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Communications

ESMTB
European Society for Mathematical
and Theoretical Biology

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Letter from the President

Dear fellow mathematical and theoretical biologists,

Once more, the ESMTB board has been renewed and I am writing to you after my first year in office as president. First of all, my cordial thanks go to the outgoing members Andrea deGaetano, Susanne Ditlevsen, Torbjörn Lundh, and Anna Marciniak-Czochra, for their six years of selfless service to the community. Together with the continuing board members (Maíra Aguiar, Luděk Berec, Sílvia Cuadrado, Bob Planqué, and myself), they have, under the able guidance of Andrea, achieved a major administrative overhaul (modern member administration system, professional bank account, new logo, new web page, a new prize, new guidelines for various procedures, …, new everything), so we are now all shiny, fresh, and in good shape for the future. This gives the new board the privilege to concentrate more on scientific issues.

Tom Britton, José Antonio Carrillo, Elisenda Feliu, Benoît Perthame, and Angélique Stéphanou have joined the board as new members. José is vice president and our representative with ICIAM, the International Consortium of Industrial and Applied Mathematics, where ESMTB is a member. Likewise, Benoît is our delegate with EMS, the European Mathematical Society. Angélique takes care of the Communications you are just reading, and Elisenda is responsible for the email newsletter; moreover, Elisenda and Maíra jointly care about society communication and promotion. Tom is the master of our prizes (the Ovide Arino Outreach Award and the Reinhart Heinrich Prize), while Sílvia is the new secretary. Bob continues as treasurer, while Luděk takes care of the new colloquium and remains responsible for summer schools and educational matters. But these roles only tell part of the story. Much of what we do is the joint work of all of us.

Let me briefly mention the main cornerstones of our work in this first year. Early in 2021, and with the specific involvement of Benoît and José, we finalised the renegotiation of our cooperation contract with SpringerNature about ESMTB's official journal, the Journal of Mathematical Biology (JoMB). Among other things, this implies substantial influence of the society on the development of the journal; in particular, it means that we are involved in the choice of the editors in chief. I am happy to report that, after Anna Marciniak-Czochra was appointed successor of Mats Gyllenberg in 2020 (and took office in 2021), Thomas Hillen was appointed successor of Mark Lewis in 2021 (and will take office in 2022). This is in an excellent tradition, not least because Thomas is a scientific son of Karl Hadeler, who was a founder of both ESMTB and JoMB, the second president of ESMTB, and managing editor of JoMB for about 25 years. I am happy to see the journal in Anna's and Thomas' hands and look forward to a fruitful collaboration.

Some other actions may have been more visible to the majority of our members. In spring, we started the ESMTB online colloquium, with top-level speakers and substantial resonance in the community. The first bunch of talks for 2022 is already on our web page. Next, with Bob, Maíra, and myself as members of the organising committee, we were deeply involved in the preparation and the running of the virtual SMB 2021 meeting, where SMB (the Society of Mathematical Biology) partnered with KSIAM (the Korean Society for Industrial and Applied Mathematics) and ESMTB. And when that was done, we started thinking about the next European conference, ECMTB 2022 in Heidelberg (once more a joint endeavour with SMB), under conference chair Anna Marciniak-Czochra and with Bob, Sílvia, and Maíra (and Torbjörn Lundh from the previous board) as members of the scientific committee. Since the last ECMTB (2018 in Lisbon), we had to postpone our flagship conference twice due to Covid and now sincerely hope that it will take place (September 19-23, 2022), but the effort required is multiplied due to the insecure perspective and the planned (partial) hybrid option. All this is a heroic effort for Anna, and we will support her in all possible ways.

You will also have noticed that we cut our membership fees in half (thus passing on to our members the reduced expenses on conference and travel support due to Covid) and that Elisenda untiringly supplies you with information via the email newsletter, which, by the way, members and non-members alike may subscribe to. Indeed, we have come a long way — I still remember stuffing the very first edition of the printed Biomathematics Newsletter into envelopes in 1988, as a PhD student in Wolfgang Alt's group in Bonn. The entire group was sitting on the library floor, paper scattered everywhere. It took forever, but we had a lot of fun!

With cordial regards

Ellen Baake

Ellen Baake

Meet the new board of ESMTB

The continuing board members

Maíra Aguiar is a biologist by training and she holds a double PhD degree in Population Biology (by Lisbon University, Portugal) and Life Sciences (by VU Amsterdam, The Netherlands). 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-born (and other) diseases and develop and evaluate the introduction of intervention strategies including vector control and vaccination. With a large experience in scientific meetings' organization, she has organized and celebrated, for the past ten years, the Workshop DSABNS with wide national and international participation. She was also part of the Scientific Committee of the 11th European Conference of Mathematics and Theoretical Biology, that took place in Lisbon in 2018, and was co-Chair of this event.

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 stochastics (branching processes, interactive particle systems, duality, large deviations, and stochastic simulations) and discrete and continuous dynamical systems (in particular bifurcation theory). She is the speaker of the Research Centre for Mathematical Modelling (RCM^2), the central academic institution of Bielefeld University that provides a common platform for applications of mathematics, in particular in the sciences. She has coordinated the Priority Programme 'Probabilistic Structures in Evolution' (2011-2020), a research consortium funded by DFG (German Research Foundation) devoted to the in-depth theoretical study of stochastic processes in population genetics, stochastic models of adaptive dynamics, and probabilistic aspects of evolutionary game theory. She is an associate editor of the Journal of Mathematical Biology.

Luděk Berec 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 emphasis 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 was one of the organizers of the *Intensive Research Program in Mathematical Biology* (Centre de Recerca Matemàtica), one of the three theme semesters of the Year of Mathematical Biology.

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 postdoc 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.

The new board members

Tom Britton holds the Cramér chair in Mathematical statistics, at the Department of Mathematics at Stockholm University (Sweden). He did his PhD in the same university, and after this he did a Post Doc with Niels Becker in Australia, followed by Associate professor at Uppsala University (Sweden). He has written just above 100 scientific research papers and 3 research monographs, all on Epidemic modelling. Over the years his three main research areas have been epidemic modelling (both theoretically and applied to specific diseases), phylogenetics/genetics and network modelling. His background is probability and statistics. Among other things he has been using coupling, weak convergence, branching processes, diffusion theory, martingale theory, survival analysis, inference theory, MCMC and particle filtering, when addressing various problems in the fields mentioned above. He has been deeply involved in modelling and analyses of Covid-19 and he has frequently been interviewed in both national and international media. He is currently the chairman of the Cramér Society (the Swedish academic statistical society). He has been associate editor for Journal of Mathematical Biology for 10 years, and he is a Deputy Editor for PLoS Computational Biology.

José A. Carrillo is currently Professor of the Analysis of Nonlinear Partial Differential Equations of the OxPDE group in the Mathematical Institute at the University of Oxford and affiliated to the Wolfson Center of Mathematical Biology. He previously held academic positions at Imperial College London, Universitat Autònoma de Barcelona, and Universidad de Granada, where he also did his PhD. He works on kinetic and aggregation-diffusion equations. He has contributed to the theoretical and numerical analysis of PDEs, and their simulation in different applications such as granular media, semiconductors and lately in collective behavior models in Mathematical Biology and Computational Neuroscience. He was the chairman of the Year of Mathematical Biology Committee in 2018 organized by the ESMTB and the EMS.

