

Prize talks

Prize talks, Wednesday, 21.09.2022, 11:00–12:40

Winners of the Reinhart Heinrich award (DKFZ Big)		
11:00	Lisa Kreusser (University of Bath, UK)	TBA
11:30	Lukas Eigentler (University of Dundee, UK)	Modelling dryland vegetation patterns: the impact of non-local seed dispersal and mechanisms of species coexistence
12:00	Martina Conte (Politecnico di Torino, Italy)	TBA
12:30	Poster prize	

Mini-symposia

MS1, Monday, 19.09.2022, 11:00–12:40

Mathematical modeling in radiation oncology – an RRS/SMB minisymposium (DKFZ Big)		
11:00	Carmen Villagrasa (Institute for Radiological Protection and Nuclear Safety, Paris, France)	Methods to study the correlation between the topology of energy transfers and the biological consequences of exposure
11:25	David Hormuth (University of Texas, Austin, TX, USA)	Personalizing spatial-temporal forecasts of high-grade glioma response to radiotherapy via multi-parametric MRI
11:50	Francesco Cordini (University of Trento, Trento, Italy)	The Generalized Stochastic Microdosimetric Model (GSM2): exploring different levels of stochasticity in radiation biophysical modeling
12:15	Mohammad U. Zahid (Moffitt Cancer Center, Tampa, FL, USA)	Mathematical models of tumor volume dynamics in response to radiotherapy: implications of model selection
Investigating the dynamics of many - Mathematical modeling and parameter estimation for multi-cellular systems (BioQuant SR42)		
11:00	Lutz Brusch (Center for Information Services and High Performance Computing, TU Dresden, Germany)	Modeling multi-cellular morphodynamic feedback loops during tissue morphogenesis
11:25	Jan Hasenauer (Faculty of Mathematics and Natural Sciences, University of Bonn, Germany)	Statistical Inference for Computational Models of Multi-cellular Processes
11:50	Franziska Matthäus (Frankfurt Institute for Advanced Studies, Goethe University Frankfurt, Germany)	Towards virtual biological systems - From image analysis to mathematical multi-particle models
12:15	Frederik Graw (BioQuant - Center for Quantitative Biology, Heidelberg University, Germany)	Analyzing multi-cellular dynamics of host-pathogen interactions
Boolean networks and related modeling frameworks - Part I: Model Design and Analysis (BioQuant SR43)		

11:00	Mohit Kumar Jolly (Indian Institute of Science, Bangalore, India)	Landscape of Epithelial Mesenchymal Plasticity as an emergent property of coordinated teams in regulatory networks
11:25	Matthew Wheeler (University of Florida, USA)	Modularity and Boolean Network Decomposition
11:50	David Murrugarra (University of Kentucky, USA)	Asymptotic Results on the Dynamics of Linear vs Nonlinear Boolean Networks
12:15	Luis L. Fonseca (University of Florida, USA)	Generating ODE Approximations of Agent Based Models for Control Purposes
Mathematical biology of signaling and metabolism at synapses (BioQuant SR43)		
11:00	Michael Graupner (Saints-Pères Paris Institute for the Neurosciences, Université Paris Descartes, France)	Irregular activity reveals burst dominance over spike-timing in plasticity induction
11:25	Erik De Schutter (Okinawa Institute of Science and Technology, Japan)	Modeling the tripartite synapse at the nanoscale
11:50	Geneviève Dupont (Unit of Theoretical Chronobiology, Université Libre de Bruxelles (ULB), Belgium)	Reciprocal regulation of cytosolic Ca ²⁺ signalling and mitochondrial metabolism
12:15	Renaud Jolivet (Maastricht Centre for Systems Biology (MaCSBio), Maastricht University, Netherlands)	Energy-efficient information transfer in brain circuits
Controlling epidemics: the interplay between models and public health policies (Mathematikon Hoersaal)		
11:00	Vincenzo Capasso (ADAMSS (Centre for Advanced Applied Mathematical and Statistical Sciences), Università degli Studi di Milano "La Statale", Milano, Italy)	Optimal control methods for vector borne diseases: the case of malaria. Part I: Mathematical Modelling
11:25	Peter Rashkov (Institute of Mathematics and Informatics, Bulgarian Academy of Sciences, Bulgaria)	Mathematical analysis of a repellent-based control intervention for vector-borne diseases
11:50	Alberto d'Onofrio (Dipartimento di Matematica e Geoscienze, Università di Trieste, Italy)	Optimal control methods and algorithms in behavioural epidemiology of infectious diseases
12:15	Cristiana J. Silva (Center for Research and Development in Mathematics and Applications (CIDMA), Department of Mathematics, University of Aveiro, Portugal)	Impact of individual behaviors on epidemic spreading through hybrid mathematical models
Evolutionary dynamics in structured populations: modelling, analytics and numerics (Mathematikon A + B)		

11:00	Giulia L. Celora (University of Oxford, UK)	Modelling phenotypic and spatial heterogeneity in solid tumours
11:25	Jules Guilberteau (Sorbonne Université, France)	Asymptotic behaviour of an integro-differential selection-advection equation
11:50	Max O. Souza (Universidade Federal Fluminense, Brazil)	On a continuous approach to fixation on graphs with large populations: the star as a paradigm
12:15	Chiara Villa (Sorbonne Université, France)	Modelling the adaptive dynamics of space- and phenotype-structured populations of cancer cells
Dynamics of blood flow in microcirculation (Mathematikon C)		
11:00	George W Atkinson (Mathematical Institute, University of Oxford, UK)	Oscillatory behaviour arising as a result of stochastic fluctuations in a bistable microvasculature blood flow network
11:25	Maxime Berg (Center for Nerve Engineering, University College London, UK)	Red blood cell distribution in microvascular networks
11:50	Paul W. Sweeney (Department of Physics, University of Cambridge, UK; Cancer Research UK Cambridge Institute, University of Cambridge, UK)	Simulating the distribution of haematocrit in vascular tumours
12:15	Romain Enjalbert (Centre for Medical Informatics, Usher Institute, The University of Edinburgh, UK)	Effect of vessel compression on red blood cell partitioning at vascular bifurcations in a vessel network

MS2, Monday, 19.09.2022, 14:30–16:10

Collective cell migration in cancer growth and spread: interacting dynamics at multiple spatial scales (DKFZ Big)		
14:30	Nadia Loy (Politecnico di Torino)	Direction-Dependent Turning Leads to Anisotropic Diffusion and Persistence
14:55	Arran BJ Hodgkinson (University of Exeter)	A mathematical approach to understanding cooperative invasion of heterogeneous melanoma subpopulations

