both express their intention to run for president. After two passionate presentations and two rounds of questions from Board members, Andrea De Gaetano is elected president of ESMTB.

The ESMTB Board for the 2018-2020 term is therefore:

- Andrea de Gaetano (President)
- Maíra Aguiar (Vice president)
- Ellen Baake (Secretary)
- Bob Planqué (Treasurer)
- Luděk Berec
- Sílvia Cuadrado
- Susanne Ditlevsen
- Frank Hilker
- Anna Marciniak-Czochra
- Torbjörn Lundh

The names of the new ESMTB Board have to be registered in France as soon as possible. VV and BB will help with the registration process and provide the necessary documents. Furthermore, EMS and the Journal of Mathematical Biology need to be informed about the changes.

2. Report by the president and ad interim treasurer

RM makes a brief report on Society's current situation. The Society is in good state financially and several activities are planned in the Year of Mathematical Biology.

In absence of treasurer Frank Hilker, the Society's previous treasurer Andreas Deutsch has kindly agreed to step in and help out with Society's finances, for which the Board is most grateful. Andreas Deutsch reports that the current balance on ESMTB bank account is 28.307,72 EUR. The newly elected treasurer BP will contact AD to arrange a transition (a new ESMTB bank account is to be opened in The Netherlands).

3. Member administration

In the previous Board meeting, a decision was made to start using a professional service to handle member administration (e.g. Wild Apricot, used by the Society for Mathematical Biology). In this way, handling of the Society's website and ESMTB Infoletter will become easier as well. BP has kindly offered to arrange the transition.

SD remarks that an additional option to pay the ESMTB membership fee for several years in advance would be welcome.

4. Year of Mathematical Biology 2018

The Year of Mathematical Biology 2018 is a joint venture of the European Mathematical Society (EMS) and ESMTB. The main objectives are to celebrate the huge increase and importance of applications of mathematics to biology and life sciences in the last years and to foster the feedback-loop between life sciences and mathematics for years to come (see <http://euro-math-soc.eu/year-mathematical-biology-2018>).

RM gives an update on the planned activities. The Year of Mathematical Biology kicks off with a mathematical weekend on the 4th and 5th of January 2018 in Joensuu, Finland, a joint effort of EMS, ESMTB and the Finnish Mathematical Society (for more details see www.uef.fi/web/matematiikanpaivat2018). The main event of the Year of Mathematical Biology is the 11th European Conference on Mathematical and Theoretical Biology in Lisbon, Portugal (23-27 July 2018). More information about the planned activities can be found on

<http://euro-math-soc.eu/year-mathematical-biology-2018>.

In addition, the 10th of October was announced as the Day of Mathematical Biology, to be celebrated annually with events devoted to popularisation of Mathematical biology. The first Day of Mathematical biology in 2018 will take place during the Simons symposium at the Mittag-Leffler Institute in Sweden and will be celebrated with public lectures on mathematics in biology.

ESMTB members will be informed about the activities in the Year of Mathematical Biology via ESMTB InfoLetter and the ESMTB website will include links to events which are open for registration.

5. ECMTB 2018

MA presents a detailed update on the 11th European Conference on Mathematical and Theoretical Biology, which will take place at the Faculdade de Ciências in Lisbon, Portugal (23-27 July 2018). Plenary speakers are Helen Byrne (Oxford University, UK), Antonio DeSimone (Scuola Internazionale Superiore di Studi Avanzati, Italy), Eva Kisdi (Helsinki University, Finland), Samuel Kou (Harvard University, USA), Mirjam Kretzschmar (University Medical Centre Utrecht, The Netherlands), Eva Löcherbach (Cergy-Pontoise University, France), Andrea Pugliese (Trento University, Italy), Eörs Szathmáry (Eötvös Loránd University, Hungary) and Kees Weijer (Dundee University, UK).

The conference website www.ecmtb2018.org is fully functional and registration is open. The organisers have already received 52 applications for mini-symposia. A mentoring program will be announced soon and potential mentors will be invited to participate in the program.

Financial aspects of the conference are discussed and the Board unanimously agrees ESMTB support in the amount of 2500 EUR.

6. Future ECMTB

The 2020 ECMTB will be a joint event with SMB and will take place in Heidelberg, Germany. AMC gives an updated on the progress. The first week of August 2020 is suggested as the time slot.

For 2022, there is an initiative to organise a joint conference in China, co-organised by SMB, ESMTB, the Japanese Society for Mathematical Biology and the Chinese Society for Mathematical Biology. The Board discusses the possibility and the prevailing sentiment is that the idea is good, provided that all

Societies are well represented and involved in organisation.

