

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!

StAMBio University of St Andrews Mathematical Biology Group

The research group is based within the School of Mathematics and Statistics of the University of St Andrews. We are an interdisciplinary group of mathematicians who develop, analyse and simulate mathematical models to study the key mechanisms that underpin the dynamics of biological systems. Our current research interests include multiscale models of cancer growth and treatment, models of infectious diseases and immune competition, biological pattern formation and morphogenesis, free boundary problems in biology, stochastic models of signalling and gene regulatory networks, evolutionary dynamics in structured populations and mathematical models arising from theoretical ecology.

At present the group consists of five members of staff, four postdoctoral fellows and three PhD students, whose research profiles are briefly described below.

STAFF MEMBERS

Mark A. J. Chaplain (Head of the Group)



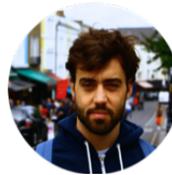
My main area of research is Mathematical Oncology the application of mathematical modelling to cancer growth and treatment. I am interested in all aspects of cancer modelling gene regulatory networks, avascular growth, the immune response to cancer, angiogenesis, invasion and metastasis, multiscale modelling techniques, chemotherapy and radiotherapy treatment. I am also interested in theoretical ecology, specifically host-parasitoid systems.

Jochen Kursawe



I develop and apply mathematical and computational methodology to understand embryonic development. I collaborate with experimental biologists to research how individual cells make decisions (e.g. to divide or differentiate) and how multiple cells interact to form healthy and viable tissues. My work includes analysing the dynamics of gene regulatory interactions and modelling mechanics of single cells and cell-cell interactions. My aim is to decipher fundamental mechanisms that underlie the robustness of embryonic patterning and morphogenesis.

Tommaso Lorenzi



The focus of my research is on mathematical models of complex living systems formulated in terms of nonlinear partial differential equations and corresponding stochastic individual-based models. These models can support a deeper theoretical understanding of the mechanisms underlying a variety of emergent behaviours observed in nature. Moreover, they pose a series of analytical and numerical challenges which make them interesting mathematical objects per se.

Giorgos Minas



I study noisy, dynamic and complex biological processes, such as gene regulation, signalling and development. The target is to develop an integrated, multi-level approach that combines stochastic modelling and mathematical analysis with computational, statistical and machine learning methods. The ultimate goal is to answer fundamental biological questions such as how cells adapt to multi-dimensional signals received in their ever-changing environments.

Nikolaos Sfakianakis

The focus of my research is the multiscale study of cancer and spans from lamellipodium dynamics and live cell motility, to cancer growth and tissue formation, and to the role of stemness in health and disease.

The tools I employ come from several (sub-)fields of Applied Mathematics: modelling, scientific computing, numerical analysis, and analysis of partial differential equations.

POSTDOCTORAL FELLOWS**Ruth Bowness**

I am a Medical Research Council Fellow and Academy of Medical Sciences Springboard Award Holder. My research involves using differential equations and individual-based models to describe infectious disease spread within the human body,

and to simulate and compare treatment strategies. My current projects include multiscale within-host modelling of tuberculosis disease progression and treatment, and within-host modelling of antimicrobial resistant infections.

Sara Hamis

As part of an interdisciplinary team with researchers at Ninewells hospital, I am currently working on developing new paradigms for overcoming drug resistance in cancer. Mathematical and computational biology are my main research interests,

and I work with multiscale, hybrid individual-based models.

Fiona R. Macfarlane

The main focus of my research is the development of individual-based models describing tumour-immune competition and tumour growth. More recently, I have been

working on the derivation of partial differential equation models from stochastic individual-based models of cell populations.

Cicely K. Macnamara

Currently I am working as part of SoftMech an EPSRC-funded centre for Mathematical Sciences in Healthcare. I work on an individual-based, force-based model for tumour growth and the interactions

with the extra-cellular matrix. My other research interests include cancer-immune dynamics; intracellular dynamics, including gene regulatory networks and cancer invasion.

PHD STUDENTS**Linnea C. Franssen**

I am an EPSRC-funded PhD student in my final year. I focus on modelling cancer cell invasion and secondary metastatic spread. For this, I use spatially explicit hybrid modelling techniques to account for the evolution of individual cancer cells and connected clusters of cancer cells, and for the transition between those states. I have developed the first cell-based spatially explicit framework of metastatic spread and currently work on a 3D in silico model that captures cancer cell invasion observed in in vitro assays.

Chiara Villa

I started my PhD in 2018, under the supervision of Mark Chaplain and Tommaso Lorenzi. I am originally from Italy and I studied in St Andrews for an MMath degree in Applied Mathematics. I work

on continuous models of phenotypic selection in vascular tumours, and mechanochemical models of pattern formation and tumour invasion.

Yunchen Xiao



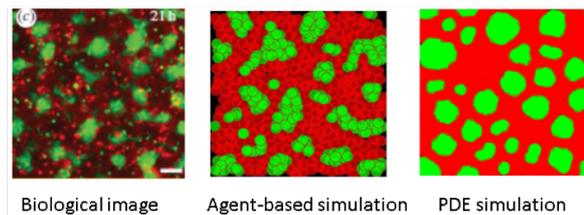
I started my PhD in 2018, under the supervision of Mark Chaplain and Len Thomas (Statistics). My interest in Mathematical Biology began during a summer research internship with Tommaso Lorenzi. My Masters dissertation was entitled 'Mathematical models of cell dynamics in acute myeloid leukaemia'. My current research interests are: parameterising mathematical models of tumour-induced angiogenesis and tumour invasion & metastasis, along with parameter estimations and selecting among competing models using Approximate Bayesian Computation methods.