15:20	Stephane Urcun (Universite du Luxembourg)	Modeling Proliferating and Invasive Behaviors of Non-Operable Glioblastoma by Multiphase Reactive Poromechanical Modeling
15:45	Dumitru Trucu (University of Dundee)	Multi-scale modelling of cancer invasion in the presence of M1 and M2 tumour associated macrophages
Multi-scale phenomena in biology: modelling and analysis (BioQuant SR41)		
14:30	Cordula Reisch (Technische Universität Braunschweig, Germany)	Modeling liver infections with reaction–diffusion equations
14:55	Linus Schumacher (University of Edinburgh, UK)	Regulation of stem cell dynamics through volume exclusion
15:20	Markus Schmidtchen (Technische Universität Dresden, Germany)	On tissue-growth models for two species
15:45	Havva Yoldaş (University of Vienna, Austria)	A probabilistic approach for the long-time behaviour of some PDE models for structured population dynamics
Stochastic Modelling of Genetic and Biochemical Systems I (BioQuant SR43)		
14:30	Christoph Zechner (Max Planck Institute of Molecular Cell Biology and Genetics & Center for Systems Biology Dresden, Germany)	Stochastic biochemical networks in compartmentalized environments
14:55	Lucy Ham (University of Melbourne, Australia)	Unravelling the correlation structure of noise in molecular pathways
15:20	Kaan Öcal (University of Edinburgh, UK)	Approximation and Reduction of the Chemical Master Equation using Statistical Machine Learning
15:45	Claudia Iglar (ETH Zurich, Switzerland)	Assessing the importance of resistance, persistence and hyper-mutation for antibiotic treatment success with stochastic modelling
Mathematics for cell migration under the influence of the microenvironment: from single cells to populations (Mathematikon Hoersaal)		
14:30	Alf Gerisch (TU Darmstadt, Germany)	On the simulation of models of cell migration involving myopic diffusion and cell-cell adhesion
14:55	Luigi Preziosi (Politecnico di Torino, Italy)	Modelling physical limits in cell migration

15:20	Juan Soler (University of Granada, Spain)	Mathematical modeling of contact-mediated signalling in cell communication
15:45	Min Tang (Shanghai Jiao Tong University, China)	Self-propelled particles in confined environment
Mathematical modeling of psychiatric disorders and addiction (Mathematikon A)		
14:30	Margaret Brandeau (Department of Management Science and Engineering, Stanford University, USA)	Cost-Effectiveness of Treatments for Opioid Use Disorder: A Model-Based Analysis
14:55	Jacob P. Duncan (Winona State University, USA)	A Fast-Slow Dynamical System Model of Addiction: Predicting Relapse Frequency
15:20	Josefien J. F. Breedvelt (National Centre for Social Research, London, UK; Dept. of Psychiatry, Amsterdam UMC, location AMC, University of Amsterdam, The Netherlands)	Advancing urban mental health research: from complexity science to actionable targets for intervention
15:45	Maria R. D'Orsogna (Dept. of Mathematics, California State University, Northridge, USA)	A mathematical model of reward-mediated learning in drug addiction
Pattern formation in developmental processes (Mathematikon C)		
14:30	Mingfeng Qiu (Laboratoire de Physique de l'Ecole Normale Supérieure Paris, France)	Actomyosin cables from active mechanical self-organization
14:55	Moritz Mercker (Institute of Applied Mathematics, Heidelberg University, Germany)	Pattern formation in biological tissues - mechanisms, experiments and models
15:20	Roman Vetter (ETH Zürich, Switzerland; Swiss Institute of Bioinformatics, Switzerland)	Spatial precision of morphogen gradients in tissue patterning
15:45	Camile Fraga Delfino Kunz (Institute of Medical Biometry and Statistics, University Hospital Freiburg, Germany)	Mathematical analysis and simulation of a model coupling (Turing) reaction-diffusion and chemotaxis and implications for hair follicle formation in mice

NSF panel

18:10–19:00 Founding opportunities for Mathematical Biology at the NSF and the NIH (DKFZ Big)	
	Zhilan Feng (NSF/DMS/Math Bio)
	Joseph Whitmeyer (NSF/SBE/SES)
	Han Nguyen (NIH/NIGMS)

MS3, Tuesday, 20.09.2022, 11:00–12:40

Single-cell dynamics and longitudinal landscapes in cancer drug resistance and clonal evolution, part I (DKFZ Big)		
11:00	Sidhartha Goyal (University of Toronto, Canada)	Statistical dynamics of tumor initiation and progression
11:25	Jeremie Roux (University Cote d'Azur (Nice-Sophia Antipolis), CNRS, France)	Profiling cell decision at the molecular level, using predictive single-cell dynamics
11:50	Nataly Kravchenko-Balasha (The Institute of Biomedical and Oral Research, The Hebrew University of Jerusalem, Israel)	Modeling intra-tumor and inter-patient signaling heterogeneity in cancer using thermodynamic-based approaches
12:15	Lisa Tucker-Kellogg (Duke-NUS Medical School, Singapore)	Computational modeling of drug-resistance evolution, studying how the speed of developing resistance to a combination of drugs can be affected by the non-additivity of the drug combinations
Modeling the female reproductive system at different scales (DKFZ Small)		
11:00	Leopold Franz (Computational Biology Group (CoBi), D-BSSE, ETH Zurich, Switzerland; Swiss Institute of Bioinformatics, Switzerland)	FollicleFinder & FollicleTracker to monitor ovarian follicle growth and selection in individual women
11:25	Aurelio A. de los Reyes V (Biomedical Mathematics Group, Institute for Basic Science, Daejeon 34126, Republic of Korea; Institute of Mathematics, University of the Philippines Diliman, Quezon City 1101, Philippines)	A model-based hormonal contraception strategy

11:50	Susanna Röblitz (Computational Biology Unit (CBU), Department of Informatics, University of Bergen, Norway)	Modelling ovarian follicle competition
12:15	Romain Yvinec (PRC, INRAE, CNRS, Université de Tours, 37380 Nouzilly, France; Université Paris-Saclay, Inria, Inria Saclay-Ile-de-France, 91120, Palaiseau, France)	Time scale separation in life-long ovarian follicles population dynamics model
Insights on collective migration using agent-based modeling (BioQuant SR41)		
11:00	W. Duncan Martinson (University of Oxford, UK)	Extracellular matrix remodelling by lead chick cranial neural crest cells is a major determinant of robust collective migration
11:25	Stuart Johnston (University of Melbourne, Australia)	Modelling collective navigation via non-local communication
11:50	Aashrith Saraswathibhatla (Stanford University, USA)	Coordinated tractions control the size of a collectively moving pack in an epithelial monolayer
12:15	Viktoria Freingruber (Heriot Watt University, University of Edinburgh, UK)	How cells work together to migrate more efficiently
Stochastic biochemical reaction networks (BioQuant SR42)		
11:00	Grzegorz Rempala (The Ohio State University, USA)	Approximating bio-chemical dynamics using survival models
11:25	Hye-Won Kang (University of Maryland at Baltimore County, USA)	Determining a computational cell size in stochastic chemical systems with spatial patterns
11:50	Radek Erban (University of Oxford, UK)	Chemical reaction networks: systematic design, noise control, bifurcations, efficient simulations and identifiability
12:15	Boseung Choi (Korea University)	Statistical inference of hierarchical Bayesian model for the stochastic chemical reaction with time delay
Boolean networks and related modeling frameworks - Part II: The Role of Canalization (BioQuant SR43)		
11:00	Claus Kadelka (Iowa State University)	Canalization in gene regulatory networks: an in-depth analysis
11:25	Luis M. Rocha (State University of New York at Binghamton)	The effective graph: a weighted graph that captures nonlinear canalization in biochemical systems