7. ESMTB Communications / InfoLetter / Promotion

VV introduces ESMTB Communications to new Board members and reports on the preparations of the latest issue. With the election of the new Board, VV will step down as the main editor of the Communications, as will many others involved. ADG suggests to appoint an ESMTB communications officer, who will be in charge not only of ESMTB Communications but will also supervise all activities related to promotion of the Society (e.g. via Twitter and Facebook). Susanne Ditlevsen kindly agrees to take over as the main editor of ESMTB Communications, Silvia Cuadrado and Luděk Berec kindly offer to join the editorial board. SD and SC will jointly be in charge of promotion activities. All Board members will be given access to the ESMTB Facebook and Twitter accounts.

LB suggests promotion of mathematics in biology via booklets, which are to be presented and distributed in schools, companies etc. The Board welcomes the idea.

8. ESMTB travel grants

ADG presents the current evaluation process for ESMTB travel grants. The automated evaluation procedure has not been entirely satisfactory and various alternatives are discussed. It is agreed that travel applications will be evaluated by a small committee of Board members. The committee will be supervised by Luděk Berec, who has kindly offered to be in charge of the ESMTB travel grants system. The new evaluation system should be clarified on ESMTB website as soon as possible. The budget planned for 2018 ESMTB travel grants is 3000 EUR for the ECMTB in Lisbon and an additional 3000 EUR for (possibly) other meetings.

ESMTB received one further request for financial support of the workshop, i.e. the 9th Workshop on Dynamical system applied to Biology and Natural Sciences in Torino (DSABNS, February 7-9, 2018). The Board agrees to support the workshop with 500 EUR.

9. Ties with EMS and ICIAM

Ties with EMS are good. EMS and ESMTB jointly organise the biggest event in the Year of Mathematical Biology, the ECMTB 2018 in Lisbon.

In addition, EMS-ESMTB summer schools in mathematical and theoretical biology are annually organised.

In the last few years, ADG was ESMTB's contact with ICIAM and attended ICIAM meetings regularly. Now that ADG has been elected new ESMTB president, a new delegate will represent ESMTB. Suggestions are discussed and a delegate will be confirmed in due course.

10. ESMTB Summer schools

The joint EMS-ESMTB summer school 2018 will take place between 19 and 26 August 2018 in Linnasmäki Conference Centre, Turku. This will be the 6th in the series of very successful summer schools "The Helsinki Summer School on Mathematical Ecology and Evolution".

Suggestions for the organisation of the 2019 EMS-ESMTB summer school are made. The final decision is to be made via e-mail before the end 2017.

11. The Reinhart-Heinrich award

RB remarks that, with the end of his term, there will be no ESMTB Board member in the Reinhart-Heinrich price committee. When one of the current prize committee members steps down, ESMTB will need to consider nominating one of their own to join the prize committee.

12. Closing

RM closes the meeting with a word of thank you to departing Board members and to Ryszard Rudnicki, who has kindly hosted the meeting.

The meeting ends at 16.30.

Barbara Boldin
ESMTB Secretary

Meet the new Board of ESMTB



Máira Aguiar is a biologist by training and she holds a double PhD degree in Population Biology (by Lisbon University) and Life Sciences (by VU Amsterdam). She is highly trained in nonlinear dynamics, bifurcation analysis and biostatistics and her scientific interests

address significant mathematical problems and fundamental questions in public health, which requires a highly multidisciplinary approach. Her research crosses the different epidemiological areas of infectious diseases, with special focus on disease control and prevention, by developing mathematical models which can be used by public health authorities as a tool to understand and predict the transmission of the vector-borne (and other) diseases and develop and evaluate the introduction of intervention strategies including vector control and vaccination.



Ellen Baake is full professor for biomathematics and theoretical bioinformatics at the Faculty of Technology at Bielefeld University, and also a member of the Faculty of Mathematics. Her main area of research today is mathematical population

genetics, seeking to understand the dynamics of genes in populations under the joint influence of mutation, selection, recombination and genetic drift; the main tools come from stochasticity (branching processes, interactive particle systems, duality, large deviations, and stochastic simulations).



Luděk Berc is an associate professor at the Biology Centre CAS & University of South Bohemia, České Budějovice, Czech Republic. His long-term research interests include mathematical modelling in ecology, epidemiology and evolutionary biology, with a particular em-

phasis on mating dynamics, dynamics of sex-structured populations, Allee effects, and sexually transmitted infections. By means of epidemiological models, he seeks to understand how infectious diseases affect and are themselves affected by population dynamics, both on ecological and evolutionary time scales. The modelling approaches he uses range from differential equations to stochastic, individual-based simulations.



Sílvia Cuadrado is an associate professor at the Department of Mathematics of the Universitat Autònoma de Barcelona. Her research interests are mainly in the field of population dynamics and biological evolution. She is particularly interested in continuously structured

population dynamics and the use of partial differential equations and delay equations to model and analyze complex situations like for instance cell population growth, bacteria-phage interaction or evolutionary dynamics. She is one of the organizers of the *Intensive Research Program in Mathematical Biology* (CRM), one of the three theme semesters of the Year of Mathematical Biology.



