HAUSDORFF SCHOOL FOR ADVANCED STUDIES IN MATHEMATICS

UNIVERSITÄT BONN

Workshop

"Young Women in Mathematical Biology"

April 1-3, 2025

organized by
Eugenia Franco, Anna Logioti

Abstracts

Minicourses

Marie Doumic Jauffret (INRIA and Ecole Polytechnique)

Asymptotic analysis and estimation problems in population dynamics

Abstract: The aim of this course is to present asymptotic direct and inverse problems coming from modelling biological populations. We first give a general overview of the models, their mathematical analysis and their application domains, detailing the correspondence between the population view, described by a Partial Differential Equation (PDE), and the underlying stochastic branching tree, as well as the scaling limits between the models. We then focus on the inverse problems consisting in the estimation of the initial distribution of the population and of the birth and death characteristics, as well as the choice of a "best-fit" model, for two types of applications: polymer breakage and cell division cycle. .

Vivi Rottschäfer (Leiden University)

Lecture 1: Modelling drug dynamics in the brain

Lecture 2: Can you always determine parameters from data in a unique way?

Abstract: Many drugs need to bind to receptors in the brain to have an effect. In this talk, I will present various models that we developed to study drug distribution into the brain and the central nervous system (CNS). In these models we take the physiology of the CNS and the pharmacokinetic properties of the drugs into account. We developed a compartmental model as well as a spatial model for drug distribution into the brain. We compare the results of the models to results of experiments (in rats). The future aim is to use the compartmental model for prediction of drug concentrations in the brain and their resulting effect in case no experimental data is available for a drug. In the second part of the talk, I will consider the question of whether parameters in a mathematical model can be determined *uniquely* from available data. This is often overlooked when models are analysed

and simulated. I will give a brief overview of some of the available methods to determine parameters in a model *uniquely*.

Mariya Ptashnyk (Heriot-Watt University Edinburgh)

From individual cells to tissues: multiscale modelling, analysis and simulation of chemical and mechanical interactions in biological tissues.

Abstract: In this minicourse we will consider multiscale modelling, analysis and simulation of mechanical and chemical interactions between cells. In the microscopic models the biological processes will be defined on the level of a single cell. Using multiscale analysis techniques, we will derive macroscopic tissue level description of intercellular signalling in and growth of biological tissues. Techniques of nonlinear analysis are applied to analyse the microscopic models and rigorously derived the macroscopic effective equations in the limit of many cells. The two-scale (bulk-surface) finite element method is used for the approximation and numerical simulation of the macroscopic models. As specific examples we will discuss intercellular signalling processes involving receptor movement on cell membranes, mechanical interactions and growth in multicellular systems, and stress-based growth of plant tissues.

Talks

Inmaculada Benítez (University of Granda)

Asymptotic behavior of solutions to the Becker-Döring equations

Abstract: Coagulation and fragmentation equations are mathematical models that describe the processes of particle aggregation (coagulation) and division (fragmentation) within a population. These equations play a fundamental role in various scientific fields, including chemistry, physics, and biology, as they provide essential insights into the dynamics of particle systems. Coagulation equations describe how particles combine to form larger clusters, while fragmentation equations govern the disintegration of larger entities into smaller components. The Becker-Döring equations, introduced by Becker and Döring (1935), serve as a key framework for modeling first-order phase transitions in diverse chemical and physical systems, such as vapor condensation and lipid aggregation. While significant research has focused on the nonlinear case, including the study of metastable states by Penrose (1989) and the exponential convergence results in the sub- critical case by Cañizo & Lods (2013), the linear scenario remains an area of interest. In this work, we focus on the linear Becker-Döring equations, given by:

$$\frac{d}{dt}c_i = W_{i-1} - W_i \text{ for all } i \geq 2,$$

where c_1 remains constant for all $t \in \mathbb{R}$, and the fluxes W_i depend on the coagulation and fragmentation coefficients a_i and b_i as follows:

$$W_i = a_i c_1 c_i - b_{i+1} c_{i+1}.$$

Our primary objective is to analyze the asymptotic behavior of solutions approaching equilibrium, refining previous estimates of the convergence rate, particularly improving upon the results established by Kreer (1993). To this end, we employ spectral theory and entropy methods, utilizing the free energy framework also introduced by Kreer (1993).

