

ECMTB 2018

*Celebrating the Year of
Mathematical Biology 2018*

CO-ORGANIZED BY:



23 TO 27 JULY

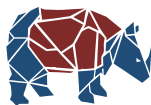
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<http://ecmtb2018.org/>



WELCOME!

The European Conference on Mathematical and Theoretical Biology (ECMTB) is organized regularly by the European Society for Mathematical and Theoretical Biology (ESMTB) and is a major worldwide scientific event in this field, attracting researchers from all over the world.

The 11th European Conference on Mathematical and Theoretical Biology (ECMTB 2018) is taking place in the exciting city of Lisbon, Portugal, from 23 to 27 July, 2018, and it is the main event of the YEAR OF MATHEMATICAL BIOLOGY (YMB; <http://euro-math-soc.eu/year-mathematical-biology-2018>), set up by ESMTB and by the European Mathematical Society (EMS). For that reason, ECMTB 2018 will, for the first time, be a joint ESMTB-EMS conference and will be co-organized by SPM (Portuguese Mathematical Society). The venue is the Faculty of Sciences of the University of Lisbon and its research centre CMAF-CIO will host the event. ECMTB 2018 has the high patronage of the President of the Portuguese Republic, and the seal of the Portuguese National Commission of the United Nations Educational, Scientific and Cultural Organization (UNESCO).

To all these institutions, as well as to all the other supporters (please see their logos at the end of this booklet), the Organizing Committee is deeply grateful.

Early conference check in starts on July 22th, 2018 afternoon, where a complimentary welcome drink during this afternoon and the conference material will be delivered to the participants.

The ECMTB 2018 invited speakers are:

Helen Byrne (Oxford University, UK)

Antonio DeSimone (Scuola Internazionale Superiore di Studi Avanzati, Italy)

Eva Kisdi (Helsinki University, Finland)

Samuel Kou (Harvard University, USA) | BS-EMS JOINT LECTURE

Mirjam Kretzschmar (University Medical Centre Utrecht, The Netherlands)

Eva Löcherbach (Cergy-Pontoise University, France)

Andrea Pugliese (Trento University, Italy)

Eörs Szathmáry (Eötvös Loránd University, Hungary)

Kees Weijer (Dundee University, UK).



Besides the invited talks by these remarkable scientists, we are happy to announce that this ECMTB 2018 will have an exciting programme, from cutting-edge minisymposia to the many contributed talks and posters on recent research developments in all areas of Mathematical Biology, as well as lectures from the recent winners of the Reinhart Heinrich Best Doctoral Theses Award. We are also happy to inform that, thanks to the support of several scientific publishers, there will be 4 poster prizes.

This Conference is a great opportunity for fruitful interactions among members of our scientific community, taking advantage of the coffee and lunch breaks and of the poster parties, as well as of the Mentorship Program designed to help young researchers establishing contacts with more senior members. Of course, participants are also able to enjoy the nice optional excursions and the Conference Dinner (please visit the Conference website for more information).

ESMTB will held its General Assembly meeting during the Conference. Conference participants that are not yet members are also invited to attend this meeting and to join our scientific community, benefiting from the following special invitation offer:

SPECIAL INVITATION: The ESMTB, to celebrate the Year of Mathematical Biology 2018 and wishing to extend its membership to other researchers in the area, invites every participant registered for the ECMTB 2018, that is not yet an ESMTB member, to become a member and welcomes those accepting such invitation by exempting them of the first year membership fee. NOTE: If you accept this invitation, it only takes effect after you becoming a Conference participant, that is, after payment of the ECMTB 2018 registration fee, so the Conference fee should be according to your current status (prior to becoming an ESMTB member).

To know more about ESMTB, visit the Society webpage <http://www.esmtb.org>

To stay updated on the latest news on the ECMTB 2018, follow us at <https://www.facebook.com/ecmtb2018/>. In case of any need, please do not hesitate in contacting us by **email (info@ecmtb2018.org)**.

We wish all participants a nice stay in Lisbon and a fruitful conference.
Enjoy ECMTB 2018!

MAIRA AGUIAR, CARLOS BRAUMANN, NICO STOLLENWERK
Conference Chairs



ECMTB 2018 SCIENTIFIC PROGRAMME

PRACTICAL INFORMATION

PARTICIPANTS ARE REQUESTED TO HAVE
THEIR IDENTIFICATION BADGE ALL THE TIME.

For the ECMTB 2018, 36 Minisymposia, 307 Contributed talks, divided in 60 parallel sessions, and 119 posters, divided in 2 Poster Sessions, are going to be presented. The Scientific programme is very exciting and since we will have a very tight agenda, please note:

MINISYMPOSIA SESSIONS (MS):

◆ **MS** Organizers are responsible for designating a "Session Chair" to introduce the speakers and to keep the session on time.

◆ Should one of the speakers be missing, make a 20 min interval and keep the times prescribed in the programme for the remaining speakers.

◆ A desktop computer, a laser pointer and a 5 min warning and "Time is over" warning signs will be available in the seminar room. Presentations in PDF format are advised.

◆ When using the Desktop of the seminar room, please be sure to have your presentation uploaded in the session folder "MS-xSessionName_x_JulyXX_Morning/Afternoon" ► example: "MS-MathematicalMethods_July22_Morning_EinsteinAlbert"

and tested well in advance. The Organizing Committee will be able to receive your presentations as well, during the morning/afternoon prior you session starts. We will be available in BUILDING C6 (on July

22nd, 2018) and in Building C3 from 23-27 of July, during the whole conference period.

◆ **When using your own computer, please remember to bring a VGA adapter.**

PROJECTOR IN THE SEMINAR ROOM HAS A VGA ENTRANCE AND THERE IS NO ADAPTER AVAILABLE FOR LAPTOPS.

◆ Talks are 20 min long (15 talk +5 min for Q&A). After 20 min, the talk must be stopped.

◆ In case a talk still needs to be uploaded at the last minute or a computer needs to be connected, please use the Q&A time to organize that.

PARALLEL SESSIONS (PS):

◆ Parallel sessions will have 2 (two) "Session Chairs": The last speaker (who chairs all the talks except his/her own) and the first speaker (who chairs the last talk). **In case you are one of those and do not feel comfortable with that, please let us know immediately.**

The session chairs are responsible to introduce the speaker and to keep the session on time.

◆ Should one of the speakers be missing, make a 20 min interval and keep the times prescribed in the programme for the remaining speakers.





◆ A desktop computer, a laser pointer and a 5 min warning and "Time is over" warning signs will be available in the seminar room. Presentations in PDF format are advised.

◆ When using the Desktop of the seminar room, please be sure to have your presentation uploaded in the session folder "PS-xSessionName_x_JulyXX_Morning/Afternoon" -> example: "PS-EpidemiologyV_July25_Morning_AguiarMaira"

and tested well in advance. The Organizing Committee will be able to receive your presentations as well, during the morning/afternoon prior you session starts. We will be available in BUILDING C6 (on July 22nd, 2018) and in Building C3 from 23-27 of July, during the whole conference period.

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POSTER SESSIONS:

◆ Double-tape will be available for you to fix your poster in the poster panels.

◆ Poster presenters are requested to **display the poster on his/her poster panel**, that will be identified with a number (PXX) and name, **in the morning of the session your poster is scheduled to take place.**

◆ Poster maximum size: A0 Portrait orientation, or A1 Landscape orientation

◆ If you have applied for a poster prize, please do not forget to mark your panel with the orange stick that will be given to you during your check in. The awarding committee will look for that sign.

◆ **All posters must be removed immediately after the poster session is over, around 7:00pm of each day when poster sessions are taking place.**



Monday ♦ July 23	
08h15	Registration
09h00-09h45	Opening Session
09h50-10h10	Odo Diekmann, Utrecht University, The Netherlands
TRIBUTE TO KARL PETER HADELER	
10h10-11h10	Samuel Kou, Harvard University, USA
(BS-EMS JOINT LECTURE) BIG DATA, GOOGLE AND DISEASE DETECTION: A STATISTICAL ADVENTURE	
11h10-11h40	Coffee Break
11h40-13h00	Mini-Symposia and Parallel Sessions
13h00-14h20	Lunch Break
14h20-16h00	Mini-Symposia and Parallel Sessions
16h10-17h10	Eva Löcherbach, Université de Cergy Pontoise, France
MODELING INTERACTING NETWORKS OF NEURONS AS PROCESSES WITH VARIABLE LENGTH	
17h20-18h50	Poster Session I Coffee Break + Cocktail

Tuesday ♦ July 24	
09h00	Registration
09h00-10h00	Eörs Szathmáry Eötvös Loránd University, Hungary
MODELS OF LEARNING AND EVOLUTION: WHAT DO THEY HAVE IN COMMON?	
10h00-10h30	Coffee Break
10h30-12h30	Mini-Symposia and Parallel Sessions
12h30-14h00	Lunch Break
14h00-15h40	Mini-Symposia and Parallel Sessions
15h50-16h50	Eva Kisdi Helsinki University, Finland
ADAPTIVE DYNAMICS AND THE EVOLUTION OF DIVERSITY	
17h00-18h30	Poster Session II Coffee Break + Cocktail

Wednesday ♦ July 25	
09h00	Registration
09h00-10h00	Andrea Pugliese University of Trento, Italy
EPIDEMIC MODELS STRUCTURED BY PARASITE LOAD AND IMMUNE LEVEL	
10h00-10h30	Coffee Break
10h30-12h30	Mini-Symposia and Parallel Sessions
12h30-14h00	Lunch Break
14h00	Social Program

BUILDING C3

MAIN AUDITORIUM

RECEPTION

ATRIUM



ECMTB 2018 PROGRAMME

Thursday • July 26	
09h00	Registration
09h00-10h00	Mirjam Kretzschmar, University Medical Center, Utrecht, The Netherlands
MODELLING THE WANING AND BOOSTING OF IMMUNITY	
10h00-10h30	Coffee Break
10h30-12h30	Mini-Symposia and Parallel Sessions
12h30-14h00	Lunch Break
14h00-15h20	Mini-Symposia and Parallel Sessions
15h30-16h30	Helen Byrne, University of Oxford, UK
MATHEMATICAL APPROACHES TO MODELLING AND REMODELLING BIOLOGICAL TISSUES	
16h40-17h30	ESMTB GENERAL ASSEMBLY 2018
17h30-18h00	Coffee Break and ESMTB GA' Wine Tasting
19h30	ECMTB 2018 CONFERENCE DINNER*

*MONTES CLAROS
BUSES LEAVE FROM THE
CONFERENCE VENUE AT 19:30

Friday July 27, 2018	
09h00	Registration
09h00-10h00	Antonio DeSimone, Scuola Internazionale di Studi Avanzati, Italy
BIOLOGICAL AND BIO-INSPIRED MOTILITY AT MICROSCOPIC SCALES: LOCOMOTION BY SHAPE CONTROL	
10h00-10h30	Jochen Kursawe, Manchester University, UK
(RH BEST THESIS AWARD TALK) QUANTITATIVE APPROACHES TO INVESTIGATING EPITHELIAL MORPHOGENESIS	
10h30-11h00	Coffee Break
11h00-12h40	Mini-Symposia and Parallel Sessions
12h40-14h00	Lunch Break
14h00-15h00	Kees Weijer University of Dundee, UK
ANALYSIS OF COLLECTIVE CELL BEHAVIOURS UNDERLYING PRIMITIVE STREAK FORMATION IN THE CHICK EMBRYO	
15h10-16h00	Poster prizes ECMTB 2020 Announcement Conference closing
16h00-16h30	Coffee Break
16h30-17h30	ESMTB BOARD MEETING

BUILDING C8

VARIOUS ROOMS

BUILDING C6

INDOOR GARDEN



◆HELEN BYRNE

Wolfson Centre for Mathematical Biology, Mathematical Institute, University of Oxford, Oxford OX2 6GG, United Kingdom

“Mathematical approaches to modelling and remodelling biological tissues”

ABSTRACT: As the eld of mathematical biology has matured, closer collaboration with experimentalists and clinicians has become more wide common, these changes bringing multiple bene ts to both communities. For example, the mathematical models can increase our understanding of biological systems while the biological questions can stimulate new theoretical challenges. This symbiotic relationship can be exemplified by studies of biological tissues.

