

Monday

9:00–10:00: PLENARY

Arthur Sherman, “Type 2 diabetes: New equations, new thinking”

10:30–12:30: MINISYMPOSIA

Z-110: Recent advances on modelling and dynamics of vector-borne diseases

Vector-borne diseases are a big threat to public health since some of them can kill an unprotected individual very quickly like malaria. The study of vector-borne diseases has become one of the most promising interdisciplinary areas in mathematical biology. This mini symposium will focus on recent advances on a variety of modeling and computational developments for studying vector-borne diseases. Topics cover malaria, West Nile virus, Lyme disease and etc. We highlight the importance of potential collaboration between mathematicians, entomologists, epidemiologist, and modelers in the prediction, prevention, and control of vector-borne diseases.

- 10:30–11:00: Jacques Bélair, “Waning immunity, distributed delays, multiple serotypes and reinfection”
- 11:00–11:30: Jie Gao, “Detecting Early Warning Signal of Complex Diseases Based on Dynamical Network Biomarkers”
- 11:30–12:00: Xi Huo, “Using Trap Data to Study *Aedes aegypti* Population in South Florida”
- 12:00–12:30: Ling Xue, “Modeling Mitigating Strategies for Dengue Virus Transmission”

Z-200: Immunobiology and Infection Subgroup

The Immunobiology and Infection Subgroup was created to bring together researchers in the SMB community who are interested in the modeling and analysis of immune processes in human disease and of host-pathogen interactions. Our broad objective is to discuss various topics including - within-host infectious diseases - host immune responses - causes and effects of inflammation - disease progression and outcome - integration of experimental and clinical data into models - model-driven experimental design In our 2019 minisymposium, we will focus on infection and host immune responses to both infectious and non-infectious insults. We will have 7 speakers with expertise in these areas. The talks will also showcase diverse modeling styles and

integration with data.

- 10:30–11:00: Elissa J. Schwartz, “Dynamics of lentiviral infection in vivo in the absence of adaptive immune responses”
- 11:00–11:30: Esteban Hernandez-Vargas, “Immune therapy for treating secondary bacterial infections during severe influenza infections”
- 11:30–12:00: Rosemary Aogo, “Dissecting drug action and host responses during malaria infection”
- 12:00–12:30: Carmen Lia Murall, “Modelling the evolution of viral oncogenesis”

Z-205: Using ecological theory to understand cancer

The complexity of cancer has inspired the use of ecological thinking to understand the network of cell-cell and cell-environment interactions that make up the cancer ecosystem. Ecologists have long embraced the challenge of making sense of complex systems despite incomplete information about underlying mechanisms, and shown that carefully crafted theories provide precisely the tools needed to integrate the multiple streams of partial information into a useful whole. Speakers in the minisymposium will examine cancer from multiple theoretical perspectives, ranging from community ecology, behavioral ecology, restoration ecology, and evolutionary ecology.

- 10:30–11:00: Jason Griffiths, “Cancer-immune ecology, treatment resistance and the role of within patient cellular variability”
- 11:00–11:30: Irina Kareva, “Modeling of replicator - genetic parasites dynamics and coexistence”
- 11:30–12:00: Robert Beckman, “Genetic Instability, Neutral Evolution, and Dynamic Precision Medicine of Cancer”
- 12:00–12:30: John Pepper, “Does the Ecology of Somatic Tissue Normally Constrain the Evolution of Cancer?”

Z-209: Recent perspectives on mathematical epidemiology

This minisymposium will bring together researchers to examine up-to-the-minute disease problems that showcase the usefulness and applicability of mathematical modelling to a world far beyond the mathematical community. The audience is the mathematical biologist with an interest in infectious disease. This includes students and researchers, mathematicians interested in seeing applications and biologists who wish to see how mathematics can be used to solve real problems. The minisymposium is interdisciplinary in nature and includes those trained as mathematicians, epidemiologists and immunologists.