Elisenda Feliu is Associate professor at the Department of Mathematical Sciences, University of Copenhagen. Her current research field primarily concerns the development of mathematical theory for the analysis of models in molecular biology, mainly using algebraic approaches. In this context, her fascination for biology and pure mathematics nicely meet: she holds a PhD in Mathematics, followed by a master in Bioinformatics. A tipping point in her career was the competitive Sapere Aude Starting Grant from the Danish Research Council (2015), which allowed her to start her own research group, and led to her admittance to the Young Academy of Denmark. In 2018-2019, she was secretary of the SIAM activity group on algebraic geometry, mainly in charge of communication with members, and she gained good insight into SIAM's organization.

Benoît Perthame is a professor at Sorbonne Universite, formerly known as Paris 6, and was head of the Jacques Louis Lions laboratory 2013-2019. He has been elected to the french Académie des Sciences in 2018 and he is currently running the Adora ERC advanced grant. He is co-editor in chief of Acta Applicandae Mathematicae. His scientific background is on nonlinear Partial Differential Equations, from control theory, Boltzmann theory and conservation laws. At the end of the previous century he decided to fully re-orient his research to the direction of mathematical biology. For that purpose he organized an Inria team (now called Mamba) on this subject and an option of master degree in his university. He is a theoretician and his interests are broad in terms of biology fields (bacterial movement, tissue growth, chemotaxis, neuroscience, evolution).

Angélique Stéphanou is a CNRS researcher at the TIMC Laboratory in Grenoble since 2004. She initially trained as a physicist and then did a PhD in Mathematical Biology jointly in the Universtity of Dundee and Joseph Fourier University in Grenoble. Her initial scientific interest was towards morphogenetic processes using mathematical and computational approaches, coupling PDEs and agent-based systems. She studied cell deformations and motility, vascular development and angiogenesis. That progressively led her to consider tumour growth and anticancer therapies using hybrid multiscale and multiphysics models. She is a member of the editorial board of Acta Biotheoretica and member of the board of the French-Speaking Society for Theoretical Biology (SFBT).

News from the Journal of Mathematical Biology

For nearly 14 years, ESMTB's official journal, the Journal of Mathematical Biology (JoMB), has been steered by Mats Gyllenberg (University of Helsinki) and Mark Lewis (University of Alberta, Edmonton) as Editors in Chief. With their remarkable insight and clever judgement, they have managed the challenging task to navigate the journal on its high-quality track.

We now have a change at the top: Anna Marciniak-Czochra and Thomas Hillen follow in Mats' and Mark's footsteps as the new Editors in Chief.

Anna Marciniak-Czochra is a professor of applied mathematics at Heidelberg University, Germany, and head of the research group *Applied Analysis and Mathematical Modelling in Biosciences* at the Institute of Applied Mathematics (IAM), Interdisciplinary Center for Scientific Computing (IWR) and the Bioquant Center. Her research focus is mathematical modelling and analysis of dynamics of self-organisation and structure formation in multicellular systems. Specific applications include stem cell basis of hematopoiesis, neurogenesis, organ development and cancer, and molecular and mechano-chemical mechanisms of developmental pattern formation. Her mathematical toolbox includes partial differential equations, dynamical systems, and multiscale and singular perturbation analysis, with emphasis on methods of model upscaling and reduction. Pursuing developments on the confluence of mathematics and biosciences, she was a member of the ESMTB board in 2014–2020 and is the chair of the 12th European Conference on Mathematical and Theoretical Biology (ECMTB), a joint ESMTB-SMB enterprise to be held in Heidelberg in September 2022. Her term as co-Editor in Chief of JoMB has started in March 2021.

Thomas Hillen (he/him) is a professor in the Department of Mathematical and Statistical Sciences at the University of Alberta. His main research interests include the mathematical modeling of cancer, cancer growth, diagnosis, and treatment with an emphasis on cell movement behaviour. He applies these movement models to a much wider range of fields beyond cancer, such as chemotaxis, wolf movement on inhomogeneous habitats, sea turtle orientation, and forest fire spread. His tools range from dynamical systems via partial differential equations to stochastic models. Over the years, he has developed a keen interest in the scientific publication landscape, cherishing traditional publications in high profile journals and exploring new media such as online blogs and online videos. As Associate Editor of 10 scientific journals and co-founding editor in chief of *Mathematics in Science and Industry* he gained valuable experience in journal publishing. Thomas obtained his PhD in 1995 under the supervision of Karl Hadeler, one of the founders of the journal. It is a great honour for him to continue this legacy. His term as co-Editor in Chief of JoMB has started in January 2022.

Mats' term has ended in December 2021. After an interim phase, Mark will step down in the course of 2022. We cannot thank Mats and Mark enough for their commitment and service to the journal and the community.

The 1927 epidemic model of Kermack and McKendrick : a success story or a tragicomedy?

By Odo Diekmann
Mathematical Institute, Utrecht University,
the Netherlands

1. How it started

At the end of the 19th century, it was suspected that malaria was not caused by bad air, as the Italian name suggests, but by a parasite. It was, however, a mystery how the parasite was transmitted. In 1897 Ronald Ross resolved this mystery by establishing that mosquitos acted as a vector. Ross received the 1902 Nobel prize for physiology/medicine for this discovery and in 1911 he was knighted.

Ross had many talents (he wrote poems and novels, composed music, made drawings, ...). He also was a keen mathematician and after his discovery he used mathematical models to show that malaria could be eliminated by bringing the ratio of mosquito - to human density below a certain threshold value.

In 1901, Ross went on a mission to Sierra Leone to improve the local anti-malarial measures. Among the other people taking part in the mission, was the 25-year-old Anderson Gray McKendrick, who, after completing medical studies at the University of Glasgow, had entered the Indian Medical Service and was trained in military and tropical medicine. It seems safe to conclude that Ross instilled into the young McKendrick a sincere interest in both infectious diseases and mathematics (the former being natural and to be expected, the latter being catalysed by the coincidence that McKendrick possessed a probably even greater talent for mathematics than Ross himself).

After the Sierra Leone mission, McKendrick served for almost two decades in India, where he investigated rabies in particular (the treatment of patients and the preparation of vaccine being an important part of these investigations). In 1920 he returned to Scotland for health reasons and then he started to work at the Royal College of Physicians in Edinburgh. In 1921, the 23-year-old (bio)chemist William Ogilvy Kermack joined the college. In 1924, Kermack (who had safely completed service in the Royal Airforce during the First World War) lost the sight in both of his eyes in a lab explosion. It is not known to the writer of this story when and how the collaboration between McKendrick and Kermack started, but in 1927 the Proceedings of the Royal Society A contained the joint paper "A contribution to the mathematical theory of epidemics" [1]. A truly brilliant paper !

2. The model

The incidence of an infectious disease is defined as the number of new cases per unit of time (e.g., per day) in a specified population or geographical area (or per unit of area). The force of infection on a susceptible individual is defined as the probability per unit of time of the susceptible becoming infected. A key assumption of the Kermack-McKendrick model states

incidence = force of infection times size of the susceptible subpopulation

(this is a variant of the Principle of Mass Action of chemical kinetics, see [2]; often 'size' is measured in terms of spatial density, but alternatively one can consider the number of inhabitants of a certain geographical area, for instance a country; the main requirement is that 'incidence' and 'susceptible subpopulation' use the same measuring stick).