Biological tissues are complex, evolving structures, characterised by multiple interactions that act across diverse space and time scales. In this talk I aim to illustrate how theoretical studies of biological tissues can provide new mechanistic insight into their behaviours while also acting as a source of mathematically challenging problems. I will take my inspiration from recent studies of cancer, wound healing, tissue engineering and retinitis pigmentosa, a degenerative disease that causes blindness.

KEYWORDS: Mathematical Modelling, Wound healing, Tissue engineering, Cancer

◆ANTONIO DESIMONE

MathLab@SISSA-International School for Advanced Studies, Italy

“Biological and bio-inspired motility at microscopic scales: locomotion by shape control”

ABSTRACT: Cell motility is key to many biological functions, and it is accomplished by coordinated shape changes. Locomotion strategies employed by unicellular organisms are particularly interesting because they are invisible to the naked eye, and offer surprising new solutions to the question of how shape can be programmed. In recent years, we have studied locomotion by shape control using a variety of methods: modeling, theory, and numerical simulation, observations at the microscope, manufacturing of prototypes. A concrete case study is provided by

PLENARY

THURSDAY,
JULY 26TH

15:30- 16H30

BUILDING C3
-MAIN
AUDITORIUM

CHAIR :
SUSANNE
DITLEVSEN

PLENARY

FRIDAY,
JULY 27TH

09:00 - 10:00

BUILDING C3
-MAIN
AUDITORIUM

CHAIR :
ANDREA DE
GAETANO



our results on *Euglena gracilis*, a unicellular protist that is able to move both by agellar propulsion and by highly coordinated changes of the shape of the whole cell body [1, 2]. We will survey the most recent findings within this stream of research, and point out to current directions and challenges for the future.

KEYWORDS: Cell motility, Shape control, Mechano-biology, Active matter.

Acknowledgements: This work has been supported by the ERC Advanced Grant 340685-MicroMotility.

REFERENCES:

[1] M. Rossi, G. Cicconofri, A. Beran, G. Noselli, A. DeSimone (2017). Kinematics of agellar swimming in *Euglena gracilis*: Helical trajectories and agellar shapes, *Proc Nat Acad Sci USA* 114,13085{13090

[2] G. Noselli, A. Beran, M. Arroyo, A. DeSimone (2018). Experimental and theoretical study of metaboly in *Euglena gracilis*. Preprint.

♦EVA KISDI

Department of Mathematics and Statistics, University of Helsinki, Finland

“Adaptive dynamics and the evolution of diversity”

ABSTRACT: Natural selection is usually paraphrased as the survival of the fittest - or the demise of all others. How can natural selection explain the enormous diversity of variants living together in Nature? Adaptive dynamics finds the answer in deriving fitness explicitly from models of population dynamics. This leads to an ever-changing fitness landscape, which facilitates not only the coexistence of multiple species but also the formation of new lineages through a process called evolutionary branching. After a brief introduction to the mathematical framework of adaptive dynamics, I consider three questions relating to diversity. First, is there an upper bound to the number of species, and if so, how does a “saturated” community evolve? Second, can natural selection lead to extinction? Third, when diversity evolves, it may be just variation but not speciation. Will natural selection lead to the origin of new species?

KEYWORDS: Adaptive dynamics, Evolutionary branching, Evolutionary suicide, Speciation.

PLENARY

**TUESDAY,
JULY 24TH**
15:50 - 16:50
BUILDING C3
-MAIN
AUDITORIUM

CHAIR :
FABIO CHALUB



♦SAMUEL KOU

Department of Statistics, Harvard University, USA

“Big data, Google and disease detection: a statistical adventure”

ABSTRACT: Big data collected from the Internet have generated significant interest in not only the academic community but also industry and government agencies. They bring great potential in tracking and predicting massive social activities. We focus on tracking disease epidemics in this talk. We will discuss the applications, in particular, Google Flu Trends, some of the fallacy and the statistical implications. We will propose a new model that utilizes publicly available online data to estimate disease epidemics. Our model outperforms all previous real-time tracking models for influenza epidemics at the national level of the US. An extended version of the model gives accurate tracking of Dengue fever in Asian and South American countries. We will also draw some lessons for big data applications.

KEYWORDS: Influenza, Dengue fever, Internet search, Forecasting.

PLENARY

BS-EMS JOINT
LECTURE

MONDAY
JULY 23RD

10:10 - 11:10

BUILDING C3
-MAIN
AUDITORIUM

CHAIR :
JOSÉ A.
CARRILLO

♦MIRJAM KRETZSCHMAR

Julius Center for Health Sciences and Primary Care, University Medical Center, Utrecht, The Netherlands

“Modelling the waning and boosting of immunity”

Joint work with Odo Diekmann (Utrecht University), Wilfred de Graaf (Utrecht University) and Peter Teunis (RIVM).

ABSTRACT: The immune status of an individual host is determined by the increase of immunity during infection, waning of immunity after clearing the infection, and boosting by renewed exposure to the pathogen. The process of boosting, the rate at which immunity wanes, and the level of protection it confers, all influence the transmission dynamics of the pathogen. Information about the immune status of a population is often available from serological studies, but it may be unclear what this means for the level of protection against infection or symptomatic disease. We would like to understand how an intervention changes a pop-

PLENARY

THURSDAY
JULY 26TH

9:00 - 10:00

BUILDING C3
-MAIN
AUDITORIUM

CHAIR :
JULIA GOG



ulation's immune status and the incidence of symptomatic infection for an infectious disease with waning immunity. In this talk I will introduce a mathematical model for the waning and boosting of immunity. The model is defined on two levels. On the within-host level we defined a model that distinguishes between episodes of infection and time periods of waning of immunity (De Graaf et al. 2014). During infection, a simple 2-dimensional system of ODE's describes the time evolution of pathogens and immunity within the host. Between infection episodes immunity wanes until a new exposure triggers the next infection episode. We then lift the model to the population level by studying the distribution of immune states in a population under the assumption of a constant force of infection. The events of exposure and infection are described by a time-homogeneous Poisson process, between exposures immune status wanes deterministically. This model can be formulated in terms of a renewal equation, for which a stable stationary distribution can be derived. The modelling framework will be illustrated with applications to pertussis epidemiology. For pertussis, longitudinal and cross-sectional serological data are available, which can be used to parameterize the model. We were interested in obtaining estimates for the incidence of symptomatic infections, the ratio of symptomatic to asymptomatic infections, and the immune level at which protection from symptomatic infection occurs. We found remarkable correspondence between predictions of the within-host model with observations reported in the literature concerning the serological correlate of protection. The modelling framework has strong links with a statistical model used for estimating incidence from serological data.

KEYWORDS: Mathematical model, Waning immunity.

REFERENCES:

- [1] de Graaf WF, Kretzschmar ME, Teunis PF, Diekmann O. (2014). A two-phase within-host model for immune response and its application to serological profiles of pertussis, *Epidemics* 9:1-7.



◆EVA LÖCHERBACH

Laboratoire AGM UMR CNRS 8088 Université de Cergy-Pontoise, France

Modeling interacting networks of neurons as processes with variable length

ABSTRACT: A class of recently introduced models to describe networks of neurons as stochastic processes with memory of variable length will be presented. These are non-Markovian processes in high or infinite dimension in which the past dependence of transition probabilities or intensities has a range that is finite but depends on the particular history. Starting from existence results, we study related mean-field models in continuous time and their large population limits, and discuss the relation with associated Piecewise Deterministic Markov Processes (PDMP's) and state results concerning their longtime behavior. Finally, two important problems of statistical inference in such models will be considered: estimation of the spiking rate function and estimation of the neuronal interaction graph. The talk is based on joint work with Susanne Ditlevsen, Aline Duarte, Antonio Galves and Guilherme Ost.

KEYWORDS: Multivariate nonlinear Hawkes processes, Mean-field approximations, Piecewise deterministic Markov processes, Multi-class systems, Oscillations.

◆ANDREA PUGLIESE

Department of Mathematics, University of Trento, Italy

Epidemic models structured by parasite load and immune level

ABSTRACT: A growing number of researchers are developing models that link within-host infection dynamics to population-level epidemic dynamics [2]. Multiscale immunoepidemiological are relevant, for instance, in evolutionary epidemiology [4] where they also naturally allow for host heterogeneity [5], or for describing the dynamics of infections with temporary immunity [1] more accurately than SIRS models. Another area of likely interest are infections, such as varicella/zoster [3] where severe disease depends on immunological status. The development of

PLENARY

**MONDAY
JULY 23RD**

16:10 - 17:10

**BUILDING C3
-MAIN
AUDITORIUM**

CHAIR :
**NICO
STOLLENWERK**

PLENARY

**WEDNESDAY
JULY 25TH**

9:00 - 10:00

**BUILDING C3
-MAIN
AUDITORIUM**

CHAIR :
MAÍRA AGUIAR



useful multiscale immunoepidemiological models poses strong mathematical and numerical challenges. Within this broad area, I will present some simple models whose analysis have led to interesting biological insights, and discuss some instances where a feedback arises from epidemic to within-host processes resulting into new dynamical features.

KEYWORDS: Immunoepidemiology, Evolutionary epidemiology, Immunity boosting and waning.

REFERENCES:

- [1] W.F. de Graaf, M.E.E. Kretzschmar, P.F.M. Teunis, P. F. M., O. Diekmann. A two-phase within-host model for immune response and its application to serological profiles of pertussis. *Epidemics* 9, 1-7.
- [2] J. R. Gog et al. (2015). Seven challenges in modeling pathogen dynamics within-host and across scales, *Epidemics* 10, 45-48.
- [3] G. Guzzetta et al. (2013). Hope-Simpson's progressive immunity hypothesis as a possible explanation for Herpes Zoster incidence data. *Am. J. Epidemiol.* 177, 1134-1142.
- [4] N. Mideo, S. Alizon, S., T. Day. (2008). Linking within- and between-host dynamics in the evolutionary epidemiology of infectious diseases. *TREE* 23, 511-517.
- [5] A. Pugliese (2011). The role of host population heterogeneity in the evolution of virulence. *J. Biol. Dyn.* 5, 104-119.

◆ **EÖRS SZATHMÁRY**

Evolutionary Systems Research Group, MTA Ecological Research Center, Tihany, Hungary, and Parmenides Center for the Conceptual Foundations of Science, Pullach, Germany

Models of learning and evolution: what do they have in common?

ABSTRACT: In the past several scholars have noted some relationship between learning and evolution and various levels of abstraction. William James was wondering about the possible role of a process analogous to evolution of natural selection in the brain, whereby adaptive answers to complex problems might arise. Changeux and Edelman were considering selectionist approaches to brain dynamics during its development: while their approach has been experimentally validated, replicator dynamics has not been entertained by them. The first question is then whether true evolutionary dynamics can unfold in the brain (evolution in learning). On the flip side of the coin Richard Watson has raised the idea whether associative,

PLENARY

**TUESDAY
JULY 24TH**

9:00 - 10:00

**BUILDING C3
-MAIN
AUDITORIUM**

**CHAIR :
MATS
GYLLEMBERG**



reinforcement and deep learning dynamics could play a role in the evolution of ecosystems, developmental genetic regulatory networks and evolutionary transitions in individuality (learning in evolution). A third, potentially unifying theme is the analogy between Bayesian inference and the discrete-time replicator equation: here the question is whether similar algorithms could realize either of them in some natural systems. I shall review the relevant concepts and mathematical formulations behind these ideas. Open questions will be raised that, if answered positively, could entail that there will ultimately be only one unified theory including evolution and learning as subcases.

KEYWORDS: replicator equation, Bayesian models, Hebb synapse, reinforcement, adaptation.

Acknowledgements: This project is supported by the Templeton World Charity Foundation (Learning in evolution, evolution in learning) and by funded by National Research, Development, and Innovation Office Grants NKFI-K119347 and GINOP-2.3.2-15-2016-00057.

