

Communications



ESMTB

European Society for Mathematical
and Theoretical Biology

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Letter from the President

Dear fellow mathematical and theoretical biologists,

What a year! After two years of activities stifled by some strange virus, the community burst back to life. This was most visible at THE event of the year, the 12th ECMTB in Heidelberg. After having been cancelled twice, the conference now resurrected in a format that topped all expectations — indeed, three times the expected number of participants (44 of them supported by ESMTB travel grants) filled the lecture halls and seminar rooms of the campus in Neuenheimer Feld. I have never before experienced such a happy atmosphere at a big conference! While the official report is on page 21, let me take the opportunity to express my heartfelt thanks to the organisers here. Anna Marciniak-Czochra and her team did a superhuman job in developing a high-quality scientific programme, implementing a hybrid option, organising catering for the crowd (in a time where caterers tend to decline orders due to shortage of staff) and coping with uncountable unforeseen (and inconceivable) difficulties.

The conference also provided the first opportunity for the ESMTB board to meet in person. Indeed, it gave me a burst of joy to see all members, some of them for the very first time, after one and a half years of intense and constructive joint work via virtual interactions.

Furthermore, the conference pointed to the future: at the closing ceremony, José Carrillo announced that the 13th ECMTB will be organised by Victor Manuel Pérez García in Toledo, Spain (the historic city is a UNESCO World Heritage Site!).

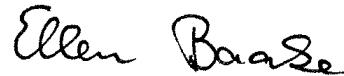
Also apart from the big events, good things have happened in 2022. In a joint venture, the publisher (SpringerNature), the Editors in Chief (Anna Marciniak-Czochra and Thomas Hillen), and the ESMTB board have newly established the Karl-Peter-Hadeler Prize of the Journal of Mathematical Biology (JoMB) to recognise outstanding publications in the journal. Our online colloquium has become widely visible, with seven top-level speakers this year and substantial resonance in the community; we plan to continue the format during the ‘low-conference high-risk season’ with about 3 colloquia per semester. We are currently planning the talks for early 2023; they will soon appear on our web page.

At the administrative level, we have overhauled the statutes of the society, which had fallen out of time. The new version has arrived in the 21st century and was accepted by our members with large

majority (77 votes for and 2 against it); they are available on our web page. Importantly, the new statutes allow us to replace a board member who resigns; the next candidate on the list who obtained the most votes in the last election may then join the board. In fact, this did happen in 2022: alas, Maíra Aguiar resigned (cordial thanks for all she did for ESMTB, and specifically for organising the unforgettable 11th ECMTB in Lisbon in 2018!) and was replaced by Tommaso Lorenzi (Torino). Tommaso is involved in managing ESMTB social media and provides technical support for the colloquium; and he, like all of us, actively engages in the many things that profit from being done together.

Finally, I’d like to break the good news that the number of active ESMTB members has climbed to 429 — an alltime high, but hopefully not yet the summit.

With cordial regards



Ellen Baake

Meet our new ESMTB board member



Tommaso Lorenzi is Associate Professor of Mathematical Physics in the Department of Mathematical Sciences of Politecnico di Torino. He is an applied mathematician and he works in mathematical biology. The focus of his research is on the development,

analysis and numerical simulation of deterministic models formulated as partial differential equations, or partial integro-differential equations, and corresponding stochastic individual-based models. These models complement empirical research by enabling extrapolation beyond scenarios which can be investigated through experiments and by revealing emergent phenomena that would otherwise remain unobserved. Moreover, they pose a series of analytical and numerical challenges which make them interesting mathematical objects per se. He collaborates with researchers in the natural sciences. His current research interests include mathematical models of evolutionary dynamics, cell movement, tissue development, tumour growth and invasion, and immune response to cancer. He joined the board of the ESMTB in Autumn 2022.

Current (2021-2023) board members

- Ellen Baake, Bielefeld, Germany (President)
 - José A. Carrillo, Oxford, UK (Vice President)
 - Bob Planqué, Amsterdam, Netherlands (Treasurer)
 - Sílvia Cuadrado, Barcelona, Spain (Secretary)
 - Luděk Berec, České Budějovice, Czech Republic
 - Tom Britton, Stockholm, Sweden
 - Elisenda Feliu, Copenhagen, Denmark
 - Tommaso Lorenzi, Torino, Italy
 - Benoît Perthame, Paris, France
 - Angélique Stéphanou, Grenoble, France
-

published in JoMB every year.

Springer will offer the prize winner EUR 500 as a cash prize or EUR 1000 in books of their choice. The winner will also be invited to give a talk in the ESMTB online colloquium, as long as it is continuing.

So, don't hesitate to submit your best work to the Journal of Mathematical Biology!

Procedures. The EiCs collect nominations from the Associate Editors and recommend a small number (around 3 to 5) to the ESMTB board. The ESMTB board will then form an ad hoc committee of 3-5 persons who will select the winning paper (and possibly the runners-up, who will receive honourable mention).

News from the Journal of Mathematical Biology



In a joint venture, the publisher (SpringerNature), the Editors in Chief (Anna Marciniak-Czochra and Thomas Hillen), and the ESMTB board have newly established the **Karl-Peter-Hadeler Prize** of the Journal of Mathematical Biology (JoMB). It recognises outstanding publications in the journal.

Karl Peter Hadeler (1936-2017) was a pioneer in mathematical biology. He co-founded JoMB (1974) and the ESMTB (1991), and was a leading editor of JoMB for many years.

His lifelong passion for mathematical biology was driven by his love of mathematics and biology alike. He saw that mathematical modelling can help understand biological processes on a deep level, identify new structures, generate new insight, and even inspire new mathematics. It is in this vision that we recognise the outstanding research

The Reinhart-Heinrich Doctoral Thesis Award 2020

The 2020 Reinhart-Heinrich Doctoral Thesis Award goes to **Lukas Eigentler** with a PhD thesis from Heriot-Watt University (UK). Lukas PhD Thesis is entitled *Modelling dryland vegetation patterns: nonlocal dispersal, temporal variability in precipitation and species coexistence* and was realised under the supervision of Jonathan A. Sherratt.

Lukas presented his very nice work at the ECMTB conference in Heidelberg and formally received his award at the dedicated ceremony.

Lukas Eigentler Personal statement

I have been intrigued by the application of mathematics in biology and ecology since my undergraduate studies in mathematics at the University of Dundee, Scotland. The fascination sparked by my undergraduate courses made transitioning to a PhD on the subject an easy choice. I pursued a PhD under the supervision of Jonathan A. Sherratt between 2016 and 2020 at the Maxwell Institute Graduate School in Analysis and its Applications, a centre for doctoral training jointly run by Heriot-Watt University and The University of Edinburgh, Scotland. My PhD research focussed on the development and analysis of models for dryland vegetation patterns, a classical example of a self-organising principle in ecology.



My fascination with the project is twofold. First, I am intrigued by the significance of mathematical modelling of the subject. Due to the long time scales associated with the dynamics of desert plants and the large spatial scales of vegetation patterns, field and experimental data are notoriously difficult to obtain. This leaves mathematical modelling and analysis as the only feasible method to develop a comprehensive understanding of this phenomenon.

Second, I am fascinated by the rich solution structure exhibited by the deliberately phenomenological models used in my research and the associated power of mathematical analysis. In my opinion, my work highlights how intentional focus on a small number of key ecosystem processes that makes a mathematical model amenable to analytical treatment can reveal a much deeper understanding than a highly-detailed, high-dimensional model that can solely be investigated by numerical simulations.

The focus on deliberately phenomenological models to advance our understanding of fundamental ecosystem processes is a key tenet of my past and current work as well as future research plans. Currently, I am applying this principle to microbial range expansion as part of an interdisciplinary team at the University of Dundee, Scotland, led by microbiologist Nicola R. Stanley-Wall and mathematician Fordyce A. Davidson.

Thesis summary: ‘Modelling dryland vegetation patterns: nonlocal dispersal, temporal variability in precipitation and species coexistence’ by Lukas Eigentler

Introduction and Overview

More than 2.5 billion people live in drylands that cover approximately 41% of the Earth’s land mass. A ubiquitous feature of many drylands is spatiotemporal patterns of vegetation, characterised by alternating patches of high biomass and patches of bare soil (Fig. 1). First documented through aerial photography in the 1940s, observations of vegetation patterns have been reported from all continents except Antarctica. Understanding their dynamics is of crucial global socio-economic importance. In particular, many economies in drylands rely on the livestock and agriculture sectors, whose developments are affected by future vegetation levels. For example, in Chad, the livestock sector contributes around 20% of the country’s GPD and involves about 40% of its population.

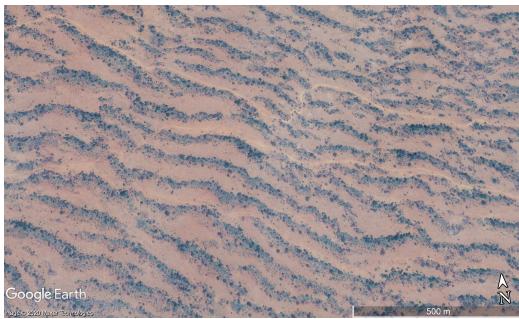


Figure 1: Satellite image of vegetation bands. A satellite image of vegetation stripes in the Horn of Africa ($7^{\circ}50' \text{ N}$, $47^{\circ}04' \text{ E}$) is shown. It visualises the characteristic separation of plants into stripes of high biomass and bands of bare soil in between. The photograph, taken in 2013, has been obtained from Google Earth. Image © Maxar Technologies.

Vegetation patterns are a classical example of a self-organisation principle in ecology. The separation into patches of dense biomass and areas of bare soil is induced by a positive feedback between local vegetation growth and water redistribution towards areas of high biomass. Depending on soil properties and plant species,

a number of different mechanisms are involved in this pattern-inducing feedback loop. For example, overland water flow towards dense biomass patches is induced by the formation of infiltration-inhibiting biogenic soil crusts on certain soil types; or laterally extended root systems as well as a combination of vertically extended roots and a soil type supporting fast water diffusion can cause water redistribution below ground. As a consequence, vegetated patches act as resource sinks, which drives further plant growth and closes the feedback loop.

The self-organisation of plants can result in patterns of different shapes, including gap patterns, labyrinth patterns and spot patterns. On gentle slopes (up to approximately 2% gradient), vegetation patterns occur as regular stripes parallel to the contours of the terrain, and this type of pattern is the focus of the thesis. Some field studies report uphill migration of bands over a generational timescale. This property emerges from the positive feedback between local vegetation growth and water redistribution towards dense biomass patches. Due to the sloped terrain, the uphill edges of vegetation stripes profit most from this water redistribution, intercepting most of the water run-off from the upslope interband region. The resulting hydrological distribution promotes upslope expansion and downslope contraction of the bands. However, other observations suggest that vegetation bands can also be stationary.

