

Reports from 2018 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 an ESMTB member at the moment of submitting the application. The maximum amount of travel support provided by the ESMTB per single application is currently set to 350 euro. However, funding will in most cases be only partial, in order to support a greater number of applicants. In general, preference will be given to:

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

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

In 2018, 20 travel grants were awarded, with total support of 4610 EUR. Most applications concerned participation at the ECMTB2018 conference in Lisbon, followed by the ESM-ESMTB Summer School on Mathematical Ecology and Evolution 2018 in Turku.

The awardees are asked to write a brief report about the event. Here we present some of the reports the awardees sent to us upon returning from the event they were attending. The original reports are slightly edited and shortened yet their spirit remains unchanged.

Report by Aurélien Velleret on the ESM-ESMTB Summer School on Mathematical Ecology and Evolution 2018, Turku

This school was one of the best opportunities for me to advance in my future career. It was quite dense but very well organized. The conditions were optimal for us to learn a lot and exchange between the students and the teachers in a very friendly and open manner. The fact that we were all staying for the week in this rather remote place – with a nice forest nearby – contributed much to this atmosphere. Indeed, I liked much the informal meetings during lunches, dinners or in the evenings (more than the breaks where I rather wanted some rest). The expeditions at Turku and the experience of sauna were also great and made me feel at ease in the group, leading to easier interactions (probably also in the future!). The lessons were of great quality and variety. Since I consider these methods and topics as potential future area of research, it was a wonderful opportunity to consolidate my knowledge.

Among all presented courses, the Sebastian Schreibers course was probably the one I expected the most, since it dealt with these issues of maintenance of ecological diversity in the context of a (usually random) changing environment. In fact, my PhD deals with the survival of populations submitted to a risk of extinction given a change of the environment and the stochastic emergence of new fixed mutations in the population. So there is clearly some insight that I could have through the models he presented, notably on this notion of a species being able to invade a stochastic dynamics with possibly many others. Even after my PhD, I would really enjoy to work on more carefully on these subjects, possibly wondering about an extinction of a species not completely excluded and yet a priori very exceptional.

I was also very glad we could have an opportunity to work between the students on articles related to one of the course and present at the end some conclusions to the other groups. Quite naturally, I've chosen Schreibers group and the

articles were very interesting (in fact, we chose to focus only on one of the two for the presentation). I must say I was probably the most familiar with the probabilistic notions presented (branching processes, generating functions), so that I was often in charge of explaining them. Yet, there was a real dynamics of group and we were left very autonomous on the way we managed the job, with of course the support of Sebastian Schreiber to deal with our difficulties in understanding. It was a great experience and a very nice way to interact with the other members of my group.

Finally, the short presentation of each students, done in the two first evenings, was a useful way to present ourselves to the others and present our main subject of interest for following discussions. As we were quite numerous (above 30), it was indeed quite dense and I was glad it was at least split in two evenings. In conclusion, I highly appreciated the contents I studied thanks to this Summer School and the wonderful conditions we were in!

Report by Sara Hamis on the “Mathematical perspectives in the biology and therapeutics of cancer” workshop at CIRM, Marseille The workshop brought together mathematicians, clinicians and biologists, comprised a symposium, a series of invited and contributed talks and posters, the majority of which investigated aspects of cancer mathematically. An impressive array of invited speakers from well-renowned cancer research institutes and universities shared their expertise to a highly interested audience. Multiple cancer-related concepts of clinical importance were discussed, such as tumour growth, intratumoural heterogeneity, angiogenesis, drug resistance, treatment responses and treatment optimisation. In an effort to portray these cancer aspects sensibly using mathematics, several mathematical modelling techniques were proposed. Mechanistic and phenomenological, discrete and continuous, deterministic and probabilistic models were all presented and motivated. Mathematically, problems were solved both analytically and numerically and cancer

was investigated, on various scales, ranging from macroscopic population scales down to patient, tumour, cell and subcellular scales. Overall, the great variety mathematical techniques to investigate various cancer issues provided a nice up-to-date overview of what fellow researchers are working on right now.

In addition to mathematical presentations, more biology-centered talks were presented by clinicians and biologists, providing us mathematicians with useful insights. These talks instigated well-needed discussions attempting to answer the questions (1) What can we (mathematicians) do to help clinicians/scientists advance cancer research and clinical protocols? (2) What information do we (mathematicians) need from clinicians/scientists in order to progress mathematical oncology?

Furthermore, in the spirit of interdisciplinary collaborations, a fruitful symposium was held on Wednesday morning. Speaking at the symposium were people from French cancer research institutes including Christine Chomienne, the director of ITMO Cancer Aviesan and Research and Innovation department INCA. We (the audience) received useful advice on how to establish successful collaborations with clinicians/scientists, and how to formulate prosperous grant applications. Personally, as a young researcher who wishes to continue in the field of mathematical oncology, I found this symposium to be highly interesting and important as it provided useful information on how to achieve successful research (beyond mathematical aspects).

To summarise the scientific content of this workshop in three words, it was interdisciplinary, well-delivered and current. I enjoyed every single talk and poster. In addition to learning from other peoples presentations, I was gratefully given the opportunity to present my research on modelling effects of hypoxia-activated prodrugs (talk) and chemotherapeutic drug resistance (poster). Presenting my work in front of an audience of experts (most of whom I have cited) was a humbling and exciting experience. Scientific content aside, the workshop was fantastically well-organised, fun and friendly. The conference center and the geographical lo-

cation is absolutely gorgeous, and an unforgettable hike in the Calanques was arranged for adventurous conference participants. I would highly recommend fellow young researchers in the field of mathematical oncology to attend any upcoming similar events.