Luce Breuil (Ecole Polytechnique)

Mathematical modeling and statistical study of a two-phased ageing model in drosophila

Abstract: For around ten years, M. Rera and his team have been studying the biological mechanisms of ageing using a phenotype that predicts the onset of natural death in Drosophila and other model organisms : the Smurf phenotype. In this work, we propose a stochastic mathematical model of the two-phase ageing framework where the life of each individual is defined by the rate at which it turns Smurf and the rate at which it dies once Smurf. We use both non-parametric and parametric estimations of these rates on in-vitro data to determine the dynamics of the model, investigate the potential dependence between time spent non-Smurf and Smurf and assess the relevance of modeling ageing as a two phase process. The non-parametric estimations are performed with kernel estimators. As the most commonly used kernels suffer from boundary bias near 0 when estimating hazard rates, we work with non-classical kernels for which we also present convergence results.

Giada Fiandaca (INRIA)

Overcoming Hypoxic Radiotherapy Resistance: Can Eco-Evo insights improve Dose Painting?

Abstract: In the study of therapeutic strategies for cancer treatment, eco-evolutionary dynamics play a crucial role, as tumor population characteristics, environmental interactions, and treatment effects

shape both the spatial and epigenetic heterogeneity of the tumor. These factors directly impact therapy efficacy and influence the likelihood of relapse. In the context of radiotherapy, oxygen concentration is a key determinant of treatment effectiveness and hypoxia-driven selective pressure, often leading to radiotherapy resistance. To address this challenge, Dose Painting, a radiotherapy approach that delivers spatially heterogeneous radiation doses based on biological tumor features, offers a promising strategy to enhance treatment precision and mitigate resistance.
In this talk, we will present a mathematical model within the framework of epigenetically structured population dynamics, formulated through coupled non-linear integro-differential equations, designed to capture and investigate the eco-evolutionary interactions driving tumor response to radiotherapy. Our simulations illustrate how environmental selection and therapeutic interventions shape tumor evolution, explaining observed phenomena such as relapses and treatment failures. The results further suggest that integrating Dose Painting strategies with eco-evolutionary insights, by spatially adapting radiation delivery to hypoxic-resistant tumor subpopulations, may optimize radiotherapy and potentially improve treatment outcomes.
This modeling framework, supported by experimental data, provides a first step toward the development of adaptive radiotherapy strategies that account for spatial and evolutionary tumor heterogeneity. Future studies incorporating quantified clinical data could refine this approach, leading to a decision-support tool for optimizing personalized radiotherapy protocols and advancing the application of Dose Painting to counteract hypoxia-induced resistance.

Work done in collaboration with: Giulia Chiari, and Marcello Delitala.

Burcu Gürbüz (Johannes Gutenberg-Universität Mainz)

Dynamics and qualitative analysis of photosynthetic reactions

Abstract: In this talk, a mathematical model of the Calvin cycle, a fundamental chemical reaction network in photosynthesis, is explored. By incorporating ATP diffusion, the model is formulated as a system of reaction-diffusion equations. Through rigorous mathematical analysis, we demonstrate the existence of multiple spatially inhomogeneous positive steady states under appropriate parameter settings. Furthermore, it is shown that all positive steady states - homogeneous or inhomogeneous - are nonlinearly unstable, with the exception of a trivial steady state where only ATP has a non-zero concentration. In the spatially homogeneous scenario, linearisation shows that certain steady states have complex eigenvalues, suggesting oscillatory dynamics. Numerical simulations highlight temporal variations in concentrations, showing non-monotonic behaviour over time.

Hui Yu (Xiangtan University)

Traceability of Water Pollution: An Inversion Scheme Via Dynamic Complex Geometrical Optics Solutions

Abstract: We investigate the identification of the time-dependent source term in the diffusion equation using boundary measurements. This facilitates tracing back the origins of environmental pollutants. Employing the concept of dynamic complex geometrical optics (CGO) solutions, a variational formulation of the inverse source problem is analyzed, leading to a proof of uniqueness result. Our proposed two-step reconstruction algorithm first determines the point source locations and subsequently reconstructs the Fourier components of the emission concentration functions. Numerical experiments on simulated data are conducted. The results demonstrate that the proposed two-step reconstruction algorithm can reliably reconstruct multiple point sources and accurately reconstruct the emission concentration functions. Additionally, by partitioning the algorithm into online and offline computations, and concentrating computational demand offline, real-time pollutant traceability becomes feasible. This method, applicable in various fields - especially those related to water pollution, can identify

the source of a contaminant in the environment, thus serving as a valuable tool in environmental protection.