Due to the long temporal and large spatial scales involved in vegetation pattern dynamics, the acquisition of high-quality empirical data is notoriously difficult. While it is possible to obtain data on some properties, including pattern wavelength, terrain elevation and historical rainfall data, I am not aware of methods that enable the collection of other relevant types of data, such as biomass densities or species composition, over long periods of time and wide areas of space. In isolation, datasets that are currently available can only provide limited information

on the complex ecosystem dynamics.

As a consequence of the challenges associated with the acquisition of high-quality data on vegetation patterns, mathematical modelling plays a crucial role in the development of a better understanding of dryland ecosystem dynamics. In my thesis, I present results of a theoretical investigation on the impact of a number of different processes and phenomena on vegetation stripes. Mathematical models used include reaction-advection-diffusion models, an integrodifference model and a model consisting of impulsive differential equations that represent vegetation stripes as periodic travelling waves (Fig. 2). Results are obtained using a combination of analytical and numerical methods. The main focus lies on revealing the bifurcation structure of the models. Particular emphasis is put on determining the existence and stability of periodic travelling wave solutions (Fig. 2), using algorithms based on numerical continuation. The thesis is split into three main parts. In part I, I highlight the impact of nonlocal dispersal of seeds; in part II, I disentangle the effects of temporal variability in precipitation regimes; in part III, I reveal mechanisms of species coexistence despite competition for a limiting resource.

Part I: Nonlocal seed dispersal

For mathematical simplicity, plant dispersal is modelled by diffusion in many theoretical models for vegetation patterns. In the thesis, I replace plant diffusion by a convolution term to account for nonlocal effects, backed up by empirical data. An asymptotic analysis of the model is possible, due to a scale difference between plant dispersal and water transport. Using a specific dispersal kernel, a condition for pattern onset can be found analytically, valid to leading order in a large parameter describing water flow downhill on sloped terrain. Assuming an evolutionary trade-off between dispersal distance and dispersal rate, a convergence result allows for a comparison to results for the model with local plant diffusion. Finally, numerical schemes can be utilised to show that results remain qualitatively unaffected by the choice of kernel func-

tion.

The main finding is that both longer dispersal distances and faster dispersal rates inhibit the onset of spatial patterns by stabilising a spatially uniform vegetated state for lower precipitation volumes. Auxiliary results include information on the patterns' properties, such as wavelength or migration speed in the uphill direction, close to onset. Some limited empirical data exists for both pattern wavelength and uphill migration, and thus theoretical results may provide useful complements to future empirical studies.

Contents of this part are separately published in the Journal of Mathematical Biology [3].

Part II: Rainfall intermittency and seasonality

Most continuum approaches of modelling vegetation patterns are based on PDEs and thus assume that rainfall occurs continuously and uniformly in time. In reality, however, precipitation in drylands is seasonal, intermittent or a combination thereof. The temporal non-uniformity in precipitation regimes also has significant effects on other biological processes. For example, seed dispersal typically occurs in the latter stages of the dry season or is synchronised with a rainfall event, while plant growth predominantly occurs during and shortly after precipitation occurrences. Experiments with small numbers of individual plants show that such rainfall regimes have a significant impacts on the plants, but its effects on an ecosystem-wide scale have not been addressed in detail using theoretical models before.

In the thesis, I describe seasonality of precipitation and seed dispersal using a discrete integrodifference system to show that such an approach is insufficient to capture effects of nonuniformity in precipitation on vegetation patterns. Motivated by this, I next investigate the effects of rainfall intermittency, by proposing a model of impulsive differential equations. The idea of using such a hybrid model is to combine processes occurring continuously in time (e.g. plant mortality, water transpiration) with pulse-

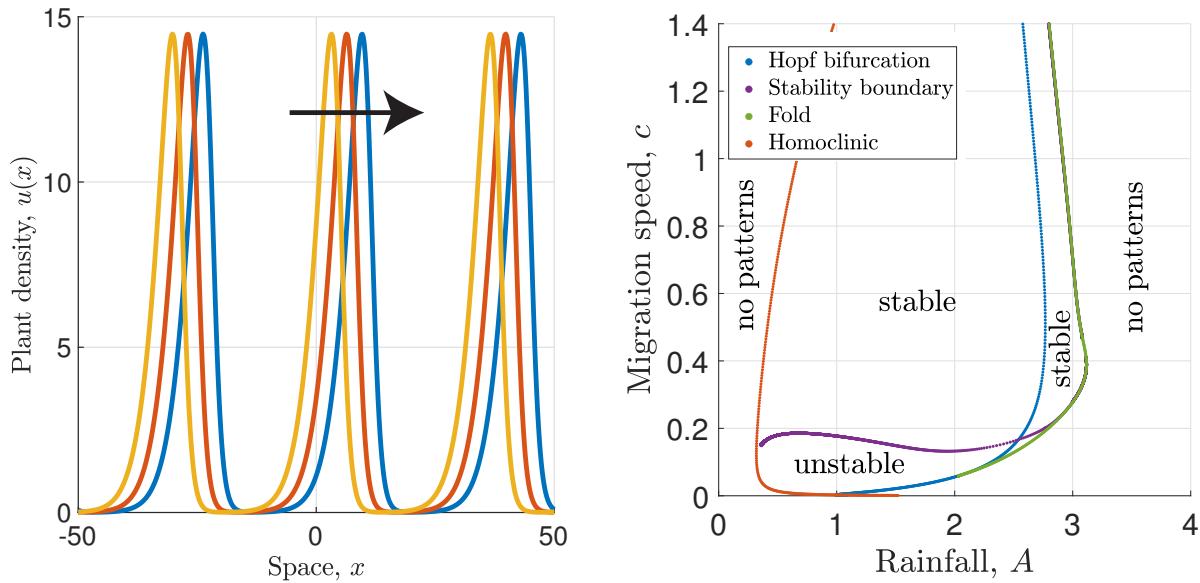


Figure 2: Vegetation stripes represented as periodic travelling waves. Mathematical models represent vegetation stripes as periodic travelling waves (left). Different colours show solutions at different time points and visualise the migration of patterns consistent with some field data. Existence and stability results on periodic travelling waves are typically visualised through stability diagrams in a parameter plane spanned by the main bifurcation parameter (here, rainfall) and one of the emergent solution properties (here, migration speed) (right - reproduced with permission from [1]). For decreasing rainfall, pattern onset occurs via a Hopf bifurcation, but patterns exist for higher rainfall levels due to a fold in the branch of pattern solutions. Transition from patterned vegetation to uniform desert at low rainfall levels occurs via a homoclinic orbit. The pattern existence region is separated into stable and unstable regions by stability boundaries.

type processes triggered by high-intensity precipitation events (e.g. plant growth, seed dispersal). The focus of the analysis lies on a derivation of conditions for pattern onset, which can be found analytically under strict assumptions on the plant dispersal kernel and functional responses in the system. The effects of relaxing those assumptions is further investigated using numerical simulations. The main finding is that a detailed knowledge about a plant species' response to low soil moisture levels is key in understanding the effects of intermittent precipitation on the ecohydrological dynamics. If plant growth is only triggered under sufficiently high water levels, a low frequency of high-intensity rainfall events inhibits pattern onset compared to a more frequent addition of water under the same total annual precipitation volume.

Contents of this chapter are separately published in the Journal of Mathematical Biology [6] and Physica D [5].

Part III: Species coexistence

Herbaceous and woody species generally coexist in dryland ecosystems (both in patterned vegetation and arid savannas), despite their competition for the same limiting resource. Classical results such as the principle of competitive exclusion and Tilman's R^* rule thus postulate the existence of other coexistence-promoting mechanisms, which can be revealed through the analysis of mathematical models. In the thesis, I present several multispecies models to propose potential mechanisms that can enable species coexistence in both savannas and vegetation patterns.

In the context of arid savannas, model solutions are also characterised by spatial patterns, but in stark contrast to solutions representing a vegetation pattern, they oscillate between two nonzero biomass densities. As a consequence, tools and methods from pattern formation theory can also be applied to solutions representing a savanna biome. I utilise this by applying numerical continuation techniques to investigate the onset, existence and stability of coexistence states in a mathematical model. This reveals that coexistence is facilitated by spatial heterogeneities in the environmental conditions (water density), induced by the positive feedback between local plant growth and water redistribution. A crucial condition for the occurrence of coexistence states is a balance between the species' local competitive abilities and their mean dispersal distances. In other words, species coexistence between two species requires the superior local competitor to be inferior in its colonisation abilities. Ecologically, the crucial importance of these results becomes clear through a comparison with results of the corresponding single-species model: despite competition for a limiting resource, the coloniser species facilitates the superior local competitor under precipitation volumes that would not allow the latter to exist on its own. This is an example of ecosystem engineering, a modification of environmental conditions by one species that facilitates the growth of a competitor species.

For lower precipitation volumes, the same model captures coexistence solutions that represent patterned vegetation (i.e. the oscillation of biomass between a vegetated and a bare soil state). In contrast to the savanna-type solutions discussed above, these patterns are not stable solutions of the mathematical model. Instead, coexistence patterns occur as long transient states. I derive that such metastable states are characterised by small growth rates of spatially uniform perturbations to equilibria and occur if the average fitness difference between two species is small. An in-depth analysis of the system's dispersal relation highlights that the formation of spatial patterns occurs on a much shorter timescale due to the existence of a

spatial mode for which growth rates of perturbations are much larger. These results emphasise an important issue often ignored in the analysis of mathematical models, but regarded as highly important by ecologists. In many ecosystems, it may be insufficient to only consider equilibrium dynamics. Instead, the understanding of transient states is of utmost importance as many ecosystems never reach an equilibrium state due to frequent disturbances, such as changes in environmental conditions.

On the other hand, coexistence patterns occur as a stable model solution if intraspecific competition dynamics other than those for the limiting resource are considered. I show that strong intraspecific competition of one species only (the coloniser species) suffices to enable coexistence in vegetation patterns. Strong intraspecific competition among the superior coloniser reduces its advantages under severe environmental stress, thus stabilising coexistence for a wider range of rainfall regimes. Moreover, this approach allows for a statistical analysis of the spatial distribution of both species under changes to the system's parameters, based on the numerical continuation of model solutions. Additionally, the extent to which two species differ has a significant impact on the bifurcation structure, in particular the transition from a desert state to a vegetated state, if intraspecific competition dynamics are considered. This result is of crucial ecological significance since an understanding of this state transition is key for successful vegetation-recolonisation programs.