11:50	Elena Dimitrova (Cal Poly, San Luis Obispo, USA)	Unraveling the canalizing structure of Boolean functions
12:15	Hamza Coban (Koc University, Istanbul, Turkey)	Minimum sensitivity of nested canalizing functions and gene networks at the edge of chaos
Modelling of intra- and inter-hospital transmission of multidrug-resistant Enterobacteriaceae (Mathematikon Hoersaal)		
11:00	Johannes Horn (Martin Luther University Halle-Wittenberg, Germany)	Creating artificial profiles of patients based on existing health data
11:25	Mirjam Kretzschmar (University Medical Center Utrecht, Utrecht University, The Netherlands)	Relevance of intra-hospital patient movements for the spread of healthcare-associated infections: a mathematical modelling study
11:50	Konrad Sakowski (University of Warsaw; Institute of High Pressure Physics PAS, Poland)	On prevalence in healthcare facilities and modelling of healthcare-associated infection spread
12:15	Agata Lonc (University of Warsaw, Poland)	Modelling transmission of drug-resistant bacteria by hospital-community model with patient risk groups
Non-local models in mathematical biology (Mathematikon A)		
11:00	Valeria Caliaro (Laboratoire Jacques-Louis Lions, Sorbonne Université, France)	Mathematical modeling of regenerative processes in axolotl spinal cord
11:25	Maria Bruna (University of Cambridge, UK)	Excluded-volume and order in systems of Brownian needles
11:50	Carles Falcó (Mathematical Institute, University of Oxford, UK)	Nonlocal models of cell-cell adhesion and their Cahn-Hilliard approximation
12:15	Zuzanna Szymańska (University of Warsaw, Poland)	Bayesian inference of a non-local proliferation model
Quantitative investigation of the immune system's functions: from molecules to organisms, part 1 (Mathematikon B)		
11:00	Flavia Feliciangeli (Department of Applied Mathematics, School of Mathematics, University of Leeds, UK)	Why are cell populations maintained via multiple intermediate compartments?
11:25	Shabaz Sultan (Department of Tumor Immunology, RIMLS, Radboud University Medical Centre, Nijmegen, The Netherlands)	A parallelized cellular potts model that preserves system kinetics and enables simulations at tissue scale
11:50	Kevin Thurley (Institute of Experimental Oncology, Biomathematics division, Bonn University Hospital, Germany)	Response-time modeling of immune-cell interaction networks in acute and chronic inflammation

12:15	Hassan (Sam) Jamaledine (Department of Physiology, McGill University, Montreal, Canada)	How the evolving T cell avidity profile differentially impacts acute vs. chronic viral dynamics
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MS4, Tuesday, 20.09.2022, 14:30–16:10

Single-cell dynamics and longitudinal landscapes in cancer drug resistance and clonal evolution, part II (DKFZ Big)		
11:00	Qing Nie (Department of Mathematics, Department of Developmental and Cell Biology, NSF-Simons Center for Multiscale Cell Fate Research, University of California, Irvine, USA)	Multiscale spatiotemporal reconstruction of single-cell genomics data
11:25	Carmen Ortega Sabater (University of Castilla-La Mancha, Spain)	Single-cell analysis as a tool to reveal how phenotypic plasticity shapes tumour evolution
11:50	Maalavika Pillai (Centre for BioSystems Science and Engineering, Indian Institute of Science, Bangalore, India)	Quantifying cell state transitions and landscapes in melanoma tumors
12:15	Anja Voß-Böhme (University of Applied Sciences Dresden, Technische Universität Dresden, Germany)	Data-driven quantification of stochastic cell state transitions in tumor cell lines
Recent Progress and Open Frontiers in Turing's Theory of Morphogenesis (DKFZ Small)		
14:30	Mariya Ptashnyk (University of Edinburgh, UK)	Interactions between chemical and mechanical pattern formation during developmental processes
14:55	Mohit Dalwadi (University College London, UK)	Robustness of biological pattern formation in spatio-temporal morphogen variations
15:20	Chandrasekhar Venkataraman (University of Sussex, UK)	Pattern formation in cell biology
15:45	Frits Veerman (University of Leiden, The Netherlands)	Beyond Turing with mechano-chemical pattern formation
Quantitative investigation of the immune system's functions: from molecules to organisms, part 2 (BioQuant SR41)		

14:30	Amber M. Smith (Department of Pediatrics, University of Tennessee Health Science Center, Memphis, USA)	Modeling immunopathology during influenza-bacterial coinfection
14:55	Bevelynn Williams (Department of Applied Mathematics, School of Mathematics, University of Leeds, UK)	Mathematical modelling of anthrax infection
15:20	Veronika Zarnitsyna (Department of Microbiology and Immunology, Emory University, Atlanta, USA)	Estimating waning of vaccine-induced immunity and protection
15:45	Michal Or-Guil (Systems Immunology Lab, Department of Biology, Humboldt-Universität zu Berlin, Germany)	Advancing discovery of clinical knowledge by exploitation of functional antibody landscapes
Bistable genetic switches across time, space, and disciplines (BioQuant SR43)		
14:30	Pau Formosa-Jordan (Max Planck Institute for Plant Breeding Research, Cologne, Germany)	A stochastic bistable switch model can account for variability in seed germination time
14:55	Daria Stepanova (Laboratorio Subterráneo de Canfranc, Spain; Centre de Recerca Matemàtica, Barcelona, Spain)	A method to coarse-grain multi-agent stochastic systems with regions of multistability
15:20	Francisco Berkemeier (University College London, UK)	The dynamics of long-range signalling via the Notch-Delta pathway
15:45	Irene Otero Muras (Computational Synthetic Biology Group. I2SysBio Institute for Integrative Systems Biology Spanish National Research Council, València, Spain)	Detection and Design of Biomolecular Networks for Cell Decision Making
SMB Writing Groups: Showcasing the research of one group to highlight the role of writing groups in the development of early-career researchers. (BioQuant SR44)		
14:30	Shelby M. Scott (University of Tennessee, Knoxville. Guidehouse, LLP)	COVID-19 and crime: Analysis of crime dynamics amidst social distancing protocols
14:55	Jessica Crawshaw (The University of Oxford, The Mathematical Institute; The University of Melbourne, School of Mathematics and Statistics)	Examining the mechanical forces driving vascular regression using a fluid-structure-growth model
15:20	Joan Ponce (University of California, Los Angeles)	Realistic model assumptions increase the applicability of epidemiological models