- 10:30–11:00: Robert Smith?, “Modelling the Effects of Stigma on Leprosy”
- 11:00–11:30: Aili Wang, “Dynamics of a non-smooth epidemic model with three thresholds”
- 11:30–12:00: Cameron Browne, “Multi-strain immuno-epidemiological model of dengue structured by dynamic host antibody level”
- 12:00–12:30: Katie Vogt Geisses, “Immigration and Tuberculosis in Chile: A deterministic mathematical model”

Z-210: Mathematical modeling of normal and abnormal tissue growth and development

The minisymposium is intended to describe the contributions of mathematical modeling and computation to topics at the interface between developmental biology and oncology. Topics of 1) brain tumor development, 2) growth regulation in intestinal crypts, 3) pancreatic cancer invasion in extracellular matrix and 4) cell intercalations during *Drosophila* germband extension will be presented to gain a broader understanding of the similarity and difference between normal growth and abnormal growth.

- 10:30–11:00: Vivek Shenoy, “Regulation of nuclear architecture, mechanics and nucleo-cytoplasmic shuttling of epigenetic factors by cell geometric constraints”
- 11:00–11:30: Clinton Durney, “Dynamics of PAR Proteins Explain the Oscillation and Ratcheting Mechanisms in Dorsal Closure”
- 11:30–12:00: Axel Almet, “Biomechanics of Intestinal Crypt Morphogenesis”
- 12:00–12:30: Meghan Hall, “A DTI-based continuum mechanics computational model of glioma”

Z-215: Spatial and evolutionary dynamics in mathematical ecology

This workshop will focus on the spatial and evolutionary dynamics of organisms submitted to a changing environment. An interdisciplinary approach to the modeling and analysis of the problem will shed new light to this area. It is the goal of this mini-symposium to bring together biologists and mathematicians working on those problems, and to foster the development of new ideas and tools to understand the ecology of organisms in a changing world.

- 10:30–11:00: Xiaoying Wang, “Turing patterns in a predator-prey model with seasonality”
- 11:00–11:30: Yuan Lou, “Ideal free distribution in two patches”
- 11:30–12:00: Zhisheng Shuai, “Impact of Asymmetric Movement on Population

Dynamics”

- 12:00–12:30: Guo Hongjun, “On the Mean Speed of Bistable Transition Fronts in Unbounded Domains”

Z-220: Global Dynamics : Coexistence and Extinction in Mathematical Models from Ecology and Epidemiology

This minisymposium is intended to bring into discussion two fundamental outcomes of mathematical models from ecology and epidemiology : coexistence and extinction. A variety of aspects of analysis, including modeling techniques, numerical methods and the use of mathematical tools (such as stability analysis, bifurcation theory, persistence theory) are expected to be represented.

- 10:30–11:00: Linda Allen, “Stochastic Epidemic Model for Zoonotic Spillover”
- 11:00–11:30: Ruiwen Wu, “A reaction-diffusion model of vector-borne disease with periodic delays Ruiwen Wu”
- 11:30–12:00: Shugui Ruan, “On a Nonlinear Age-structured Model for Tumor Cell Populations with Quiescence”
- 12:00–12:30: Xiunan Wang, “A PREDATOR-PREY MODEL WITH SEASONALITY AND MATURATION DELAY: AN APPLICATION TO PHAGE-BACTERIA DYNAMICS”

Z-245: Applications of mathematical techniques to neuroscience: from molecules to networks

The brain is a highly complex system. To understand its behavior under (ab)normal conditions, researchers explore brain activity at many different levels: genetic, molecular, cellular, circuit, and network. Traditional biological approaches are not well adapted to complex, nonlinear interactions or large data sets, both of which are inherent to many areas of brain research. In this minisymposium, we intend to bring together scientists who take interdisciplinary approaches to answer questions related to brain dynamics. Topics covered in the minisymposium include all those that apply mathematical techniques to solve problems at various spatial and temporal scales of the brain in health and disease.