◆ **KEES WEIJER**

School of Life Sciences, University of Dundee, Dundee, DD1 5EH, UK

Analysis of collective cell behaviours underlying primitive streak formation in the chick embryo

Joint work with Silke Henkes (CSMB, University of Aberdeen, Aberdeen, UK), Rastko Sknepnek (School of Science and Engineering, University of Dundee, Dundee, UK) and Ping Lin (School of Science and Engineering, University of Dundee, Dundee, UK)

ABSTRACT: How dynamic cell behaviours such as differentiation, division, cell shape change and movement are integrated at the tissue, organ and organism level is a key question in biology. This is particularly important during gastrulation, a key process during the early embryonic development of all higher organisms involving large scale tissue deformations and cell movements. During gastrulation the three germ layers, the ectoderm, mesoderm and endoderm take up their correct topological positions in the embryo. In amniotes including humans the mesoderm precursors are formed from a single layered epithelial

PLENARY

FRIDAY

JULY 27TH

14:00 - 15:00

BUILDING C3

-MAIN

AUDITORIUM

CHAIR :

ROELAND

MERKS



sheet of cells, the epiblast. During gastrulation these mesoderm and endoderm precursors ingress through a structure known as the primitive streak to form the inner layers of the embryo [1]. The mesendoderm precursor cells in the epiblast move in two large scale vortex flows towards and along the midline of the embryo to form the primitive streak [2]. We investigate the cellular mechanisms that drive these large scale tissue flows in the chick embryo, as well as the mechanisms that integrate these cell behaviours during streak formation on an embryo wide scale. Using a dedicated lightsheet microscope we are able to follow detailed cell behaviours such as cell division, ingression, cell-shape change and cell-cell intercalations of over 200.000 cells in the chick embryo epiblast. Our experiment have shown that the large scale epiblast tissue cortex flows resulting in the formation the primitive streak are driven by localised anisotropic pulling forces generated by mesendoderm cells. These forces appear to be generated by two main cellular mechanisms: directional cell-cell intercalation and apical contraction followed by ingression of mesendoderm cells [3]. We currently investigate the interplay between mechanical and chemical cell-cell signalling mechanisms that integrate these key behaviours at the tissue scale, using a combination of experimentation and cell based and continuous modelling approaches [4]. Specifically we test the hypothesis that junctional Myosin II accumulation resulting in apical contraction and cell-cell intercalation is a tension sensitive process and that this mechanosensitive process is a key part of the mechanism of tissue wide integration of cell behaviours during primitive streak formation.

KEYWORDS: Gastrulation, Collective Cell behaviours, Cell-based modelling

REFERENCES:

- [1] Stern, C.D., Gastrulation, from cells to embryo's, ed. C.D. Stern. 2004, New York: Cold Spring Harbor Laboratory Press.
- [2] Chuai, M., D. Hughes, and C.J. Weijer, Collective epithelial and mesenchymal cell migration during gastrulation. *Curr Genomics*, 2012. 13(4): p. 267-77.
- [3] Rozbicki, E., et al., Myosin-II-mediated cell shape changes and cell intercalation contribute to primitive streak formation. *Nat Cell Biol*, 2015. 17(4): p. 397-408.
- [4] Barton, D.L., et al., Active Vertex Model for cell-resolution description of epithelial tissue mechanics. *PLOS Computational Biology*, 2017. 13(6): p. e1005569.



♦JOCHEN KURSAWE

Faculty of Biology, Medicine and Health, University of Manchester,
Michael Smith Building, Oxford Road, M13 9PT, Manchester,
UK

Quantitative approaches to investigating epithelial morphogenesis

Joint work with Ruth E. Baker (University of Oxford) and Alexander G. Fletcher (University of Sheffield)

ABSTRACT: Morphogenesis - the generation of biological shape and form - is fascinating, and its study promises to shed light on a wide range of developmental defects and inform strategies for the artificial growth of organs. Recently, the experimental study of morphogenesis has thrived due to a rise in quantitative methods. The resulting avalanche of quantitative data requires us to rethink the scientific method. We need to design quantitative hypotheses through mathematical models, make quantitative experimental predictions, devise methods for quantitative data analysis, and design methods for quantitative inference using models and data. Our work aims to enable this transition for the integrative analysis of morphogenesis in epithelia, one of the major tissue types in animals. We conduct the first systematic numerical analysis of a widely used cell-based model of epithelia, the vertex model, and estimate to what extent quantitative model predictions may be influenced by parameter values and implementation details. We then apply this model to a key question in developmental biology by constructing a quantitative theory for tissue size control in the embryonic epidermis of the fruit fly *Drosophila*, using the model to predict the outcomes of future experiments. We further devise a method for estimating mechanical parameters of vertex models from imaging data and quantify the uncertainty associated with such estimates. Finally, we propose a novel algorithm for robust cell tracking in live-imaging microscopy videos of epithelial tissues that illustrates how graph theoretic concepts may be used to overcome challenges in quantitative data analysis. Together, these contributions will enable the quantitative study of epithelia for a wide range of applications.

KEYWORDS: replicator equation, Bayesian models, Hebb synapse, reinforcement, adaptation.

RH BEST
THESIS
AWARD'
TALK

FRIDAY

JULY 27TH

10:00 - 10:30

BUILDING C3

-MAIN

AUDITORIUM

CHAIR :

TORBJÖRN

LUNDH



Acknowledgements: JK acknowledges funding from the Engineering and Physical Sciences Research Council through a studentship.

REFERENCES:

- [1] J. Kursawe, R. E. Baker, A. G. Fletcher. (2017). Impact of implementation choices on quantitative predictions of cell-based computational models J. Comp. Phys. 345, 752-767
- [2] J. Kursawe, P. A. Brodskiy, J. J. Zartman, R. E. Baker, A. G. Fletcher (2015). Capabilities and Limitations of Tissue Size Control through Passive Mechanical Forces. PLoS Comput. Biol. 11, e1004679
- [3] J. Kursawe, R. E. Baker, A. G. Fletcher. (2018). Approximate Bayesian computation reveals the importance of repeated measurements for parameterising cell-based models of growing tissues J. Theor. Biol. 443, 66-81
- [4] J. Kursawe, R. Bardenet, J. J. Zartman, R. E. Baker, A. G. Fletcher. (2016). Robust cell tracking in epithelial tissues through identification of maximum common subgraphs J. R. Soc. Interface 13, 20160725

NOTES

MS	A MULTISCALE APPROACH TO `GROWTH AND FORM	ROOM C8.2.02
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Organizers: Chandrasekhar Venkataraman and Mariya Ptashnyk	11:40-13:00
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John King "Multiphase approaches to tissue growth"

Harsha Hutridurga "Evolution by competition-diffusion in heterogeneous environments"

Dagmar Iber "How to shape an Organ? Computational models of organogenesis"

Fred Vermolen "Cell-based and continuum scale models for the contraction of burns"

MS	HYBRID MODELLING IN BIOLOGY	ROOM C8.2.03
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Organizers: Francesco Giannino and Christian E. Vincenot	11:40-13:00
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Francesco Giannino "Vegetation pattern formation: system dynamics, individual-based hybrid modelling exercises"

Gudrun Wallentin "Dynamic coupling of Individual-based with system-dynamics models to represent multi-scale systems"

Constantinos Siettos "Bridging scales: from the atomistic simulations to the systematic numerical analysis of the emergent behaviour"

Dimitrios Gkousis "Valid reduced Michaelis-Menten models"

MS	MATHEMATICAL NEUROSCIENCE	ROOM C8.2.06
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Organizers: Daniele Avitabile and Reuben O'Dea	11:40-13:00
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Susanne Ditlevsen "Inferring visual processing in the brain"

Krasimira Tsaneva-Atanasova "Individual motor signatures and socio-motor biomarkers in schizophrenia"

Elif Köksal Ersöz "Canard mediated mixed-mode bursting oscillations in a rate model"

Michael Forrester "TMS-induced synchronisation in human brain networks"

MS	DYNAMICS AND OSCILLATIONS OF REACTION NETWORKS	ROOM C8.2.10
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Organizer: Josef Hofbauer	11:40-13:00
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Josef Hofbauer "Dynamics of generalized mass-action systems"

Alan D. Rendall "Bounded and unbounded oscillations in the Selkov model of glycolysis"

Anne Shiu "Multisite phosphorylation systems: bistability, oscillations, and a rational parametrization of steady states"

Maya Mincheva "Parametric sensitivity analysis of a gene regulation delay model"

MS	TOPICS IN STRUCTURED POPULATION DYNAMICS	ROOM C8.2.11
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Organizers: Sílvia Cuadrado and Jordi Ripoll	11:40-13:00
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Carles Barril "From individuals to populations: densities versus histories"

Raluca Eftimie "A kinetic modelling approach for tumour-macrophages interactions in heterogeneous cell populations"

Jordi Ripoll "Limit procedure for the computation of R_0 in structured population models"

Laurent Pujo-Menjouet "Language competition: analysis and qualitative simulations of a deterministic age-structured mathematical model"



MS QUANTIFYING GENETIC AND NON-GENETIC HETEROGENEITY IN CANCER EVOLUTION ROOM **C8.2.13**
11:40-13:00

Organizers: Ryan Schenk and Mohit Kumar Jolly

Benjamin Werner “Measuring single cell divisions in human cancers from multi-region sequencing data”

Mingyang Lu “Understanding the robustness and plasticity of gene regulatory circuits”

Gregory Kimmel “Dynamics of non-Hodgkin lymphoma CAR-T cell therapy”

Lorand Gabriel Parajdi “Mathematical modeling of cell dynamics and optimization problems in chronic myeloid leukemia therapy”

PS CANCER I 11:40-13:00 ♦ ROOM **C8.2.15**

Martina Conte “Kinetic-based models for tumor-immune system competition”

Agnieszka Bartłomiejczyk “Travelling waves in modelling chemotherapy for low grade gliomas”

Stefano Avanzini “Probabilistic models of cancer: an estimate for the time to relapse”

Qi Ma “Genome wide study of glucocorticoid receptors’ role in estrogen receptors regulated enhancers in breast cancer”

PS EVOLUTIONARY DYNAMICS I 11:40-13:00 ♦ ROOM **C8.2.17**

David Cheek “Mutation frequencies in a birth-death branching process”

George W. A. Constable “The effect of adult sex ratio on transitions between male and female heterogamety”

Omri Tal “Bet hedging models: a reappraisal”

Alexandre Blanckaert “In search of the Goldilocks zone for hybrid speciation”

PS MATHEMATICAL METHODS IN BIOLOGY I 11:40-13:00 ♦ ROOM **C8.2.19**

Paulo Amorim “Reaction-diffusion and individual-based models for ant movement”

Timothy Whiteley “An integro-differential equation model for urban population dynamics predicting emergent pattern formation”

Kenta Ishimoto “Hydrodynamic modelling of human sperm clustering”

Masakazu Akiyama “A mathematical model of collective cell migrations based on cell polarity”

PS PHYSIOLOGY I 11:40-13:00 ♦ ROOM **C8.2.23**

Valeriia Kaneva “Particle-based model of microvascular thrombus formation demonstrates the role of the interplay between platelet adhesive receptors”

Christopher D. Marcotte “Tuning critical excitations in stiff cardiac models”

Aleksey V. Belyaev “Computer simulations of cell adhesion to surfaces with microrelief”

Hisao Honda “Appearance of a chiral structure in cardiac looping of the embryonic heart”



PS MATHEMATICAL METHODS IN BIOLOGY II 11:40-13:00 ♦ ROOM C8.2.38

Katharina Franziska Becker “Modelling hierarchical pattern formation in epidermal appendage development”

Thomas E. Woolley “Pattern production through a chiral chasing mechanism”

Sungrim Seirin-Lee “Pattern formation induced by dynamic deformation of domain”

Ricardo Martinez-Garcia “Cell adhesion and fluid flow jointly initiate biofilm spatial structure”

PS EPIDEMIOLOGY I 11:40-13:00 ♦ ROOM C8.2.39

Gisele H. B. Miranda “Towards the prediction of influenza-like illness cases in Belgium”

Edward Hill “Assessing intervention responses against H5N1 avian influenza outbreaks in Bangladesh”

David Haw “Should we expect attack rates for infectious disease to vary across small spatial scales?”