Contents of this chapter are separately published in the Journal of Theoretical Biology [7], the Bulletin of Mathematical Biology [4], Oikos [2] and Ecological Complexity [1].

Impact and outlook

The long-term goal of the study of dryland vegetation patterns by both ecologists and mathematical modellers is the creation of predictive frameworks that provide forecasts of future developments of such ecosystems, in particular to combat the threat of irreversible desertification processes. A fundamental ingredient for this is

the understanding of the effects of basic ecological mechanisms on the ecosystem dynamics. The chapters of my thesis provide examples of theoretical investigations using deliberately simple phenomenological models into the qualitative impact of such processes. Results are expected to be regarded as the bases for more detailed and potentially quantitative approaches in the future.

The work on rainfall intermittency and seasonality is only the starting point to address a bigger question: *How can mathematical modelling be utilised to investigate ecosystem responses to variations in precipitation regimes?* In reality, the arrival of a precipitation pulse is best described as a Poisson process with the intensities of such events being exponentially distributed. However, current modelling frameworks are unsuitable to incorporate a non-deterministic description of precipitation, as the eventual occurrence of a long drought period would lead to low biomass levels from which recovery is impossible. Recovery processes, such as seed banks, need to be accounted for in any mathematical model attempting to investigate effects of a more realistic description of rainfall.

Intraspecific competition dynamics have both a qualitative and quantitative impact on both single-species and multispecies vegetation patterns. To this date, mathematical models incorporate these dynamics in a general way by combining them into one single variable, the maximum standing biomass, for each species. The significant impact of strong intraspecific competition proposed by previous results motivates a more detailed investigation of their dynamics in the future, such as the explicit consideration of autotoxic soil compounds released by plants into the soil.

Finally, my work on nonlocal seed dispersal promises to provide a resolution to contrasting field observations on the migration of vegetation stripes: at some sites patterns are reported to gradually move uphill while on others they are stationary. Numerical continuation suggests the occurrence of almost stationary patterns (migration speed $\ll 1$) provided seed dispersal distances are sufficiently large. In a forthcoming

paper, I will provide analytical results, obtained through a perturbation theory approach that provide analytical confirmation of these numerical observations.

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The Reinhart-Heinrich Doctoral Thesis Award 2021

The 2021 Reinhart-Heinrich Doctoral Thesis Award goes to **Martina Conte** with a PhD thesis from the University of the Basque Country (Bilbao, Spain). Martina defended her PhD Thesis *Mathematical models for glioma growth and migration inside the brain* in 2021 at the Basque Center for Applied Mathematics/Basque Country University, under the advisor of Juan Soler and Luca Gerardo-Giorda (Johannes Kepler University and RICAM, Linz).

The prize committee had the following motivation: *The prize goes to Martina Conte for her important contributions to building mathematical theory and integrating it with biological and clinical data to increase understanding of Glioma (brain tumor) growth and migration, potentially leading to new treatments.*

Martina presented her inspiring work at the ECMTB conference in Heidelberg and formally received her award at the dedicated ceremony.

Martina Conte Personal statement

Glioma migration and invasion into the brain tissue is a complex phenomenon and little is still known about the underlying mechanisms that lead to tumor progression. Although the evident scientific progress obtained over the years, both in the area of early diagnosis and in the development of specific and innovative therapies, the world mortality rate for these tumors has not experienced a decrease proportional to the research efforts and investments. Gliomas are often resistant to treatment, the median survival ranges between 9 and 12 months, and recurrence is the main cause of mortality. Thus, with this Ph.D. thesis, we propose and develop several mathematical models that study various aspects of glioma progression for providing possible answers to the problems of tumor growth and invasion into the brain tissue. Exploiting the inherently multiscale nature of glioma evolution allows us to define different classes of models. The integration of biological and clinical data with mathematical theory has always been one of the key focus in order to increase the understanding of tumor progression and potentially lead to new treatments. The research I have undertaken during this Ph.D. was the first step towards this goal.



Thesis summary: ‘Mathematical models for glioma growth and migration inside the brain’ by Martina Conte

Gliomas are the most prevalent subtype of primary brain tumors originating from mutations of the glia cells in the central nervous system. Classified by the World Health Organization into three main types and four grades, the most common and aggressive variety is called glioblastoma (GB). Gliomas, and especially GBs, are characterized by fast cell growth, strong invasion capability, and well-developed tumor vasculature, which is responsible for hypoxia-driven mechanisms and for sustaining proliferation and spread. Although the research advances and the newly implemented clinical trials have allowed significant progress, these tumors are still characterized by a poor prognosis. Therefore, research on the mechanisms driving glioma progression remains an emerging field.

Motivations and main objectives

The advancements in technology have created a considerable amount of clinical and biological data about glioma evolution. However, the high complexity of the invasion process remains a challenge to face and several important questions are still unanswered. Moreover, there is a need to integrate theoretical and empirical knowledge towards the investigation of the mechanisms that contribute to tumor growth and invasion. In this context, mathematical models emerge as powerful tools to face these challenges, as they can provide significant insights into the processes characterizing tumor progression. In this dissertation, we propose different mathematical approaches for the description of some relevant mechanisms involved in glioma growth and spread inside the brain, with a special interest in integrating clinical and biological data in the model settings.

Aims: The main aim of this thesis concerns the study of specific processes involved in tumor cell *migration and invasion*, *tumor angiogenesis*, and in the *outcomes of different treatments*. Firstly, we looked into the capability of cells to invade the extracellular matrix (ECM),

analyzing the role of the anisotropic brain fiber structure in influencing the direction of cell migration as well as the role of the cell protrusions in mediating cell-ECM interactions, and integrins and proteases activity. Then, we described the process of tumor angiogenesis, describing the interaction between tumor and endothelial cells (ECs) and the effects of hypoxia and acidity on the formation of a necrotic core in the tumor mass. Finally, concerning treatment administration, we analyzed different multimodal therapies, mainly focused on the effect of integrin inhibitors in reducing cell-ECM binding capability, and of anti-angiogenic drugs in decreasing vasculature support to the tumor mass.

Data: The integration of biological and clinical data in the mathematical models is one of the key objectives of this thesis. The experimental data at hand were obtained from magnetic resonance (MRI) and diffusion tensor images (DTI) of the human brain and from in-vivo immunofluorescence analysis of protein distributions in a *Drosophila* model of GB, a reliable model for the study of GB dynamics. The latter was obtained from some experimental studies performed in collaboration with researchers of the Instituto de Salud Carlos III (Madrid, Spain).

Mathematical framework: The process of glioma evolution features an inherently multiscale nature due to characteristic phenomena that occur on different spatial and temporal scales. Therefore, in this thesis, we used a multiscale mathematical framework based on three specific levels of description to characterize glioma progression. The *microscopic level*, generally defined in terms of ODE systems, describes the single-cell level processes. The *mesoscopic level*, modeled by kinetic equations, models several interactions between tumor cells and the extracellular environment, including the mechanisms responsible for phenotypic hetero-

geneity, cell velocity changes, or blood vessel formation. The *macroscopic level*, involving PDEs for the macroscopic quantities, describes diffusive or drift phenomena leading to tumor progression and reflects the main features of tumor evolution observable in the clinical context. The equations at this level can be properly derived from the lower levels of description via asymptotic methods, or they can be phenomenologically stated directly at the macroscopic scale, especially when the nature of the involved mechanisms does not allow for a formal derivation from first principles. In particular, in this dissertation, we proposed different approaches relying on both the deduction of the continuous macroscopic systems from a kinetic description of cell behaviors and on their definition directly at the macroscopic scale.

Cell-tissue interactions and their influence on glioma progression

Brain structures, and mainly white matter tracts, are critical factors involved in the highly anisotropic migratory dynamics of glioma cells. These structures enable glioma cells to extensively invade the brain tissue, causing the emergence of heterogeneous patterns in the tumor mass observable from the images and determining the formation of not well-delineated outer tumor borders, which can impact the outcomes of clinical treatments. Therefore, it is essential to account for the characteristics of the brain fibers in the development of reliable models for glioma progression [1]. We first defined a kinetic-based model for the evolution of glioma cells to investigate the impact of the brain fibers and the role of integrin receptors as mediators of the migration process. In particular, for this study we relied on DTI data to identify the aligned structures along which cell migration is more likely to occur. Preliminary results showed the impact of the description of the brain fiber structure and the microscopic dynamics on the extension of the neoplastic area and its shape, on tumor infiltration, and on the emergence of heterogeneous patterns in the tumor evolution (Figure 3), providing the ground floor for our study

of tumor cell invasion [2].

In parallel, we analyzed the role of cell protrusions on tumor front dynamics, looking at the interplay between integrins, proteases, and ECM. This proposed framework integrates the mathematical description of the population dynamics with experimental data about protein distribution obtained from a *Drosophila* model of GB. The experimental results determined the localization and the profile of protease and integrin distributions in different brain regions (Figure 4). The resulting mathematical setting showed the dynamical evolution of the GB front and the emergence of organized patterns in the population profiles, which were in good agreement with experimental measurements. It also allowed us to study the impact of tissue porosity variability on the appearance of front abnormalities and separations. These results highlighted the capability of the proposed approach to reproduce phenomena related to front heterogeneity and provided a potential framework for deeper analysis of the impact of these mechanisms on tumor progression [3].

The impact of brain vasculature and intratumor heterogeneity

Angiogenesis is a key event in the progression of malignant gliomas. It refers to the formation of new blood vessels by rerouting or remodeling existing ones, and it is believed to be the primary method of vessel formation in gliomas [5]. Angiogenesis is promoted by limitations in oxygen and nutrient supply (hypoxia) as well as by low pH conditions (acidosis) and it sustains tumor progression. Based on the kinetic model for tumor progression above described, we proposed a first extension to include intratumor heterogeneity aspects and the study of the interdependency between acidity and vascularity, which are two key ingredients in the process of tumor angiogenesis. Precisely, the defined multiscale mathematical model was based on the phenotypic switch between moving and proliferating tumor cells, relying on the biological *Go-or-Grow* assumption [4], and on the in-

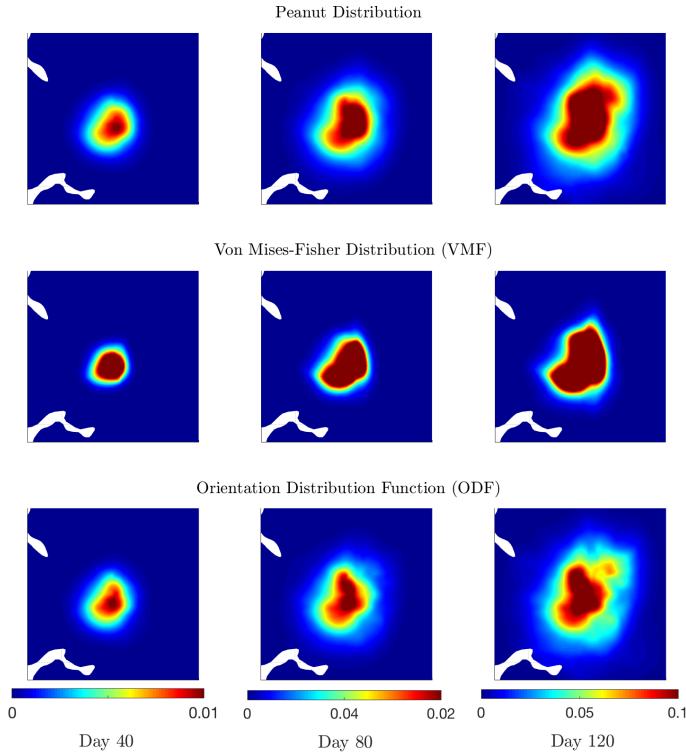


Figure 3: Impact of the brain fiber structure. Study of the impact of different descriptions of the brain fiber structure on the extension of the neoplastic area, its shape, and on tumor infiltration.