- 10:30–11:00: Niklas Brake, “Voltage-sensor domains modulate Nav1.5 inactivation via domain IV coupling”
- 11:00–11:30: Saeed Farjami, “Dynamics of Cerebellar Stellate Cells in Response to A Pair of Inputs”
- 11:30–12:00: Jonathan Rubin, “Effects of I_{NaP} block in respiratory circuits depend on the pharmacological mechanism”

- 12:00–12:30: Sue Ann Campbell, “Slowly varying modulation of neural networks”

Z-255: Wave propagation in biological media

Since the pioneer work of Fisher and KPP, Wave Propagation in Biological Media has been widely studied in various mathematical models establishing the movement or invasion of species in heterogenous media or the spread of infectious disease among species. Recently, there have been tremendous advancements in the theory of traveling wavefronts itself, with considerable applications to competition or predation models in the biological field. The purpose of this session is to invite mathematical researchers with biological backgrounds to work together and contribute to the study of biological waves. It will serve as a platform to report new breakthroughs, exchange research ideas and extend academic networks. New collaborations are also expected during and after the meeting. Speakers and talks are carefully selected to make the session attractive to a diverse audience. Especially, PhD students or post-doctoral fellows are encouraged to attend this session for getting research insight in their recent study.

- 10:30–11:00: Zhe Huang, “Speed Selection for Traveling Waves of a Reaction-diffusion-advection Equation in a Cylinder”
- 11:00–11:30: Wan-Tong Li, “Spatial Propagation of Nonlocal Dispersal Equations”
- 11:30–12:00: Zhongwei Shen, “Spreading speeds in random environments”
- 12:00–12:30: Tianyuan Xu, “Traveling Waves on Time-delayed Reaction Diffusion with Degenerate Diffusion”

Z-260: Mathematical modeling of cellular transitions en route metastasis: epithelial-mesenchymal plasticity and associated cellular traits

Metastasis the cause of almost all cancer-related deaths is a highly dynamic process where cells need to adapt to changing biochemical and biomechanical surroundings. No unique mutational signature has yet been associated with metastasis, emphasizing the importance of phenotypic plasticity the ability of genetically identical cells to alter their phenotypes in response to many signals in driving metastasis. Recent studies have identified the role of epithelial-mesenchymal plasticity in driving multiple facets of metastasis : collective cell migration, tumor-initiation, resistance against therapies including immunotherapy etc. A mapping of signaling networks driving this plasticity has motivated many mathematical models to elucidate the dynamics of such plasticity, to suggest experiments to quantify such plasticity, and to design treatment strategies to restrict this plasticity. This minisymposium focuses on inviting leaders in modeling cellular transitions during metastasis, and is proposed to last for two periods. The first

period will involve speakers who have offered valuable insights into the intracellular and tissue-level dynamics of epithelial-mesenchymal plasticity, while the second period will gather experts who have investigated the emergence of EMT-associated cellular traits such as therapy/drug resistance and tumor-initiation potential, through mathematical modeling approaches.

- 10:30–11:00: Loukia G. Karacosta, “A Single-Cell Resolution Map of EMT and Drug Resistance States in NSCLC”
- 11:00–11:30: Shubham Tripathi, “A Mechanism for Epithelial-Mesenchymal Heterogeneity in Cancer Cell Populations”
- 11:30–12:00: Melissa Davis, “miRNA combinatorial regulation of networks driving EMT”
- 12:00–12:30: Mingyang Lu, “Modeling the heterogeneity of EMT network dynamics with single cell RNA-seq data”

Z-305: Mentoring Room

12:30–13:30: LUNCH

Pavillon Jean-Coutu (???? probably???)

Panel Discussion (Z-110): Rules of life in the context of future math biology

13:30–14:30: PLENARY

Kim Cuddington, “Transients, autocorrelated variation, and invasive species impact”

14:30–15:30: CONTRIBUTED TALKS

Z-200

- Andreas Buttenschoen, “Spatio-temporal heterogeneities in a mechano-chemical model of collective cell migration”
- Jennifer Owen, “Understanding zebrafish pigment pattern formation using mathematical modelling”
- Cole Zmurchok, “Modeling cell shape diversity arising from complex Rho GTPase dynamics”

Z-205

- Matthew Faria, “Determination of a kinetic model of nanoparticle-cell interaction”
- Pauline Ruegg-Ereymond, “Pre-menstrual inflammatory processes in the uterine endometrium”
- Leonie Van Steijin, “Modeling zebrafish metabolism”