The next step is to elaborate the idea that the current force of infection is generated by individuals that were themselves infected some time ago (note that now we focus on direct host-to-host transmission rather than on vector transmission). So we want to relate the current force of infection to the incidence in the past. Here, following earlier work by Ross and Hudson (see [2,3], also for the precise references), [1] adopts a top down approach and introduces as the one-and-only model ingredient a description of the expected contribution to the force of infection at time tau after infection. Here tau varies from zero to infinity, but common sense suggests that the contribution vanishes for both small and large values of tau. For any specific disease one may, in principle, use a within-host model of the struggle between parasite and immune system to provide a quantitative version of this description bottom up. The aim of the Kermack-McKendrick paper [1], however, is to derive the qualitative consequences of the assumption, to develop a general theoretical framework as a backbone for studies of specific diseases.

The next assumption is that the population is demographically closed, meaning that transmission of the infectious disease happens on a fast time scale relative to the time scale of demographic turnover, i.e., the time scale of birth, death and migration of host individuals (think of an influenza epidemic hitting a human population in, say, a period of half a year, while humans have a life expectancy of, say, 80 years).

The final assumption is that infection ends with complete immunity, i.e., a host individual cannot be infected a second time.

As a consequence of the last two assumptions the susceptible subpopulation only changes due to the infections that happen. More precisely: the rate at which the size of the susceptible subpopulation diminishes exactly equals the incidence.

As shown in [1,4,5] one can derive, from these assumptions, a scalar nonlinear renewal equation [6] for the force of infection as a function of time. An analysis of this equation then yields the following epidemiological insights:

i) if a newly infected individual is introduced in an otherwise susceptible population, the expected number of secondary cases, called the Basic Reproduction Number and denoted by the symbol R_0 (pronounce as “R nought”), equals the product of the total population size and the expected cumulative (i.e., integrated over all tau) contribution to the force of infection; if $R_0 < 1$ the introduction does NOT lead to an epidemic, but if $R_0 > 1$ it may very well lead to an epidemic outbreak and, if it does, a fraction $1 - x$ of the host population will become infected, with x the positive solution of the equation

$$x = \exp(-R_0(1 - x))$$

ii) In the initial phase of an outbreak the incidence grows exponentially with rate r (the so-called Malthusian parameter) implicitly defined as the positive root of a relatively simple (characteristic) equation. Note that data about a newly emerging infectious disease yield estimates of r while estimating the control effort needed to stop the outbreak requires information about R_0 (control reduces R_0 with a certain factor and the aim is to bring R_0 to a value below one). So it is of paramount importance to understand how R_0 and r relate to each other and here the dependence of the contribution to the force of infection on the time tau elapsed since infection plays a crucial role.

Once again we refer to [1,4,5] for a detailed exposition.

3. A very special case of the model

If one assumes that a newly infected individual 'enters' the compartment of infectious individuals and

- provides a constant contribution to the force of infection while being in this compartment
- does stop contributing when leaving the compartment
- leaves the compartment with a constant probability per unit of time (or, in other words, has an exponential sojourn time)

one can substitute the renewal equation by an equivalent system of ordinary differential equations (ODE), called the S-I-R compartmental system (with S standing for 'susceptible', I for 'infectious' and R for 'removed'). This S-I-R system is nowadays the prototype epidemic model, figuring in countless textbooks.

4. Success (somewhat overshadowed by misconception)

On September 15 2020, [1] had 7940 citations on Google Scholar and the website of the Royal Society mentioned that the paper was downloaded 38194 times since first published online. These figures suggest that the paper is immensely successful. Yet there are reasons to doubt that it is ever read ! Indeed, an incessant community-enforced misconception is that the paper is just about the very special case, the S-I-R model. A comical consequence is that time and time again manuscripts are submitted, and often even published, about a "generalization" that is in fact only a slightly less special case of the true Kermack-McKendrick model.

One may wonder why this misconception is so persistent. No doubt the tendency to parrot plays an important role. But another factor is, very likely, the fact that ODE are the standard modeling formalism for most applied mathematicians and that a wealth of theory and a multitude of tools exist for ODE, while, in contrast, renewal equations occupy an obscure infinite-dimensional corner of the world of dynamical systems (but see [7] for recent developments). It is tempting to deny the unfamiliar ...

Anyhow, the 1927 Kermack-McKendrick paper is, in my opinion, definitely a success story, but with a tragicomical lining because the true gem remains mostly unnoticed, despite the spotlights.

5. About motivation and attitude

When authors of 'generalization' manuscripts are told about the real contents of [1], they tend to be irritated. Quite recently, the information even triggered a somewhat aggressive reaction: you are whining about a paper from 1927, that is prehistory! The aim of our paper is to show that we are smarter than all those other young scientists that compete for a tenure track position and only recent papers matter for us. (Admittedly this is a rather free and subjective translation of the literal text, but I claim that it captures the essence.)

Now contrast this with the picture of Anderson Gray McKendrick that W.M. Hirsch sketches in [8]. It is clear that McKendrick's motivation was to fight infectious diseases while building on general insights derived in the context of mathematical models. His goal was to develop knowledge and understanding and, ultimately, control. As far as one can guess, he was not thinking in terms of competition. The quote of Hirsch

"McKendrick was a truly Christian gentleman, a tall and handsome man, brilliant in mind, kind and modest in person, a skilful counsellor and administrator who gave of himself and knew how to enable others."

in fact suggests the opposite!

So the most tragical aspect of the Kermack-McKendrick story is probably not that, despite the many citations, the paper is hardly ever read, but that the story illustrates how we developed a system of evaluation of scientific research that drives young talents to publish quickly and profusely without much attention for meaning or for 'old' papers in which tremendous wisdom lies hidden.

Acknowledgement
Suggestions by Hans Heesterbeek and KaYin Leung are gratefully acknowledged. This article was reprinted with the friendly permission of the Japanese Society for Mathematical Biology (JSMB), from SMB Newsletter No.92, pp.8-11, 2020.

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[8] `http://mathshistory.st-andrews.ac.uk /DNB/McKendrick.html` (accessed on September 15, 2020)

Based on a lecture for the Finnish Society of Science and Letters, delivered in Helsinki, October 21, 2019.

Meanwhile a lot of activity was triggered by the outbreak of Covid-19. For the present context the following publications seem most relevant:

Alexei V. Tkachenko, Sergei Maslov, Ahmed Elbanna, George N. Wong, Zachary J. Weiner, Nigel Goldenfeld, Time-dependent heterogeneity leads to transient suppression of the COVID-19 epidemic, not herd immunity, *PNAS* (2021) 118(17): e2015972118 `DOI: 10.1073/pnas.2015972118`

Mircea T. Sofonea, Bastien Reyné, Baptiste Elie, Ramsès Djidjou-Demasse, Christian Selinger, Yannis Michalakis, Samuel Alizon, Memory is key in capturing COVID-19 epidemiological dynamics, *Epidemics* 35 (2021) 100459 ISSN 1755-4365, `https://doi.org/10.1016/j.epidem.2021.100459`

O. Diekmann, H.G. Othmer, R. Planqué, M.C.J. Bootsma The discrete-time Kermack-McKendrick model: A versatile and computationally attractive framework for modeling epidemics *PNAS* (2021) 118: 39 e2106332118

M. Kreck, E. Scholz Back to the roots: A discrete Kermack-McKendrick model adapted to Covid-19 `https://arxiv.org/abs/2104.00786`

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!