Silvério Rosa “Optimal control of a fractional epidemic model with application to HRSV disease”


MS CROSS-TALK BETWEEN CELLS AND EXTRACELLULAR MATRIX IN PLANT AND ANIMAL DEVELOPMENT ROOM C8.2.02
14:20-16:00

Organizer: Eva Deinum

Eva Deinum “On growth and form in plants and animals: crosstalk between cytoskeleton and extracellular matrix”

Julio Belmonte “A theory that predicts behaviors of disordered cytoskeletal networks”

Adam Runions “Why plants make puzzle-shaped cells”

Louis Daniel Weise “Mechanical model to study plant development”

Diego A. Vargas “Discrete element model of the cell to explore how HUVECs respond to mechanical properties of the substrate”

MS REDUCTION AND STRUCTURE OF REACTION NETWORKS ROOM C8.2.03

Organizer: Carsten Wiuf

14:20-16:00

Carsten Wiuf “Model reduction and the QSSA”

Murad Banaji “Inheritance of oscillation in chemical reaction networks”

Casian Pantea “Bistability in mass action: inheritance from small subnetworks”

AmirHosein Sadeghimanesh “Intermediates, binomiality and multistationarity”

János Tóth “Further inverse problems”



MS	PLANT MODELS (A): PLANT DEVELOPMENT	ROOM C8.2.06
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Organizers: Mariya Ptashnyk and Lionel Dupuy	14:20-16:00
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Leah R Band "Modelling auxin dynamics in the plant root: cell-based and continuum approaches"

Arezki Boudaoud "Understanding the robustness of morphogenesis using stochastic mechanical models of organ growth"

George Bassel "The interplay between global and local rules regulates multicellular morphogenesis"

Yann Guédon "Identifying developmental patterns in plant phenotyping data"

Henry Allen "Mathematical modelling and analysis of the interplay between auxin and brassinosteroid in plant tissues"

MS	MULTI-SCALE MATHEMATICAL MODELS IN ENDOCRINOLOGY	ROOM C8.2.10
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Organizers: Margaritis Voliotis and Eder Zavala	14:20-16:00
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David Rand "Stochastic transcriptional dynamics and spatial signalling for the prolactin gene in single cells and tissue"

Frédérique Clément "Middle-out multi-scale modelling of the development of ovarian follicles"

Eder Zavala "Developing a multiscale mathematical understanding of the HPA axis"

Duncan J. MacGregor "Population-based signal processing and stimulus-response in oxytocin neurones"

Benoit Huard "Multiple scale analysis and periodic solutions in a model of ultradian glucose regulation"

PS	ECOLOGY I	14:20-16:00 ♦ ROOM C8.2.11
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Aisling J. Daly "An individual-based model of coexistence and competition between cryptic nematode species"

Anna Poskrobko "On mathematical model for fission-fusion bats population"

Danish Ali Ahmed "Analysing the impact of trap geometry on pitfall trap counts"

Dmitrii O. Logofet "Averaging the population projection matrices overestimates the stochastic growth rate"

Andrew Dean "Toxin-mediated competition in bacterial communities"

PS	CELL AND INTRA-CELL DYNAMICS I	14:20-16:00 ♦ ROOM C8.2.13
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Nikolaos Sfakianakis "The FBLM-FEM: from cell-cell adhesion to the cluster of cells and cell monolayers"

Mauricio Moreira-Soares "Modelling cell shape and migration: a phase-field approach"

Alexander Leonard "The evolution of symmetric and asymmetric protein binding interfaces"

Haru Negami "Topological analysis of penicillin-binding proteins"

Anastasia A. Anashkina "Scoring, analysis and ranking of protein-protein docking models by QASDOM server on the example of nef-calnexin interaction"



PS POPULATION BIOLOGY I

14:20-16:00 ♦ ROOM C8.2.15

Atheeta Ching “The carrying simplex in non-competitive Lotka-Volterra systems”

Cecilia Berardo “Analysis of a functional response with prey-density dependent handling time under an evolutionary perspective”

John R. Ellis “Formation of population clusters in density dependent random walks”

Nurdan Cabukoglu “Reaction-diffusion models for populations with kinesis”

Peter Jagers “How might a population have started?”

PS PHYSIOLOGY II

14:20-16:00 ♦ ROOM C8.2.17

Anahita Bayani “Modelling anti-inflammatory systems – spatial considerations in the resolution of inflammation”

Eleni Moraki “Modelling corneal epithelium maintenance and recovery”

Johanne Gudmand-Hoeyer “The influence of transport proteins and competing steroids on the plasma cortisol dynamics”

Mariia Dvoriashyna “Mathematical model of fluid and CO₂ transport across the retinal pigment epithelium”

Zuzanna Szymańska “Mathematical modelling of the tendon healing process: blow-ups mean healing”

PS IMMUNOLOGY I

14:20-15:40 ♦ ROOM C8.2.19

Akane Hara “Theoretical study of interaction between allergy and intestinal microbiome”

Arran Hodgkinson “Both high and low affinity interferons necessary for effective immune response: a mathematical modelling approach”

Sophie Ip “Kinetics of innate immunity within the cell: mathematical parallels with prions”

Sahamoddin Khailaie “Characterization of CTLA4 trafficking: a combined in silico and in vitro approach”

PS GENETICS AND GENOMICS I

14:20-16:00 ♦ ROOM C8.2.23

Andre S. Ribeiro “Stochastic modeling and inference of temperature-dependent transcription supercoiling dynamics”

Monika Kurpas “A simulation study of the relationship between DNA damage detection pathways and the cell cycle”

Jonathan Harrison “Experimental verification of a coarse-grained model predicts production rate limits mRNA localization”

Eva Stadler “Eigensolutions for a model of vertical gene transfer of plasmids”

Alexey V. Doroshkov “Molecular evolution and meta-transcriptomic approaches to access the plant oxidative stress resistance enzymes”



PS

EVOLUTIONARY DYNAMICS II14:20-16:00 ♦ ROOM **C8.2.38**

Mario E. Veruete “Evolutionary branching via replicator-mutator equations”

Pietro Landi “Variability in life-history switch points across and within populations explained by adaptive dynamics”

Frédéric M. Hamelin “Gene-for-gene epidemic models, systemic acquired resistance, and the evolution of plant parasites”

Coralie Fritsch “Food web models with evolution of two traits”

Kalle Parvinen “The effect of spatial heterogeneity on evolution in spatial models”

PS

MATHEMATICAL METHODS IN BIOLOGY III14:20-16:00 ♦ ROOM **C8.2.39**

Simon Syga “A new lattice-gas cellular automaton model for cell aggregation”

Alexander Tam “The effect of nutrient-limited growth on floral pattern formation in yeast biofilms”

Ulrich Dobramysl “Determining the probability flux from a Brownian source to small absorbing windows via a mixed analytical-stochastic simulation method”

Clemens Kreutz “An intuitive and efficient approach for testing parameter identifiability”

Jean-Luc Gouze “Reduction of metabolic networks keeping core dynamics”

NOTES

MS EXPLORING THE TISSUE REGENERATION PROCESSES THROUGH MATHEMATICAL MODELLING ROOM **C8.2.02**
10:30-11:50

Organizers: Diane Peurichard and Dirk Drasdo

Oswaldo Chara "Data-driven multi-scale model of tissue regeneration in axolotl"

Aur lie Carlier "In silico clinical trials for pediatric orphan diseases: a case study"

Yanlan Mao "Wound edge fluidity promotes epithelial wound healing"

Anotida Madzvamuse "Recent advances in mathematical modelling of cell migration"

MS MATHEMATICAL MODELING OF LEUKEMIA AND MYELOPROLIFERATIVE NEOPLASMS ROOM **C8.2.03**
10:30-11:50

Organizers: Morten Andersen and Thomas Stiehl

Thomas Stiehl "Modeling feedback signals in acute leukemias: biological insights and clinical applications"

David Dingli "Hematopoietic stem cell dynamics and paroxysmal nocturnal hemoglobinuria"

Johnny T. Ottesen "The Cancitis model: a coupled leukemic-inflammatory response"

Doron Levy "The role of the autologous immune response in chronic myelogenous leukemia"

MS EPIDEMIC MODELS: FROM INDIVIDUAL DECISION TO COLLECTIVE DYNAMICS ROOM **C8.2.06**
10:30-11:50

Organizers: Gabriel Turinici

Bruno Buonomo "Public health intervention in behavioral vaccination models: analysis and control"

Alberto d'Onofrio "Vaccine opinion dynamics: imitation game reloaded"

Tim Reluga "Social distancing epidemic games, diagnosis, and incomplete information"

Francesco Salvarani "A mean field games approach to imperfect vaccination"

PS CELL AND INTRA-CELL DYNAMICS II 10:30-12:30 ♦ ROOM **C8.2.10**

Reuben O'Dea "Multiphase and morpho-poro-elastic multiscale models of biological tissue growth"

Martin Lercher "Accurate prediction of intracellular concentrations in E. coli from a simple optimality principle"

Julian Rode "Proliferation rate inference with continuous labelling assays"

Daniel Sanchez-Taltavull "Architectures of differentiation cascades with asymmetric and symmetric stem cell division"

Abhyudai Singh "Exact lower and upper bounds on moments of biochemical systems"

Simon P. Pearce "Curvature-sensitive kinesin binding can induce rings and chaotic dynamics in microtubules"

PS CANCER II 10:30-12:30 ♦ ROOM **C8.2.11**

Pietro Mascheroni "Modeling the influence of compressive stresses on the efficacy of anticancer treatments"



Léolo Gonay "Structure and dynamics of a gene regulatory network driving hepatocellular carcinoma"

Dumitru Trucu "Multiscale modelling of cancer growth and spread: a multiscale moving boundary approach"

Alvaro Köhn-Luque "Personalized cancer treatment simulation: a multi-scale model informed by multi-source clinical data"

Bertin Hoffmann "Radiotherapy and chemotherapy change vessel tree geometry and metastatic spread"

Mark Robertson-Tessi "Evolution of competing diversities: tumor vs. immune"

PS **EVOLUTIONARY DYNAMICS III**

10:30-12:30 ♦ ROOM **C8.2.13**

Georgiy Karev "Evolutionary games: natural selection of strategies"

Jacek Miękisz "Social dilemmas in simple evolutionary games"

Frédéric Grogard "Uninvadable strategies for biotrophic pathogens, from dynamic games to adaptive dynamics"

Piret Avila "Sex-ratio conflict disrupts colony growth in annual haplodiploid social insects"

Yuhua Cai "Resident-invader dynamics of similar strategies in noisy environments"

Barbara Boldin "An extension of the classification of evolutionarily singular strategies in adaptive dynamics"

PS **ECOLOGY II**

10:30-12:30 ♦ ROOM **C8.2.15**

Alexander Medvinsky "Direct and indirect effects of temperature on the dynamics of lake plankton"

Giancarlo Consolo "Secondary seed dispersal in the Klausmeier vegetation model for sloped semi-arid environments"

Simona Panunzi "A novel advection-diffusion-reaction model of the spatio-temporal mercury dynamics in water and sediments"

Arnina Goodlad "Collective movement of marine animals: the effect of anthropogenic noise on pattern formation"

Aleksandra Z. Płochocka "Homing of green sea turtles across various geographical locations"

Vincent Calcagno "Foraging under predation risk: a marginal value approach"

PS **EPIDEMIOLOGY II**

10:30-12:10 ♦ ROOM **C8.2.17**

Ryosuke Omori "Predictability of prevalence of sexually transmitted infection on complex network"

Max von Kleist "Hybrid stochastic framework predicts the prophylactic efficacy of antivirals against HIV-infection"

Hee-Dae Kwon "Feedback control of an HBV model based on a nonlinear Kalman filter"

Ganna Rozhnova "Impact of pre-exposure prophylaxis on the Dutch HIV epidemic among men who have sex with men"

Cristiana J. Silva "Hopf bifurcation and optimal control of a delayed HIV model"



PS GENETICS AND GENOMICS II10:30-12:30 ♦ ROOM **C8.2.19**

Krzysztof Puszynski “The influence of the stochastic gene switching on effectiveness of the metronomic therapies”

Alessandra Micheletti “A comparison of singular values decomposition and functional statistics for the analysis of omics data”

Frits Veerman “A hybrid analytical-numerical method for parameter inference in stochastic gene expression models”

Núria Folguera-Blasco “Unlocking the stem cell phenotype: a multi-scale model of the epigenetic regulation of cell fate and plasticity”

Abhishek Gupta “Extrinsic noise leads to phenotypic transitions in stochastic gene expression”

Nikos Kavallaris “Data driven model selection and parameter estimation for DNA methylation”

PS EPIDEMIOLOGY III10:30-12:30 ♦ ROOM **C8.2.23**

Alberto Pinto “Evolutionary vaccination dynamics”

José Martins “Learning strategies in a rumor spreading model based on the SIR epidemic model”

Paulo Doutor “Rational behavior and social cost for vaccination in childhood diseases”

Ka Yin Leung “Epidemics on networks with social distancing”

Joe Hilton “Household models for endemic diseases”

Ana P. Lemos-Paião “Optimal control of a SIQRB cholera delayed model”