15:45	Laura F. Strube (Virginia Tech, United States)	A mechanistic ODE model of the integrated stress response reveals a "tug-of-war" motif that produces an analog-digital response tuned by eIF2B
Disease Models: Modeling, Analysis, and Simulation (Mathematikon Hoersaal)		
14:30	Ben Adams (Bath University, UK)	Some insights into the entwined eco-epidemiology of <i>Borrelia burgdorferi</i> and <i>Babesia microti</i>
14:55	Rachel Jennings (Applied Research Associates, Inc., USA)	A within-host modeling framework for SARS-CoV-2 infection to support vaccine strategies
15:20	Jordi Ripoll (University of Girona, Spain)	Evolution of infection transmission prior to symptom onset
15:45	Gergely Röst (University of Szeged, Hungary)	Temporal variation of contact structures during COVID-19 outbreak
Novel techniques for spatial analysis of biological data (Mathematikon A)		
14:30	Simon P. Castillo (Centre for Evolution and Cancer, The Institute of Cancer Research, UK)	Breast tumour eco-immunology: the importance of being spatial
14:55	Joshua A. Bull (University of Oxford, UK)	Mathematical tools for multiscale spatial analysis of multiplex images
15:20	Jesús J. Bosque (Universidad de Castilla-La Mancha, Spain)	Using topological data analysis to unveil traits of interaction among immune cells in colorectal lesions
15:45	Abigail Hickok (University of California Los Angeles, USA)	Analysis of Spatial and Spatiotemporal Anomalies Using Persistent Homology
Anisotropy and finite-size effects in the emergence of collective behaviour (Mathematikon B)		
14:30	Michael Faran (Tel Aviv University, Israel)	Nonequilibrium driven self-assembly: from micro to macro-scale
14:55	Jean-François Joanny (Collège de France, Paris, France)	Mixtures of hot and cold particles
15:20	Laura Kanzler (LJLL Sorbonne Université, Paris, France)	A model for myxobacteria colonies: Connecting microscopic to kinetic and macroscopic scales
15:45	Suwendu Mandal (TU Darmstadt, Germany)	Crowding-enhanced diffusion of highly entangled self-propelled stiff filaments

DEI Panel, Tuesday, 20.09.2022, 16:30–18:10

16:30–17:20 Panel Discussion: Equity of paths into mathematical biology (DKFZ Big)	
Miranda Lynch (Staff Scientist, High-Throughput Crystallization Screening Center, Hauptman-Woodward Medical Research Institute)	
Luis Sordo Vieira (Research Assistant Professor, College of Medicine, University of Florida)	
Aur�lie Carlier (Assistant Professor, MERLN Institute for Technology-Inspired Regenerative Medicine, Maastricht University)	
Adam L. MacLean (Moderator, University of Southern California, USA)	
17:20–18:10 Panel Discussion: Building inclusive graduate programs in mathematical biology (DKFZ Big)	
Alun Lloyd (Director of Biomathematics Program at North Carolina State University North Carolina State University)	
Alla Borisyuk (Lead faculty in the Mathematical Biology Program at the University of Utah University of Utah)	
Juliane Liepe (Lead faculty in Quantitative and Systems Biology at MPI Max-Planck Institute for Biophysical Chemistry)	
Gibin Powathil (Deputy Director of Mathematics at the Centre for Biomathematics at Swansea Swansea University)	

MS5, Thursday, 22.09.2022, 11:00–12:40

Mathematical and computational modeling of cancer evolution (DKFZ Big)		
11:00	Khanh Dinh (Department of Statistics, Columbia University, New York, USA)	Modeling and simulation of cancer evolution in single cells
11:25	Thomas O. McDonald (Department of Data Sciences at Dana-Farber Cancer Institute, Boston, USA)	Modeling of evolution of resistance to anti-cancer drugs as an evolutionary process
11:50	Donate Weghorn (Centre for Genomic Regulation, The Barcelona Institute of Science and Technology, Barcelona, Spain)	Probabilistic approaches to inference of mutation rate and selection in cancer

12:15	Benjamin Werner (Centre for Cancer Genomics and Computational Biology, Barts Cancer Institute, Queen Mary University of London, UK)	Somatic evolutionary dynamics in hierarchical tissue structures
Physical Determinants of Subcellular Processes (DKFZ Small)		
11:00	Aur�lie Carlier (University of Maastricht, The Netherlands)	Computational modelling of the fundamental building blocks of life
11:25	Anotida Madzvamuse (University of Sussex, UK)	A mechanobiochemical model for 3D cell migration
11:50	Marko Vendelin (Tallinn University of Technology, Estonia)	Molecular movement in cardiomyocyte: how do we use combination of mathematical models and experiments to describe diffusion
12:15	Hilary Hunt (University of Oxford, UK)	A transcriptome-guided analysis of phloem metabolism
Non-local mathematical models for collective migration: insights from analytical methods (BioQuant SR41)		
11:00	Valeria Giunta (School of Mathematics and Statistics, University of Sheffield, UK)	Detecting stability and multi-stability in multispecies non-local advection-diffusion models
11:25	Gissell Estrada-Rodr�guez (Department of Mathematics, Universitat Polit�cnica de Catalunya, Barcelona, Spain)	Macroscopic description of non-local movement of biological systems
11:50	Martina Conte (Department of Mathematical Sciences, Politecnico di Torino, Italy)	Non-local kinetic models for cell migration in multi-cue environments
12:15	Sara Bernardi (Department of Mathematical Sciences, Politecnico di Torino, Italy)	Non-local hyperbolic models for leader-follower systems
The SMB Immunobiology and Infection Subgroup mini-symposium (BioQuant SR42)		
11:00	Marta Schips (Department Systems Immunology, Helmholtz Centre for Infection Research, Braunschweig, Germany)	How does T-FR limit autoreactivity despite being outnumbered in the GC?
11:25	Hind Zaaraoui (Inserm and Universit� de Paris, France)	Modeling the efficacy of antiviral strategies in households
11:50	Mario Castro (Instituto de Investigaci�n Tecnol�gica (IIT), Universidad Pontificia Comillas, Madrid, Spain)	BCR-antigen catch bond behavior

12:15	Andrea Cavalli (Institute for Research in Biomedicine, Università della Svizzera Italiana)	Modelling human antibody repertoires with LSTMs
From single cells to populations: models and experiments (BioQuant SR44)		
11:00	Tomasso Bianucci (Center for Systems Biology Dresden; MPI-CBG, Dresden, Germany)	Moment-expansion methods for compartmentalized biochemical systems
11:25	Dimitrios Volteras (Mathematics, Imperial College London, UK)	Exploring transcription variability along the cell cycle with metabolic labelling data and stochastic modelling
11:50	Paul Pihø (Mathematics, Imperial College London, UK)	Modelling selection on stochastic gene expression in clonal populations
12:15	Chetan Aditya (Inria, Paris, France; Department of Computational Biology, Institut Pasteur, Paris, France)	Mechanistic interrogation of stochastic cell-fate decisions at the single cell level
Multiscale mathematical models of infectious disease (Mathematikon Hoersaal)		
11:00	James Doran (University of Bath, UK)	From within-host to between-host: immuno-epidemiological models of infectious disease
11:25	Francesca Lovell-Read (University of Oxford, UK)	Assessing the effects of outbreak interventions in an age-structured population: what can we learn from COVID-19?
11:50	Stephanie Evans (Public Health England, UK)	Estimating the impact of testing and infection prevention and control measures on the transmission of SARS-CoV-2 in English hospitals
11:15	Juliano Ferrari Gianlupi (Indiana University, USA)	Modeling the effect of dose interval, potency, and cell-to-cell heterogeneity on the effectiveness of an antiviral
Recent advances in mathematical modelling in neuroscience (Mathematikon A)		
11:00	Mattia Sensi (Inria Sophia Antipolis - Méditerranée Research Centre)	A generalization of the full SNARE-SM model
11:25	Panagiotis Kaklamanos (Maxwell Institute of Mathematical Sciences and School of Mathematics, University of Edinburgh, UK)	Geometric singular perturbation analysis of the multiple-timescale Hodgkin-Huxley equations