Mathematical Medicine at Swansea University

Our group is based in the Mathematics Department in Swansea University - consisting of two faculty members, one postdoctoral research assistant, and six PhD students - each of their research areas detailed below. We use interdisciplinary multi-scale approaches and utilise mathematics to understand the underlying complexity of various biological and biomedical problems in medicine. Our aim is to find new ways in which medicine can improve the chance of survival and quality of life for patients that suffer from various diseases. Our research focuses on a number of topics such as multi-scale modelling of cancer progression and multimodality treatment responses, radiation ecology, modelling and understanding of sepsis and problems in development, evolution and disease. We are part of the Covid-19 pandemic modelling group at Swansea University and we closely collaborate with clinicians, experimentalists and industrial partners such as AstraZeneca.

STAFF MEMBERS

Dr Noemi Picco

I work at the interface between mathematics and biology. My main focus is on mathematical modelling of health and disease with a particular focus on cancer, sepsis, and the developing brain. I use a range of theoretical and computational tools to describe the dynamical interactions occurring at different spatial and temporal scales. My work in mathematical oncology uses individual-based models coupled to partial differential equations to study the interactions between a tumour and its environment. I am also using population dynamics to study the development of the cerebral cortex and to map the divergent evolutionary trajectories that give rise to differences between mammalian species. I am actively working on ways to integrate experimental data into mathematical models in order to quantitatively describe the processes of interest and make testable predictions.

I enjoy working in close contact with experimentalists and developing new collaborations to study problems in development, evolution and disease.

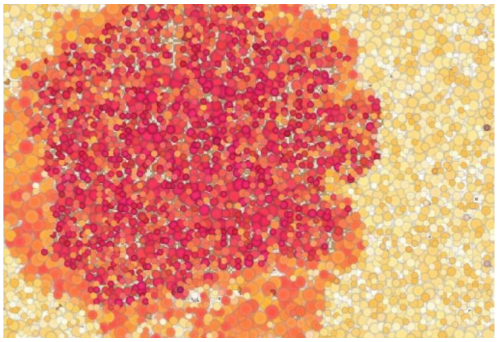
Dr Gibin Powathil

My primary research interests are in mathematical biology and mathematical oncology. In particular, I am interested in multiscale mathematical modelling of cancer and associated therapies, which will eventually help towards Model Assisted Personalised Medicine. These mathematical and computational models can be very helpful in gaining valuable insights into the mechanisms and consequences of various complex intracellular and intercellular changes during and after therapy. I am also interested in radiation ecology and works closely with multidisciplinary experts to understand the effects of low dose radiation and its role in clinical radiation and environmental protection. My work is in the interface of mathematics and medicine and I have active collaborators in clinical oncology, cancer biology and pharmaceutical industry.

POSTDOCTORAL RESEARCH ASSISTANT

Dr Carla White

My current research is studying the effects of small molecule drugs on solid tumours. This involves the development of a multi-scale/multi-cell model, combining agent-based tumour models with ODE drug binding models. I am also part of the Covid-19 modelling team at Swansea University. I completed my PhD, entitled ‘Contributions to mathematical pharmacology: new receptor theory with dimeric receptor models’, in 2021. During this time, I developed a number of models for drugs interacting with receptors and analysed these using techniques such as asymptotic analysis and structural identifiability analysis.



Hybrid cellular automata model of tumour-stroma interactions. 2D section of an *in silico* tissue with heterogeneous populations of fibroblasts (yellow) and cancer (orange/red).

PHD STUDENTS

Tabitha Lewis

I am a first-year Mathematics PhD student. My project is titled 'Machine Learning-Guided Dynamical Systems Modelling of Sepsis' and is under the primary supervision of Dr Noemi Picco. Sepsis is highly complex and unpredictable, where patients with mild symptoms can very quickly degenerate into those requiring resuscitation. By exploring sepsis in mice, I aim to identify possible biomarkers and turning points through machine learning and mathematical techniques.

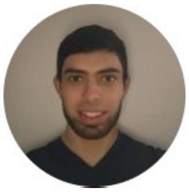
Leonardo Lonati

I am currently a third-year PhD student at the University of Pavia under the primary supervision of Dr Giorgio Baiocco and a visiting student at Swansea University under the supervision of Dr Gibin Powathil. Currently, I am working on studying alteration of cell cycle progression due to X-ray radiation, both implementing a mathematical model to predict the delays in time as a function of dose, with supporting experimental measurements on an in vitro system on a colorectal adenocarcinoma cell line (Caco-2).

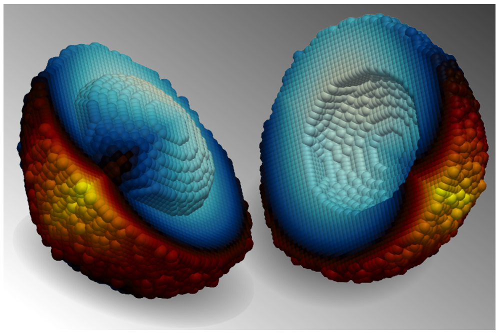
Amy Milne

I am in my first year of my PhD under the supervision of Dr Noemi Picco. My area of research is modelling the spatial ecology of cancer. I will consider the spatial and evolutionary aspects of the tumour and its microenvironment that affect the efficiency of intermittent treatments through the development and maintenance of resistance due to environment-mediated drug resistance.

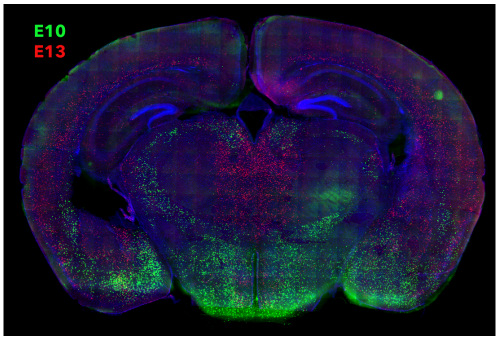
Sam Oliver



I am a first-year PhD student under the supervision of Dr Gibin Powathil. My area of research is looking into how adipose tissue and its composition can play a role in the development and progression of certain types of cancer. I am particularly interested in using mathematical models to predict how tumours will respond to different methods of treatment as this can give an important insight into what results can be expected when administered to a patient.



The image demonstrates how oxygen levels vary amongst cancer cells in a simulated, cracked open tumour spheroid where the different colours correspond to various oxygen concentrations. Cells with high oxygen concentrations are displayed in warm colours such as yellow and red whilst cells with low oxygen concentrations are displayed in cold colours such as blue. Springer, `https://doi.org/10.1007/978-3-030-33471-0_25`.

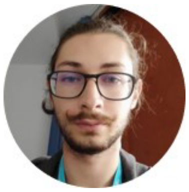


A cross-section of the developing mouse brain. Staining reveals location and birth time of neurons. In green, early-born neurons at embryonic day 10 (E10), in red, neurons born at mid-neurogenesis (E13). Mathematical modelling can help us integrate the spatio-temporal dynamics occurring during neurogenesis in brain development, giving us a mechanistic understanding of the processes involved. Image courtesy of Dr Fernando García-Moreno (Achucarro Basque Center for Neuroscience).

Kira Pugh

I am a second-year PhD student under the primary supervision of Dr Gibin Powathil. I am working on developing a mathematical model to study the effects and responses of DNA Damage Response (DDR) inhibiting drugs. The goal of the model is to predict the effects of the DDR inhibitor drugs in combination with each other, and in combination with other DNA damaging therapies such as radiation therapy or chemotherapy – with the aim to predict optimal scheduling, sequencing and dosage of the drugs.