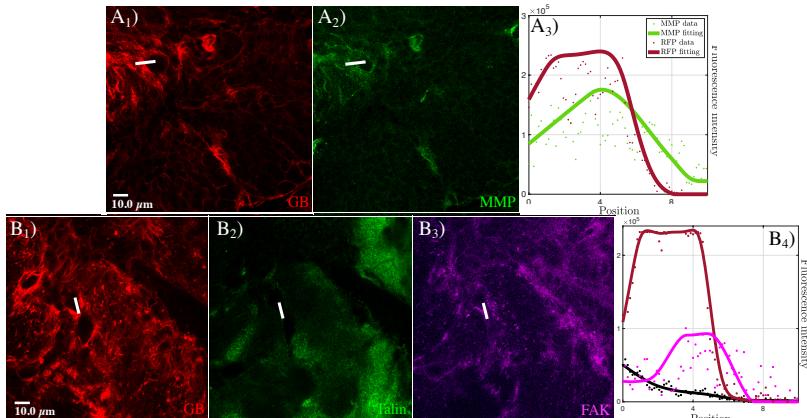


Figure 4: MMP and integrin distributions. Fluorescent confocal images of a Drosophila 3rd instar larval brain with GB marked in red (A_1 and B_1), and stained with anti-MMP (first row in green, A_2), anti-Talin (second row in green B_2), and anti-FAK (second row in magenta B_3). A_3 shows the quantification and the graphical representation of the fluorescent intensity for GB and MMP signals along the white lines in A_1 - A_2 , while B_4 shows the quantification and the graphical representation of the fluorescent intensity for GB, Talin, and FAK signals along the white lines in B_1 - B_3 . Both A_1 - A_2 and B_1 - B_3 refer to tumor front regions.

teractions between tumor and endothelial cells. In this setting, tumor evolution involved, at the microscale, the dynamics of two types of membrane receptors, mediating cell interactions with

the ECM and with the extracellular protons (responsible for environmental acidity). The component of intratumor heterogeneity modeled a phenotypic switch driven by nutrient availabil-

ity (supplied by vasculature), extracellular pH (determined by the acidity), and the crowding of the environment. Altogether these mechanisms determined a macroscopic setting characterized by nonlinear, myopic self-diffusion, involving the anisotropic description of the local tissue structure, and multiple taxis for both cell populations (tumor and endothelial cells). The numerical results first highlighted the capability of the proposed model to reproduce hypoxia-related histopathological features typical of GB evolution (e.g. microvascular hyperplasia with glomeroloid bodies) and, then, showed the impact of the go-or-growth dichotomy on the overall system behavior. Precisely, we noticed a general slowdown of the tumor dynamics compared to the case in which this dichotomy was neglected. Moreover, we proposed a possible extension of this model that involved the dynamics of healthy and necrotic tissue. This opened the way for the description of a necrosis-based tumor grading. We used it for determining and quantifying the evolution of the tumor in different scenarios and the influence of tumor heterogeneity and vasculature supply on the progression of the neoplasia (Figure 5) [6].

Tumor response to combined therapeutic treatments

The treatment of gliomas for a patient takes into account several aspects, such as tumor location, potential symptoms, and potential benefits versus risks of different treatment options. Over the past decades, the treatments have become more multi-modal, combining the three most used interventions (surgery, radiation, and chemotherapy) with new therapeutic targets. New treatments are emerging to target molecules involved in various signaling pathways and, among them, in this thesis we focused on angiogenesis inhibitors, tested as anti-migratory agents for ECs, and on integrins inhibitors, which reduce cell-tissue interactions and binding affinity. Based on the previously described results about tissue and vasculature influence on tumor progression, we presented a complementary analysis centered on tumor and ECs response to

multi-modal therapies. In the specific, we modified the described micro-meso formulations to include the effects of different treatments. We started from the model without vasculature and we included a combination of integrin inhibitors-based therapy with radiations. This choice allowed us to numerically reproduce the reduction of tumor infiltration, due to the integrin inhibitors, and the reduction of the tumor volume, due to radiation impact. Then, in the model with EC dynamics, we included the effects of treatments combining radiations, chemotherapy, and anti-angiogenic therapy with different timing. Precisely, radiations were aimed at affecting tumor, ECs, and healthy tissue, whose degradation also depended on the activity of tumor cells, chemotherapy impacted the tumor population only, while the anti-angiogenic therapy affected ECs, reducing their proliferation ability and their affinity with specific growth factors. The comparison between the progression of the tumor when no treatments were applied and the tumor outcomes for different schedules of the multi-modal therapy showed how tumor cells could better respond to specific choices of the type of treatment and its timing [7]. In particular, this suggest that letting the clinical studies have a longer follow-up might provide more useful information for the clinician about the possible outcomes of specific treatments.

Conclusions

The central problem addressed in this thesis concerned the modeling of the complex dynamics driving tumor cell progression inside the brain. Specifically, referring to the case of gliomas, we analyzed cell growth and migration in relation to several factors, such as brain fiber network, brain vasculature, membrane dynamics, and therapeutic treatments. We started looking into the anisotropic characteristics of the brain tissue, showing how the information on the fiber alignment can be obtained from the DTI data, quantified, and included in the models. This analysis represented the ground floor to the development of different micro-meso formulations for glioma invasion, each of which considered

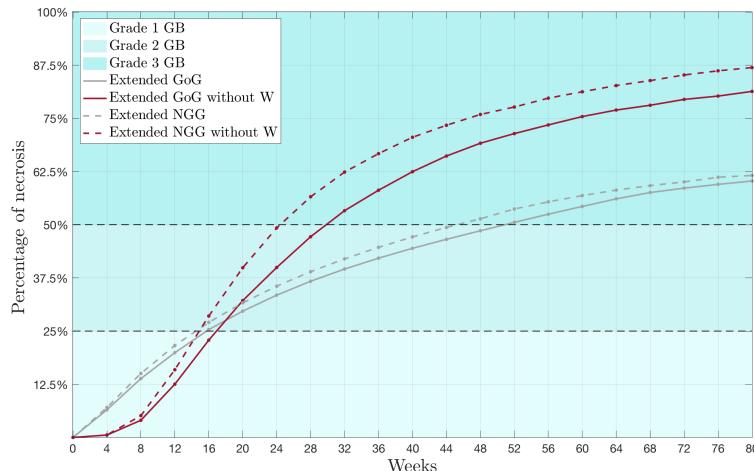


Figure 5: Tumor grading. Evolution of a grade function evaluating the fraction of necrosis with respect to the fraction of living cells in the visible tumor volume. Grey curves relate to the extended full model (including dynamics of endothelial cells) in the case with go-or-grow (solid line) and without the migration/proliferation dichotomy (dotted line). The red curves refer, respectively, to the same model variants, but without vascularization.

additional and different mechanisms influencing tumor progression (e.g., vasculature, acidity, or phenotypic heterogeneity). At the same time, measurements of protein levels and distribution performed in a *Drosophila* model of GB provided us further elements to analyze the evolution of tumor propagation fronts in relation to the dynamics of several other agents (i.e., ECM, proteases, or integrin receptors). We finally presented different results concerning the analysis of tumor response to different therapeutic treatments. All the proposed settings showed several advances in the study of the processes driving tumor invasion and they provided important contributions to building mathematical theory and integrating it with biological and clinical data, increasing the understanding of glioma growth and migration. Nevertheless, different extensions and improvements of these settings may be proposed, leaving plenty of room for further analysis that could be beneficial for getting a greater understanding of the mechanisms behind glioma progression.

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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 Oncology Laboratory - MOLAB

Our group is based at the departments of Mathematics of the University of Castilla-La Mancha and the University of Cádiz, Spain. We use a variety of tools from applied mathematics, including differential equations, discrete methods, statistical and data-analysis techniques, artificial intelligence, etc. Our goal is to answer compelling questions in medicine with a focus on oncology. The group is highly multidisciplinary with applied scientists complementing researchers with a more mathematical profile. We collaborate with more than 40 hospitals and biomedical research centers either by leading clinical studies or by integrating into existing initiatives to provide computational and data analysis support.

STAFF MEMBERS

Victor Pérez-García



Víctor M. Pérez-García is a full professor in Applied Mathematics at the University of Castilla-La Mancha and MOLAB director. He has worked on the mathematical description of physical and biological systems. His research has led to over 150 publications receiving more than 10,000 citations. He is currently editor-in-chief of the multidisciplinary journal 'Physica D: Nonlinear Phenomena' and coordinator of the 'Mathematics' board at the Spanish National Research Agency. His main current research interests are the use of mathematical methodologies to optimize the design of clinical trials in-silico for pediatric cancers, lymphomas, brain tumors, and fibrous dysplasia, and the identification of novel predictive and prognostic biomarkers based on imaging and molecular data.

Dr Gabriel F. Calvo



Gabriel F. Calvo is an Associate Professor in Applied Mathematics and a senior research member at

MOLAB. He has worked on the mathematical explanation of different physical and biological phenomena, including the quantum field theory of photons, quantum information processing, and different problems in oncology. His current research interests in mathematical oncology include the tumor microenvironment, the emergence of drug resistance, evolutionary dynamics and scaling laws, and the identification of image-based biomarkers. He also works in characterizing the behavioral landscapes of the immune system, with particular emphasis on neutrophils. His research has led to over sixty publications in JCR-indexed journals including *Nature* and *Cell*.