Z-209

- Hana Dobrovolny, “An agent-based model of viral transmission”
- Caitlin Hult, “Understanding the role of neutrophils in *M. tuberculosis* infection: Modeling approaches and visualization techniques”
- MD Rafiul Islam, “Identifying the dominant transmission pathway in a multi-stage infection model of the emerging fungal pathogen *Batrachochytrium salamandrivorans* on the Eastern Newt”

Z-210

- Amy Hurford, “Eliminating stage-structured pests with temperaturedependent life histories”
- Eunok Jung, “Dynamical Models of the 2009 A/H1N1 Influenza and Effective Intervention Strategies in the Republic of Korea”
- Ryosuke Omori, “Difference in seasonal variations between transmission rate and re-activation rate explains the epidemic curves of Varicella and Zoster”

Z-215

- Annabelle Ballesta, “P-glycoprotein (*Abcb1*) expression and activity are sex-, feeding-, and circadian time-dependent, implications for mechanistic pharmacokinetics modeling”
- Brendan Fry, “Modeling bloodflow and oxygenation in a retinal microvascular network”
- Valerie Voorluijs, “Impact of mitochondrial exchanges on calcium wave propagation in astrocytes”

Z-220

- Daniel Abler, “Capturing variability of tumor-induced mass-effect in glioma growth models”

- David Basanta, “Evolutionary tempo and the tumor microenvironment”
- Chakib Jerry, “Controlled Switched System for Cancer Model”

Z-245

- Georgiy Karev, “Struggle for Existence: models for Darwinian and nonDarwinian selection”
- Guanlin Li, “Why be Temperate: On the Fitness Benefits of Lysis vs. Lysogeny”
- Igor Rouzine, “Evolutionary footprint of epistasis”

Z-255

- Paulo Campos, “Functional speciali”
- Paul Hurtado, “A General Linear Chain Trick for building ODE models with flexible dwell times”
- Michael Kelly, “Marine Reserves and Optimal Dynamic Harvesting When Fishing Damages Habitat”

Z-305: Mentoring Room

15:30–16:00: BREAK

16:00–18:00: MINISYMPOSIA

Z-110: Recent advances on modeling and dynamics of vector-borne diseases

Vector-borne diseases are a big threat to public health sine some of them can kill an unprotected individual very quickly like malaria. The study of vector-borne diseases has become one of the most promising interdisciplinary areas in mathematical biology. This mini symposium will focus on recent advances on a variety of modeling and computational developments for studying vector-borne diseases. Topics cover malaria, West Nile virus, Lyme disease and etc. We highlight the importance of potential collaboration between mathematicians, entomologists, epidemiologist, and modelers in the prediction, prevention, and control of vector-borne diseases.

- 16:00–16:30: Binxiang Dai, “The IGP Model and Free Boundary Problems”
- 16:30–17:00: Shujing Gao, “Transmission Dynamics and Optimal Control of

Stage-structured HLB Model”

- 17:00–17:30: Rongsong Liu, “Intra-specific Competition and Insect Larval Development: a Model with Time-dependent Delay”
- 17:30–18:00: Dane Patey, “Multiple Dose Pharmacokinetic Models Predict Bioavailability of Toxins in Vertebrate Herbivores”

Z-200: Algebraic tools for the analysis of biochemical reaction networks

It is common to model the dynamical behavior of biochemical reaction networks such as signal transduction pathways and gene regulatory networks with a system of ordinary differential equations. The analysis of such systems has been crucial in understanding the biological mechanisms underlying such processes as apoptosis, circadian rhythms, and the cell cycle, and diseases like diabetes and cancer. Nevertheless, mathematical analysis of such models is challenging as a result of the high dimensionality of the systems, parameter uncertainty, significant nonlinearities, and time-scale separations between reactions. To address these challenges, tools from computational algebra and numerical algebraic geometry have been particularly fruitful and significant progress towards answering some of the more challenging questions in this area has resulted. In this session, we will give a forum to the latest advances on the analysis of such systems, with an emphasis on contributions from dynamical systems theory, algebraic geometry, and symbolic/numeric computation.