11:50	Annalisa Iuorio (University of Vienna, Austria)	A new E-GLIF model for hippocampal CA1 pyramidal neurons and interneurons
12:15	Daniele Avitabile (Vrije Universiteit Amsterdam, The Netherlands)	Bump Attractors and Waves in Networks of Integrate-and-Fire Neurons
Computational Models of Biological Fluid-Structure Interaction Systems (Mathematikon B)		
11:00	Alexander Hoover (Cleveland State University, USA)	Neuromechanical Wave Resonance in Fluid Transport
11:25	Fabian Pallasdies (Institute for Theoretical Biology, Berlin, Germany)	From Single Neurons to Behavior in Two Computational Models of Jellyfish
11:50	Wanda Strychalski (Case Western Reserve University)	Computational modeling of adhesion-independent confined cell migration
12:15	Thomas Fai (Brandeis University)	Theoretical model of nuclear size control regulated by osmotic pressure

MS6, Thursday, 22.09.2022, 16:30–18:10

How to get a big picture of cancer? Recent advances in mathematical oncology (DKFZ Big)		
16:30	Thomas Höfer (Division of Theoretical Systems Biology, German Cancer Research Center, Heidelberg, Germany)	Stem cell hierarchy and cancer risk
16:55	John Metzcar (Departments of Intelligent Systems Engineering and Informatics, Indiana University, USA)	A novel model of multicellular communication through extracellular matrix microstructure
17:20	Bernadette Stolz (University of Oxford, UK; EPFL, Lausanne, Switzerland)	Persistent homology for the spatial characterisation of tumour blood vessel networks
17:45	Matthias Kloor (Department of Applied Tumor Biology, Heidelberg University Hospital, Germany)	Cancer-preventive vaccines in Lynch syndrome
Bridging scales between the cytoskeleton and tissue mechanics (DKFZ Small)		
16:30	Serge Dmitrieff (Institut Jacques Monod, Université Paris Cité/CNRS, Paris, France)	Cytoskeleton modeling: bridging molecular details, continuous theory, and experiments

16:55	Dennis Wörthmüller (Institute for Theoretical Physics, Universität Heidelberg, Germany)	Modelling optogenetic control of cell contractility and force propagation in epithelial tissue
17:20	Gonca Erdemci-Tandogan (Institute of Biomedical Engineering, University of Toronto, Canada)	Role of cellular rearrangement time on the rheology of tissues
17:45	Alexander Nestor-Bergmann (Department of Physiology, Development and Neuroscience, University of Cambridge, UK)	From molecules to tissues: a multiscale understanding of active tissue dynamics in a morphoelastic model
Multi-scale and data-driven modeling approaches in ecology, immunology, and epidemiology II (BioQuant SR41)		
16:30	Hayriye Gulbudak (Assistant Professor, Department of Mathematics, University of Louisiana at Lafayette)	Modeling across-scale feedbacks of infectious diseases
16:55	Edward Hill (The Zeeman Institute for Systems Biology & Infectious Disease Epidemiology Research, School of Life Sciences and Mathematics Institute, University of Warwick, UK)	Possible future waves of SARS-CoV-2 infection generated by variants of concern with a range of characteristics
17:20	Jennifer Lord (Liverpool School of Tropical Medicine, UK)	Mechanistic modelling in empirical studies of arboviruses: from within mosquito dynamics to between species transmission
17:45	Andrea Pugliese (Department of Mathematics, University of Trento, Italy)	Epidemic dynamics with multiple strains and waning immunity
Modeling and analysis of within-host influenza infection and vaccination dynamics (BioQuant SR42)		
16:30	Molly E. Gallagher (Emory University and Johns Hopkins University Applied Physics Lab)	A macroparasite within-host framework accommodating spatial structure can recapitulate key aspects of influenza A infection dynamics
16:55	Michael A. Martin (Population Biology, Ecology, and Evolution Graduate Program, Laney Graduate School, Emory University, Atlanta, GA, USA; Department of Biology, Emory University, Atlanta, GA, USA)	Leveraging genomic diversity to gain insights into within-host influenza dynamics
17:20	Ke Li (School of Mathematics and Statistics, The University of Melbourne, Australia)	Using mathematical models to understand viral pathogenicity of 1918 pandemic and H5N1 influenza virus infection

17:45	Andreas Handel (University of Georgia)	The impact of seasonal influenza vaccine dose on homologous and heterologous immunity
Modelling and Estimation in Mathematical Biology (BioQuant SR44)		
16:30	Prajakta Bedekar (Johns Hopkins University)	Optimal time-dependent classification for diagnostic testing
16:55	Rayanne A. Luke (Johns Hopkins University)	Optimal multiclass classification and class prevalence estimation with applications to SARS-CoV-2 antibody assays
17:20	Ryan M. Evans (National Institute of Standards and Technology)	A Mathematical Model for Biological Field Effect Transistors
17:45	Luis A. Melara (Shippensburg University)	Optimal Bandwidth Selection in Bio-FET Measurements
Digital twins in medicine: where we are, where we are heading, and what is needed (Mathematikon Hoersaal)		
16:30	Anna Niaraki (Université Paris-Saclay & INRIA Saclay - Île-de-France)	Development of a virtual Rheumatoid Arthritis synovial fibroblast for large-scale dynamic analysis and efficient drug-target identification
16:55	María Rodríguez Martínez (IBM Zurich Research Laboratory, Zurich, Switzerland)	Artificial intelligence approaches for cancer personalized medicine
17:20	Maral Budak (Department of Microbiology and Immunology, University of Michigan, USA)	Virtual clinical trials to identify improved regimens for treatment of TB
17:45	Reinhard C. Laubenbacher (Division of Pulmonary, Critical Care, and Sleep Medicine, University of Florida, USA)	Mathematics in 21st Century Medicine: Digital Twins
Brain Rhythms in Health and Disease, part 1 (Mathematikon A)		
16:30	Anmar Khadra (McGill University)	Characterizing the underlying dynamics of traveling waves in area V4 of the visual cortex
16:55	Axel Hutt (INRIA Nancy - Grand Est)	Impact of transcranial Direct Current Stimulation on brain networks in the context of a ketamine-animal model of psychotic disorder
17:20	Jaroslav Hlinka (Czech Academy of Sciences)	On complex explanations for complex brain network dynamics

