

Reports from 2019 travel grant awardees supported by an ESMTB travel grant

ESMTB Travel Support

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

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

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

In 2019, nine travel grants were awarded, with total support of 1850 EUR.

The awardees are asked to write a brief report about the event. Here we present some of the reports. The original reports are slightly edited and shortened yet their spirit remains unchanged.

Yvonne Krumbeck: Mathematical Biology on the Mediterranean Conference (MBMC)

In September 2019, University of the Aegean hosted the first Mathematical Biology on the Mediterranean Conference (MBMC), located on the beautiful Greek island Samos. With great efforts by the organising committee, Stelios Xanthopoulos and Jean Clairambault, the conference has become a grand success and was received positively by the participants. Attendees from Universities of different countries created a culturally diverse atmosphere and encouraged exciting exchanges.

The conference was split into 1 week of a summer school and a 1-week long workshop, where participants could attend either one or both events. During the first week, 5 lectures covered a range of topics in mathematical biology. The lecturers, Benoît Perthame, Nicolas Vauchelet, James Sneyd, José Antonio Carrillo and Nikolaos Sfakianakis addressed mathematical models and methods for evolutionary and bio-chemical dynamics, cell kinetics, collective motion and many more. For me personally, the lecture on an epidemiological model for the spread of Wolbachia bacteria in mosquito populations held by Vauchelet was the most insightful lecture. A well-balanced mix of lectures made the summer school accessible for those who are more mathematically as well as more biologically oriented students. It offered many opportunities to ask and discuss questions and exchange knowledge of different expertise.

The workshop during the second week added more interesting talks by researchers from various fields of mathematical biology. Among all, Mats Gyllenberg, Charalambos Makridakis, Anna Marciniak-Czochra, Luigi Preziosi and Christian Schmeiser have been invited as keynote speakers. Up to 45-min long presentations offered a great opportunity - especially for PhD students - to speak more in depth and have longer discussions about the research.

Unfortunately, there was only a small number of participants who presented a poster. Thus, the sessions to view and discuss them was rather short. Nonetheless, attendees had many opportunities to gather in small groups and discuss their research in more depth.

Excursion days were organised to explore the island Samos and learn more about its history and culture, including the life of the famous mathematician Pythagoras. First, we visited the archaeological site of the ancient temple of Hera, followed by a stop

at the museum in Pythagoreio. After that, we were offered to taste the sweet wine from Samos and learn about its production at the wine museum. The location of the conference close to the sea, beautiful hiking areas and delicious local food made the overall experience even more enjoyable.

To conclude, interdisciplinary gatherings like MBMC always offer a pleasant opportunity for researchers from various fields to meet and exchange their knowledge. The diversity of participants helped to reinforce the network of those interested in mathematical biology. After the great success of this conference, I hope that other Universities will follow up and soon host the next of this series.

Diana-Patricia Danciu: Mathematical Biology on the Mediterranean Conference (MBMC) I attended the MBMC, held between 1-14 September 2019 at the University of the Aegean, Karlovasi on the Greek island of Samos, the island of Pythagoras. The first week of the event consisted of a summer school, with lectures on various topics in mathematical biology presented by renowned professors in the field. The lecturers taught complementary subjects inspired by their own research: Attractive-repulsive mathematical models in collective motion by José Antonio Carrillo, Models of adaptive dynamics in mathematical biology and their analysis by Benoît Perthame, Mathematical problems in evolutionary theory and associated numerical questions by Nikolaos Sfakianakis, Topics in mathematical physiology by James Sneyd and Control of vector-borne diseases and their epidemics by Nicolas Vauchelet. Not only did I learn something from each lecture, but I also had the possibility to further discuss the topics with the lecturers. Working with compartmental models myself, I found the lectures by Nicolas Vauchelet particularly interesting and helpful, and it was very rewarding to see once again the power of relatively simple deterministic models when applied to specific biological systems: in this case, modelling the dynamics of disease-carrying mosquito populations and the techniques used for preventing the spread of the disease. On the other hand, the lectures by James Sneyd were very entertaining, and even though there were no similarities to my projects, I enjoyed not only learning about the mathematical methods used and about the importance of calcium in living organism, but also about the importance of having a goal, a question to answer when starting to develop a mathematical model a concept which I have been supporting, as well. The lectures by Nikos Sfakianakis

taught me, among others, about certain optimization techniques, and were very inspiring, showing how certain mechanisms from physics can explain evolution, for example how one can use the brachistochrone problem to explain limb regeneration in salamanders.