Juan Belmonte-Beitia



Juan Belmonte-Beitia is a full professor in biomathematics at the School of Engineering at the University of Castilla-La Mancha. He graduated in Mathematics and Physics at the University Complutense de Madrid and got his Ph.D. in Mathematics (2008) at the University of Castilla-La Mancha. His research interests are dynamical systems, differential equations, and partial differential equations and their applications to Mathematical Biology, specifically the mathematical modeling of tumor growth, the application of optimal control theory to therapy scheduling, stochastic processes applied to cancer, and numerical simulations of tumor growth and therapies. He is also interested in the mathematical modeling of diabetes and infectious disease dynamics.

María Rosa Durán



María Rosa Durán is an associate professor of Applied Mathematics at the University of Cádiz (Spain), where she obtained her Ph.D. in Mathematics. She has worked on methodological aspects of PDEs and mathematical models of tumor growth and the development of resistance. Currently, her research focuses on the development of mathematical models to optimize Acute Lymphoblastic Leukemia (ALL) treatments in children in collaboration with different hospitals. She is leading several clinical studies and research projects on pediatric malignancies incorporating data and model-based mathematical approaches.

Her mathematical toolbox includes partial differential equations, Lie symmetries, dynamical systems, and discriminant analysis.

David Molina-García



David Molina-García holds double degrees in Computer Science and Mathematics (University Autónoma de Madrid). He is an Associate Professor at the Department of Mathematics at the University of Castilla-La Mancha. His Ph.D. thesis dealt with the fields of Discrete Mathematics and Machine Learning. His postdoctoral research at MOLAB was related to the development of biomarkers in glioblastoma and other cancers using pre-treatment medical imaging. He is also interested in the field of Mathematical Education.

Julián Pérez-Beteta



Julián Pérez-Beteta is a BSc in Electrical Engineering (2014), with an MSc and Ph.D. in Applied Mathematics (2016 and 2019) from the University of Castilla-La Mancha, where he is now working as a post-doc and coordinating several clinical studies. His research involves medical image processing for the development of new morphological and metabolic imaging biomarkers, based on mathematical models of tumor growth.

Odelaisy León-Triana



BSc and MSc in Mathematics (Havana, Cuba, 2014 and 2017) and Ph.D. in Mathematics (UCLM, 2022). She is a postdoc in an industry-funded project led by Hospital Universitario de La Paz (Madrid) and MOLAB and together with the Spanish National

Group for Cellular Therapies. Her research involves using mathematical models to describe the response to immunotherapies and has worked on modeling tumor growth and response to radiation therapy.

Salvador Chulián-García



Salvador Chulián is a graduate (University of Cádiz) and a Ph.D. (University of Castilla-La Mancha) in Mathematics and is now a postdoctoral researcher at the Univer-

sity of Cádiz. He is also developing collaborations with Oxford University and the Moffitt Cancer Research Center. His research has focused on the dynamics and biomarkers of relapses in Acute Lymphoblastic Leukemia (ALL) using topological data analysis, differential equations, and machine learning methods.

Soukaina Sabir



Soukaina Sabir (Ph.D. in Mathematics, Morocco 2021) is a postdoctoral researcher at the MOLAB. Her research interests are mainly in the field of population dynamics, optimization and mathematical modeling applied to oncology. She is currently working on the development of data-based mathematical models for cellular immunotherapy against cancer, and more specifically on CAR T cell immunotherapy treatments in lymphomas and other B cell malignancies.

Mariia Soloviova



Mariia Soloviova is a graduate (Karazin Kharkiv National University, Ukraine, 2014) and a Ph.D. (University of Padova, Italy, 2020) in Mathematics (2020) working as a postdoctoral researcher at MOLAB. She is developing ODE-, PDE-based, and discrete mathematical models for bone regeneration to describe fibrous dysplasia in collaboration with researchers from the University of Córdoba (Spain) and the National Institute of Health (Bethesda, USA).

Jesús J. Bosque



BSc and MSc in Mechanical Engineering (University Politécnica de Madrid, UNED) and MSc in Applied Mathematics (UCLM). His Ph.D. thesis delved into the macroscopic footprints of cancer metabolism identifiable in PET images and the interplay of oxygen and temperature in cancer using mathematical models. He is now working on the in-silico design of clinical trials by means of hybrid computational modeling approaches fed with data from experimental animal models.

Juan Jiménez-Sánchez

BSc in Biotechnology (UPM), MSc in Biophysics (UAM), and MSc in Applied Mathematics (UCLM). He is now a post-doc at MOLAB working on evolutionary dynamics and virtual clinical trials in cancer. The discrete stochastic tumor growth models developed in his Ph.D. thesis (2022) have been used for human data-based studies on evolutionary dynamics, to discover new biomarkers in different cancers, and to optimize glioblastoma treatments.

Beatriz Ocana-Tienda

Beatriz Ocana-Tienda holds a BSc in Physics (Córdoba University) and MSc in Biomedical Engineering. She is now a Ph.D. student at MOLAB currently developing mathematical models of brain metastases growth and image-based biomarkers using data from large clinical datasets. She is also working on microscopic models to understand the initiation of brain metastases in collaboration with Oxford University and the Spanish National Cancer Research Center (CNIO).

Carmen Ortega-Sabater

Carmen Ortega-Sabater (BSc in Biology and MSc in Experimental Oncology, University of Murcia and MSc in Applied Mathematics) is a Ph.D. student funded by the Spanish Association Against Cancer (AECC). She is studying mathematically the mechanisms behind phenotypic plasticity and also malignancy evolution in pediatric leukemias and brain metastases using single-cell karyotyping and scRNA-seq data from CNIO and Josep Carreras Foundation.

Álvaro Martínez Rubio

Álvaro Martínez-Rubio (BSc in Physics, University of Córdoba; MSc in Applied Mathematics, Imperial College London) is a Ph.D. student funded by Pablo Ugarte Foundation. He uses statistical and machine learning methods to predict relapses in pediatric leukemias using flow cytometry data. He also develops differential equation models to simulate ALL and lymphoma

response to immunotherapies, the latter in collaboration with the Max Planck Institute for Evolutionary Biology.

Ana Nino López

Ana Nino-López holds an MSc in Mathematics and is now a Ph.D. Fellow at MOLAB-University of Cádiz. She is working on the development of mathematical models for chemotherapy optimization in Childhood Acute Lymphoblastic Leukemia and the clinical automation of diagnosis using mathematical tools. Her goal is to find the ALL type and risks of each patient from the initial bone marrow sample.

David G. Aragonés

David G. Aragonés (BSc and MSc in Civil Engineering, and MSc in Applied Mathematics) is a Ph.D. student working at MOLAB. His research focuses on developing mathematical models in immunology, combining computational statistics, numerical optimization, and network theory. Currently, he is working on the development of dimensionality reduction techniques for high-dimensional data.

Luis E. Ayala Hernández

Luis E. Ayala-Hernández (BSc and MSc in Biochemical Engineering, University of Guadalajara, México) is a Ph.D. student at MOLAB. His area of research is modeling the response of low-grade gliomas to chemotherapy and radiotherapy treatments. By performing computational simulations, his aim is to identify more effective combination therapy administration protocols.

José A. Romero Rosales

José A. Romero Rosales (BSc in Physics, University of Córdoba; MSc in Applied Mathematics, UCLM), is a Ph.D. student at MOLAB. He has worked on the development of new image biomarkers and on the generation of large public imaging datasets for brain metastases. His Ph.D. thesis will focus on understanding the resistance to treatment in

glioblastomas through cellular plasticity in collaboration with researchers from Institute Curie, Paris.

José García Otero



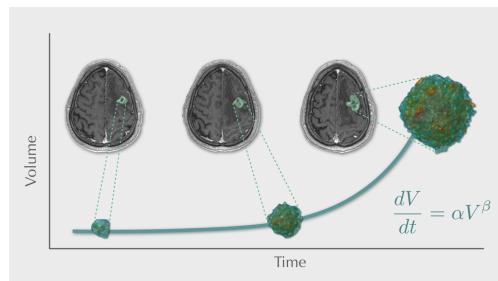
José García Otero (BSc in Mathematics, Basque Country University; MSc in Applied Mathematics, UCLM) is a Ph.D. student interested in the field of mathematical modeling in cancer. He is currently modeling the relationship between cancer, the immune system, and a novel treatment with mesenchymal cells loaded with an oncolytic virus called Celyvir. His goal is to understand the dynamics to suggest in-silico the best treatment scheme.

María Jesús Pérez Moraga



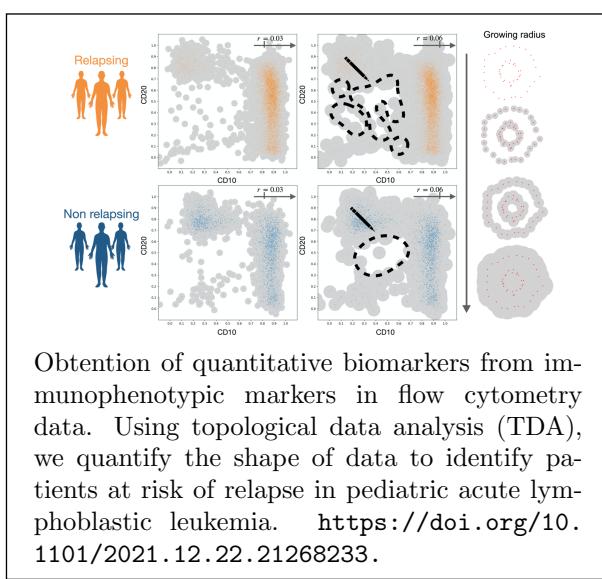
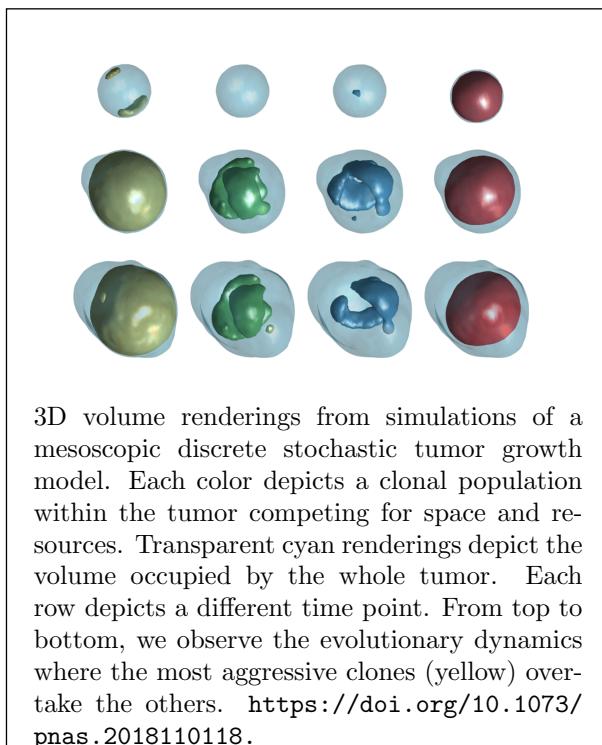
María Jesús Pérez Moraga is the Staff Manager at MOLAB. She has developed her activity since the inception of MOLAB, arranging all aspects of MOLAB organization and managing extra scientific setups. She is in charge of the organization and outreach of the lab scientific events. She provides services to

MOLAB research members and external collaborators (visiting professors, researchers, and students), as well as assistance in the development of ongoing projects and partnering with national and international research institutions.