17:45	Stephen Coombes (University of Nottingham)	The importance of gap junctions and the extracellular space in modelling seizure dynamics: a new neural mass approach
The Next Frontier in Mathematical Biology: Learning from Complex Biological Data (Mathematikon B)		
16:30	Laleh Haghverdi (Computational Methodologies and Omic Analytics Group Leader, Max Delbrück Center for Molecular Medicine)	Towards Reliable Quantification of Cell State Velocities
16:55	Dhananjay Bhaskar (Post Doctoral Researcher and Boehringer-Ingelheim Fellow, Yale University)	Grappling with 10^{60} : A Representation-First Approach for Drug Discovery and Lead Optimization
17:20	Elisabetta Mereu (Josep Carreras Research Institute)	Technical and biological variability in single-cell and spatial genomics
17:45	Mohammad Lotfollahi (Post Doctoral Researcher at Helmholtz Center Munich, German)	Deep Learning for Single-Cell Genomics

MS7, Friday, 23.09.2022, 9:00–10:40

Modeling inflammation and cancers (DKFZ Big)		
9:00	Natalia Komarova (University of California Irvine)	Aspirin and Colorectal Cancer
9:25	Doron Levy (University of Maryland)	An Overview of Mathematical Modeling of Tumor Promoting Inflammation
9:50	Thomas Stiehl (Aachen University)	Determinants of clonal evolution in blood cancers – insights from mathematical modeling
10:15	Yangjin Kim (Konkuk University)	Mathematical Modeling of tumor growth: OV Therapy
Cell and Developmental Biology Subgroup minisymposium: Spatial cell heterogeneity across scales (DKFZ Small)		
9:10	Zena Hadjivasiliou (The Francis Crick Institute, London, UK)	Growth and patterning in development and evolution

9:25	Sabine Fischer (Center for Computational and Theoretical Biology, Universität Würzburg, Germany)	Cell differentiation in mouse blastocysts exhibits complex spatio-temporal patterns
9:50	Vivienne Leech (University College London, UK)	A modelling framework to describe the dynamics and scaling of nuclear growth
10:15	Ruben Perez-Carrasco (Imperial College London, UK)	Stator dynamics of the bacterial flagellar motor
COVID-19 Across Multiple Scales (BioQuant SR41)		
9:00	Stanca M. Ciupe (Virginia Tech University, USA)	Modeling within-host and aerosol dynamics of SARS-CoV-2: the relationship with infectiousness
9:25	Chapin S. Korosec (York University, Canada)	Modeling long-term durability of SARS-CoV-2 immune response from vaccines and infection
9:50	Libin Rong (University of Florida, USA)	Modeling COVID-19 dynamics: From within-host to between-host
10:15	Jonathan Forde (Hobart and William Smith Colleges)	Multiscale Modeling of Interrelated Dynamics of COVID-19 Vaccination and Testing Strategies
Multi-scale and data-driven modeling approaches in ecology, immunology, and epidemiology (BioQuant SR43)		
9:00	Joshua Macdonald (Research Assistant, Department of Mathematics, University of Louisiana at Lafayette)	Evidence for antibody dependent enhancement in secondary Dengue via intermediate cross-reactive antibody level
9:25	Erin Gorsich (The Zeeman Institute for Systems Biology & Infectious Disease Epidemiology Research, School of Life Sciences, University of Warwick)	Modelling endemic Rift Valley fever
9:50	Amanda Laubmeier (Department of Mathematics, Texas Tech University)	Ecosystem impacts of feedback between social and ecological networks
10:15	Simon Gubbins (Transmission Biology, The Pirbright Institute)	From within hosts to between farms: modelling the dynamics of foot-and-mouth disease virus across scales
Dynamical modeling of respiratory virus propagation (Mathematikon Hoersaal)		
9:00	Jane Heffernan (York University)	Modelling SARS-CoV-2 immunity
9:25	Julien Arino (University of Manitoba)	Investigating the existence of multiple epidemic waves with variants and vaccination

9:50	James Watmough (University of New Brunswick)	Alternate stable states in immune system models
10:15	Huaiping Zhu (York University)	Dynamics of the asymptomatic infection in spreading of SARS-CoV-2
Brain Rhythms in Health and Disease, part 2 (Mathematikon A)		
9:00	Niklas Brake (McGill University)	A biophysical model to correct for the EGG spectral trend
9:25	Jonathan Rubin (University of Pittsburgh)	Oscillations in the basal ganglia in parkinsonism: delta enters the picture
9:50	Gihan Weerasinghe (University of Oxford, UK)	A Strategy for closed-loop deep brain stimulation using multi-contact electrodes
10:15	Richard Gao (University of Tübingen, Germany)	Mechanistic model inference from observed neurodynamics
Sneak peak at the future of mathematical biology: biology-driven machine learning (Mathematikon B)		
9:00	Dimitris G. Patsatzis (School of Chemical Engineering, National Technical University of Athens, Greece)	System-level understanding in multi-scale systems: analysis of a pharmacokinetics model
9:25	Célestin Bigarré (COMPUtational pharmacology and clinical Oncology Department, Inria Sophia Antipolis – Méditerranée, Cancer Research Center of Marseille, Inserm UMR1068, CNRS UMR7258, Aix Marseille University UM105, Marseille, France)	Mechanistic modeling of metastatic free relapse in breast cancer to investigate the biological impact of diagnosis biomarkers
9:50	Josue Manik Navas Sedeno (Department of Mathematics, Universidad Nacional Autonoma de Mexico, Mexico City, Mexico)	Technique development for the definition and analysis of discrete biological models
10:15	Simon Martina-Perez (Mathematical Institute, University of Oxford, UK)	Efficient Bayesian inference for mechanistic modelling with high-throughput data

Contributed talks

CT1 - Monday, 19.09.2022, 16:30–18:10

DKFZ big		
16:30	Fabian Froehlich (Harvard Medical School, USA)	A Mechanistic model of EGFR and ERK signaling reveals how allostery and rewiring contribute to RAF and MEK inhibitor resistance
16:50	Alexander Paul Browning (Queensland University of Technology, University of Oxford, UK)	Mathematical, statistical, and experimental analysis of tumour spheroid structure
17:10	Juan Jiménez-Sánchez (Mathematical Oncology Laboratory (MOLAB), University of Castilla-La Mancha, Spain; Institute of Applied Mathematics in Science and Engineering (IMACI), University of Castilla-La Mancha, Spain)	On optimal temozolomide scheduling for slowly growing gliomas
17:30	Julia Grajek (Nalecz Institute of Biocybernetics and Biomedical Engineering, Polish Academy of Sciences, Poland)	An in silico model to study CAIX as a biomarker for immune checkpoint inhibitor therapy
17:50	Even Moa Myklebust (Oslo Centre for Biostatistics and Epidemiology, Faculty of Medicine, University of Oslo, Norway)	Phenotypic deconvolution in heterogeneous cancer cell populations using drug screening data
BioQuant SR41		
16:30	Shalu Dwivedi (Department of Bioinformatics, Matthias Schleiden Institute, Friedrich Schiller University, Jena, Germany)	A game-theoretical description of defense and counter defense in host-pathogen interactions
16:50	Gil Ariel (Bar Ilan University, Israel)	Chaos and Levy walks in swarming bacteria
17:10	Kalle Parvinen (University of Turku, Finland; International Institute for Applied Systems Analysis (IIASA), Laxenburg, Austria)	Evolution of dispersal under spatiotemporal heterogeneity
17:30	Philip Gerlee (Chalmers University of Technology, Sweden)	Weak selection and the separation of eco-evo time scales using perturbation analysis