Andrea De Gaetano is an Italian biomathematician working with the National Council of Research of Italy in Rome. He is an M.D. with a specialty in Emergency Surgery, M.Sc. and Ph.D. in Applied Mathematics, and Juris Doctor admitted to the Italian Bar.

He is Director of Research with CNR's Institute for Systems Analysis (IASI) and adjunct professor of Mathematical Statistics with the Dept. of Mathematics at Mahidol University Bangkok. With his colleagues at CNR IASI BioMatLab in Rome he has studied mainly dynamical system problems in mathematical physiology, using ODEs, DDEs, SDEs and now FDEs (fractional order deterministic and stochastic differential equa-

tions), authoring some 150 papers so far. He is particularly interested in parameter estimation and model validation, and would like to learn much more about these aspects of the use of mathematical models in concrete clinical situations, such as diabetes and surgical shock. He has been a more or less proud member of ESMTB since 1996.



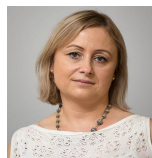
Susanne Ditlevsen is professor in Statistics and Stochastic Models in Biology at the Department of Mathematical Sciences at University of Copenhagen. Her main research interests are statistical inference for stochastic processes, mathematical modeling of physio-

logical systems, nonlinear dynamics, biostatistics and mathematical neuroscience. She is head of the Dynamical Systems Interdisciplinary Network, a larger project with participants from mathematics, statistics, bioinformatics, econometrics, psychology, physiology and neuroscience. The project network encompass visual cognition, neuronal signalling and networks, renal and cardiovascular physiology, molecular dynamics and econometrics. The research focusses on developing mathematical models and statistical methods suited for the analysis of empirical data obtained from such systems.



Torbjörn Lundh is Professor in Mathematics at Chalmers and University of Gothenburg, Sweden. Having a background with a master in Engineering Physics and a PhD in pure mathematics from Uppsala, Torbjörn Lundh has progressively become

more involved in biomathematics via contacts with “real” biologist at his post-docs at Cambridge, UK and Stony Brook, NY. He is now working on problems from various fields such as Artificial Life, Ecology, Morphology and Collective Behaviour and on medtech problems from vascular surgery needs.



Anna Marciniak-Czochra is professor of Applied Mathematics at the Heidelberg University. She is director of the Institute of Applied Mathematics, member of the Interdisciplinary Center

for Scientific Computing (IWR) and of the Bioquant Center. Her research is devoted to mathematical modelling, analysis and simulation in biology and medicine. Specifically, her field of focus is (1) mechanisms of symmetry breaking and pattern formation in development and disease and (2) dynamics of stem cell self-renewal, differentiation and clonal evolution. The work is based on a close collaboration with experimentalists and clinicians, and analytical investigations of the mathematical problems arising in the modelling. The mathematical areas of focus are partial differential equations (pattern formation and structured population dynamics) and multiscale analysis (upscaling and model reduction).



Bob Planqué is a mathematical biologist at the Vrije Universiteit Amsterdam, in the Department of Mathematics. After a PhD in Mathematics at the CWI in Amsterdam and a post-doc in Bristol, UK, on collective behaviour in ants, he landed

back in Amsterdam. His main motivation has always been to ask biological questions first, and try to use the mathematical techniques appropriate for the problem at hand, whether analytical, stochastic, or computational. Bob is currently chiefly interested in a wide array of systems biology problems in microbial growth, gene expression and control, together with the Systems Bioinformatics group at the VU Amsterdam.

Frank Hilker from Universität Osnabrück was elected Board Member starting 2015, but has unfortunately resigned from the Board. The Statutes of the Society do not foresee the substitution of a Board member between elections and therefore the Board will count nine members until the new mandate starting 2021.

Reinhart-Heinrich Doctoral Thesis Award



ESMTB announces the annual Reinhart Heinrich Doctoral Thesis Award to be presented to the student submitting the best doctoral thesis within the current year 2018 in any area of Mathematical and Theoretical Biology.

Professor Reinhart Heinrich (1946 – 2006) started his research career in theoretical physics and then moved into biochemistry, becoming a full professor and head of theoretical biophysics at the Humboldt University, Berlin in 1990. He is considered a father of the field that is now named Systems Biology, since he investigated various topics such as modelling metabolic networks and metabolic control theory, modelling of signal transduction networks, nonlinear dynamics as applied to biological systems, protein translocation, lipid translocation, vesicular transport, and even DNA repair. Reinhart Heinrich was always searching for the principles that underlie observations, looking for different perspectives and connecting theoretical abstraction with biological evidence. In this way, he inspired numerous students, gave them insight and direction for future research in modern mathematical and theoretical biology, and organized a large number of memorable conferences. Gratefully acknowledging his stimulating support of our interdisciplinary field and, in particular, his way of guiding students and young scientists, the Board of ESMTB decided to offer a Doctoral Thesis Award annually to commemorate Reinhart Heinrich and his legacy in mathematical and theoretical biology.