In the second week of the event, we took part in a workshop hosting talks on various advanced topics in mathematical biology, presented by researchers at various stages of their career. The plenary talks, in particular, were very interesting, offering a general overview of methods in applied mathematics used in understanding various biological aspects. From among the other talks, I found those by Emeric Bouin, Diane Peurichard and Nikolaos Kavallaris particularly interesting, once again discovering the impact that relatively simple mathematical models can have in explaining biological mechanisms. I also had the opportunity to present the work I did during my doctoral studies and my talk was well received, with many follow-up questions from interested persons. One participant told me she would like to find out more details, as she could use some methods that I presented for her own project.

During the two weeks I had the possibility to interact with fellow researchers and made many new friends, extending my network of scientific connections. It was extremely rewarding to learn about their projects and the various methods that they use, thus paving the way towards possible future collaborations. I usually find it difficult to do networking in big conferences, but during these two weeks I had no such problems, as the MBMC event nicely facilitated and encouraged the interactions through the good organization.

In conclusion, I consider that participating in this event was very rewarding, having had the opportunity to learn many new things, to make a lot of new connections, even friends, and to get ideas for possible future research topics.

Lin Wang: Croucher Summer Course on Computational Genomics of Viral Evolution and Epidemiology This summer school introduced mathematical and computational concepts, methods and analytical tools for dealing with genomic sequencing data, which are very important in pathogen surveillance, clinical diagnosis, treatment, vaccination, risk assessment, disease prevention, etc. The school had three modules: Phylogenetic Inference (PI) Module, Evolutionary Hypothesis Testing (EHT) Module, and Next Generation Sequencing (NGS) Analytics Module. PI module focused on

the sequence alignments and maximum likelihood methods for building phylogenetic trees, EHT module focused on the likelihood and Bayesian inference (e.g. coalescent theory, phylogenetics, phylodynamics, phylogeographic analyses), and NGS module covered more complex analysis of full genomes and huge datasets of pathogens with a focus on Next Generation Sequencing data.

I attended the EHT Module led by Professor Philippe Lemey and Professor Marc Suchard. This module not only provided a comprehensive overview of the Bayesian inference and hypothesis testing theory, but also instructed their computational implementation, e.g. BEAST, HyPhy, Spread3, ggTree. I also attended several lectures about the alignment algorithms, transcriptomics, RNASeq, metagenomics, molecular adaptation, large-scale visualization offered by the other modules. These lectures have been highly relevant to my studies in the evolution and transmission of arboviruses such as dengue.

During the summer school, I presented a poster ‘Characterizing the dynamics underlying global spread of epidemics’. The co-director, Professor Anne-Mieke Vandamme, mentioned that all poster abstracts will be published as a special issue by the journal ‘Virus Evolution’ (<https://academic.oup.com/ve>). I discussed with several course instructors about collaborations on combining molecular evolution, phylogenetic and epidemic dynamics together for jointly estimating virus evolution and epidemic transmission.

In sum, “Croucher Summer Course on Computational Genomics of Viral Evolution and Epidemiology” was very informative and provided an excellent opportunity for connecting with experts in the fields of mathematical modelling, infectious disease dynamics, molecular epidemiology, genomic analysis, evolution, phylogenetics and phylodynamics. I very much appreciate the ESMTB to support my attendance of the Croucher Summer Course on Computational Genomics of Viral Evolution and Epidemiology.

Chakib Jerry: Mathematical Models in Ecology and Evolution (MEEE) The conference was divided into several working sessions. Each session was distinguished by a field of applied mathematics. I attended several plenary lectures and presentations during various sessions where I was able to enrich my scientific culture especially on the different fields of applications of mathematics such as epidemiology, evolution, decision-making, ecol-

ogy, population and ecosystems dynamics as well as emerging trends such as population genetics and game theory.

This conference gave me the opportunity to meet several researchers including Johann Bauer, Dibyendu Sekhar Mandal, Katherine Heath and Katerina Stankova who are interested in my field of application and other areas for possible scientific collaborations that will help me in my research and preparation of my authorisation.

During the session “Epidemiology I”, I presented my work entitled “Simple cancer model as controlled switched system” in which we investigated a simple mathematical population model of Proliferative/Quiescent cells interactions where chemotherapy treatment was considered as a control variable. The feature thing in this work is that the control variable is not considered continuous by time but piecewise-continuous which is introduced in our work by an impulsive control. This kind of control is motivated by the fact that chemotherapy is not applied continuously (day by day treatment) but piecewise continuous (a break between two chemotherapy applications). Furthermore, we study an optimal control problem to find the best strategy to minimise the size of tumor cell which mean maximising health state of the treated person. We discuss also numerical results for chemotherapy regimens.