Kévin Spinicci



I am a second-year PhD student under the supervision of Dr Gibin Powathil, at the University of Swansea, and Dr Angélique Stephanou, at the TIMC laboratory in Grenoble. I am studying the effect of the Hypoxia Inducible Factor (HIF) on cellular metabolism heterogeneity in the tumour. My work will combine two approaches: pathway enrichment analysis, to determine which precise pathways are deregulated in the case of cancer, and the development of a multi-agent mathematical model, to simulate tumour growth in 2D/3D. The aim will be to perform drug repurposing to find potential candidates in cancer therapy.

Centre for Biomathematics

We are also a part of the **Centre for Biomathematics** at Swansea University. The Centre for Biomathematics provides an interdisciplinary community for researchers from across various faculties with interests on the interface between mathematics and biology or medicine. The primary aim of the centre is to foster interdisciplinary collaborations which are mutually interesting, leading to new developments in both fields, from biologically-informed predictive models for applied questions across biology and medicine to new theoretical developments in mathematics and computer science. The centre organises frequent colloquia and supports interdisciplinary projects. For more details, please visit `https://biomaths.swansea.ac.uk`

For more information on the work we do, please visit `https://mathematicalmedicine.swansea.ac.uk`

SMB 2021 Report

As all SMB meetings, SMB2021 covered all aspects of mathematical biology. Special emphasis this year was on the impact of Mathematical Biology on Translational Science & Promotion of Diversity, Equity, and Inclusion.

Meeting Partner Societies: Society for Mathematical Biology (SMB), European Society for Mathematical and Theoretical Biology (ESMTB) and Korean Society for Industrial and Applied Mathematics (KSIAM).

Webpage: `https://www.smb2021.org/home`

Contributions of Individual Members of the Organizing Committee and Judges: `https://www.smb2021.org/acknowledgments`

International Sub-Committees of the Organizing Committee:

Cooperation with ESMTB: Mark Alber, Ellen Baake, Weitao Chen, Lisette de Pillis, Amber Smith, Roeland Merks, Maíra Aguiar, Daniele Avitabile, Robert Planqué

Cooperation with Asia & Oceania and KSIAM: Weitao Chen, Heyrim Cho, Jae Kyoung Kim, Peter Kim, Gen Kurosawa, Lei Zhang

Conference Information: While COVID-19 was spreading across the world, the Society for Mathematical Biology kept the health and safety of its members as the top priority. We held the 2021 Annual Meeting in a virtual form between June 13-17, 2021. The meeting was held 24 hours a day to maximize the participation of people across the world.

Dates (in Americas and Europe/Africa): Monday, June 13 – Thursday, June 17, 2021

Dates (in Asia/Oceania): Monday, June 13 – Friday, June 18, 2021

Online platforms used:

- Webinars hosted and recorded with Zoom.
- Sococo used to coordinate webinar links, host poster sessions, networking, and provide industry interface.
- Slack for announcements, support, and discussion.
- Support provided by Mathdept.org

Leadership of the Organizing Committee:
Mark Alber (Chair), Univ. of California, Riverside, USA
Amber Smith (Vice Chair), Univ. Of Tennessee Health Science Center, USA
Weitao Chen (Associate Chair), Univ. of California, Riverside, USA

Jolene Britton (Assistant Chair), Univ. of California, Riverside, USA
Francesco Pancaldi (Assistant Chair), Univ. of California, Riverside, USA

Scientific Committee:
Mark Alber, Univ. of California, Riverside, USA
Ruth Baker, Univ. of Oxford, UK
Reinhard Laubenbacher, Univ. of Florida, USA
Suzanne Lenhart, Univ. of Tennessee, Knoxville, USA
Philip Maini, Univ. of Oxford, UK
Anna Marciniak-Czochra, Heidelberg Univ., Germany
Gibin Powathil, Swansea Univ., UK
Santiago Schnell, Univ. of Michigan, USA
Amber Smith, The Univ. of Tennessee Health Science Center, USA

Organizing Committee:
Maíra Aguiar, Basque Center for Applied Mathematics, Bilbao - Basque Country, Spain
Mark Alber (Chair), Univ. of California, Riverside, USA
Paul Atzberger, Univ. of California, Santa Barbara, USA
Daniele Avitabile, Vrije Universiteit Amsterdam, The Netherlands
Ellen Baake, Bielefeld Univ., Germany
Mario Banuelos, California State Univ., Fresno, USA
Mikahl Banwarth-Kuhn, Univ. of California, Merced, USA
Jolene Britton (Assistant Chair), Univ. of California, Riverside, USA
Sunny Canic, Univ. of California, Berkeley, USA
William Cannon, Pacific Northwest National Laboratory, USA
Weitao Chen (Associate Chair), Univ. of California, Riverside, USA
Heyrim Cho, Univ. of California, Riverside, USA
Yat Tin Chow, Univ. of California, Riverside, USA
Lisette de Pillis, Harvey Mudd College, USA
Amina Eladdadi, The College of Saint Rose, Albany, USA
German Enciso, Univ. of California, Irvine, USA
Marcella Gomez, Univ. of California, Santa Cruz, USA
Melissa Gomez, Univ. of California, Riverside, USA
Jia Gou, Univ. of California, Riverside, USA
Robert Guy, Univ. of California, Davis, USA
Alexander Hoffmann, Univ. of California, Los Angeles, USA
Chiu-Yen Kao, Claremont McKenna College, USA
Jae Kyoung Kim, KAIST, South Korea
Peter Kim, Univ. of Sydney, Australia
Denise Kirschner, Univ. of Michigan Medical School, USA
Natalia Komarova, Univ. of California, Irvine, USA
Gen Kurosawa, RIKEN, Japan
Doron Levy, Univ. of Maryland, USA
James Marberry, Univ. of California, Riverside, USA
Alison Marsden, Stanford Univ., USA
Roeland Merks, Leiden Univ., The Netherlands
Andrew D. McCulloch, Univ. of California, San Diego, USA
Christian Michael, Univ. of California, Riverside, USA
Qing Nie, Univ. of California, Irvine, USA
Francesco Pancaldi (Assistant Chair), Univ. of California, Riverside, USA
Mykhailo Potomkin, Univ. of California, Riverside, USA
Gibin Powathil, Swansea Univ., UK
Robert Planqué, Vrije Universiteit Amsterdam, The Netherlands
Russell Rockne, Beckman Research Institute of City of Hope, USA
Suzanne Sindi, Univ. of California, Merced, USA
Amber Smith (Vice Chair), Univ. Of Tennessee Health Science Center, USA
Kevin Tsai, Univ. of California, Riverside, USA
Qixuan Wang, Univ. of California, Riverside, USA
Dominik Wodarz, Univ. of California, Irvine, USA
Roya Zandi, Univ. of California, Riverside, USA
Lei Zhang, Peking Univ., China

Registered Participants and Talks:
Registered Attendees: **2585**
Number of countries involved: **47**
Attending the Early Career workshop: **867**
Maximum number of parallel sessions: **12**
Number of talks: **744** Mini-Symposium talks and **275** Contributed Talks
Number of posters: **196**
Number involved in mentoring program: **466** as mentees, **153** as mentors, and **130** both

Plenary Speakers:
Sandra Loerakker, Eindhoven Univ. of Technology, Netherlands
Carrie Diaz Eaton, Bates College, USA
Denise Kirschner, Univ. of Michigan Medical School, USA
George Karniadakis, Brown Univ., USA
Michael Savageau, Univ. of California, Davis, USA
Jennifer A. Flegg, Univ. of Melbourne, Australia
Timothy Elston, Univ. of North Carolina, USA
Leah Edelstein-Keshet, Univ. of British Columbia, Canada
Anita Layton, Univ. of Waterloo, Canada
David Basanta, Moffit Cancer Center, USA
Christian A. Yates, Presentations from Best Paper Prize Winner
Alexander P. Browning*, Presentations from Best Student Paper Prize Winner