Finally, I would like to add that I am very thankful to the workshop organisers for accommodation funds and to ESMTB for the travel grant. Without the support I could not have attended this workshop.



Participants of the “Mathematical perspectives in the biology and therapeutics of cancer” workshop organized at CIRM, Marseille

Report by Tatjana Jakushina on the Lisbon ECMTB2018 conference The 11th European Conference on Mathematical and Theoretical Biology (ECMTB 2018) was one of the most important events related to the Year of Mathematical Biology 2018. The organization of the conference and the quality and diversity of presented researches was very impressive. This event gathered around 700 participants from 60 countries, including both influential scientists and young specialists. It was an invaluable experience to attend such a broad range of sessions and have an opportunity to discuss the most relevant problems in mathematical biology.

The conference program included nine plenary talks, one of which was the BS-EMS Lecture by Samuel Kou. Among other impressive lectures, I found the talk Models of learning and evolution: what do they have in common? by Eors Szathmaary one of the most inspir-

ing. In this presentation, three main questions shedding light on the relation between evolution and learning processes were discussed. First, whether true evolutionary dynamics can unfold in the brain. Second, whether associative, reinforcement and deep learning dynamics could play a role in the evolution of ecosystems, developmental genetic regulatory networks and evolutionary transitions in individuality. Third, whether similar algorithms could realize either of them in some natural systems. This talk was thought-provoking, providing many ideas for further research in artificial evolution and multilevel selection.

Another plenary speaker that I want to mention specifically was Eva Kisdi with a talk Adaptive dynamics and the evolution of diversity. This presentation was dedicated to an important approach in evolutionary theory and its possibility to explain the enormous diversity of living forms. That lead to a series of problems: the existence of the upper bound to the number of species, the possibility of natural selection to lead to extinction, and the difference between variation and speciation.

More than 400 contributed talks were arranged in parallel and contributed sessions and minisymposia, covering a wide range of cutting-edge topics. I attended talks in Evolutionary Dynamics, Mathematical methods in Biology, and Population Biology sessions, prioritizing the fields that are relevant to my current projects. Moreover, I still address the conference materials for useful references. A series of results on replicator equations, host-parasite dynamics, and spatially distributed populations was especially interesting. Many different techniques represented the spatial evolution problem: Wright island models, static and random graphs for replicator dynamics, Wright-Fisher diffusions. New modeling frameworks were suggested, such as numerical simulations of non-local agent-based models can be combined with the analysis of corresponding continuum models or spatially explicit 3D-individual-based models. One minisymposium dealt with the dynamical behavior of systems of ordinary differential equations arising from chemical reaction net-

works. In particular, the authors investigated the boundaries and general techniques to find first integrals and conservative oscillations.

This conference provided fantastic networking opportunities due to its social program and an extensive poster session. I found this experience has improved my presentation skills and more importantly, my confidence in the current project.

Report by Sophie Meakin on the 10th Summer Institute in Statistics and Modelling in Infectious Diseases (SISMID), University of Washington, Seattle The school offered fifteen 2.5 day courses in a range of methods of statistical analysis and modern modelling techniques. ESMTB kindly awarded me a travel grant to help cover the expenses of the summer school; I was also awarded a scholarship from the Department of Biostatistics at the University of Washington. I elected to take courses on Markov chain Monte Carlo methods, integrating novel data streams into epidemiology, and contact network epidemiology.

The first course I attended was an introduction to Markov chain Monte Carlo (MCMC) methods for infectious diseases, taught by Elizabeth Halloran, Vladimir Minin and Kari Auranen. MCMC is widely used in epidemiological modelling research and thus an important technique to be able to understand and apply. I took this course specifically to learn how to implement MCMC for parameter estimation and data augmentation. The course covered both the theory behind MCMC methods and computer sessions implementing various results in R. This latter part of the course was particularly useful, especially being able to discuss the practical choice of the sampling distribution and convergence with the module leaders. I will use the methods in my research in modelling emerging infectious diseases to estimate key epidemiological parameters.

The second course I attended covered topics in modelling with novel data streams, such as Google trends and Twitter, into epidemiological modelling. The course was led by Mauricio Santillana, Alessandro Vespignani and Elaine

Nsoesie. I took this course primarily to learn a new approach to epidemic modelling, as well as to understand the challenges and limitations of using online data. The course covered a wide range of topics, including: accurate estimation of current disease incidence using data from Google trends and Twitter; using the Global Epidemic and Mobility Model (GLEAM), a worldwide metapopulation model for infectious diseases that draws together real-world population and mobility data; and practical web-scraping methods to collect Twitter, Amazon and Yelp data. I was especially interested to learn how to use GLEAM as it ties in well with my own research and will be a very useful tool. In addition, I have learnt a range of practical methods such as data management using Python's Pandas library.

The final course I attended was on contact network epidemiology, led by Joel Miller and Thomas Hladish. Contact networks are one modelling paradigm used to describe the mixing patterns of a population: nodes represent individuals and edges between nodes represent disease-transmitting interactions. The course was a balance of both analytic and computational methods in network epidemiology, for example: deriving analytic epidemiological models on contact networks; finding closed-form expressions for the basic reproduction number and final size distribution for these models; an introduction to NetworkX, a Python library that can be used to simulate epidemics on networks. I found all aspects of this course both interesting and relevant: my own research is currently focussed on metapopulation models (networks where nodes are populations rather than individuals), but I found that many of the analytic methods for contact networks could be translated to think about metapopulation models, which has given me ideas how to approach some challenges I am facing in my own research.

Overall, my experience at SISMID was fantastic: I learnt a lot of new statistical and mathematical methods that will be very useful in the rest of my PhD, and met many wonderful people (staff and fellow students) who I look forward to meeting at future conferences.