Several researchers and specialists attended my presentation and at the end of it numbers of relevant questions were asked mainly about tools used to study the model, perspectives of my work and the degree of experimentation with the results obtained.

I hope that my contribution to this conference, as well as the many discussions held with several researchers, will be able to contribute to possible collaboration, in particular with Dibyendu Sekhar Mandal, Katherine Heath and Katerina Stankova. I hope that our Moulay Ismail University will made more effort to give opportunities to different professors and researchers to distinguish themselves in the international scientific world.

Lukas Eigentler: Mathematical Models in Ecology and Evolution (MEEE) I have been awarded a travel scholarship from the ESMTB to partially fund my travel to and attendance of the 7th edition of Mathematical Models in Ecology and Evolution (MMEE 2019), which took place in Lyon from 16th July 2019 to 19th July 2019.

The meeting was the latest of a series of biennial workshops that brings together theoretical ecologists, theoretical biologists and mathematical

biologists to discuss their advances in the modelling of problems arising in ecology and evolution. The conference consisted of five plenary talks by Joanna Masel (Arizona), Florence Debarre (Sorbonne), Thomas Hansen (Oslo), Jeremy Draghi (New York) and Thomas Lenormand (Montpellier); a public lecture by Steven Frank (UC Irvine); ten minisymposia; 16 parallel sessions of contributed talks; and a poster session.

I actively participated in the meeting by contributing my talk *Metastability as a coexistence mechanisms in a model for dryland vegetation patterns* in one of the parallel sessions. The talk emerged to be the foundation for many fruitful discussions afterwards, including some suggestions for further work that may well prove to be useful in the future.

In general, the event provided me with a good networking opportunity, allowing me to discuss my work with fellow researchers and learning about their recent advances. The conference organisers also provided a large poster with one column to which anyone looking for postdoc positions could add their names and a short description of their work, while a second column was being used by senior researchers to list any open postdoc positions. I believe that this was a fantastic idea and may well provide a good reference point as I am in the process of funding a postdoc position.

Further, the conference allowed me to broaden my knowledge across different topics in mathematical biology since presentations covered a wide area of topics, some of which were completely new to me. It was of particular interest to learn how similar methods (including methods closely related to those used in my research) can be applied to a wide range of different problems in ecology and biology.

I would like to kindly thank the ESMTB for the award of this travel scholarship which enabled my participation at the conference.

Simon Syga: Annual Conference of the Society for Mathematical Biology (SMB) I attended the Annual Conference of the Society for Mathematical Biology (SMB) in Montreal, Canada, from July 21 to July 26, 2019 and was supported by the ESMTB. I presented a poster titled *A new lattice-gas cellular automaton model explains plasticity in breast cancer invasion*, that summarized a model that is part of a joint publication with Peter Friedl, Nijmegen, which is currently in preparation. For the outstanding poster, I was awarded a poster prize. Besides the ECMTB, SMB is one of the

biggest and most important conferences on mathematical biology, which allowed me to get in touch with many researchers of his field working outside of Europe.

Aleksandra Plochocka: Annual Conference of the Society for Mathematical Biology (SMB) I would like to thank the ESMTB for awarding me a travel scholarship to attend the Annual Meeting of the Society for Mathematical Biology (SMB) in Montreal, Canada between the 21st and 26th of July 2019. The SMB 2019 meeting was the largest SMB gathering of researchers in Mathematical Biology since its foundation with over 360 attendees. A plethora of research topics meant that many of the plenary talks were given by individuals in research areas unfamiliar to me. This provided a great opportunity to get a glimpse at the cutting edge work in other fields. The highlights of these talks for me included Lindin Wahl (bottlenecks in influenza), Arthur Sherman (reversing vs. preventing type 2 diabetes) and Nick Monk (philosophical discussion of teaching in mathematical biology). Aside from this, the meeting included seminar on “how to get a tenure track position”, interactive discussion of presenting research in short digestible formats and a women’s lunch which discussed the unconscious bias in academia and how to overcome it.

Personally, since I am starting a postdoc in New York in October I found this meeting to be particularly apt for me since it enabled me to meet many academics from North America. Through giving a talk at the mini-symposium on intracellular transport I was able to meet many academics whose research formed the basis of my PhD thesis literature review. It was exciting to discuss my research in detail with academics such as Eric Cytrynbaum and Adam Hendricks. Various mini-symposiums captured my interests, with two highlights including the ‘Mathematical modeling of normal and abnormal tissue growth and development’ and ‘Multiscale modeling of cytoskeleton-mediated cellular transport and aggregation’. SMB provided a great atmosphere to meet both new and familiar academics in an stimulating environment. SMB 2019 was a truly rewarding experience, thank you.