- 16:00–16:30: Elizabeth Gross, “Mixed volumes of steady-state systems”
- 16:30–17:00: Nicolette Meshkat, “Absolute Concentration Robustness: Algebra and Geometry”
- 17:00–17:30: Matthew Johnson, “Steady State Parametrizations for Biochemical Reaction Systems”
- 17:30–18:00: Adrian Tudorascu, “Convergence to equilibrium for a complex balanced system with boundary equilibria”

Z-205: Modeling and analysis of the endocrine and neuroendocrine systems

The endocrine system is composed of glands that contain hormone-secreting cells. The secretion of some hormones is under the direct control of the hypothalamus in the brain, forming the neuroendocrine system. Examples of endocrine glands are the pituitary, the adrenal, the pancreas, and the gonads. The hormones travel through the blood stream to target tissues throughout the body, including the brain, and regulate their function. They are responsible for mood, reproduction, sexual behavior, temperature and water regulation, growth, and glucose homeostasis, among many other things. The

speakers in this minisymposium will discuss recent research utilizing mathematical models to understand the activity of cells in the endocrine or neuroendocrine system, and the effects of the released hormones on target tissue. The minisymposium is held in honor of Arthur Sherman, this years Winfree Award recipient and a pioneer in the modeling and analysis of these systems.

- 16:00–16:30: Anmar Khadra, “Local and Global Regulation of GnRH Secretion: A Potential Neuroendocrine Mechanism for Pulsatile Release”
- 16:30–17:00: Eder Zavala, “A First Generation Model of Stress and Metabolic Axis Interactions”
- 17:00–17:30: Joon Ha, “A New Predictor of Diabetes from a Longitudinal Mathematical Model”
- 17:30–18:00: Cecilia Diniz Behn, “Quantifying Insulin Sensitivity in Obese Adolescent Girls”

Z-209: Data-driven methods for biological modeling

In the advent of big data and increased data availability in biology, mathematical modelers are faced with many opportunities and challenges, such as capturing heterogeneity, model selection and refinement, and utilizing multiscale models with data. This minisymposium will present advances in the development or novel application of statistical and machine learning methods towards modeling. These methods enable the use mathematical models to assess hypotheses and propose biological mechanisms leading to the observed data. The first session applies data-driven methods to cancer, while the second session considers applications to a variety of biological phenomena such as wound healing, disease spread, and epidemiology.

- 16:00–16:30: Lee Curtin, “A multifaceted approach to characterizing glioblastoma subpopulation dynamics”
- 16:30–17:00: Yang Kuang, “Predictive Mathematical Models of Hormone Treatment for Prostate Cancer”
- 17:00–17:30: Erica Rutter, “Modeling, Estimating, and Quantifying Uncertainty in Heterogenous Cancer Models”
- 17:30–18:00: Christina Vaghi, “Combining Population Modeling and Bayesian Inference for Tumor Growth Prediction”

Z-210: Resource explicit population models

We present a collection of biological and mathematical findings in novel mathematical models where resource quantities are explicitly incorporated. The research presented

will include an assortment of mathematical models based on biological stoichiometry where limiting resource quantity and quality are both present. Biological stoichiometry is the study of the balance of energy and multiple chemical elements in living organisms. Stoichiometric modeling, a relatively young branch of mathematical biology, has been greatly expanded in the past two decades, and population models inspired by biological stoichiometry have produced complex but strikingly realistic dynamical behaviors. Applications of resource explicit population models range from aquatic and terrestrial food webs, as well as within host systems such as cancer dynamics.