PS POPULATION BIOLOGY II10:30-12:30 ♦ ROOM **C8.2.38**

Benoit Sarels “Interactions of traveling waves in the context of population genetics”

Reinhard Bürger “Two-locus clines maintained by diffusion and recombination in a heterogeneous environment”

Ilya Timofeyev “Large deviations theory with application to rare events in bacterial populations”

Carlos A. Braumann “Constant effort harvesting models with Allee effects in randomly varying environments”

Nuno M. Brites “Performance of fishing policies for populations with weak Allee effects in a random environment”

Tim Rogers “Strength in numbers: how demographic noise can reverse the direction of selection”

PS MATHEMATICAL METHODS IN BIOLOGY IV10:30-12:30 ♦ ROOM **C8.2.39**

Burcu Gürbüz “Laguerre polynomial solutions of a class of nonlinear reaction diffusion equation and its applications in biology”

Chengming Huang “An efficient numerical algorithm for auto-convolution Volterra integral equations”

Rossana Vermiglio “Polynomial Chaos expansions for stability, uncertain quantification and sensitivity analysis of equilibria of uncertain delay differential equations”

Luís Mateus “Prediction and predictability in population biology”



Carlos Correia Ramos “Animal movement: symbolic dynamics and topological classification”

Claus Haeteringer “Sustainability indicator system for assessment of dairy farms at Vale do Taquari-RS (Brazil)”



MS CURRENT DIRECTIONS IN HOST-PARASITE COEVOLUTION ROOM C8.2.02

Organizers: Alex Best **14:00-15:20**

Chaitanya Gokhale “Antagonistic coevolution, population dynamics, and implications for the Red Queen”

David Dingli Sona John “From coevolutionary dynamics to genomics and back: inferring the speed of the Red Queen”

Michael Sieber “Evolution of parasite host ranges - going beyond trade-offs”

Alex Best “Host-parasite coevolution within communities”

MS CURRENT DIRECTIONS IN HOST-PARASITE COEVOLUTION ROOM C8.2.03

Organizers: Tony Humphries and Laurent Pujo-Menjouet **14:00-15:20**

Tony Humphries “Modelling granulopoiesis with state-dependent delays”

Mostafa Adimy “Age-structured and delay differential-difference model of hematopoietic stem cell dynamics”

Anna Marciniak-Czochra “Clonal evolution and emergence of resistance in acute leukemias: insights from mathematical modeling”

Adélia Sequeira “Modeling and simulations of the blood coagulation process”

MS MULTI-SCALE MODELS OF CELL BEHAVIOUR ROOM C8.2.06

Organizers: Enrico Gavagnin and Christian A. Yates **14:00-15:20**

Enrico Gavagnin “Modelling persistence in motion of interacting cells at multiple scales”

Andreas Deutsch “Biological lattice-gas cellular automaton models for the analysis of collective behaviour in interacting cell populations”

Anna Marciniak-Czochra Linus J. Schumacher “Semblance of heterogeneity in collective cell migration”

Christian A. Yates “Incorporating a multistage representation of the cell cycle into models of cell migration”

MS FREE BOUNDARY PROBLEMS IN MATHEMATICAL BIOLOGY ROOM C8.2.10

Organizers: Raquel Barreira and Chandrasekhar Venkataraman **14:00-15:20**

José Carrillo “Attractive-repulsive models in collective behavior models and applications”

Tobias Kies “Numerical simulation of membrane mediated particle clustering in an elastic model”

Chandrasekhar Venkataraman “Free and moving boundary problems in cell biology”

Euripides J. Sellountos “Boundary domain integral methods for the solution of the Navier-Stokes equations”



MS	PARTIAL DIFFERENTIAL EQUATION MODELS IN ECOLOGY AND EVOLUTION	ROOM C8.2.11 14:00-15:20
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Organizers: Max Souza e Reinhard Bürger

Max Souza “Continuous approximations of finite-population stochastic models: the PDE viewpoint”

Gaël Raoul “Dynamics of an asexual population facing climate change”

Linlin Su “Clines with partial panmixia across a geographical barrier in an unbounded unidimensional habitat”

Silvia Cuadrado “Asymptotic behavior of some selection-mutation equations”

MS	VEGETATION INTERPLAY OF WATER AND TOXICITY IN VEGETATION PATTERN FORMATION	ROOM C8.2.13 14:00-15:20
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Organizers: Frits Veerman and Koen Siteur

Johan van de Koppel “Multi-scale patterns in self-organized ecosystems: a new hype or something really important?”

Annalisa Iuorio “Interplay of water and toxicity in pattern formation vegetation”

Lukas Eigentler “How does long-range dispersal affect pattern formation in semi-arid vegetation?”

Koen Siteur “Vegetation patterns and ecosystem degradation: towards a complete indicator framework”

PS	EVOLUTIONARY DYNAMICS IV	14:00-15:40 ♦ ROOM C8.2.15
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Dániel Czégel “Major evolutionary transitions as structure learning of Bayesian belief networks”

Nathalie Gontier “Can we define life by how it evolves?”

Nicole Fortuna “Modelling the evolution of generalist vs. specialist pathogens spreading on a clade of host species”

Tadeas Priklopil “When does an invasion of a novel trait imply fixation?”

Inês Fragata “Predictability of long-term, but not short-term phenotypic evolution of *Drosophila*”

PS	PHYSIOLOGY III	14:00-15:40 ♦ ROOM C8.2.17
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Claudiu-Cristi Antonovici “Dynamic model of stomatal development and patterning with auxin regulation”

Isabella Marinelli “Analysis of different bursting modes in the integrated oscillator model for pancreatic beta-cells”

Yannis Kalaidzidis “Bile flux quantification by intra-vital microscopy”

Linda Irons “Effect of deep inspirations on airway smooth muscle cell-matrix adhesions”

Leo Creedon “A mathematical model of bovine progesterone based on corpus luteum measurement”



PS IMMUNOLOGY II**14:00-15:40 ♦ ROOM C8.2.19**

Connor White “The protectiveness of HLA Alleles against infection in the presence of multiple pathogen strains”

James Preston “Exploring the dynamics of an enterpathogenic *Escherichia coli* infection via a computational model”

Lito A. Papaxenopoulou “Model-driven experiments induce elimination of *Staphylococcus aureus* chronic infection”

Suzanne Touzeau “Investigating viremia rebounds using a PRSS data-supported model of immune response”

Bruno M. P. M. Oliveira “Concentration of T cells and antigenic stimulation”

PS CELL AND INTRA-CELL DYNAMICS III**14:00-15:40 ♦ ROOM C8.2.23**

Aldo E. Encarnacion Segura “Cellular decision making models in microorganisms”

J. Krishnan “Temporal and spatial information processing in cell signalling networks”

Anne-Sophie Giacobbi “Modelling of the ERK pathway in hepatocellular carcinoma cells exposed to sorafenib”

Carla White “Cooperativity across dimers and the effect on ligand binding: linear and non-linear models”

Mariya Ptashnyk “Multiscale modelling and analysis of intercellular signalling processes in biological tissues”

PS EPIDEMIOLOGY IV**14:00-15:40 ♦ ROOM C8.2.38**

Thi Mui Pham “Mathematical modelling of *P. aeruginosa* transmission routes in intensive-care units”

Sara Jabbari “Exploiting the antibiotic-induced morphological transition of *Pseudomonas aeruginosa*”

Martín López-García “A unified stochastic modelling framework for the spread of nosocomial infections”

Paul A. Roberts “Using predictive models to optimise the treatment of bacterial infections: combining a novel anti-virulence therapy with antibiotics”

Míriam García “Modeling the dynamics of antimicrobial resistance in a Morbidostat”

PS EVOLUTIONARY DYNAMICS V**14:00-15:40 ♦ ROOM C8.2.39**

Thi Mui Pham Peter Czuppon “Disentangling ecological noise and evolutionary dynamics during trait fixation”

Celia García-Pareja “Exact simulation of coupled Wright Fisher diffusions”

Hye Jin Park “Fate of populations in a stochastic system with mutations”

Meike Wittmann “Stable polymorphisms due to seasonally fluctuating selection and their genetic footprint”

Tatiana Yakushkina “Near-neutrality in evolutionary models: the first arrival time problem”



MS	BRAIN NETWORKS: A WINDOW ON BRAIN FUNCTION AND DYSFUNCTION	ROOM C8.2.02 10:30-11:50
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Organizers: Marinho A. Lopes

Joana Cabral "Whole-brain network dynamics: mathematical models and mechanistic scenarios"

Ernesto Pereda "Multiplex network fingerprints of the risk of evolution from early stages of Alzheimer's disease"

Timothée Proix "Spatiotemporal modeling of seizure propagation and termination in human focal epilepsy"

Gorka Zamora-López "Understanding the relation between structural and functional brain connectomes"

MS	MATHEMATICS AT THE INTERFACE OF COLLECTIVE BEHAVIOR AND EMERGENT PHENOMENA IN BIOLOGY	ROOM C8.2.03 10:30-12:10
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Organizers: Jason M. Graham and Simon Garnier

Gonzalo Polavieja "Models of collective behavior"

Richard P. Mann "Rational collective decision making, in the lab and in the wild"

Violet Mwaffo "Determining cause-and-effect relationships from raw trajectory data of collective behavior"

James A.R. Marshall "When Condorcet is wrong (almost always) and what to do about it"

Daniel Strömbom "A comparison of polarization inducing mechanisms for modeling collective motion"

MS	PLANT MODELS (B): MODELLING LIFE IN SOIL	ROOM C8.2.06
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Organizers: Lionel Dupuy and Mariya Ptashnyk 10:30-11:50

Dani Or "Microbial life in soil aggregates - from hotspots to soil biogeochemical fluxes"

Matthias Mimault "A SPH model for growth of plant roots"

Siul Ruiz "Mechanical and biophysical constraints affecting soil bioturbation by earthworms and plant roots"

Lionel X. Dupuy "The random walks of roots in a granular media"

MS	ALGEBRAIC, ANALYTIC, AND ALGORITHMIC APPROACHES TO STEADY STATES OF REACTION NETWORKS	ROOM C8.2.10 10:30-12:10
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Organizers: Elisenda Feliu

Elisenda Feliu "Node balanced steady states: unifying and generalizing complex and detailed balanced steady states"

Stefan Müller "Characterizing generalized mass-action systems with a unique complex-balancing equilibrium"

Georg Regensburger "Computing sign-vector conditions for bounding the number of complex-balancing equilibria"

Balázs Boros "Weak reversibility implies existence of a positive steady state"

Gheorghe Craciun "Polynomial dynamical systems and reaction networks: persistence, permanence and global stability"

MS	MULTI-SCALE MODELING AND SIMULATIONS OF STOCHASTIC SYSTEMS IN BIOLOGY	ROOM C8.2.11 10:30-12:10
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Organizers: Jae Kyoung Kim

Jae Kyoung Kim "Reduction of multiscale stochastic biochemical reaction networks"



Ankit Gupta "Adaptive hybrid simulation and sensitivity estimation for multiscale stochastic reaction networks"

Stefan Hellander "Mesoscopic-microscopic spatial stochastic simulation with automatic system partitioning"

Christopher Lester "Robustly simulating biochemical reaction kinetics using multi-level Monte Carlo approaches"

Stephen Smith "The effect of cell-cell coupling on single-cell noise"

MS

MATHEMATICAL MODELING IN PHYSIOLOGY: ONE MAIN ROAD TOWARDS PERSONALIZED MEDICINE

ROOM **C8.2.13**
10:30-12:10

Organizers: Andrea de Gaetano and Jerry Batzel

Franz Kappel "Challenges for mathematical modelling in view of personalized medicine"

Thomas Heldt "Model-based estimation for noninvasive intracranial pressure monitoring"

Andrea de Gaetano "Modeling of ventilator-patient interaction"

Luciano Curcio "A simple cardiovascular model for the study of haemorrhagic shock"

Irina Pashchenko "Personalized mathematical modeling of whole body glucose metabolism for insulin therapy adjustment"

PS

CELL AND INTRA-CELL DYNAMICS IV

10:30-12:10 • ROOM **C8.2.15**

Tomasz Lipniacki "Limits on information transmission through biochemical networks in response to the pulsed stimuli"

Valentina Baldazzi "Unravelling the contribution of cell cycle and cell expansion in an integrated model of tomato fruit development"

Abhishek Pal Majumder "Long term behavior of some non-regular stochastic reaction networks"

Robert Schwieger "Investigation of Boolean monotonic model pools"

Philipp Thomas "Stochastic gene expression in growing cell populations"

PS

EPIDEMIOLOGY V

10:30-12:30 • ROOM **C8.2.17**

Antoni Leon Dawidowicz "Mathematical model of Lyme disease caused by the bacterium *Borrelia burgdorferi*"

Winfried Just "Should I get a flu shot? How well did this go last year?"