Medical images from cancers are collected, processed and analyzed at MOLAB to reconstruct the volumes, shapes and metabolic activities of individual tumors. We use these datasets to parametrize mathematical models of tumor growth and response to treatment, which we use later to perform simulations. This workflow allows us to study the understand the growth dynamics of different tumors, discover new biomarkers of prognosis and response to treatments, optimize therapy schedules, and

perform clinical trials in silico.



For more information, please visit:
<https://molab.es>

ECMTB 2022



The **12th European Conference on Mathematical and Theoretical Biology (ECMTB2022)** took place in Heidelberg, Germany, between 19.09.-23.09.2022 and was a joint event of the European Society for Mathematical and Theoretical Biology (ESMTB) and the Society for Mathematical Biology (SMB). It was supported by the Heidelberg Cluster of Excellence “Structures” and the MAThematics Center Heidelberg (MATCH). ECMTB, formerly known as ECMBM – the European Conference on Mathematics applied to Biology and Medicine – was organized for the first time in Grenoble-Alpes D’Huez in 1991, followed by Lyon in 1993, and Heidelberg in 1996. After 26 years, ECMTB returned to Heidelberg. The event took place at the University Campus located among the fields on the Neckar River in three main buildings, where research in Mathematical Biology is carried out: Mathematikon (housing the Faculty of Mathematics and Computer Science and the Interdisciplinary Center for Scientific Computing), BioQuant (the Center for Quantitative Analysis of Molecular and Cellular Biosystems) and DKFZ (the German Cancer Research Center).

The ECMTB2022 brought together researchers and students interested in mathematical modelling with applications to life sciences. It was a large scientific meeting with over 740 participants from more than 40 countries around the world, among which more than 640 attended on site in Heidelberg. Virtual participation was also possible, and online participants were able to follow all plenary talks and oral presentations in webinar format, as well as submit online posters which were hosted on our platform.

The program offered a variety of interesting presentations on mathematical and computational modelling and methods applied to an array of biological and medical fields, such as developmental biology, immunobiology, epidemiology, neuroscience, physiology, and oncology, among others. Novel results of these topics were presented in 51 minisymposia of 4 talks each, 120 contributed talks and 205 posters, as well as 50 online posters. The program was enriched by six keynote talks by prestigious researchers: Daniel Forger, Julijana Gjorgjieva, Heather Harrington, Roeland Merks, Benoît Perthame and Padmini Rangamani, presenting cutting-edge results ranging from developing models in precision medicine, to understanding cell behaviour and collective pattern formation in developmental biology, and deciphering connectivity patterns and synaptic plasticity in neuroscience.

Additionally, the ECMTB2022 hosted talks by three Reinhart Heinrich Award recipients: Lisa Kreusser, Lukas Eigenthaler, and Martina Conte, a Diversity, Equity, and Inclusion (DEI) Panel, a National Science Foundation (NSF) panel and a meeting with editors from Springer Publishing Company. Over 200 posters were presented in four sessions grouped thematically, and 16 awards for the best posters from various sessions were awarded: 12 by ESMTB, 1 by the Journal of Theoretical Biology and 3 by the SMB Cell and Developmental Biology subgroup. The winning posters can be found on our website: <https://ecmtb2022.org/program/bookofabstracts/>

The Sunday before the official start of the conference, the Early-Career Workshop, traditionally organized by SMB every year, took place, with

the aim of providing tools for students, postdocs and junior faculty members who are entering the job market, or planning to do it in the future. A separate mentoring program also offered an excellent way for early-career scientists to obtain advice on career objectives, interdisciplinary approaches, work-family balance, networking, and other.

The scientific program was accompanied by a social program which allowed participants to network informally, while exploring and discovering the beauty of Heidelberg city. The weather was on our side and participants were able to enjoy a boat ride on the Neckar River, a tour of the Heidelberg old town, a tour of the Heidelberg castle or a hike along the Philosophers' Path.

Overall, the ECMTB2022 was an exciting worldwide scientific event, connecting researchers with similar research interests and the common goal of advancing the field of mathematical and theoretical biology. We are glad that the 12th ECMTB finally took place in person, after being postponed twice, and are thrilled to hear that participants had a great time exchanging scientific ideas and reconnecting throughout the week!

Anna Marciniak-Czochra



ECMTB 2022 in Heidelberg – Travel grants reports

44 travel grants were awarded mostly to young researchers to present their research at the 12th European Conference on Mathematical and Theoretical Biology (ECMTB), taking place in Heidelberg, Germany, on 19-23 September 2022. About 15kEUR was provided in total in this support. We have now obtained travel reports from some of the awardees and are glad to share their experience with you. The following text highlights the themes that recur in the reports, without any specific order of importance.

The awardees of the travel grants have expressed that they enjoyed the possibility to present their work in the form of posters quite a lot. They were less stressful relative to when they would present their research as a talk and could feel presence of fellows at the same career stage. As Kira Pugh says for all: “The poster session really helped me develop the skills of presenting my research in a short space of time and gave me a lot of confidence in talking to people and instead of being shy, sharing our ideas together. During this event, I was able to make genuine connections with people in the same field as me and we continued discussions over lunch and dinner during the week of the conference. I will stay in contact with everyone and potentially collaborate in the future or continue future research studies with them.” Sara Sottile adds: “Several researchers asked for more explanations of my work and I was very happy to share my results with them. I really appreciated the two poster sessions organized during the conference, since they were places of exchange of knowledge in a very friendly atmosphere.” Also David Morselli appreciates the poster sessions: “The poster sessions were another great opportunity to gain a general overview of the different approaches that are currently used in mathematical biology, as well as to get a one-to-one interaction with researchers in my own field.” And similarly Xiaoxi Pang: “I really enjoy giving talks in a less formal scenario, allowing me to interact with my audience, and most of whom have showed appreciation of my current work.”

Virtually all awardees enjoyed visiting sessions on other topics than is their own, stating that this was inspiring, extending horizons, enabling them to learn new methods that might be useful in various contexts. For many, this was a little taster for other topics, allowing them to think about what to possibly do in the future. For example, Molly Hawker says: “I enjoyed seeing the methods I use within my own research being applied to other areas of mathematical biology. For example, the use of Markov models to model opioid use disorder and anthrax infection and ordinary differential equations to model the female reproductive system.” Carmen Ortega Sabater adds: “One of the strong points of the conference lies in its multidisciplinary character. It was nice to see work from people outside our field, it refreshed my brain and I got new ideas for my work.” And Maria Gutierrez nods: “ECMTB22 has helped me to understand better what are the main research areas in mathematical biology outside of my field (epidemiology).”

Many of those providing us with travel reports enjoyed the mentoring program, highlighting a friendly and non-stressful atmosphere during the lunch meetings. Andrew Mair says: “Finally, the mentoring lunch provided the chance for groups of three researchers, at different career stages, to discuss their work and life in academia. I found this very useful from a career planning perspective, and it was nice to do it in such a relaxed environment.” Daria Stepanova specifically discussed “how to find a balance between a successful career in academia (in the field of mathematical biology) and family (work-family balance)”.

For many PhD students it was amazing to meet, for the first time, people that they have known just from reading their papers. In the words of Carmen Ortega Sabater: “This week was an amazing opportunity to meet in person many of the researchers and professors who are behind the articles that we thoroughly read.” And Dimitrios Katsounis adds: “One of the most important aspects of the conference was that I had the ability to expand my scientific network. . . . Getting to know PhD students and early career researchers and connecting with senior professors and researchers that I had only read their work these past years, enhanced the experience and brought up many fruitful conversations that will be continued in the future.”

One of the key moments for many PhD students was apparently attending the Reinhart Heinrich award talks. For many it has represented a position where they would like to be in a year or two and was thus an inspiring and path-forming experience. Andrew Mair says: “Another highlight of mine was the session of talks from the winners of the Reinhart Heinrich award. The speakers all presented their work in a very engaging way, and it was impressive to see the body of work that they had produced throughout their PhDs.”

Last but not least, all respondents agree that a possibility to meet people in person in such a big and important event was a real relief. As Sara Sottile says: “I also had the possibility, after these two past years of pandemic, to meet several researchers in this area, both old collaborators and new people. I hope that my contribution to this conference and the discussions held with several researchers will lead to fruitful collaborations.”

But conference is not only talks and posters, but it is also a free program. Our respondents generally appreciated the organized tours, but I am sure that many others enjoyed just free walking here and there. As Carmen Ortega Sabater aptly expressed it: “Walking around Heidelberg and eating local food was undoubtedly an added bonus to the conference.”

Other moments that were highlighted in the reports include the Early career workshop organized by SMB and wonderful plenary sessions. Let me close this short text by the final sentence of Giulia Chiari’s report which I believe represents the voice of many others: “I very much appreciated the general setting of the conference, the selected themes and the organization and I would be happy to participate in the next ECMTB event.” So, hope to see you all at ECMTB 2024 in Toledo, Spain.

Luděk Berec

The Helsinki Summer School on Mathematical Ecology and Evolution 2022



After a break due to the pandemic, the last week of August 2022 saw once again students of biomathematics converge to Finland for The Helsinki Summer School on Mathematical Ecology and Evolution. As its previous editions, this seventh school of our biennial series was a week-long, high-speed effort of five lecture courses and their associated working groups. The groups studied research papers ahead of the school, discussed them during the school and each group prepared a presentation to report back

to the entire school at the end.

On the more theoretical side of the school, Josef Hofbauer (University of Vienna) lectured on dynamical systems in mathematical ecology, with emphasis on saturated equilibria and permanence. It was impressively clear and a lot to learn also for myself! From an acutely applied angle, Gergely Rost (University of Szeged) taught the mathematics of infectious diseases and also showed us how he, as a mathematician, stepped up to the pandemic as the head of the COVID-19 Epidemiological Analysis and Modelling Response Team, the body that advised the government of Hungary during the crisis. While Gergely's lectures were concerned with deterministic dynamics, Pieter Trapman (who was just moving from Stockholm University to the University of Groningen and gave the school his full attention while distance-managing the transition in the breaks) concentrated on stochastic models of epidemics. After covering the background of branching processes, he taught us about epidemics in well-mixed populations; then we got an introduction to random graphs to move on to epidemics on networks.