17:50	Giulia Belluccini (University of Leeds, UK)	Multi-type branching processes to study cell population dynamics
BioQuant SR42		
16:30	Philip Pearce (University College London, UK)	Bacterial quorum sensing in spatio-temporally heterogeneous environments
16:50	Francesco Puccioni (Imperial College of London, UK)	Stochastic modelling of agent-based populations
17:10	Marie Haghebaert (Université Paris-Saclay, INRAE, MaAGE, 78350, Jouy-en-Josas, France)	Modelling interactions between host and gut microbiota
17:30	Michael Raatz (Max Planck Institute for Evolutionary Biology, Germany)	Avoiding extinction or maximising growth? The impact of treatment on trait trajectories in evolving populations
17:50	Ezio Venturino (University of Turin, Italy)	Mathematical explanation of hyperpredation between invasive Eastern cottontail and native European hare
BioQuant SR43		
16:30	Maria Carla Tesi (University of Bologna, Italy)	Dynamics of proteins in Alzheimer's disease: a mathematical model
16:50	Mustafa Sayli (University of Nottingham, UK)	Effects of delays on neuronal dynamics
17:10	Urszula Forys (University of Warsaw, Poland)	Neuronal population model of decision-making: influence of distributed delays
17:30	Qiyao Peng (Leiden University, The Netherlands; Hasselt University, Belgium; Delft University of Technology, The Netherlands)	A Mathematical Model describing Cell Shape Evolution and the Impact of Cellular Forces on the Extracellular Matrix during Cell Invasion through a Flexible Channel
17:50	Yue Liu (Mathematical Institute, University of Oxford, UK)	Parameter identifiability for extensions of the Fisher-KPP model
Mathematikon Hörsaal		
16:30	Usman Sanusi (Technical University of Munich, Germany)	Quiescence generates delay and moving average in a stochastic epidemiological model
16:50	Md Nurul Anwar (The University of Melbourne, Australia; Bangabandhu Sheikh Mujibur Rahman Science and Technology University, Bangladesh)	Optimal interruption of vivax malaria transmission using mass drug administration

17:10	Pauline Clin (INRAE, UMR IGEPP, France)	Host mixtures for plant disease control: benefits from pathogen selection and immune priming
17:30	Prashant Kumar Srivastava (Indian Institute of Technology Patna, India)	Multiple stability switches and Hopf-Hopf bifurcation in an SIRS model with information under influence of two time delays
17:50	Tom Britton (Stockholm University, Sweden)	Optimal intervention strategies for minimizing total incidence during an epidemic
Mathematikon A		
16:30	Benjamin J. Walker (1: University College London, UK)	Multiscale analysis for microscale swimming
16:50	Torbjörn "Toby" Lundh (University of Gothenburg, Sweden; Chalmers University of Technology, Sweden)	Biological image data augmentation using Möbius transformations
17:10	Ryszard Rudnicki (University of Silesia, Poland)	Dynamics of immune status: asymptotic properties of a stochastic model
17:30	Katarzyna Pichór (University of Silesia, Poland)	Asymptotic properties of Stein's neuronal model
17:50	Radosław Wieczorek (University of Silesia, Poland)	A hybrid stochastic model of retinal angiogenesis
Mathematikon B		
16:30	Salvo Danilo Lombardo (Department of Structural and Computational Biology, Max Perutz Labs, University of Vienna, Austria; CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria)	A multi-layer network approach to investigate disease onset across different tissues and times
16:50	Karen Amaral de Oliveira (IGBMC, France)	Modelling Transcription Factors Search and Polymerase Recruitment Dynamics within a complex chromatin structure
17:10	Hamza Faquir (Computational Synthetic Biology Group. I2SysBio Institute for Integrative Systems Biology (UV-CSIC), Spain)	Optimal Control of Stochastic Gene Regulatory Networks in Bacterial Populations.
17:30	Robyn Araujo (Queensland University of Technology, Australia)	A Universal Integral Control Implementation for Biochemical Reaction Networks that Exhibit Robust Perfect Adaptation

17:50	Pablo Rojas (Theoretical Physics, University of Kassel, Germany)	Diffusion enhanced oscillations in biochemical networks
Mathematikon C		
16:30	Roberto Barrio (University of Zaragoza, Spain)	A dynamical systems analysis of the generation of early afterdepolarizations in cardiomyocytes: insights from "in silico" electrophysiological models
16:50	Sofia Farina (University of Luxembourg, Luxembourg)	3D Modelling of a Spatially Resolved Energy Metabolism in Physiological Astrocytic Morphology
17:10	Siting Miao (Wolfson Centre for Mathematical Biology, Mathematical Institute, University of Oxford, UK)	Modelling IL-2 signalling dynamics on the individual cell scale
17:30	David M. Versluis (Institute of Biology, Leiden University, The Netherlands)	Multiscale modelling helps analyze the effect of colonic mucus types on the infant gut microbiota
17:50	Magali Ribot (Institut Denis Poisson, Université d'Orléans, CNRS, France)	Modeling adipocyte dynamics with differentiation

CT2 - Thursday, 22.09.2022, 09:00–10:40

DKFZ big		
9:00	Stefano Pasetto (H. Lee Moffitt Cancer Center & Research Institute, USA)	Breast Cancer Reaction-Diffusion from Spectral-Spatial Analysis in Immunohistochemistry
9:20	Giulia Chiari (Politecnico di Torino, Italy)	A mathematical study of the influence of hypoxia on tumour growth, phenotypic heterogeneity and radiotherapy
9:40	Chloe Audebert (Sorbonne Universite, LJLL, LCQB, Paris, France)	Mathematical model of heterogeneity in lymphocyte cell counts of CLL patients under ibrutinib treatment
10:00	Simon Syga (Center for Information Services and High Performance Computing, TU Dresden, Germany)	The interplay of spatio-temporal interactions and evolutionary dynamics during tumor growth

10:20	Tuğba Akman Yıldız (Oslo Centre for Biostatistics and Epidemiology, Faculty of Medicine, University of Oslo, Oslo; Department of Computer Engineering, University of Turkish Aeronautical Association, Etimesgut, Ankara, Turkey)	Modeling aromatase inhibitor treatment in breast cancer: from mice experiments to a clinical trial
DKFZ small		
9:00	Edgar Wilfried Delgado Eckert (University of Basel, Switzerland)	Detecting resolution of autonomic dysregulation in preterm infants using mathematical modelling
9:20	Antony R. Humphries (McGill University, Canada)	Modeling Iron Metabolism and Erythropoiesis of Blood Donors
9:40	Fenja Zell (Institute of Medical Engineering, University of Lübeck, Germany)	Comparison of the fluid-structure interaction of an airway of a sleep apnea patient with and without wearing a protrusion splint
10:00	Marco Bussoletti (Sapienza University of Rome, Italy)	A continuous mesoscale analysis of curvature-mediated protein interaction on lipid membranes
10:20	Nicholas A. Hill (University of Glasgow, UK)	Computational models of the coronary and pulmonary circulations
BioQuant SR41		
9:00	Olga Vasilieva (Universidad del Valle, Cali, Colombia)	Wolbachia invasion in wild mosquito populations: a modeling framework apt for different strains
9:20	Fordyce Davidson (University of Dundee, UK)	Growth arrest in bacterial biofilms: the pros and cons of self-starvation
9:40	Małgorzata Fic (Max-Planck Institute for Evolutionary Biology, Germany)	Collective beliefs and trust in structured populations
10:00	Hannah Götsch (Faculty of Mathematics, University of Vienna, Austria; Vienna Graduate School of Population Genetics, Austria; Vienna School of Mathematics, Austria)	An infinite sites model for polygenic adaptation in finite populations
10:20	Lucy Lansch-Justen (University of Edinburgh, UK)	Quantifying stress-induced mutagenesis using fluctuation assays
BioQuant SR42		
9:00	Adam Lampert (The Hebrew University of Jerusalem, Israel)	Optimizing the use of suppression zones for containment of invasive species