Christopher N. Davis "Village-scale persistence and elimination of HAT (gambianse human African trypanosomiasis)"

Joseph Pérez Chávez "An impulsive model for Dengue transmission dynamics with seasonal effects and pesticide control"

Theresa Stocks "Dynamic modelling of hepatitis C transmission among IDUs: revealing the undiagnosed and impact of interventions"

Maira Aguiar "Modeling the implementation of dengue vaccine"

PS

ECOLOGY III

10:30-12:30 • ROOM **C8.2.19**

Candy J. Abboud "Using post-introduction data and a mechanistic-statistical approach to date and localize an invasion"

Samuel Fischer "Optimal strategies to prevent invasive species transport"

Christelle Suppo "Range expansion of the yellow-legged hornet in Europe and the role of human-mediated dispersal"

Andy White "Conservation management in the face of disease-mediated invasion"

Sonja Radosavljevic "Poverty traps as a social-ecological phenomena: dynamical system approach"

Joe Yuichiro Wakano "Ecocultural range-expansion model of modern humans in Paleolithic"



PS

CANCER III

10:30-12:30 ♦ ROOM C8.2.23

Jeffrey West "Neoadjuvant trade-offs in ER+ breast cancer: a game theoretic approach"

Jean Clairambault "Cancer as a default of evolutionary coherence between tissues in metazoa"

Sara Hamis "Hypoxia-activated prodrugs and radiation: an in silico investigation to study the synergetic effects of bystander responses in tumour spheroids"

Marek Bodnar "Mathematical model describing low grade gliomas and its reaction to chemotherapy"

Sarah C. Brünink "A multiscale model for predicting the response of 3D spheroids to combinations of radiation and hyperthermia"

Arturo Álvarez-Arenas "An integro-differential equations model to study the development of multidrug resistance in cancer"

PS

MATHEMATICAL METHODS IN BIOLOGY V

10:30-12:10 ♦ ROOM C8.2.38

George A.K. van Voorn "Quantifying adaptive capacity of socioecological systems"

Guus ten Broeke "Using simulation models to assess resilience"

Torbjörn Lundh "Position prediction of neighbours can generate milling flocks"

Andreagiovanni Reina "Studying psychophysical laws in the superorganism through a novel automated analysis tool"

Cinzia Soresina "Cross-diffusion predator-prey models arising by time-scale arguments"

PS

EPIDEMIOLOGY VI

10:30-12:30 ♦ ROOM C8.2.39

Shingo Iwami "Quantifying antiviral activity optimizes drug combinations against hepatitis C virus infection"

Trystan Leng "Concurrency of partnerships, consistency with data, and control of sexually transmitted infections"

Christine Bürl "Population-based and individual-based modelling of *Opisthorchis viverrini*"

Yusuke Kakizoe "Evaluating the drug combination therapy against hepatitis C virus"

Geisel Alpizar-Brenes "Mathematical modeling of the interaction between wilds and *Wolbachia*-infected mosquitoes"

Urszula Skwara "Stochastic modelling of vector-borne diseases"

NOTES

PS MATHEMATICAL METHODS IN BIOLOGY VI 10:30-12:30 ♦ ROOM C8.2.02

Jake Alan Pitt "Parameter estimation in models of biological oscillators: dealing with multimodality and overfitting"

Attila Csikász-Nagy "Single molecule switches and oscillators"

Ilona Kosiuk "Geometric singular perturbation analysis of spiky oscillations in a minimal NF-kappa B signaling model"

Tomislav Plesa "Noise control and mixing in designing reaction networks"

Ruben Perez-Carrasco "Success of oscillations in negative feedback gene regulatory networks is determined by degradation rate uniformity"

Daniele Cappelletti "Designing reaction networks with a given stationary distribution"

PS POPULATION BIOLOGY III 10:30-12:30 ♦ ROOM C8.2.03

Bob W. Kooi "Sensitivity and bifurcation analysis using predator-prey models as case studies"

Vitalii Akimenko "An age-structured model with Allee effect and time delay"

Robert Planqué "Maximising microbial growth rate in changing environments: the mORAC framework"

Carmen Lia Murall "The challenges of modelling the vaginal microbiome"

J. Leonel Rocha "Stability analysis of Gompertz's logistic growth equation under strong, weak and no Allee effects"

Lucia Russo "From gradual changes to catastrophic shifts in ecosystems with human interaction"

PS CANCER IV 10:30-12:10 ♦ ROOM C8.2.06

Marina D.M. Oliveira "Growth of tumor microtubule networks in a glioblastoma"

Isabel M. Narra de Figueiredo "Space-time model for the understanding of aberrant crypt foci morphogenesis"

Gerhard A. Burger "Cell density influences clustering and migratory behaviour of triple-negative breast cancer cells"

Krzysztof Gogolewski "Pitfalls in clustering metabolic landscapes"

PS CELL AND INTRA-CELL DYNAMICS V 10:30-12:30 ♦ ROOM C8.2.10

Sophie Hecht "Incompressible limit of a continuum model of tissue growth with segregation for two cell populations"

Haralampos Hatzikirou "On a theory of cell decision-making in multicellular systems: the least microenvironmental uncertainty principle"

Alf Gerisch "Insight into a nonlocal PDE model of cellular adhesion by microscale spacejump process modelling"

Dirk Alexander Kulawiak "Poroelectric two-phase model for moving droplets of Physarum polycephalum with free boundaries"

Franziska Matthäus "On a mechanochemical model for cell polarization"

Frédérique Robin "Structured cell population dynamics: application to the morphogenesis of ovarian follicles"



PS EVOLUTIONARY DYNAMICS VI 10:30-12:30 ♦ ROOM **C8.2.11**

Christopher E. Overton "Deterministic approximations of stochastic dynamics in evolutionary graph theory"

Laura Hindersin "The effect of graph structure on fixation probability and time"

Yuriy Pichugin "Reproduction costs can drive the evolution of groups"

Ilhem Bouderbala "A spatially explicit individual based model to study the motile-phyto-plankton aggregation process"

Daniah Tahir "Modeling a two-type, asymmetric, trait-dependent diversification process, on a random species tree"

Caterina Vitale "Evolution of tolerance under selective predation"

PS EPIDEMIOLOGY VII 10:30-12:10 ♦ ROOM **C8.2.13**

Lee Benson "Direct transmission models for indirectly transmitted environmental pathogens"

Viggo Andreasen "Coexistence in a seasonal epidemic model"

Ruili Fan "Virulence management in a model with explicit within- and between-host dynamics"

Maria Vittoria Barbarossa "An in-host perspective on disease dynamics"

Eleanor Tanner "Culling causes compensatory population growth due to release from disease-induced mortality"

PS GENETICS AND GENOMICS III 10:30-12:30 ♦ ROOM **C8.2.15**

Qi Zheng "Shedding new light on random chromosome segregation"

Nicolas Privault "Modeling and estimation of substitution rates along phylogenetic trees by stochastic bridges"

Yun Jun Zhang "Revealing individual-level heterogeneity in infectivity from pathogen phylogeny"

Joanna Tyrcha "Stochastic activation in a genetic switch"

Kseniia Nikitina "Probabilistic graphical models for loss-of-function genomic screens analysis"

Christel Kamp "The right word in the right place: optimizing codon usage for protein translation"

PS PHYSIOLOGY IV 10:30-11:50 ♦ ROOM **C8.2.17**

Gabriel F. Calvo "Modelling the interplay of two glycemic biomarkers for patient-specific monitoring of diabetes"

Claudio Gaz "Design of a control law for insulin resistant patients by means of a simple glucose/insulin system model"

Adam C. Bridgewater "Perturbation analysis of a delayed model of glucose-insulin regulation"

Alessandro Borri "Structured models as a mathematical tool to describe diabetes evolution"

PS MATHEMATICAL METHODS IN BIOLOGY VII 10:30-12:30 ♦ ROOM **C8.2.19**

Jan Rombouts "Traveling pulses in a time-delayed Fitzhugh-Nagumo model"

Dominique Joubert "Determining the minimal output sets that ensure the structural identifiability of a model"



Maria Pia Saccomani "New perspectives and practical tools for local identifiability analysis of biomathematical models"

András Telcs "Inference of causal relations via dimensions"

Matthew Adamson "Anticipating nonlocal critical transitions in nearly-1D systems"

Stefan Schuster "Use of Fibonacci numbers in lipidomics - enumerating various classes of fatty acids"

PS

ECOLOGY IV

10:30-12:10 ♦ ROOM C8.2.23

Elisabeta Vergu "Analysis of the cattle trade network in France to inform epidemiological risk"

Pierre Montagnon "A stochastic SIR model for cattle diseases on a population graph"

Patrick Hoscheit "Using TempoRank to identify central nodes in cattle trade networks"

Gaël Beaunée "Inference in a metapopulation model via a composite-likelihood approximation"

Mathieu Andraud "Using field and experimental data to estimate key epidemiological parameters to decipher PRRSV epidemiology"

PS

EPIDEMIOLOGY VIII

10:30-12:30 ♦ ROOM C8.2.38

Carlene P. C. Pilar-Arceo "An edge-based SEIR model on a static random network"

Mariajesus Lopez-Herrero "Maximum epidemic size for a nonlinear SEIR model with limited resources"

Raquel Filipe "The SHAR model and its effective infection rate: analytical results on severe vs asymptomatic infection"

Sophie R. Meakin "Correlations between stochastic epidemics in multiple interacting sub-populations"

Antonio Gómez-Corral "Dynamics of epidemic models with two strains and cross immunity"

Nico Stollenwerk "Chaos via torus destruction in population biology: implications for data analysis"

PS

POPULATION BIOLOGY IV

10:30-12:30 ♦ ROOM C8.2.39

Ezio Venturino "How does herd gathering influence interacting population dynamics?"

Yuuya Tachiki "The evolution of rhizome system in bamboos under spatial heterogeneities"

Shigehide Iwata "Reconsideration about an optimal management for the migrated species"

Stefania Ragni "Optimal effort control for the harvesting of a population modeled by a parabolic PDE"

Rafael Bravo de la Parra "Discrete time multiregional stochastic models with fast migration: re-scaling survival to the fast scale"

Volkmar Liebscher "Deriving simple predator-prey models from individual based models via singular perturbation theory"



PS

PHYSIOLOGY V

14:00-15:20 ♦ ROOM C8.2.02

Alberto Otero-Cacho "Experimental and CFD numerical simulations of stenosis and atherosclerosis occurring in vessel branches"



Juan Calvo “Long time behavior for some continuous polymerization models”

Marcos Gouveia “Simulating vessel growth with extracellular matrix remodeling”

Telma Guerra “Flow control with applications to hemodynamics”

MS

MATHEMATICAL MODELS FOR PEST CONTROL

ROOM **C8.2.03**

Organizers: Andrea Pugliese and Bedreddine Ainseba

14:00-15:20

Bedreddine Ainseba “Are we able to predict pest dynamics?”