Jolien Kamphulis (Leiden University)

Effect of spatially periodic coefficients in pattern forming systems

Abstract: We are interested in the formation of patterns that arise as solutions to nonlinear partial differential equations with spatially varying coefficients. We focus on one-dimensional small amplitude patterns that bifurcate from a background state in the presence of a spatially varying heterogeneity. These nonlinear PDEs with spatially varying coefficients emerge from biological application-based models, such as ecology models, where the spatially varying coefficients represent a spatially varying terrain. In this case, the corresponding solutions can be interpreted as vegetation patches adjusting to the periodic domain, hence forming patterns on patterns. During this talk, we'll showcase along various examples of PDEs with spatially periodic coefficients, such as Klausmeier and Swift-Hohenberg, what the effect of spatially periodic patterns are on the resulting patterns and the derived modulation equation.

This is joint work with Martina Chirilus-Bruckner.

Laura Kanzler (Sorbonne Université)

First order non-instantaneous corrections in collisional kinetic models

Abstract: In this talk we introduce a new class of kinetic models, which overcome the standard assumption in kinetic transport theory that collision processes happen instantaneously. In particular, this modelling approach is interesting for applications in life-science, where the interaction-time between biological agents cannot meaningfully be neglected. On the level of the underlining stochastic processes this results in replacing the jump-process, which are defining the collisions, with continuous stochastic processes. As an example, we will investigate a kinetic model with non-instantaneous alignment collisions between particles. The collisions are described by a transport process in the joint state space of the colliding particles, where the states of the particles approach their midpoint. Moreover, we will elaborate on the question, which model can be used as an accurate first order non-instantaneous correction in the regime where the collision time is very small, implying that the collisions are almost instantaneous. Last, the instantaneous limit will be considered, where the latter leads to standard collisional kinetic models of Boltzmann type.

This is joint work with Carmela Moschella, Christian Schmeiser and Veronica Tora.

Daphne Nesenberend (Leiden University)

Mathematical models for in-vitro mechanically induced pattern formation, two case studies

Abstract: It is well known that chemical as well as mechanical cues play an important role in morphogenesis. A lot of experimental research is dedicated to understanding how mechanics, such as curvature, stresses, and strains, influence cell shape and behavior. In this talk I would like to discuss two different mathematical models that I have been working on in collaboration with experimentalists. These models help to understand the collective behavior observed in vitro and are being used to formulate new experimental designs. In the first study, we are interested in understanding the collective behavior of cardiomyocytes, radially aligning in a synthetic hydrogel. Using the strain-stiffening

properties that were measured in the hydrogel, we could tune a combined Cellular Potts - Finite Element Model. From the results of the model, we postulated the necessity of a high (enough) cell concentration to observe the collective cell behavior, which could be verified in follow up experiments. In the second study, we have been investigating Septin; a membrane binding, curvature-inducing molecule. Incubated under particular conditions, Septin can induce the formation of golf ball patterns on lipid vesicles. To understand these observations, we discussed possible energy functionals that describe the properties of Septin. Comparing to in vitro experiments of Septin reorientation on a fixed but curved membrane, the model showed promising results and provided us with insights for new experimental design, which are currently being executed.

Federica Padovano (Sorbonne Université)

The development of drug resistance in metastatic tumours under chemotherapy: An evolutionary perspective

Abstract: We present a mathematical model of the evolutionary dynamics of a metastatic tumour under chemotherapy, comprising non-local phenotype-structured PDEs for the primary tumour and its metastasis, where drug delivery is described using a physiologically-based PK model implementing a realistic delivery schedule. By means of long-time asymptotic and global sensitivity analysis, as well as numerical simulations, we explore the impact of cell migration from the primary to the metastatic site, physiological aspects of the tumour and drug dose on the development of drug resistance and treatment efficacy. Our findings provide a possible explanation for empirical evidence indicating that chemotherapy may foster metastatic spread and that metastases may be less impacted by the chemotherapeutic agent.