With the fourth lecturer, we entered new territory. Our previous schools focused entirely on mathematics and even if data were shown, data analysis was not part of the main line. This time we asked Jarno Vanhatalo (University of Helsinki) to teach Bayesian statistics to students of mathematics and thereby to show how modern statistics is able to connect potentially complex models to reality.

The last lecture series focused on the dynamics of social behaviour, in particular on cooperation. This fascinating area never ceases to excite, especially when introduced with such skill and clarity as Christian Hilbe (Max Planck Institute for Evolutionary Biology) did! With his lectures, our summer school has also reached a historic moment: Christian was a student participant of the school in 2010 and now we had him on our faculty.

A good school is made by its faculty as well as by its students. I am grateful to our 35 student participants for their enthusiasm, effort, and devotion: I very much enjoyed the week we spent together. Our usual venue, the Linnasmäki Conference Center in Turku, once again provided us with flawless and friendly service. As an EMS-ESMTB summer school, we thank both EMS and ESMTB for financial support, as well as the Magnus Ehrnrooth Foundation of The Finnish Society of Sciences and

Letters and the University of Helsinki.

Eva Kisdi

Department of Mathematics and Statistics
University of Helsinki

ESMTB Travel Support ESMTB

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)

January 20, 2022, 12:00-14:00

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

Absent (with apology): Tom Britton (TB).

- E-vote decisions: Decisions taken via email since the previous meeting (October 1, 2021)
 - November 9, 2021:
 1. The board nominates Bob Planqué and Sílvia Cuadrado as members of the scientific committee of ECMTB22.
 2. The board agrees to do the final selection for the annual prize, to be established for the best JOMB paper. The author(s) of the winning paper will be invited to give a talk in the ESMTB colloquium provided the colloquium continues.
- Report of the treasurer (RP): As a consequence of the pandemic the number of conferences supported is lower than in previous years. Nevertheless, due to the reduction of membership fees during one year, the numbers are balanced. The report will be presented in the general assembly during ECMTB 2022.
- PCI initiative: The discussion initiated at the last meeting about the petition received to support “PCI Mathematical & Computational Biology” is resumed. The board decides unanimously to decline it at this moment but is willing to reconsider it in the future when PCI has developed further.
- Communications: The new issue of the Communications is ready to be printed. The address to download it will be announced via the newsletter and hard copies will be sent to the members that requested to receive it on paper. Extra copies will be made to be handed during ECMTB 2022.
- Reinhart Heinrich Award: The prize is given yearly to the student with the best doctoral thesis in Mathematical Biology. It is decided to change the ESMTB board procedure as follows: The prize committee should consist of 3-5 members, including a chairman and a representative from the ESMTB board (which may or may not

be the same person). The committee is decided by the ESMTB board each year, and typically members belong to the committee for up to 4 years. The committee is currently composed of: Carlos Braumann, Reinhard Bürger, Helen Byrne, Mirjam Kretzschmar and Stefan Schuster. Some committee members end their period and it is decided that the next committee will consist of: Tom Britton (chair), Helen Byrne, Mirjam Kretzschmar, Josep Sardanyés and Jana Wolf.

- ECMTB 22: The 12th European Conference on Mathematical and Theoretical Biology will take place in three locations in the campus of the University of Heidelberg. The meeting is planned as an in-person conference with the possibility of participating online. The online version of the meeting will include live stream/webinar of plenary lectures and oral presentations. Online participants will be able to submit abstracts for consideration for an online poster.
- The board agrees to open the application for travel support for ECMTB 22.
- Various: ESMTB members no longer receive discounts for Springer books; but, via ESMTB’s membership in the EMS can receive a 20 percent discount on books by EMS Press. This will be advertised on our web page.

April 5, 2022, 13:00-14:15

Members present: Ellen Baake (EB), Luděk Berec (LB), Tom Britton (TB), José Antonio Carrillo (JAC), Sílvia Cuadrado (SC), Elisenda Feliu (EF), Benoît Perthame (BP), Bob Planqué (RP).

Absent (with apology): Angélique Stéphanou (AS)

- Journal of Mathematical Biology, Bulletin of Mathematical Biology, Society for Mathematical Biology.

EB and JAC had a meeting with the SMB about cooperation in society and journal matters. It was agreed to cross-advertise the journals.

The Editors in Chief of the Journal of Mathematical Biology and the Bulletin of Mathematical Biology will write a joint editorial for the two journals and EB and Heiko Enderling (president of SMB) will write two paragraphs on the societies. It was also suggested to create a mathbio blog.

Currently, ESMTB has reciprocal memberships with

- SMB (Society for Mathematical Biology),

- ISMTB (Israeli Society for Theoretical and Mathematical Biology),
- JSMB (Japanese Society for Mathematical Biology),
- NVTB (Dutch Society for Theoretical Biology),
- SFTB (Société Francophone de Biologie Théorique (French-speaking Society for Theoretical Biology).

In the longer term reciprocal memberships with some other societies could be considered.

- Reinhart Heinrich Prize

Report of Tom Britton, responsible of the prizes of ESMTB:

The deadline for the 2021 award was on March 31st and 6 nominations were received. The winner of the Reinhard-Heinrich Award Doctoral Thesis Award 2020 was decided last March and the one of 2021 will be decided in May. Due to the pandemic, two previous winners of the prize could not give a talk at ECMTB, thus there will be four slots reserved at ECMTB 2022: 2018 prize (Dan Nichol), 2019 prize (Lisa Maria Kreusser), 2020 prize (Lukas Eigenthaler) and 2021 prize winner.

- Change of statutes of ESMTB.

It is agreed to write and submit for the approval of the members of the Society a new version of the statutes in which the option of replacing resigning Board members will be included.

- ECMTB 22 and Ukraine.

It is decided to make ECMTB 2022 free for people working at Ukrainian institutions.

After two years without activity it is also decided to send a reminder of the travel support offered by the Society.

- ECMTB 24

The deadline for submission of a proposal for the organisation of ECMTB in 2024 is May 1, 2022. At this moment no proposal was received yet but some are expected to be received before the deadline.

September 5, 2022, 13:00-14:00

Members present: Ellen Baake (EB), Luděk Berec (LB), Tom Britton (TB), José Antonio Carrillo (JAC), Sílvia Cuadrado (SC), Elisenda Feliu (EF), Tommaso Lorenzi (TL, invited guest before, board member after appointment), Benoît Perthame (BP), Bob Planqué (RP), Angélique Stéphanou (AS).

- E-vote decisions: Decisions taken via email since the previous meeting (April 5, 2022)

- May 4, 2022: Two proposals were received for the organization of ECMTB 2024. The board decided unanimously to accept the proposal of Victor Manuel Perez Garcia to host ECMTB24 in Toledo, Spain.
- May 25, 2022: The board decides to name the paper prize to be established for the Journal of Mathematical Biology after Karl-Peter Hadeler.
- July 6, 2022: The board decides to support with 500 euros the initiative "The Art of Theoretical Biology" as part of Leiden City of Science 2022.
- August 3, 2022: The board agrees on the following procedure for the Karl-Peter Hadeler Prize of the Journal of the Mathematical Biology: The Editors in Chief collect nominations from the Associate Editors and then recommend a small number (around 3 to 5) to the ESMTB board. The ESMTB board will then form an ad hoc committee of 3-5 people who will select the winning paper (and possibly the runners-up, who will receive a honourable mention).

- Statutes, new board member: In August 2022 all members of the ESMTB were invited to vote on an updated version of the statutes prepared by the board. The results were 77 votes in favor and 2 against resulting in the approval of the new statutes. The next step will be their registration with the French administration.

After the resignation of former board member Maíra Aguiar in February 2022 and following the approved statutes the board takes a secret vote about replacing her by Tommaso Lorenzi, the next candidate on the list who obtained the most votes in the last election. With all votes in favor, TL is appointed board member. The composition of the board until December 2023 is: EB (president), JAC (vice president), RP (treasurer), SC (secretary), LB, TB, EF, TL, BP, AS. The composition of the new board will be registered in France.

- ECMTB Heidelberg: The next board meeting is scheduled for September 20 in Heidelberg during the ECMTB.

There will also be an informal meeting with Lynn Brandon (Springer/JMB) during the conference. It is agreed that the Society will pay the prizes for the posters that will be called ESMTB poster prizes. 12 prizes of 200 EUR will be awarded. The General Assembly will take place on Wednesday 21 September at 14.30. Invitations will be sent

beforehand to all members.

EB will speak at the opening ceremony and JAC at the closing ceremony where the location of the next ECMTB will be announced.

- Conference support: It is agreed to revise the guidelines for conference support at the next meeting in Heidelberg.
- ECMTB 2024: EB informs that the Memorandum of Understanding has been signed on both sides (ESMTB and Fundación General de la Universidad de Castilla-La Mancha and University of Castilla-La Mancha).

**Minutes of the ESMTB board meeting in Heidelberg,
September 20, 2022, 16:30-18:10**

Members present: Ellen Baake (EB), Luděk Berec (LB), Tom Britton (TB), José Antonio Carrillo (JAC), Sílvia Cuadrado (SC), Elisenda Feliu (EF), Tommaso Lorenzi (TL), Benoît Perthame (BP), Bob Planqué (RP), Angélique Stéphanou (AS) .

- E-vote decisions: Decisions taken via email since the previous meeting (September 5, 2022)
 - September 16, 2022: The board decides to maintain the reduced membership fee and also to reduce the life membership fee by 50% for 2023.
- General Assembly: The contents of the presentation that has been prepared for the General Assembly are discussed.
- ESMTB/SMB collaboration: Heiko Enderling (president of the SMB) and EB, together with Thomas Hillen (JMB) and Matthew Simpson (BMB) have written a draft about the collaboration of the societies that will be published on the web page. In the future it might also be an editorial of the journals. The whole board is in agreement with its content.
- Conference support: The guidelines for conference support are discussed. It is agreed to ask the organizers to provide the distribution list of the ESMTB to participants and to remove the requirement: *If the meeting has a registration fee, each participant gets a free one-year ESMTB membership upon registration. The event organisers are required to transfer 25 EUR for each registered participant to cover the membership fee.*

BP suggests to increase the support amount for bigger conferences. It is agreed to offer a maximum support of 3000 EUR depending on the size and the budget of the conference.

- Scientific Committee ECMTB 2024 in Toledo: It will be composed by 4 board members and 4-5 external members. JAC, EF, RP and SC will be the board members in the scientific committee. External members covering different topics (Evolution, Immunobiology, Mathematical Epidemiology, Neurobiology, Cardiovascular Systems..) will be proposed in the near future.