Conference Events:

Pre-Conference Program on June 13

- Public Lecture on Mathematical Biology & Translational Science

- Early Career Workshop
- DEI Discussion

Development of Diversity, Equity, and Inclusion Events

- Discussions Celebrating and Building Diversity in Mathematical Biology: Setting the stage for SMB2021
- Discussions Celebrating and Building Diversity in Mathematical Biology: Where do we want to go from here?
- Panel: A Conversation with Leaders in Building Equity & Inclusivity within Mathematical Biology
- Daily DEI Activity

Special Sessions

- Mathematical Biology in Industry
- Mathematics in Medicine

Special Meetings

- Meet with NSF Mathematical Biology Program Directors
- Meet with the Editors in chief of the Bulletin of Mathematical Biology & the Journal of Mathematical Biology
- Meet with the Senior Editor, Mathematics for Book Publishing @ Springer

Career Fair

- Meet with industry sponsors one-on-one in their Sococo booths
- Check out job postings
- Check out the CVs of SMB2021 registrants

Contributed Talk Prizes: Leonard Dekens, Zoe Lange and Franziska Kramer, William Martinson, Wayne Hayes, Tara Hameed, Sta Lea, Solveig Van der Vegt, Peter Thompson, Mohit Dalwadi, Mohammed Zahid, Miroslav Phan, Minseo Kim, Michael Raatz, Matthias M. Fischer, Martin Lopez-Garcia, Martjin de Jong, Johannes Borgqvist, Maalavika Pillai, Linus Schumacher, Kyle Dahlin, Kevin Murgas, John Parker, Jody Reimer, Jackie Taylor, Aniruddha Deka, Gess Iraji, Elizabeth Trofimenkoff, Dongheon Lee, Denis Patterson, Dana Kleimeier, Bevelynn Williams, Arwa Abdulla Baabdulla, Aneequa Sundus, Aden Forrow, Joshua C. Macdonald, Maíra Aguiar, Yukitaka Ishimoto.

Poster Prizes: Quynh-Anh Nguyen, Youngmin Park, Nao Yamamoto, Yun Min Song, Souvadra Hati, Sophie Fischer, Seokjoo Chae, Sara Hamis, Samarth Kadaba, Ryan Godin, Peter Nabutanyi, Pedro Henrique Pinheiro Cintra, Nicole Cusimano, Nathan Lee, Miranda Lynch, Michael Pablo, Lucy Lansch-Justen, Lucia Wagner, Lee Curtin, Laura Strube, Keith Harris, Dylan Dronnier, John Cody Herron, Hyundong Kim, Georgia Pope, Galina Kolesova, Eva Stadler, Emmanuel Adabor, Ellen Swanson, Daniel Cruz, Elba Raimundez, Daniel Cardoso Pereira Jorge, Connah Johnson, Chandler Gatenbee, Brydon Eastman, Benjamin Garcia de Figueiredo, Aparna Ramachandran, Anuraag Bukkuri, Angelica Bloomquist, Amanda Laubmeier, Alex John Quijano.

Workshop on Mathematical Modelling and Control for Healthcare and Biomedical Systems

The workshop took place online in the days 28-30 september 2021,

`http://www.biomatematica.it/mchbs2021/index.php`

The workshop covered research topics in scientific areas such as mathematical modelling in drug delivery, control strategies, biomaterials, tissue engineering, tumor growth and cancer therapeutics, smart devices and many other topics at the interface between biomedicine, bioengineering and mathematics. The aim of the workshop was to bring together young researchers and leading scientists from diverse disciplinary backgrounds interested in mathematical modelling and control for biological systems. The event provided a forum for discussion of basic aspects, new trends and challenging scientific and industrial applications on the highest level of international expertise.

Three keynote speakers were invited at the workshop:

- Levente Kovacs (Taming cancer: control engineering based tumor therapy)
- Mario Grassi (Drug delivery and mathematical modeling: an historical perspective)
- Davide Manca (Physiologically based pharmacokinetic modeling for individualized medicine with control applications)

The workshop saw the participation of about 80 attendees and 58 authors who presented the state-of-the-art research and the latest achievements in the above themes. Poster sessions were also part of the workshop that also included a Book of Abstracts with ISBN, published at the end of the event. 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.

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 member at the moment of submitting the application. The maximum amount of travel support per single application is currently 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.

Details and the application form are available at `https://www.esmtb.org/Travel-Support`

Minutes of the ESMTB board meetings (via videoconference)

November 11, 2020, 17:00-18:40

Members present: Maíra Aguiar (MA), Ellen Baake (EB; minutes), Silvia Cuadrado (SC), Andrea de-Gaetano (AdG; chair), Susanne Ditlevsen (SD; from 17:43), Toby Lundh (TL), Anna Marciniak-Czochra (AMC), Bob Planqué (BP)

absent (with apology): Luděk Berec

- ECMTB 2021, 2022: It is decided that the next ECMTB should take place in presence in Heidelberg. Given the impossibility of planning a big conference in 2021 under the spell of the pandemic, it is therefore postponed once more, to 2022; no event is planned for 2021 (not online either). ECMTB 2022 should preferrably be jointly with SMB (the normal rhythm is every four years, but the rhythm has been shattered by the current situation).

  EB will notify those who have already expressed their interest to organise the next ECMTB and solicit applications for ECMTB 2024 according to our rules. The result will be announced at ECMTB 2022. The official deadline for applications is July 2022, but we ask for bids as early as March 2022 in order to have time for questions and clarifications back and forth.

- Board elections: The end of 2020 brings about the end of a six-year term for four Board members: Andrea De Gaetano, Susanne Ditlevsen, Torbjörn Lundh, and Anna Marciniak-Czochra. The following 10 candidates ran in the 2020 Board elections:
  - Tom Britton (Stockholm, Sweden)
  - José A. Carrillo (Oxford, UK)
  - Elisenda Feliu (Copenhagen, Denmark)
  - Chaitanya Gokhale (Plön, Germany)
  - Haralampos Hatzikirou (Braunschweig, Germany)
  - Tommaso Lorenzi (Torino, Italy)
  - Benoît Perthame (Paris, France)

  - Constantinos Siettos (Naples, Italy)
  - Nikolaos Sfakianakis (St. Andrews, UK)
  - Angélique Stéphanou (Grenoble, France)

  The election took place place between 1 and 31 October, 2020; in total 113 active members expressed a preference for up to 5 candidates via their personal area within the ESMTB website.

  The results were:

  - Tom Britton: 63
  - Benoît Perthame: 63
  - José A. Carrillo: 61
  - Elisenda Feliu: 61
  - Angélique Stéphanou: 59
  - Tommaso Lorenzi: 55
  - Chaitanya Gokhale: 39
  - Haralampos Hatzikirou: 29
  - Nikolaos Sfakianakis: 29
  - Constantinos Siettos: 24

  The five newly elected board members are therefore: Tom Britton, Benoît Perthame, José Carrillo, Elisenda Feliu, and Angélique Stéphanou.