Elisa Paparelli (University of Pavia)

Mathematical modelling and optimal control of epidemiological systems across scales

Abstract: Compartmental epidemic models have experienced significant advancements since the early 1900s, allowing scientists to better understand the spread of infectious diseases and develop control strategies. However, in their classic formulation, they exhibit a critical limitation: the assumption of uniformity within population compartments. We will explore how to address this limitation by introducing the concept of heterogeneity. Specifically, I will first present a structured compartmental model that we have developed and analyzed in this direction, aimed at modeling an SI-type epidemic phenomenon. In this model, susceptible individuals are characterized by a continuous variable representing their level of resistance to infection, while infectious individuals are characterized by their viral load. I will first formulate the agent-based model to formally derive the "mesoscopic" dynamics, and finally, through an appropriate rescaling, the corresponding model that describes the evolution of certain macroscopic quantities. Additionally, by introducing control over a function involved in the system, we will examine how to plan a control policy to minimize the size of the infection, capturing the heterogeneity of the system.

Quiyao Peng (Lancaster University)

Bridging models at different scales for cellular forces and diffusive compounds in the living tissue

Abstract: In biomedical applications, there are many interactions between cells and their direct environment, for instance, mechanical interaction via cellular stress and chemical interaction via diffusive compounds such as signalling molecules. For example, in wound healing, fibroblasts (skin cells)

apply pulling forces on the extracellular matrix (ECM) to contract the wound, and these skin cells are attracted from the uninjured skin to wound by the signalling molecules secreted by the immune cells. Generally speaking, agent-based modelling and continuum-based modelling are the main categories used to describe the interactions between cells and their direct environment. While continuum-based modelling is more computationally efficient, agent-based modelling provides a more precise physical description of the biological phenomena but with higher computational cost. Hence, it is important to search for a "bridge" to upscale the agent-based models to the continuum-based models, with controlling the information loss.
In this talk, we will present how to upscale the linear momentum balance model (describing the cellular forces) and the diffusion model (describing the diffusion of the compounds), with the using of Dirac delta distributions as a representation of point forces and point sources, respectively. Both analytical and numerical results will be shown.

Diane Peurichard (INRIA Paris)

Large-scale Dynamics of Self-propelled Particles moving through Obstacles: How Environment Affects Particle Swarms

Abstract: We investigate the collective motion of self-propelled agents in an environment filled with obstacles that are tethered to fixed positions via springs. The active particles are able to modify the environment by moving the obstacles through repulsion forces. This creates feedback interactions between the particles and the obstacles from which a breadth of patterns emerges (trails, band, clusters, honey-comb structures,...). We derive a macroscopic partial differential equations model from the agent-based dynamics describing the interactions between the self-propelled particles and the obstacles, under large tether stiffness. We perform an in-depth investigation of pattern formation of the discrete and continuum models in 2D: we provide phase-diagrams and determine the key mechanisms for bifurcations to happen using linear stability analysis. As a result, we discover that the agent-agent repulsion, the agent-obstacle repulsion and the obstacle's spring stiffness are the key forces in the appearance of patterns, while alignment forces between the particles play a secondary role. We present an innovative methodology to compare discrete and continuum models that we apply here to perform an in-depth analysis of the agreement between the discrete and continuum models. Altogether, this study enables to shed light on the influence of the environment in the collective motion of self-propelled particles.

Lorena Pohl (University of Bonn)

Becker-Döring type models with a broken chain of coagulation

Abstract: The Becker-Döring equations are discrete coagulation-fragmentation equations characterized by the fact that cluster growth and fragmentation occurs only through the gain or loss of a single particle. In this talk we consider the special case of a broken chain of coagulation, meaning that no new large clusters are formed, but existing clusters continue to grow and shrink. We discuss applications in chemical and biological modelling and show the long-time behaviour of the system in the case of identical coagulation and fragmentation rates.