**Minutes of the ESMTB General Assembly in Heidelberg,
September 21, 2022, 14:30-15:20**

The current board introduces itself: members are Ellen Baake (EB, President), Luděk Berec (LB), Tom Britton (TB), José Antonio Carrillo (JAC Vice president), Sílvia Cuadrado (SC, Secretary), Elisenda Feliu (EF), Tommaso Lorenzi (TL), Benoît Perthame (BP), Bob Planqué (RP, Treasurer), Angélique Stéphanou (AS).

The president (EB) begins by introducing the Society and its objectives. Then the other board members report on current activities, namely prizes (EB replacing TB), online colloquium, travel support, summer schools and educational matters, (LB), Communications (AS) communication (web page, newsletter, social media: EF, TL, RP), administration (SC), umbrella organizations and partner societies (JAC, BP).

Afterwards the treasurer (RP) explains that the transition from the German bank to the French one is, after a long time caused by administrative troubles, finalized. Also that, as a consequence of the pandemic the number of conferences supported in the last two years has been lower than in previous ones. That was one of the reasons to decide a reduction of the membership fees. It is expected that the number of applications for support will increase considerably in the coming future. Then he presents the financial report which is approved by the General Assembly.

Finally the president (EB) informs about the meaning of the membership and the number of members of the society over the last years. The assembly ends with the president thanking the attendees for their participation and encouraging them to contact

the board with any questions, proposals or suggestions concerning the ESMTB they might have.

Sílvia Cuadrado
ESMTB Secretary

ESMTB Online Colloquia

The ESMTB online colloquia were established to promote and facilitate scientific interactions during and after the COVID-19 pandemic. In view of the success of these recurring events, evidenced by a consistently good turnout, we decided to continue organising them during 2022. Owing to the fact that many scientific meetings, workshops and conferences are now held again in person, starting from September 2022 the frequency of the colloquia has been reduced. The two next colloquia are now scheduled for February and March 2023. We are pleased to announce that our February speaker will be Victor Pérez-García, the organiser of the next ECMTB conference in Toledo.

All the details of the colloquia will be shared with the members of the ESMTB mailing list and through the dedicated page on the ESMTB website (<https://www.esmtb.org/ESMTB-online-colloquium>).

Practical information:

- *When:* last Wednesday of the month at 1pm (CET).
- *Where:* colloquia are live streamed on Zoom – the Zoom link is distributed to the members of the ESMTB mailing list.
- *After the colloquium:* colloquia are recorded (provided the speaker agrees) and a link to the recording is made available on the ESMTB webpage.

2022 speakers :

- Anna Kuparinen (University of Jyväskylä), What fishing actually selects for?
- Carsten Wiuf (University of Copenhagen), Molecular Machines and the EM algorithm
- Anotida Madzvamuse (University of Sussex), Theoretical studies of non-autonomous reaction-diffusion systems: the effects of domain growth and cross-diffusion

- Susanne Ditlevsen (University of Copenhagen), Time scales in early warnings: a probabilistic approach
- Amaury Lambert (Ecole Normale Supérieure), Stochastic models coupling the evolution of genomes and species
- Luigi Preziosi (Politecnico di Torino), Modelling Cell Reorientation under Stretch: A Mechanobiological Example
- Hanna Kokko (University of Zürich), Good reasons to live shorter lives

From idea through theoretical finding up to society at large

by Luděk Berec

Being currently a member of top management of my university (vice-rector for science and research at the University of South Bohemia, České Budějovice, Czechia), I more than clearly sense a transition from purely academic research to something that is waking up under a hard to grasp concept of societal relevance of science and research. Very broadly (as I understand it), this effort to bring science and research from universities and research institutes more to wide public revolves around three major pillars representing our three major stakeholders: business (especially technology and knowledge transfer), politics (advisory organs, methodological support, funding agencies), and public (communication with media, popularization of science). All this will more and more affect not only the future of research funding, but also evaluation of our institutions and each of us at our institutions. It is young researchers that are the future of science, and especially those should be clearly taught how to communicate our results to stakeholders.

Our traditional work regarding basic science is to conceive a real problem (and mostly we conceive the problem rather than an external stakeholder that would ask us for help), develop and analyze a corresponding model, interpret and put into context of current knowledge what we have found, and publish our research. More often than in the past we use data to illustrate and further support meaningfulness of our analyzes, and forced by circumstances, we speculate on potential applications of our results. But in an overwhelming majority of cases these are just “mock applications” that we just dream of. In “green” biology such as ecology those speculations commonly revolve around species conservation, pest control or sustainable harvesting, while in “white” biology such as cell biology one commonly imagines a potential to develop a new cure or treatment. Do not take me wrong, this is not condemnable at all, but whether we speculate or not does not change things much, it often only increases our own perception of importance of our research.

What is clearly missing is a last step, really making our results applied, seeing them used in real biodiversity protection programs or in clinical practice. This is of course not fully in our hands, is usually a long-term effort, and obviously not

every result can make it to practice. That's not where I aim for. Moreover, a standard and relevant objection of many of us might be that our models do not often aim to provide something applicable to the society. Rather, that they aim to provide understanding of what we see around us (this is typical of evolutionary biology, for example). This is perfectly fine, but the right question then goes like this: do such theoretical results that help explain the world around us make it into non-mathematical (ecological, evolutionary, cancer etc.) textbooks? This is in my opinion what in this case makes an equivalence of practical application of other results.

Imagine covid-19. Almost everyone “with hands and legs” that has ever touched mathematical modelling (and in many cases also those that did not at all) and originating from many diverse disciplines was involved in covid-19 modelling. The trail has been nicely paved: relatively easily comprehensible models, rich literature on previous epidemics, the largest data collection efforts in history. But how many of the results have made it into real policy on the public health level? And I do not talk here about politics: many of us have been sitting in the governmental advisory panels and know how difficult is to bridge the gap between expertise and politics. Still, I am sure that any of the tens of thousands of papers on modelling covid-19 ended up with a variant of phrase “our results will help mitigate current pandemics and bring the societies to a normal state”.

Axel Rossberg and his co-authors, in their paper “Let's train more theoretical ecologists – here is why”, published in 2019 in Trends in Ecology and Evolution, wrote: “Theoretical Ecology does not give the impression of an intellectually coherent field of study. Onlookers see a frighteningly diverse conglomerate of various particular models and ideas, which are at best unrelated and at worst contradictory.” In some sense this is also true of covid-19 modelling. Moreover, many talks at the ECMTB 2022 conference in Heidelberg involved a phrase like “our model is simple” or “we use a simple model”, but the models have actually been used to attempt to understand something quite difficult and in a sense potentially applicable. This is fine when heading inside our community of mathematical biologists, but is in my opinion

quite risky if aiming at onlookers and stakeholders that may say: “What? That will never gonna work!” And we should think outside, more and more.

After all this lamenting, I am eventually approaching the core of my message. We should be aware of all this and value every piece of work that has eventually made it to a real real application or to a non-mathbiology textbook. Are we really aware of such achievements? Have some of previous theoretical results indeed made it to a non-academic use? And are we waving with such examples and letting math biology students know them? Honestly, I am not sure. Let's join forces and find grand examples of using results of math biologists in practice or up-to-date textbooks. Let's create something like simple “presentation cards” that would show a way of a specific result from idea through theoretical finding up to society at large. I am sure that having and sharing these exemplary examples would help us in many respects: education of all of us as well as stakeholders, communication with public, wide recognition and thriving of our field, wider funding opportunities, invitations by non-mathematicians to participate on their projects, etc. For me, it makes sense. And I hope it will also for some of you.

Poster campaign: "The Art of Theoretical Biology" in Leiden, The Netherlands

by Roeland Merks



The Ghost, by Franziska Matthäus, Damian Stichel and Kai Breuhahn

Did you ever bump into a mathematical model of the cellular slime mold *Discoideum discoideum* when you were walking around your town? Did an advertisement ever invite you to study the mathematics underlying lateral root development? Did you ever push the breaks of your car to take a closer look at cellular automata models of cancer? Perhaps this does not sound like a very probable situation, but in the summer of 2022 this was a reality for the inhabitants of Leiden, the Netherlands.

ESMTB kindly funded the poster campaign *De kunst van theoretische biologie* (*The Art of Theoretical Biology*) as part of the year-long science manifestation *Leiden European City of Science 2022*, together with the Dutch Society for Theoretical Biology (NVTB) and the institutes of mathematics and biology of Leiden University. The poster campaign was inspired by an earlier exhibition *The Art of Theoretical Biology*, held in summer 2018 in Frankfurt, Germany. This event, organized by Franziska Matthäus, featured large banners on university buildings, showing beautiful visualizations of mathematical biology, and formed the basis for the book *The Art of Theoretical Biology*.

The exhibition in Leiden lasted from August 10 to August 23, 2022 and featured 25 different posters distributed all over Leiden. Each poster had a caption in Dutch, consisting of a one-liner of the research and its societal impact. Some posters were on display near the university hospital, others were shown in residential areas. Some of the images were part of the exhibition in Frankfurt and of the book *The Art of Theoretical Biology*, whereas others were created specifically for the exhibition in Leiden.

The Art of Theoretical Biology turned out to be a playful and low-key way to introduce the importance and the beauty of theoretical biology to the general public. I hope that many follow-up events will come!

Further Reading

- Overview of all posters in the exhibition in Leiden: <http://pub.math.leidenuniv.nl/~merksrmh2/TheArtofTheoreticalBiology/>.
- The exhibition in Frankfurt, Germany: <https://fias.news/en/press-release/the-art-of-theoretical-biology/>.

- Franziska Matthäus, Sebastian Matthäus, Sarah Harris, Thomas Hillen (Eds.) *The Art of Theoretical Biology*, Springer Nature Switzerland, 2020. <https://doi.org/10.1007/978-3-030-33471-0>.



Spectral Forms and Cosmic Storms, by Michael Colman



Guiding Spirals, by John Dallon and Hans Othmer

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**
- **Travel Support** for mathematical/theoretical biology meetings
- **Support** for the organization of scientific events
- Endowing the **Reinhart Heinrich** and the **Ovide Arino Awards**
- **Reduced fees** for selected conferences and schools
- **20% discount** on EMS Press books when ordering directly from EMS Press
- **Voting** in society elections

You receive:

- Annually printed or electronic (pdf) versions of the **Communications of the ESMTB**
- Monthly electronic **ESMTB Newsletter**

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:

375 EUR (age 40 or above), 250 EUR (age 50 or above), 125 EUR (age 60 or above)

Further information:

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