- Board transition: The joint meeting of the outgoing (AdG, AMC, SD, TL), the continuing (MA, EB, LB, SC, BP), and the newly-elected board members (Tom Britton, José Carrillo, Elisenda Feliu, Benoît Perthame, Angélique Stéphanou) will take place in the week December 7-11 via zoom. The meeting will include the election of the future president, vice president, treasurer, and secretary.
- Advertising in the Newsletter: It is decided that issues of journals will not be advertised in the Newsletter — with the exception of JOMB. Furthermore, nothing commercial will be advertised.
- Springer contract: The Board discusses the new draft of the Publishing Agreement with Springer and decides that the decision should not be taken without involvement of the new board; AdG will inform Springer accordingly.
- Conference support during COVID19 crisis: BP manages requests for support of transitions from presence to online meetings and will give out a small amount of support in recognition for mention of ESMTB.

December 11, 2020, 16:00-18:20

Participants: Maíra Aguiar (MA), Ellen Baake (EB; minutes), Luděk Berec (LB), Tom Britton (TB), José Carrillo (JC), Silvia Cuadrado (SC), Andrea deGaetano (AdG; chair), Susanne Ditlevsen (SD), Elisenda Feliu (EF), Toby Lundh (TL), Anna Marciniak-Czochra (AMC), Benoît Perthame (BP), Robert ('Bob') Planqué (RP), Angélique Stéphanou (AS)

The participants belong to the following terms:

2015–2020: AdG, AMC, SD, TL (outgoing members)
2018–2023: MA, EB, LB, SC, RP (continuing members)
2020–2026: TB, JC, EF, BP, AS (incoming members)

The outgoing and continuing members together form the 'old board', the continuing and incoming members form the 'new board'. The decisions in this meeting are to be taken by the old board, with the exception of the election of the officers of the new board, which are the responsibility of the new board alone.

- The old board briefly reports on the activities of the past three years to the incoming board members.
- JOMB:
  - The current status of the JOMB publishing agreement between Springer and ESMTB is briefly discussed. The new board will tend to this early in 2021.
  - Mats Gyllenberg will step down as editor-in-chief of JOMB at the end of 2021. Springer suggests AMC as his successor. The board agrees with this unanimously, and AdG will communicate this to Springer.
- Election of ESMTB board officers: After brief self-presentations of the candidates, namely MA (candidate, president), EB (candidate, president), JC (candidate, vice president), and RP (candidate, treasurer), EB is elected president by the new board via secret ballot (6 votes for EB, 3 votes for MA, 1 abstention). JC and RP are elected vice president and treasurer, respectively, by acclamation. SC is acclaimed secretary.
- Passage of responsibilities (to take effect Jan. 1, 2021):

  - EB automatically becomes legal representative of ESMTB for ICIAM and EMS (of which ESMTB is a member). It may be decided that one or both of these responsibilities are delegated to other board members; in the old board, AMC was EMS delegate.
  - EF takes over the responsibility for the Newsletter from SC.
  - AS takes over the responsibility for the Communications from SD.
  - MA and EF take care of Facebook and Twitter.
  - TB or BP will take over the responsibility for the prizes (Reinhart Heinrich prize and Ovide Arino outreach award) from TL.

Ellen Baake
ESMTB Secretary

March 24, 2021, 14:00-16:20

Members present: Maíra Aguiar (MA), Ellen Baake (EB), Tom Britton (TB), José Antonio Carrillo (JAC), Sílvia Cuadrado (SC), Elisenda Feliu (EF), Benoît Perthame (BP), Bob Planqué (BP), Angélique Stéphanou (AS).
Absent with apology: Luděk Berec (LB)

- E-vote decisions: Decisions taken via email since the previous meeting (December 11, 2020)
  - Jan 18, 2021: José Antonio Carrillo will serve as ICIAM delegate and Benoît Perthame will serve as EMS delegate of ESMTB. Tom Britton will take responsibility for the prizes.
  - Feb 16, 2021: The board decides ESMTB to be involved in the organization of SMB21 and to nominate Maíra Aguiar, Daniele Avitabile, Ellen Baake, Bob Planqué and Roeland Merks as members of the organising committee.
  - Feb 25, 2021: The board decides a reduction of the membership fees (except life memberships) by 50 percent for one year; combined with extension of membership to 2022 for those who have already paid for 2021.
- Springer: EB, JAC and BP had a meeting with Springer (Lynn Brandon-Executive Manager Mathematics, Marc Strauss-Editorial Director Mathematics and Michael Elf-Legal director) in which they agreed that Springer will send a new draft of the Publishing Agreement to be discussed by the board. The board also discusses the option, while having JMB as the official journal, of associating to other journals in a different way in order to have a broader coverage of topics.
- SMB21: Maíra Aguiar, Daniele Avitabile, Ellen Baake, Bob Planqué and Roeland Merks are part of the organising committee which meets weekly and is now in the process of reviewing the minisymposia.
- Recipients newsletter, membership and communication campaign: A plea was sent to renew membership to former members that did not renew it. As a consequence 33 members renewed. There are about 30 memberships pending renewal due to bureaucratic delays. The options for setting up a mailing list system in order to send information (Newsletter, Colloquium) to non-members are discussed. This list might be used in the future if undertaking a member enrolment campaign.

  BP suggests the consideration of creating a “fellow of the society” scientific award.
- Colloquium: An online colloquium will be organized taking place every last Friday of the month at 1 pm CET starting in April 2021. It will be done via Zoom meetings, keeping open the possibility of switching to webinar.
- Guidelines for support for online conferences: The standard support for face-to-face conferences is 1500 euros. The board agrees on a standard amount of up to 400 euros for requests of support for online meetings which should include a description of the destination of the money. Requests to pay for keynote speakers for online conferences will be rejected.
- Nominations for the ICIAM Prizes: The board discusses the possibility of nominating a candidate for the “Lagrange Prize” which is awarded to individual mathematicians who have made an exceptional contribution to applied mathematics throughout their careers. We aim at finding an outstanding figure whose nomination would be supported by other societies.

June 7, 2021, 12:30-13:00

Members present: Maíra Aguiar (MA), Ellen Baake (EB), Luděk Berec (LB), Tom Britton (TB), José Antonio Carrillo (JAC), Sílvia Cuadrado (SC), Elisenda Feliu (EF), Bob Planqué (BP), Angélique

Stéphanou (AS).
Absent with apology: Benoît Perthame (BP).

- E-vote decisions: Decisions taken via email since the previous meeting (March 24, 2021)
  - April 28, 2021: The board agrees unanimously on the renegotiated version of the contract with Springer about Journal of Mathematical Biology as the official journal of ESMTB. The president will sign the document.
  - June 4, 2021: The board unanimously decides to support ICIAM's participation in the international year of basic sciences for sustainable development (IYBSSD).
- The board discusses and finalises the recommendations for the successor of Mark Lewis as Editor in Chief for Journal of Mathematical Biology.

October 1st, 2021, 12:00-14:15

Members present: Maíra Aguiar (MA), Ellen Baake (EB), Luděk Berec (LB), Tom Britton (TB), Sílvia Cuadrado (SC), Elisenda Feliu (EF), Benoît Perthame (BP), Bob Planqué (BP), Angélique Stéphanou (AS).
Absent with apology: José Antonio Carrillo (JAC).

- E-vote decisions: Decisions taken via email since the previous meeting (June 7, 2021)

- July 26, 2021:
  - The reduced membership fee will be kept for 2022.
  - The board decides to move the colloquium to Wednesday, 1 pm Brussels time.

- Brief report of the last months by the president (EB):

  The board has nominated a very prominent biomathematician for the ICIAM Lagrange prize.

  Thomas Hillen will replace Mark Lewis as managing editor for Journal of Mathematical Biology from January 1st 2022.

  We are in the process of sending letters to advertise ESMTB. A letter was sent just before the summer and another one will be sent in the near future.