Milene Santos (University of Coimbra)

Numerical challenges in modelling light propagation in the cornea

Abstract: Understanding the physical basis of corneal transparency has been a subject of growing interest as corneal diseases are a major cause of visual impairment worldwide [1]. The structure of the corneal stroma, characterised by the precise organisation of collagen fibrils, plays a fundamental role in the light transmis- sion. The arrangement of these fibrils and its impact on the light scattering has been studied by the numerical simulation of the corresponding optical coherence tomography (OCT) imaging [2]. However, modelling light propagation in the cornea presents significant mathematical challenges due to its curved boundary domain and curved interfaces between fibrils. In this talk, we discuss a high-order numerical approach based on the Discontinuous Galerkin (DG) method, which is designed to effectively handle curved boundary domains without relying on traditional curved meshes [3]. Some numerical results are presented to illustrate the efficacy of this method.

References:
[1] Doutch, J., Quantock, A. J., Smith, V. A., Meek, K. M. (2008). Light transmission in the human cornea as a function of position across the ocular surface: Theoretical and experimental aspects. Biophysical Journal 95(11):5092–5099. https://doi. org/10.1529/biophysj.108.132316
[2] Araújo, A., Barbeiro, S., Bernardes R., Morgado, M., Sakić, S. (2022). A mathematical model for the corneal transparency problem. Journal of Mathematics in Industry 12, 10. https://doi.org/10.1186/s13362-022-00125-y
[3] Santos, M., Araújo, A., Barbeiro, S., Clain, S., Costa, R., Machado, G.J. (2024). Very High-Order Accurate Discontinuous Galerkin Method for Curved Boundaries with Polygonal Meshes. Journal of Scientific Computing 100, 66. https://doi. org/10.1007/s10915-024-02613-2

Cinzia Soresina (University of Trento)

Derivation of cross-diffusion models in population dynamics: dichotomy, time-scales, and fast-reaction

Abstract: In population dynamics, cross-diffusion describes the influence of one species on the diffusion of another. A benchmark problem is the cross-diffusion SKT model, proposed in the context of competing species to account for stable inhomogeneous steady states exhibiting spatial segregation. Even though the reaction part does not present the activator-inhibitor structure, the cross-diffusion terms are the key ingredient for the appearance of spatial patterns [1]. From the modelling perspective, cross-diffusion terms naturally appear in the fast-reaction limit of a "microscopic" model (in terms of time scales), presenting only standard diffusion and fast-reaction terms, thus incorporating processes occurring on different time scales [3]. This talk presents a recent application of this approach to plant dynamics with autotoxicity effects [2].

References:
[1] Breden, M., Kuehn, C., Soresina, C. (2021). On the influence of cross-diffusion in pattern formation. Journal of Computational Dynamics 8(2):213-240.
[2] Giannino, F., Iuorio, A., Soresina, C. (in preparation). Vegetation patterns driven by autotoxicity: a cross-diffusion model.
[3] Kuehn, C., Soresina, C. (2020). Numerical continuation for a fast-reaction system and its cross-diffusion limit. Partial Differential Equations and Applications 1:7.

Sofie Verhees (Heriot-Watt University)

Coupling cell signalling and mechanics: a mathematical model of RhoA-driven mechanotransduction

Abstract: Communication and interactions between cells happen mostly through intercellular signalling processes. These signalling pathways are important in all physiological activities of the cell, such as cell movement, immune response, and tissue development. In many of these signalling pathways, the chemical processes and mechanics of the cell work together. How exactly these two phenomena communicate is not well known. To better understand this process, we introduce a model of the RhoA signalling pathway with a two-way coupling between the signalling processes and cell mechanics. A common way to model the chemical processes of cell signalling pathways are reaction-diffusion equations, which include the diffusion of signalling molecules and membrane receptors, and the reactions between the molecules and receptors. This is coupled to the mechanical properties, governed by the equations of linear elasticity, such that the mechanics of the extracellular matrix influences the interaction between the signalling molecules and the results of the signalling pathways affect the deformation of the cell. Simulations results are produced using a numerical method based on bulk-surface finite elements and exhibit novel findings such as the effect of cell shape on the dynamics, a threshold-like response to changes in substrate stiffness, and the emergence of mechanical homeostasis, where the cell deformation is robust under larger changes in substrate stiffness as in agreement with experiments.