- 16:00–16:30: Christopher M Heggerud, “Multiple-scale analysis of a stoichiometric cyanobacteria model with phosphorus impulses”
- 16:30–17:00: MdNazmul Hassan, “An extension to the Toxicant mediated Predator-prey model under Stoichiometric Constraints”
- 17:00–17:30: Lale Asik, “Environmental Seasonality on Predator-Prey Systems Under Nutrient and Toxicant Constraints”
- 17:30–18:00: Angela Peace, “Compensatory foraging in stoichiometric producer-grazer models”

Z-215: Modeling to conquer: Understanding and controlling deleterious diseases using dynamical systems

The worlds most harmful human diseases are complex dynamical systems. Mathematical modeling of disease dynamics, both within and between hosts, offers new insights into disease emergence, progression, transmission, and evolution. In this minisymposium, dynamical systems models will inform control strategies for a wide range of deadly human diseases, from malaria and Zika to cancer and polio

- 16:00–16:30: Deborah Shutt, “Embedded ODE Model for the 2014 Ebola Outbreak in West Africa; An analysis of Guinea, Liberia & Sierra Leone”
- 16:30–17:00: Kamaldeen Olatunde Okuneye, “Impact of temperature and diurnal temperature range on the transmission dynamics of malaria”
- 17:00–17:30: Sara Clifton, “Lying in wait: Controlling bacterial infections using latent phage-antibiotic synergy”
- 17:30–18:00: Hayriye Gulbudak, “An Immuno-Epidemiological Vector-Host Model with Within-Vector Viral Kinetics”

Z-220: Population dynamics in heterogeneous landscapes: models, tool and data

Many populations live in heterogeneous environments, and individuals encounter habitats of significantly different quality. Fragmentation levels increase through human activities and other factors. Early models for population dynamics in such landscapes consisted of coupled systems of equations (one for each patch) and simple linear exchange terms between them. Recent modelling approaches include spatially explicit models with detailed individual-level movement descriptions. In all these models, the scale difference between regions of similar quality and the overall biological system play an important role. They allow us to study appropriate scaling limits (homogenization). This minisymposium will bring together modellers, analysts and empirical researchers to discuss the latest developments of such models, ranging from model formulation to analytical tools to data availability.

- 16:00–16:30: Christina Cobbold, “Homogenisation techniques for populations dynamics on strongly heterogeneous landscapes”
- 16:30–17:00: Chris Cosner, “Recent advances in understanding the dispersal of organisms: ideal and real”
- 17:00–17:30: Elizabeth Crone, “Population dynamics of monarch butterflies in highly fragmented landscapes”
- 17:30–18:00: Thomas Hillen, “Homogenization of Transport Equations”

Z-245: Modeling mosquito dynamics: the role of environmental variability

Vector-borne diseases such as dengue, malaria, and Zika impact billions of people around the world. An essential component of their transmission cycle involves a life-cycle stage within the mosquito. In this mini-symposium, models of mosquitoes incorporating variability in stages will inform mosquito population dynamics. Such heterogeneity, altering population dynamics, can have important impact on transmission of vector-borne diseases.

- 16:00–16:30: Megan Greischar, “The impact of mosquito population dynamics on the evolution of malaria parasites”
- 16:30–17:00: Brandon Hollingsworth, “Targeting Heterogeneity: Yard-scale Treatments to Reduce Citywide *Aedes* Populations”
- 17:00–17:30: Michael Robert, “Investigating meteorological influences on *Aedes aegypti* and dengue fever”
- 17:30–18:00: Kaitlyn Martinez, “Remote Sensing, Weather, and Demographic Data for Mosquito-Borne Disease Risk”