- Colloquium:

  The colloquium is running very satisfactorily. The first speaker was Mark Chaplain (May) followed by Marie Doumic (June) and Dagmar Iber (September). The upcoming speakers will be Alex Best in October and Reinhard Bürger in November.

  It is decided not to buy a zoom license for the moment but to continue using the licenses of the institutions of the members having it.

- ECMTB 2022, 2024

  ECMTB 2022:
  - The conference will take place in the Heidelberg Campus. The location of the plenary talks will depend on the dates of the conference.
  - The two possible dates are the week of August 22nd and the week of September 19th. After a discussion, the board considers September more suitable.
  - The scientific committee will be maintained but more members might be added.
  - Plenary speakers that were proposed for the postponed ECMTB2020 will be asked about their availability for the new date.
  - The conference will very likely be in a hybrid format.
  - The board agrees to contribute to travel support and help with the reviewing process.

  ECMTB 2024:
  - A call for applications will be issued, both in the newsletter and on the website.

- PCI (Peer Community in) initiative: ESMTB has received a petition to support "PCI Mathematical & Computational Biology". The board agrees to investigate how different open access policies develop and deal with the petition in the near future.

- Various: It is agreed that membership will be for 12 months starting on the day one becomes a member. This change will be implemented from January 1st 2022.

Sílvia Cuadrado
ESMTB Secretary

ESMTB Online Colloquia

An unarguable effect of the covid-19 pandemic is that we have been forced to change the way we communicate and interact in the scientific communities. When one after the other ESMTB scientific meeting got canceled since March 2020, we had to find new ways to disseminate research, collaborate, and exchange ideas. And we sure did! Better and better online solutions appeared, and we all quickly had to adapt and get used to them.

The ECMTB at Heidelberg 2020 was also postponed twice, and with that, the research community that ESMTB represents, was left without its main gathering in Europe. And then the ESMTB colloquium was started.

The ESMTB has established an online colloquia series featuring talks of interest to the members of the society, and at a level accessible to all. The first season of the colloquia run on Fridays, while after the summer break, the colloquium has moved to Wednesdays.

The speakers of the ESMTB colloquium so far have been Mark Chaplain (University of St Andrews), Marie Doumic (INRIA), Dagmar Iber (ETHZ), Alex Best (University of Sheffield) and Reinhard Bürger (University of Vienna). The next bunch of talks is already announced on our web page and there are more to come, so stay tuned!

Big thanks to all the speakers for their availability and excellent talks. And thanks all of you for participating. You have all contributed to the cohesion of the society and to making the colloquium series a success.

Practical aspects:

- *When:* last Wednesday of the month at 13:00.
- *Where:* the talk is streamed on Zoom, and the link is distributed to the members of the ESMTB subscription list.
- *After the colloquium:* Talks are recorded. The link is available from the ESMTB webpage.

Elisenda Feliu

The Ovide Arino Outreach Award 2021

The Ovide Arino Outreach Award is a joint ESMTB (European Society for Mathematical and Theoretical Biology) and SFBT (Société Francophone de Biologie Théorique) prize, awarded every two years to a young researcher from a Southern country, on the basis of a remarkable contribution in mathematical or theoretical biology, carried out in collaboration with a European or French-speaking country.

The prize awarding committee is happy to announce that **Israël Tankam Chedjou** has been designated as the laureate for the year 2021.

Israël has been awarded a PhD in Applied Mathematics from the University of Yaoundé in 2020. He made some very interesting contributions in the understanding and control of banana pest based on mathematical modelling approaches in collaboration with the INRIA team BIOCORE in Sophia Antipolis. In a first contribution he studied the seasonal effect on the infestation by the nematode [1] and in a second he proposed some solutions to optimize banana production by controlling the nematode via the deployment of fallows [2]. This remarkable work provides a reliable alternative to the use of pesticides and has a positive impact on the environment.

Israël is today affiliated to the EPITAG Team and Laboratory of Applied Mathematics of the University of Yaoundé.

The candidate will be invited to give a talk at one of the next SFBT virtual seminars.

The OAOA committee,
Julien Arino, Slimane Ben Miled, Rafael Bravo de la Parra, Angélique Stéphanou, Suzanne Touzeau

[1] Tankam-Chedjou I *et al.*, Optimal and sustainable management of a soilborne banana pest. Applied Mathematics and Computation (2021), 397:125883. `https://doi.org/10.1016/j.amc.2020.125883`

[2] Tankam-Chedjou I *et al.*, Modelling and control of a banana soilborne pest in a multi-seasonal framework. Mathematical Biosciences (2020), 322:108324. `https://doi.org/10.1016/j.mbs.2020.108324`

Call for the organisation of ECMTB 2024

This is a call to submit a proposal for the organisation of ECMTB in 2024. Hosting an ECMTB conference is a great opportunity to increase visibility of the local mathematical and theoretical biology community.

The guidelines for proposals can be found here:

`https://www.esmtb.org/resources/Documents/guidelines_proposal_ECMTB_2024.pdf`

The deadline for submission is **May 1, 2022**.

ECMTB 2022

The **12th European Conference on Mathematical and Theoretical Biology** will take place in **Heidelberg, Germany, from 19th to 23th September 2022**, and is a joint event organized by the European Society of Theoretical Biology (ESMTB) and the Society for Mathematical Biology (SMB).

The meeting will bring together researchers and students interested in mathematical modelling with applications to life sciences. We invite you to join us in Heidelberg to hear from leading researchers in mathematics and life sciences from around the world, to present your work and to exchange scientific ideas.

Structure

- **Plenary talks** – held by prestigious researchers from the field of Mathematical Biology
- **Mini-symposia** – four 25-minute presentations (each with 5 minutes for discussion) on a single topic of substantial current interest and importance in Mathematical Biology
- **Contributed talks** – 25-minute presentations with 5 minutes allocated for discussions
- **Posters** – all researchers, at all stages of their careers, are encouraged to opt for presenting a poster, in order to reduce the high number of parallel sessions

All contributed talks, mini-symposia and posters will be **grouped thematically**.

Mentoring scheme:
Early-career scientists will also have the opportunity to take part in our mentoring program, to be paired with well-established experienced researchers who will offer feedback on conference presentations, advice on career objectives and help with networking.

To stay updated on the latest news on the ECMTB2022, follow us on

Facebook @ecmtb2022
`https://www.facebook.com/ecmtb2022/`

and on

Twitter @ecmtb2022
`https://twitter.com/ecmtb2022`

Looking forward to seeing you in Heidelberg,

Anna Marciniak-Czochra
(on behalf of the Organizing Committee)

ESMTB
European Society for Mathematical and Theoretical Biology

CALL FOR MEMBERSHIP

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, the online colloquium, the European Communications 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** (SpringerNature)
- **Travel Support** for mathematical/theoretical biology meetings
- Endowing the **Reinhart Heinrich best doctoral thesis award**
- **Reduced fees** for selected conferences and schools
- **Reduced subscription rates** for selected journals
- **Voting** in society elections

Please register at http://www.esmtb.org.

Membership Fees per year:

The **Individual Annual Membership Fee** is:

- 25 Euro (full member)
- 20 Euro (ISTMB, JSMB, NVTB, SFBT or SMB full member)
- 12,50 Euro (student, developing country or Eastern European member)
- 10 Euro (student ISTMB, JSMB, NVTB, SFBT or SMB member)

The **Institutional Annual Membership Fee** (Includes up to 5 full memberships) is : 100 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:
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