Chiara Villa (INRIA)

Calibration and analysis of phenotype-structured PDEs of cancer adaptive dynamics

Abstract: Heterogeneity and plasticity in individual cell behaviour are key drivers of cancer progression. The phenotype of cell, i.e. the ensemble of its observable characteristics determining its behaviour, can be quantified by the level of expression of certain proteins in the cell, which are typically measured on a continuum. For this reason, PDEs describing the evolutionary and spatiotemporal dynamics of phenotype-structured cancer cell populations have become increasingly popular in the mathematical community. In this talk, I will give an overview of methods and open challenges for the calibration of these models with experimental data and their analysis, from exact solutions to formal asymptotic behaviour in well-mixed and spatially-explicit models.

Havva Yoldas (TU Deft)

Macroscopic effects of an anisotropic Gaussian-type repulsive potential on a dense system of elongated particles

Abstract: Elongated particles in dense systems often exhibit alignment due to volume exclusion interactions, leading to packing configurations. Traditional models of collective dynamics typically impose this alignment phenomenologically, neglecting the influence of volume exclusion on particle positions. I will talk about a recent work where we derive nematic alignment from an anisotropic repulsive potential, focusing on a Gaussian-type potential and first-order dynamics for the particles. We perform a hydrodynamic limit to uncover the effects of anisotropy on both particle density and direction.

This is a joint work with Sara Merino, Claudia Wytrzens both from University of Vienna and Steffen Plunder from University of Kyoto.

Posters

Viktoria Freingruber (TU Deft)

Trait-structured chemotaxis: Exploring ligand-receptor dynamics and travelling wave properties in a Keller-Segel model

Abstract: A novel trait-structured Keller-Segel model that explores the dynamics of a migrating cell population guided by chemotaxis in response to an external ligand concentration is derived and analysed. Unlike traditional Keller-Segel models, this framework introduces an explicit representation of ligand-receptor bindings on the cell membrane, where the percentage of occupied receptors constitutes the trait that influences cellular phenotype. The model posits that the cell's phenotypic state directly modulates its capacity for chemotaxis and proliferation, governed by a trade-off due to a finite energy budget: cells highly proficient in chemotaxis exhibit lower proliferation rates, while more proliferative cells show diminished chemotactic abilities. The model is derived from the principles of a biased random walk, resulting in a system of two non-local partial differential equations, describing the densities of both cells and ligands. Using a Hopf-Cole transformation, we derive an equation that characterises the distribution of cellular traits within travelling wave solutions for the total cell density, allowing us to uncover the monotonicity properties of these waves. Numerical investigations are conducted to examine the model's behaviour across various biological scenarios, providing insights into the complex interplay between chemotaxis, proliferation, and phenotypic diversity in migrating cell populations.

Carmela Moschella (University of Vienna)

Existence of steady states in a Transport-Coagulation equation

Abstract: This work is motivated by a biological phenomena known as autophagy, where cells recycle damaged cellular components, resulting in the spontaneous formation of aggregates. The model we consider involves an evolution equation for the distribution of aggregates of various sizes, denoted as $f(t, x)$ where x is the aggregate's size. This leads to a transport-coagulation equation in which we seek to examine necessary and sufficient conditions for the existence of non-trivial steady states.

Michela Sabbatino (University of Trento)

A theoretical analysis of mass testing strategies to control epidemics

Abstract: In response to the COVID-19 pandemic, many countries implemented Non- Pharmaceutical Interventions (NPIs), such as test-and-isolate strategies, often coupled with contact tracing. Several studies have evaluated the effectiveness of these approaches, showing in some cases (e.g., South Korea [2] or New Zealand [1]) the potential to contain a SARS-CoV-2 epidemic, while in others (e.g., Canada [1] or France [5]), the effectiveness appeared limited. To better understand the potential and limitations of a Test-Trace-Isolate (TTI) strategy, we aim to implement a theoretical analysis of its impact in simple epidemic models. In this work [6], we present four epidemic models based on SIR and SEIR frameworks in which it is assumed that, at fixed intervals, the entire population (or a portion of population) is tested, and if positive, isolated. The first model (SIR-1) is a homogeneous SIR model in which the entire population is tested at fixed time intervals. The second model (SIR-2) is also an SIR model, but here (following the scheme proposed in [4]) the population is divided into two groups that are tested alternately in each testing session. Finally, the third (SEIR-1) and fourth (SEIR-2) models follow the same structure as the first and second, respectively, but are based on SEIR dynamics; it is also assumed that exposed individuals cannot be detected through testing. For each of

these models, we compute the effectiveness of the testing procedure necessary to control an epidemic. We also compute the reproduction number under the control strategy, R_0^c, providing an appropriate definition according to the general principle proposed in [3]. This R_0^c can be calculated analytically or numerically, depending on the model's structure and parameters.