Z-255: Multiscale modeling of biofilms as complex ecological systems

Biofilms are microbial communities on immersed surfaces, embedded in layers of a self-produced extracellular matrix, which mainly provide increased resistance against traditional methods of disinfection and eradication. Biofilms are ubiquitous and play beneficial or detrimental roles in many industrial and medical applications. For instance, they can lead to corrosion problems in freshwater pipes, and oil pipelines; they are recognized as the main cause of infections in host tissues or medical implants; they are involved in crop disease in plants and biofouling of industrial equipments. However, the adsorption and absorption properties and enhanced mechanical stability of biofilms make them advantageous to environmental engineering technologies, such as wastewater treatment, elimination of petroleum oil from contaminated systems or biofuel production. Understanding and mastering these systems is therefore a major industrial, economic and health issue. The processes and factors affecting biofilm growth are diverse and can be highly complex. They often involve direct and indirect interaction of several (up to hundreds) species including bacteria, micro-algae, archaea and fungi, complex biochemical reactions, and often depend on the physical conditions of the surrounding environment such as fluid dynamics and shear fields. Biofilm models are critical to improve our understanding of biofilm formation, structure and function. Mathematical models in this field range from stochastic individual based models to cellular automata models to deterministic continuum models. In many cases hybrid models are proposed to bridge various length and/or time scales, including PDE-ODE coupled systems of various types, mixed hyperbolic-elliptic free boundary value problems with non-local effects, etc. This raises the questions regarding well-posedness, stability, long term behavior and numerical treatment. The aim of this minisymposium is to bring together researchers from the fields of Applied Mathematics more specifically Mathematical Biology with interest in diffusion-reaction equations, free boundary problems, mixture theory, multi-scale/multi-physics phenomena, complex systems modeling and microbial population dynamics, providing a platform to discuss techniques and innovations related to modeling biofilm formation, growth, and morphology. Major emphasis will be placed on multi-scale models which describe biofilm development and its architecture under various environmental conditions. The minisymposium is intended for those studying biofilms in the context of complex ecological systems. The talks will be useful for researchers in the aforementioned fields as well as biofluids and biomechanics.

- 16:00–16:30: David Chopp, “Asymptotic Approximation for Biofilm Growth Models”
- 16:30–17:00: Ana Carpio, “Biofilm spread on surfaces”
- 17:00–17:30: Isaac Klapper, “Combined Metabolic Modeling and Population Modeling of Microbial Communities”

- 17:30–18:00: Sara Jabbari, “Optimising an anti-adhesion treatment for a *P. aeruginosa* bacterial infection”

Z-260: Mathematical modelling of hematopoiesis under stress and disease

Hematopoietic stem cells (HSC) are responsible for life-long blood cell formation, and play a pivotal role in many diseases of the blood forming (hematopoietic) system. HSCs carrying mutations give rise to a wide range of diseases including pre-malignant and malignant diseases such as leukemias (blood cancers). Our intuitive understanding of the underlying dynamics is limited due to their complex and nonlinear nature. Mathematical models are an excellent tool to study complex phenomena and to provide insights into processes that cannot be measured directly. This minisymposium aims to bring together mathematical modellers and medical doctors contributing to a rigorous understanding of the hematopoietic system. The topics covered range from applied questions such as bone marrow transplantation, blood cancer evolution and cell-cell interactions in the stem cell niche to mathematical problems such as model reduction and multi-scale dynamics.

- 16:00–16:30: Michael Mackey, “A personal view of modeling hematopoietic regulation”
- 16:30–17:00: Peter Ashcroft, “How ageing and disease affect hematopoietic stem cell dynamics”
- 17:00–17:30: Joseph Mahaffy, “Parameter Sensitivity in Models for Erythropoiesis and Thrombopoiesis”
- 17:30–18:00: Anna Miller, “Towards a Multiscale Model of the Bone Microenvironment in Multiple Myeloma”

Z-305: Mathematical modeling in radiation oncology

Since the early days of radiotherapy, mathematical modeling has played a pivotal role in analyzing radiosensitivity and calculating radiation treatment protocols. With increasing radiobiological knowledge and numerous biological agents that synergize with radiation, mathematical modeling is poised to continue to make significant contributions to the field of radiation oncology. In this minisymposium we bring together a group of leading international researchers from different research groups and hospitals that demonstrate the integration of experimental and clinical data to build mathematical models that help optimize cancer radiotherapy.

- Sarah Bruüningk, “Heat-induced radiosensitization simulated in 3D tumour spheroids”
- Jamie Dean, “Mathematical modeling reveals improved PARPi-radiation ther-

apy administration schedules”

- Juan Carlos Lopez Alfonso, “Modeling the immunological consequences of radiation therapy”
- Clemens Grassberger, “Modeling of combined Drug-Radiation treatment regimen in Non-Small Cell Lung Cancer”

18:00–21:00: POSTER SESSION

Agora of Pavillon Jean-Coutu