Prize Awarding Committee includes:

Carlos Braumann
Andreas Deutsch
Philip Maini
David Rand
Stefan Schuster (former assistant to Reinhart Heinrich)

Award

A summary of the thesis receiving the award will be published as the lead article in the 2019 issue of the European Communications in Mathematical and Theoretical Biology. The *award* includes:

- an invitation to present a lecture at the forthcoming triennial ESMTB Conference or, alternatively, a limited travel grant by ESMTB for a scientific visit of the recipients own choice;
- 1 year's free membership of ESMTB
- A voucher for Springer books.

Application

Potential applicants may be nominated by any ESMTB member.

To nominate a person for the **Reinhart-Heinrich Doctoral Thesis Award**, the following information should be submitted to Phillip Maini (maini@maths.ox.ac.uk):

1. Name, address, phone number, affiliation, and email address of the **nominator**.
2. Name, address, phone number, affiliation, and email address of the **nominee**.
3. A detailed **statement** describing why the nominee should be considered for the award.
4. An **extended summary** of the thesis (ca. 2-5 pages plus eventual pictures).
5. A **CV** of the nominee in some form.

Closing date for nominations is **31st January 2019**, by which time the thesis should have received final acceptance by the institution granting the doctoral degree.

Shortlisted applicants will be asked to send their full thesis.

CALL FOR MEMBERSHIP FEES 2018

The **European Society for Mathematical and Theoretical Biology (ESMTB)** was founded in 1991 during the first European Conference on Mathematics Applied to Biology and Medicine in l'Alpes d'Huez, France. The mission of the ESMTB is to promote theoretical approaches and mathematical tools in biology and medicine in a European and wider context. This goal is pursued by the organization and support of summer schools and conferences, by the European Communications (the former Newsletter) and the information on our web-site. ESMTB annually honours the best PhD thesis in the field of mathematical and theoretical biology with the Reinhart Heinrich Doctoral Thesis Award. ESMTB is a nonprofit organisation. The ESMTB board organizes the activities of the society according to the ESMTB statutes.

Membership benefits include:

- Full online subscription to the **Journal of Mathematical Biology** (Springer Verlag)
- Access to **Travel Support** for mathematical/theoretical biology meetings
- **Reduced fees** for selected conferences and schools
- **Voting** in society elections

Please register at <http://www.esmtb.org> and send your payment of the required annual dues for 2018 by bank draft transfer or electronically (PayPal).

Membership Fees per year:

The **Individual Annual Membership Fee** is:

- 50 Euro (full member)
- 40 Euro (ISTMB, JSMB, NVTB, SFBT, SMB full member)
- 25 Euro (student, developing country or Eastern European member)
- 20 Euro (student SMB member)

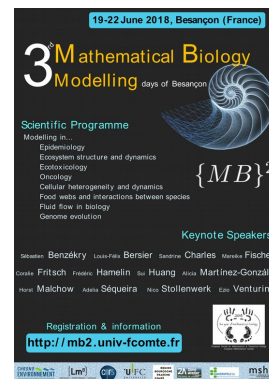
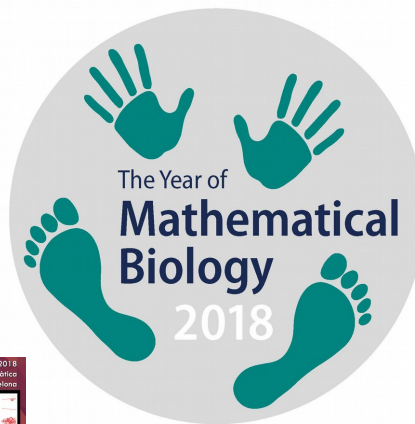
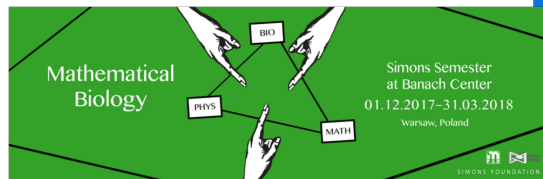
The **Institutional Annual Membership Fee** is: 200 Euro

The **Life Membership Fee** is:

1. 750 EUR (age 40 or above)
2. 500 EUR (age 50 or above)
3. 250 EUR (age 60 or above)

Further information:

Bob Planqué, ESMTB treasurer
Department of Mathematics
Vrije Universiteit
r.planque@vu.nl



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