References:
[1] Baker, M. G., Kvalsvig, A., Verrall, A. J., & Wellington, N. (2020). New Zealand's COVID-19 elimination strategy. Med J Aust 213(5): 198–200. https://doi. org/10.5694/mja2.50735
[2] Chen, Y. H., Fang, C. T., & Huang, Y. L. (2021). Effect of non-lockdown social distancing and testing-contact tracing during a COVID-19 outbreak in Daegu, South Korea, February to April 2020: a modeling study. International Journal of Infectious Diseases 110: 213–221.
https://www.sciencedirect.com/science/ article/pii/S1201971221006147
[3] Diekann, O. (1990). On the definition and the computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous populations. J Math Biol 28(4): 365–382.
[4] Liu, K., Bai, Z., He, D., & Lou, Y. (2023). Getting Jab or Regular Test: Observations from an Impulsive Epidemic COVID-19 Model. Bulletin of Mathematical Biology 85(10): 1–27.
https://doi.org/10.1007/s11538-023-01202-y
[5] Pullano, G., Di Domenico, L., Sabbatini, C. E., Valdano, E., Turbelin, C., Debin, M., ... & Colizza, V. (2021). Underdetection of cases of COVID-19 in France threatens epidemic control. Nature 590(7844): 134–139.
https://doi.org/10.1038/ s41586-020-03095-6
[6] Sabbatino, M., De Reggi, S. & Pugliese, A. A Theoretical Analysis of Mass Testing Strategies to Control Epidemics. Bull Math Biol 87, 22 (2025).
https://doi.org/10.1007/s11538-024-01387-w

Keren Tapper (Heriot Watt University)

A Multiscale Model for a Split Area Fishery with Periodic Fishing Efficiency

Abstract: The traditional fisheries of the Haenyeo Divers in the Jeju region of Korea are seeing a reduction in fishing output due to competition between fishing and tourism. We consider an ODE model for the total benefit to the Haenyeo community which assumes that the fishery is spread into two separate areas for these two competing activities. Under the additional assumption that migration between the two areas is fast, the model equations are singularly perturbed and can be analysed via an application of the dynamical systems-based geometric singular perturbation theory. This approach allows us to reduce the long-term dynamics of the model solutions to the dynamics on a globally attracting slow manifold. Finally, we extend the model by introducing seasonality of the fishing efficiency, modelled via a piecewise periodic function. By applying the desingularisation technique, known as "blow-up", we regularise and analyse the transition between the two parts of the seasonality dynamics.

Emma Verweij (Leiden University)

Pattern formation in ecosystems

Abstract: Self-organized vegetation patterns, such as stripes, spots or rings ('fairy circles'), are frequently observed in ecosystems prone to tipping. We consider two-component reaction-diffusion models to study pattern formation, driven by scale-dependent feedbacks that naturally arise in ecosystems, as ecological processes often occur on different (spatial) scales. Such a separation of scales allows for a decomposition in long- and short-range dynamics ('slow' and 'fast'), that can be studied using geometric singular perturbation theory (GSPT).

We study singular patterns in an explicit model for the autotoxic interaction between seagrass and hydrogen sulfide in the soil, however similar vegetation patterns have been studied in dryland ecosystem models. We show the existence of stationary front- and pulse-like solutions in one spatial dimension. Fast jumps between slow invariant manifolds allow for sharp transitions between bare soil and vegetation, matching observations of patterns in seagrass meadows. Using the same geometric approach, a plethora of additional singular patterns can be constructed (e.g., traveling and periodic patterns). Furthermore, the slow-fast approach also forms the foundation of the stability analysis of these singular patterns.