More about our research and possible PhD and postdoc opportunities can be found at <http://www.mcs.st-and.ac.uk/mathbiol/>

MAMBA (Inria, CNRS and Sorbonne Université)

MAMBA is not only a fast moving venomous snake but also the name of our team, an acronym for "Modelling and Analysis for Medical and Biological Applications". Located both in the Jacques-Louis Lions Laboratory of Sorbonne Université and in the Inria Paris Research Centre, our team gathers 8 permanent researchers, and 20 post-doctoral and Ph.D students. It aims at developing mathematical models, simulations and numerical algorithms to solve problems from life sciences involving dynamics of biological systems such as protein intracellular spatio-temporal dynamics, cell motion, early embryonic development, tissue growth and regeneration, cancer evolution, healthy and tumour growth control by pharmacological means, protein polymerisation occurring in neurodegenerative disorders and control of mosquito populations (to prevent epidemics of vector-borne diseases like zika or dengue). It is the evolution of the BANG project-team, headed by Benoît Perthame during 11 years (2003-2013).

Data and image analysis, statistical, ODE, PDE, SDE, stochastic processes and agent-based approaches are used either individually or in combination, with a strong focus on PDE analysis and agent-based approaches. In order to develop a unified framework to describe the systems of interest at different scales (microscopic to macroscopic scales), a large activity of the team consists in investigating the link between these different models.



Many projects within our team are guided or directly address questions or applications in biology, biotechnology or medicine and are carried out in close collaboration with specialists in biology or medicine. In this context, our ongoing collaborations with biologists and physicians, the collaboration with St Antoine Hospital within the Institut Universitaire de Cancérologie of Sorbonne Université and Hopital Paul Brousse (IUC, Luis Almeida, Jean Clairambault, Dirk Drasdo, Benoît Perthame) and close experiment-theory collaborations characterized by associated researchers at the Leibniz Institute for Working Environment and Human Factors in Dortmund (Dirk Drasdo), Germany, are key points in our project. A very strong link has also been developed with the Wolfgang Pauli Institute in Vienna, especially with C. Schmeiser and his collaborators (Marie Doumic, Benoît Perthame, Diane Peurichard), through an Inria "associated team", a format to promote close interactions and exchanges with other institutions. The mosquito population control studies (Luis Almeida, Pierre-Alexandre Bliman) are also developed in close collaboration with life scientists from Institut Louis Malardé (French Polynesia), Instituto de Medicina Tropical Pedro Kouri (Cuba) and Instituto Oswaldo Cruz (Brazil).

Our main objective is the creation, investigation and transfer of new models, methods and algorithms. In selected cases software development as that of CellSys and TiQuant (Dirk Drasdo and Stefan Hoehme) is performed. More frequently, the team develops “proof of concept” numerical codes in order to test the adequacy of our models to experimental biology.

Some very recent research examples:

Cancer:

- Proposal of strategical principles in cancer therapeutics using asymptotic analysis and optimal control for cell population dynamic models. Ref.: C. Pouchol, J. Clairambault, A. Lorz, E. Trlat, JMPA, 2018.
- Quantitative cell-based model predicts mechanical stress response of growing tumor spheroids over various growth conditions and cell lines, Ref: P Van Liedekerke, J Neitsch, T Johann, K Alessandri, P Nassoy, D. Drasdo. PLoS Comp Biol, 2019.

Protein polymerisation:

- On the asymptotic distribution of nucleation times of polymerization processes. Ref : P. Robert and W. Sun, SIAM App Math., 2019.
- A new variant of the Becker-Döring system, to model sustained oscillations observed in protein fibrils depolymerisation experiments, Ref: M. Doumic, K. Fellner, M. Mezache, H. Rezaei, JTB, 2019.

Vector-borne diseases:

- Implementation of control strategies for sterile insect techniques, P.-A. Bliman, D. Cardona-Salgado, Y. Dumont, O. Vasilieva, Math Biosci., 2019.
- Preventing epidemics of vector-borne diseases (like dengue or zika) thanks to the control of mosquito populations, Ref: L. Almeida, Y. Privat, M. Strugarek, N. Vauchelet SIAM J. Math. Anal., 2019

Cell multiscale models:

- Particle interactions mediated by dynamical networks: assessment of macroscopic descriptions, Ref : J. Barré, J.A. Carrillo, P. Degond, E. Zatorska, D. Peurichard, Journal of Nonlinear Science, 2017 (+ illustration)
- Traveling wave and aggregation in a flux-limited Keller-Segel model, V Calvez, B Perthame, S Yasuda, 2019.
- Developing a new mathematical framework to model reaction-diffusion in developing organisms: Ref : F. Rossi, N. Pouradier Duteil, N. Yakoby, B. Piccoli, Proc. 2016 IEEE CDC, 2016.



Photos from left to right then up to bottom: Luis Almeida, Federica Bubba, Marie Doumic, Gaëtan Vignoud, Jean Clairambault, Jieliang Zhao, Markus Schmidtchen, Dirk Drasdo, Julia Delacour, Mathieu Mezache, Cécile della Valle, Pierre-Alexandre Bliman, Adrien Ellis, Alexandre Poulain, Nastassia Pouradier-Duteil, Philippe Robert, Benoît Perthame, Xinran Ruan, Valeria Caliaro, Diane Peurichard

Other members: Jules Dichamp, Florian Joly, Noemi David, Jorge Estrada Hernandez, Emma Leschiera, Jesus Bellver Arnau, Giorgia Ciavolella, Gisselle Estrada Rodriguez.