Sara Pasquali “A population dynamics model as tool for pest control in vineyards”

Rachel Norman “A mathematical model of armyworm dynamics and control using a biological control agent”

Claudia Pio Ferreira “The influence of landscape diversity on insect-pest dispersal and establishment”

MS

THE INTERPLAY BETWEEN SHORT- AND LONG-RANGE INTERACTIONS IN BIOLOGY

ROOM **C8.2.06**

14:00-15:20

Organizers: José Antonio Carrillo and Maria Bruna

Alexandria Volkening “Agent-based models of pattern formation on the skin of zebrafish”

Markus Schmidtchen “Pattern formation in non-local systems with cross-diffusion”

Marco Scianna “Adhesion and volume constraints via nonlocal interactions determine cell organisation and migration profiles”

Tommaso Lorenzi “Continuum and discrete nonlocal models of spatial evolutionary games”

MS

TOPICS ON DRUG RESISTANCE IN CANCER

ROOM **C8.2.10**

Organizers: Jean Clairambault and Luis Almeida

14:00-15:20

Cécile Carrère “Growth speed of heterogeneous tumours: a competition-diffusion spreading result”

Denis Horváth “Ecological context of coevolutionary dynamics between cancer and therapeutic intervention”

Shensi Shen “Anti-cancer therapy: blazing the trail with melanoma”

Marc Sturrock “Mathematical modelling of emergent gene expression”

MS

NEW TRENDS IN MODELLING CARDIOVASCULAR DISEASES

ROOM **C8.2.11**

Organizers: Nader El Khatib and Adélia Sequeira

14:00-15:20

Vitaly Volpert “Reaction-diffusion waves of blood coagulation in quiescent plasma and in flow”

Jorge Tiago “Towards patient specific blood flow simulations: a velocity tracking approach”

Nader El Khatib “Patient specific 3D numerical fluid-structure interaction model for blood flow in an atherosclerotic artery”

Oualid Kafi “Mathematical modeling of the hydrodynamics of a free-flowing leukocyte toward the endothelial wall”



MS HOW TO DESIGN EVOLUTION-PROOF PUBLIC HEALTH INTERVENTIONS? ROOM **C8.2.13**
14:00-15:20

Organizers: Samuel Alizon and Carmen Lía Murall

Erida Gjini “Mathematical perspectives on host immunity and antibiotic treatment”

David A Kennedy “Why does drug resistance readily evolve but vaccine resistance does not?”

Christian Selinger “Multiple infections on networks”

Monika Piotrowska “Towards simulation of inter-hospital spread of multidrug-resistant Enterobacteriaceae based on real healthcare system data”

MS COMPUTATIONAL STATISTICS AND BAYESIAN INFERENCE FOR STOCHASTIC BIOLOGICAL MODELS ROOM **C8.2.15**
14:00-15:20

Organizers: Massimiliano Tamborrino and Evelyn Buckwar

Massimiliano Tamborrino “Likelihood-free methods for the inference of non-renewal point processes arising from neuroscience”

Irene Tubikanec “Structural preserving numerical method and Bayesian inference for stochastic neuronal mass models”

Annalisa Cadonna “Bayesian spectral estimation methods for multiple time series and application to multichannel EEG”

Moritz Schauer “Bayesian estimation of diffusions applied to compartment models”

MS MIGRATION AND INVASION OF EUKARYOTIC CELLS: FROM EXPERIMENTS TO MODELS ROOM **C8.2.17**
14:00-15:20

Organizers: Christophe Deroulers

Roelend Merks “Modeling of mechanical and chemical cell-matrix interactions driving cell migration and invasion”

Yi Jiang “Leading the pack: leader and follower in collective cancer invasion”

Anja Voss-Böhme “Impact of cell migration plasticity on tumor growth and invasion: a cell-based approach”

Christophe Deroulers “Fronts in populations of self-regulating cells”

PS EPIDEMIOLOGY IX 14:00-15:20 ♦ ROOM **C8.2.19**

Esteban A. Hernandez-Vargas “Advances in multiscale modeling of infectious diseases”

David Gerberry “An exact approach to calibrating infectious disease models to surveillance data”

Chakib Jerry “Economical epidemic model as controlled switched system”

Yibeltal A. Terefe “Mathematics of a sex-structured model for Trichomoniasis transmission dynamics”

PS NEUROSCIENCE I 14:00-15:20 ♦ ROOM **C8.2.23**

Voliotis Margaritis “Understanding the hypothalamic network that controls the pulsatile secretion of reproductive hormones: from theory to experiments”



Gabriela Capo Rangel “A computational model integrating brain electrophysiology and metabolism”

Lucía Pérez “The Hindmarsh-Rose neuron model: global homoclinic structure of squarewave bursters”

Marinho A. Lopes “Elevated ictal brain network ictogenicity enables optimal epilepsy surgery prediction”

MS COLLECTIVE MIGRATION IN INTERACTING CELL SYSTEMS

ROOM C8.2.38

Organizers: Andreas Deutsch and Luigi Preziosi

14:00-15:20

Josué Manik Nava-Sedeño “The role of persistency in single and collective cell migration”

Medhavi Vishwakarma "Influence of group decisions on collective cell migration"

Andras Czirok "Collective effects of cell motility within stratified epithelia"

Annachiara Colombi “Non-local hybrid model for collective cell migration during zebrafish posterior lateral line development”

PS MATHEMATICAL METHODS IN BIOLOGY VIII

14:00-15:20 ♦ ROOM C8.2.39

Gissell Estrada-Rodriguez "Space-time fractional diffusion equations in chemotaxis and immunology"

Maria Rosaria Mattei “A modeling and simulation study of the invasion phenomenon in biofilm reactors”

Cameron A. Smith “The auxiliary region method for coupling PDE and Brownian-based dynamics for reaction-diffusion systems”

Cordula Reisch “Gaining information from submodels: modeling liver infections with reaction-diffusion equations”

NOTES



PS EPIDEMIOLOGY XI 11:00-12:40 ♦ ROOM C8.2.02

Egberanmwen Barry Sunday Iyare “Mathematical modeling and analysis of the transmission dynamics of tuberculosis and lymphatic Filariasis co-infection”

Eunok Jung “Dynamical models of tuberculosis transmission and optimal treatment strategies in the Republic of Korea and Philippines”

Tatiana E. Sannikova “Mathematical modeling of sex differences in TB epidemiology”

Delfim F. M. Torres “Stability of a fractional tuberculosis model”

Carla Pinto “Non-integer order analysis of the impact of diabetes and resistant strains in a model for TB infection”

MS LOGICAL MODELLING OF (MULTI)CELLULAR NETWORKS ROOM C8.2.03

Organizers: Pedro T. Monteiro and Claudine Chaouiya 11:00-12:40

Claudine Chaouiya “Logical modelling of cellular networks, introduction and methodological challenges”

Elisa Tonello “Local negative circuits and cyclic attractors: a Boolean satisfiability approach”

Elisabeth Remy “Boolean dynamics of compound regulatory circuits”

Heike Siebert “Approximating the behavior of Boolean networks”

Denis Thieffry “Logical modelling of the regulatory network governing dorsal-ventral axis specification in the sea urchin *P. lividus*”

MS RECENT TRENDS IN THE MODELING AND CONTROL OF THE GLUCOSE-INSULIN SYSTEM ROOM C8.2.06 11:00-12:40

Organizers: Pasquale Palumbo and Alessandro Borri

György Eigner “Blood glucose regulation possibilities by modern robust control methodologies”

Claude Moog “Clinical assessment of a new biomathematical model for decision making in functional insulin therapy”

Jiaxu Li “An integrated system towards artificial pancreas and its numerical trials”

Jorge Bondia “Physiological modelling of counterregulatory response to hypoglycaemia in type 1 diabetes”

Gunnar Cedersund “Multi-level modelling of diabetes for improved treatments and understanding”

PS CANCER V 11:00-12:20 ♦ ROOM C8.2.10

Morten Andersen “Mathematical modeling of blood cancer evolution”

Andrey V. Kolobov “Investigation of reasons for transient alleviation of tumor hypoxia during antiangiogenic therapy”

Liam V. Brown “Predicting observed patient responses to a short-peptide cancer vaccine via clinical trial simulations”

Maxim B. Kuznetsov “Investigation of metastatic cell dominance phenomenon via modeling of tumor progression”



PS PHYSIOLOGY VI**11:00-12:40 ♦ ROOM C8.2.11****Jakub Köry** “The impact of geometry on effective models of nutrient uptake by root hairs”**Govind Menon** “Engineering compartmentalisation in biochemical pathways - analysis and design”**Yuting Lou** “Multicellular aging as a nonequilibrium phase transition”**Doris Schittenhelm** “Mathematical modelling of cellular response pathways for oxidative stress”**Ana M. Portillo** “Mathematical model to relate telomerase activity and telomere length with the human follicular aging”**PS ECOLOGY V****11:00-12:40 ♦ ROOM C8.2.13****Yves Fotso Fotso** “Modelling and control of coffee berry borer infestation”**Israël Tankam** “An agricultural control of *Radopholus similis* in banana plantations”**Ana P. D. Marques** “Spatial dispersal patterns of citrus disease (HLB) and its vector”**Ruairi Donnelly** “Viruses that modify plants: manipulation of vector density and transmission at several scales”**Samuel Nilusmas** “Sustainable management of root-knot nematodes by modelling and optimizing resistance deployment”**PS CELL AND INTRA-CELL DYNAMICS VI****11:00-12:20 ♦ ROOM C8.2.15****Ulyana S. Zubairova** “Computational modelling of wheat leaf epidermal morphogenesis based on large-scale LSM data”**Lucie Chambon** “Qualitative control for a genetic negative feedback loop”**Lyubov Chumakova** “Cytoskeleton self-organization is robust and depends on cell geometry alone”**Shaon Chakrabarti** “Why cousins are more similar than mother-daughters: implications for circadian-controlled cell fate”**PS EVOLUTIONARY DYNAMICS VII****11:00-12:40 ♦ ROOM C8.2.17****Karan Pattni** “Evolutionary dynamics and the evolution of multiplayer cooperation in a subdivided population”**Martin Pontz** “Evolutionary dynamics in the two-locus two-allele model with weak selection”**Peter Nabutanyi** “The Wright-Fisher model for exponentially growing populations”**Mark Roberts** “Genetic diversity in rapidly growing populations”**Tat Dat Tran** “Information geometry and its application to the Wright-Fisher population with recombination”**PS “NEUROSCIENCE II”****11:00-12:20 ♦ ROOM C8.2.19****Julia M. Kroos** “Patient-specific modeling of cortical spreading depression”**Noemi Picco** “Modelling transient traits of cortex formation: the importance of evolving cell division strategies”

Roberto Barrio “Synchronization patterns, bifurcations and control strategies in central pattern generators”

Beatriz Costa-Gomes “ALFRED: automated image analysis of microtubule networks in nerve cells”

PS

MATHEMATICAL METHODS IN BIOLOGY IX11:00-12:40 ♦ ROOM **C8.2.23**

Patrícia A. Filipe “A nonparametric estimation method for SDE models: an application to cattle growth”

Carlos Toscano-Ochoa “On the feasibility of complex synthetic biological circuits”

Hernan Morales-Navarrete “3D geometrical models of liver tissue uncover unknown features of non-alcoholic fatty liver disease”

Yumino Hayase “A 3D mathematical model of centipede locomotion on rough terrain”

Hiroshi Fujisaki “Weighted ensemble simulations of biomolecules”

PS

EPIDEMIOLOGY X11:00-12:40 ♦ ROOM **C8.2.38**

Hyun Mo Yang “Modelling the role between antibody-dependent enhancement and heterologous secondary infection in severe dengue”

Fabio Sanchez “Comparative analysis of dengue versus chikungunya outbreaks in Costa Rica”

Helio Schechtman “A first glimpse on insecticide resistance development”

Adrian E. Denz “Mathematical modelling of mosquito movement for malaria vector control”

David Greenhalgh “Estimation of the expected number of cases of microcephaly in Brazil as a result of Zika”

MS

ASSUMING COMPARTMENTAL MODELS IN INFECTIOUS DISEASE DYNAMICS. DOES IT HURT?ROOM **C8.2.39**
11:00-12:40

Organizers: Ka Yin Leung

Odo Diekmann “Renewal equations should be ubiquitous in the world of epidemic models”

Gergely Röst “Pairwise approximations of non-Markovian network epidemics”

Tom Britton “Epidemic models with symptomatic and asymptomatic cases: who causes most infections?”

Julia Gog “The importance of within-host dynamics for the population level evolution of influenza in a non-Markovian model”

Lorenzo Pellis “Modelling the individual-level transmission process: do the details matter?”

MS+PS

FRIDAY



	PRESENTER	POSTER
P1	Adamer, Michael	Coloured noise in stochastic Turing systems
P2	Andò, Alessia	Collocation methods for complex delay models of structured populations
P3	Ausmees, Kristiina	Investigating the effects of low coverage and reference set bias on phasing and imputation - applications in the field of ancient DNA
P4	Azevedo, Sofia	The advantage of being flexible: comparison of survival regression models for fruit flies interacting with the bacteria Wolbachia and viruses
P5	Bakshi, Suruchi	Systems pharmacology modelling of the alternative pathway to study target suitability
P6	Berezovskaya, Faina	On “replicators-genetic parasites” models
P7	Brown, Sarah K.	An in silico study of altered airway smooth muscle and extracellular matrix structure in the remodelled asthmatic airway.
P8	Buckingham-Jeffery, Elizabeth	Calculating normal tissue complication probabilities from microscopic models
P9	Buder, Thomas	CellTrans: an R package to quantify stochastic cell state transitions
P10	Carlos, Clara	Effects of Allee effects on extinction times of populations in random environments
P11	Carvalho, Ana R.M.	Analysis of a non-integer order model for the coinfection of HIV and HSV-2
P12	Chae, Min-Kyung	Super-helical filaments at surfaces: dynamics and elastic responses
P13	Coelho, Isabel	A prescribed curvature model for the corneal shape
P14	d'Onofrio, Alberto	Non-spatial first-order phase transitions in the self-activation transcriptional network motif
P15	Duarte, Jorge	Analytical solutions of a cancer model with Shilnikov's chaos
P16	Duchesne, Ronan	Toward a mixed effects model of the in vitro erythroid differentiation
P17	Endo, Akira	Reservoir of avian influenza: a multi-site multi-species model
P18	Gandarias, María Luz	Conservation laws and exact solutions of a time-delayed Burgers-Fisher equation
P19	Gjini, Erida	Inferring bacterial heterogeneity from time-kill in-vitro dynamics under antibiotics
P20	Gong, Chen Chris	Forbidden yet observed clustering in ensembles of repulsively coupled phase oscillators subject to common noise
P21	Graham, Jason M.	Optimization properties in the construction of living bridges by army ants
P22	Guo, Dianjing	Computational model for prediction of human branch point sequence with TNA structure
P23	Hamis, Sara	What does not kill a tumour may make it stronger: an in silico investigation into drug resistance in cancer
P24	Kettle, Helen	Modelling stage-structured populations (R-package stagePop)
P25	Kim, Jae Kyoung	Two types of transcriptional repression leads fundamentally different biological oscillators
P26	Kim, Yunha	Free energy estimation from non-equilibrium pulling experiments of model biopolymers
P27	Lack, Cameron	Modelling the interactions between macrophages and bacteria in Mycobacterium tuberculosis infections
P28	Leocata, Marta	Deciphering the effect of phenotypic and intrinsic heterogeneity in tumor development
P29	Mailleret, Ludovic	An individual based model to optimize natural enemies deployment in augmentative biological control
P30	Marini, Giovanni	Modelling West Nile virus transmission and human infection risk in Veneto (Italy)
P31	Montaseri, Ghazal	Impulsive control-based rule to tailor radiation doses in cancer radiotherapy
P32	Monteiro, Pedro	Reconstruction and analysis of the global transcriptional regulatory network in yeast



	PRESENTER	POSTER
P33	Mórèh, Àgnes	The additivity of multi-species perturbations in food webs
P34	Moreno-Zambrano, Mauricio	Development of a mathematical model of cocoa bean fermentation
P35	Mota, Manuel	Approximate Bayesian computation in branching processes: application to Black Vulture colonies
P36	Mykowiecka, Agnieszka	Metagenomics: inferring gene-species assignments via tree reconciliation
P37	Nekka, Fahima	Dose and timing individualization strategy to adapt ADHD treatment to children daily activities
P38	Odagiri, Kenta	Mathematical model for wound healing caused by exogeneous mechanical forces
P39	olde Scheper, Tjeerd V.	Criticality control of glucose-insulin release
P40	Omari, Mohamed	The impact of nutritional glucose on the bovine Estrous cycle investigated with a mathematical model
P41	Ormerod, Carl	Application of mixed boundary, polar diffusion to controlled release drug delivery models.
P42	Pájaro, Manuel	Effective stochastic approach to gene regulatory networks and the role of intrinsic noise
P43	Park, Jeong-Man	Demographic-noise-induced fixation in subdivided populations with migration
P44	Paupério, Francisco F.S.	How antibiotics and host immune responses interact in the clearance of intracellular infections
P45	Pedersen, Rasmus K.	Modelling of quiescent stem cells in relation to myeloproliferative neoplasms
P46	Pereira, Luis	Modeling heterogeneity in cell death dynamics at the receptor level
P47	Ramos, Alfonso	The bisexual Galton-Watson branching process with population-size-dependent mating
P48	Rodrigues, Luiz Alberto D.	A metapopulation model for the dynamics of the howler monkeys (<i>Alouatta guariba clamitans</i>) affected by sylvatic yellow fever
P49	Rörich, Anna	data reconstruction from electromyographic signals in biomechanics
P50	Sajid, Zamra	Modelling the myeloproliferative neoplasms(mpngs): stability analysis & sensitivity analysis
P51	Schenck, Ryan O.	Clonal architecture of the epidermis: homeostasis limits keratinocyte evolution
P52	Selvaggio, Gianluca	Modelling approach to relate epithelial-to-mesenchymal transition and cancer stem cells
P53	Seymenoglu, Belgin	Invariant manifolds of the selection-recombination model from population genetics
P54	Summers, Kim	Evolutionary strategies of <i>Bdellovibrio bacteriovorus</i> predators and prey
P55	Varela, Pedro L.	Logical modelling to explore communication network features influencing pattern formation
P56	Volkening, Alexandria	A hybrid model of mechanical stress-induced varicosity formation in axons
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P58	Wieteska, Malgorzata J.	Comparison of two techniques describing mRNA and hormone levels in bovine granulosa cells of dominant follicles
P59	Yang, Hyun Mo	The transovarial transmission in the dynamics of dengue infection: epidemiological implications and thresholds
P60	Zhang, Enpei	Evolution of maturation time in a delay Gause model

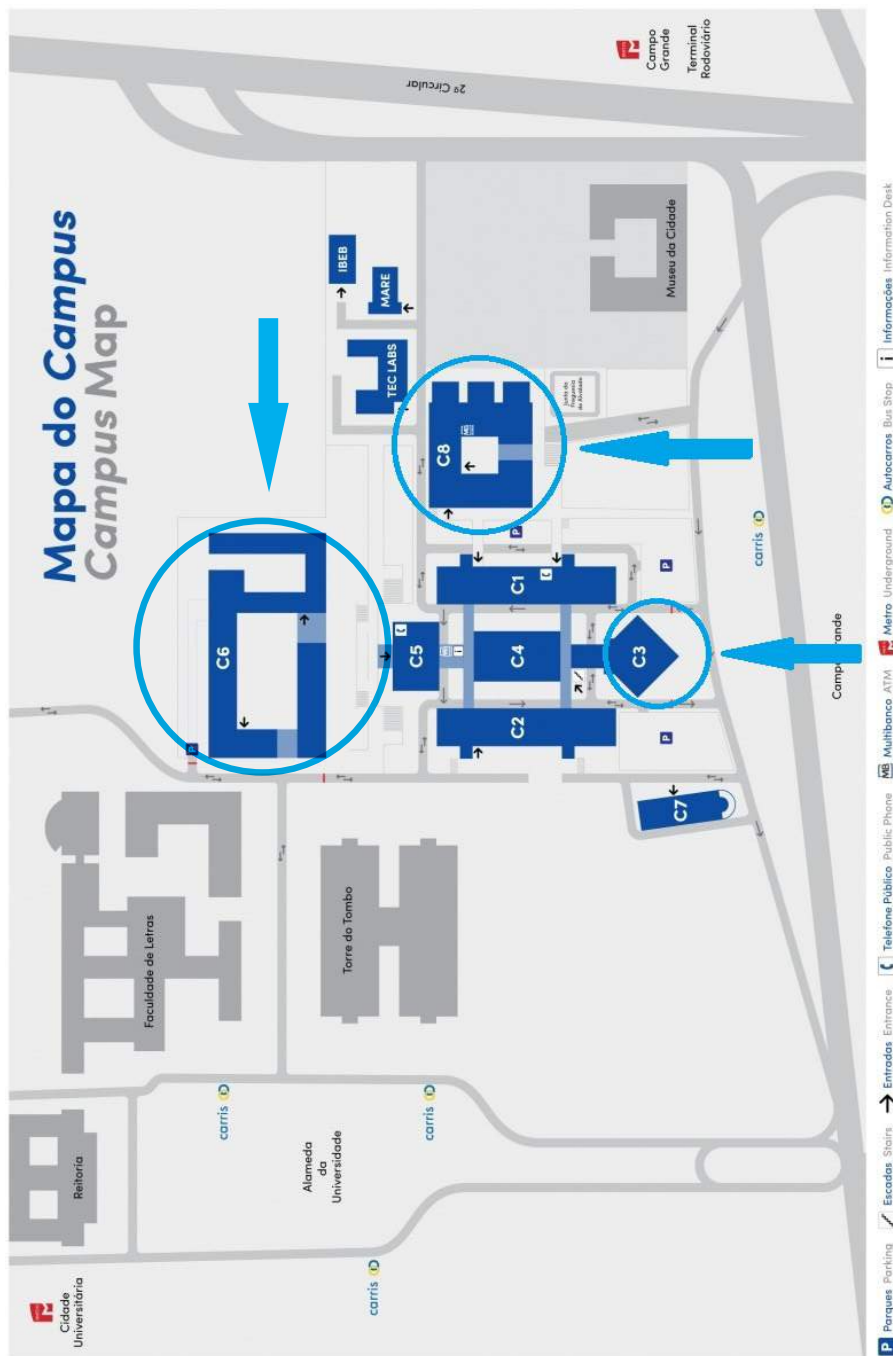


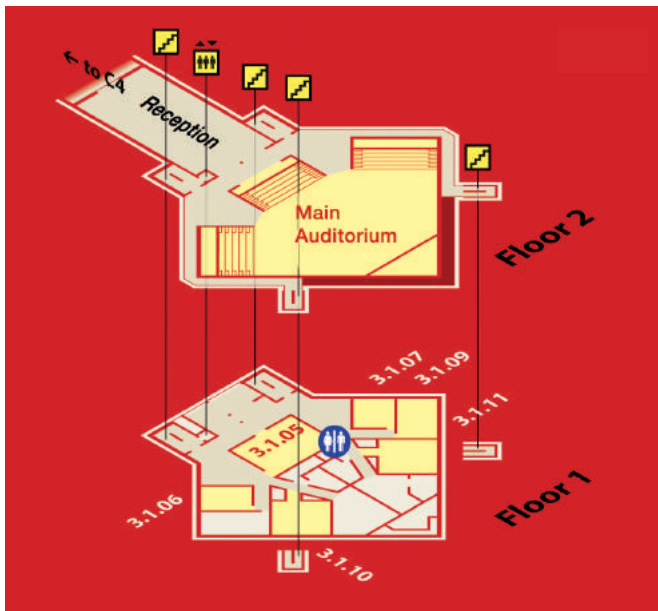
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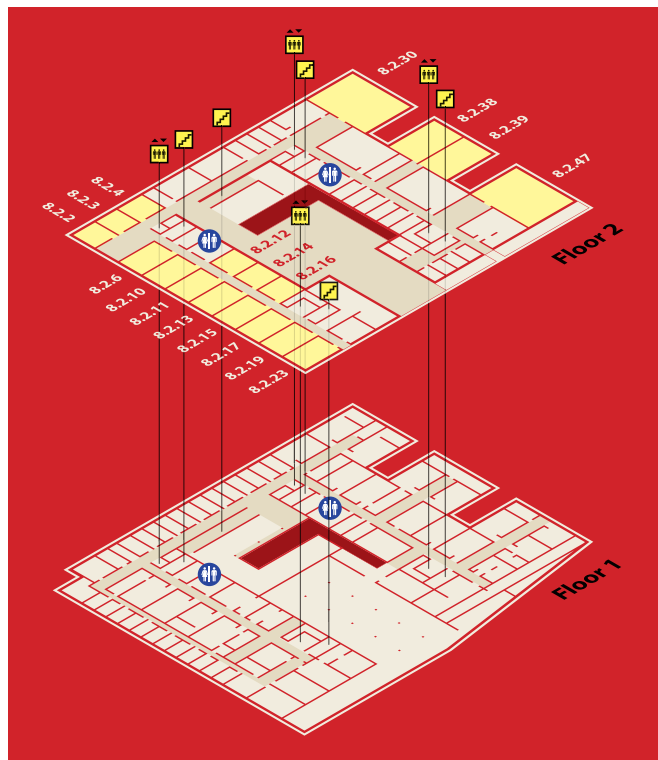
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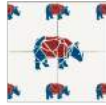




Building C3



Building C8



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