9:20	Andrew Mair (Maxwell Institute for Mathematical Sciences, Edinburgh, UK)	Modelling the influence of root-oriented preferential flow and root architectural traits on drought resistance in plants
9:40	Ludek Berec (University of South Bohemia, Czech Republic)	Evolution of hosts and their sexually transmitted pathogens
10:00	Rodrigo García-Tejera (University of Edinburgh, UK)	Regulation of stem cell dynamics through volume exclusion
10:20	Ernesto Berríos-Caro (Max Planck Institute for Evolutionary Biology, Germany)	Bottlenecks and antibiotic resistance evolution: stochastic modelling of experiments in bacteria
BioQuant SR43		
9:00	Luis Sordo Vieira (University of Florida, USA)	There is blood in the water: modeling the effects of hemorrhaging in invasive pulmonary aspergillosis
9:20	Daniel Rüdiger (Max Planck Institute for Dynamics of Complex Technical Systems, Germany)	Modeling the intracellular replication of a new type of defective interfering particle of influenza virus with genomic nucleotide substitutions
9:40	Erwing Fabian Cardozo-Ojeda (Fred Hutchinson Cancer Research Center, USA)	Mathematical modeling of gene and cell therapy approaches for HIV cure
10:00	Harsh Chhajer (Indian Institute of Science, India)	Modelling cellular lifecycle of positive-sense (+)RNA viruses suggests strategies for inhibiting productive cellular infection
10:20	Giada Fiandaca (Department of Cellular, Computational and Integrative Biology (CIBIO), University of Trento, Italy)	A knowledge-oriented approach to drive mRNA-vaccine design via QSP modelling
Mathematikon Hörsaal		
9:00	Hendrik Nunner (Department of Sociology/ICS, Utrecht University, The Netherlands; Centre for Complex System Studies (CCSS), Utrecht University, The Netherlands)	Health behavior homophily can mitigate the spread of infectious diseases in small-world networks
9:20	Francesca Scarabel (The University of Manchester, UK)	A renewal equation model for disease transmission dynamics with contact tracing
9:40	Zhijun Wu (Iowa State University, USA)	Social Distancing as a Social Dilemma Game
10:00	Todd Lawrence Parsons (CNRS & Sorbonne Université, France)	The Persistence of Emerging Pathogens
10:20	Thomas Allan House (University of Manchester, UK)	Mathematical Methods for Large Community Infection Surveys

Mathematikon A		
9:00	Rosemary A. Aogo (Viral Epidemiology and Immunity Unit, Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892-3203, USA)	Using serological and case data to model the effect of re-exposure to flaviviruses on epidemic dynamics in Nicaragua
9:20	Rasmus Kristoffer Pedersen (PandemiX Center, Department of Science and Environment, Roskilde University, Denmark)	Model-based approach for determining COVID-19 incidence for different testing intensities
9:40	Ewan McTaggart (University of Strathclyde, UK)	The effect of pests and pathogens on forest harvesting regimes: a bioeconomic model
10:00	Clotilde Djuikem (Université Côte d'Azur, Inria, INRAE, CNRS, Sorbonne Université, BIOCORE, France)	Bifurcation analysis in a coffee leaf rust epidemiological model
10:20	Ross Carter (Sainsbury Laboratory, Cambridge University, UK)	The Mechanical Control of Differential Growth in Plants
Mathematikon B		
9:00	Matteo Bottacchiari (Sapienza University of Rome, Italy)	Topological transitions in fluid lipid membranes: activation energy and force fields
9:20	Giuseppe Pontrelli (Consiglio Nazionale delle Ricerche, Italy)	A drug release model for functionally graded spherical micro-capsules
9:40	Josephine Solowiej-Wedderburn (University of Surrey, UK)	Working within constraints: Possible feedback mechanisms for cellular mechanosensation
10:00	Fraser R. Waters (University of Bath, UK)	Minimal Reaction Schemes Exhibiting Turing Instabilities
10:20	Vasco Marius Worlitzer (Bar-Ilan University, Israel; Physikalisch-Technische Bundesanstalt Braunschweig und Berlin, Deutschland)	Biophysical aspects underlying the swarm to biofilm transition

CT3 - Thursday, 22.09.2022, 14:30–16:10

DKFZ big		
14:30	Salvador Chulian Garcia (Department of Mathematics, University of Cadiz, Spain; Biomedical Research and Innovation Institute of Cádiz (INiBICA), Spain)	Persistence homology applied to data from relapsing leukaemia patients
14:50	Thomas Dombrowski (Department of Integrated Mathematical Oncology, H. Lee Moffitt Cancer Center and Research Institute, Tampa, USA)	Tumor-immune ecosystem dynamics define an individual Radiation Immune Score to predict pan-cancer radiocurability
15:10	Subhayan Chattopadhyay (Division of clinical genetics, Lund University, Sweden)	Chaos dictates clonal landscapes in cancer model systems
15:30	Anna-Dorothea Heller (Max Planck Institute of Colloids and Interfaces, Potsdam, Germany)	A Stochastic Cellular Automaton Approach for Modeling Bone Metastasis
15:50	Runpeng Li (Department of Mathematics, University of California Riverside, Riverside, USA)	Modeling interaction of Glioma cells and CAR T-cells considering multiple CAR T-cells bindings
DKFZ small		
14:30	Philipp M. Altrock (Max Planck Institute for Evolutionary Biology, Germany)	Cell-competition and stochastic extinction in chimeric antigen receptor T cell therapy
14:50	Moriah L. Echlin (Prostate Cancer Research Center, Faculty of Medicine and Health Technology, Tampere University, Tampere, Finland)	Dynamic network analysis of single-cell data-driven Boolean network models of prostate cancer
15:10	Dimitrios Katsaounis (University of St Andrews, UK)	Bridging the gap between individual cell movement and macroscopic cancer invasion models
15:30	Daniel James Glazar (Moffitt Cancer Center & Research Institute, USA)	Dynamically predicting treatment response using tumor growth inhibition model with response criteria
15:50	Leonardo Lonati (University of Pavia, Department of Physics, Pavia, Italy)	Computational model of cell cycle perturbations on adenocarcinoma cell line exposed to X-rays radiation
BioQuant SR41		
14:30	Tim Rogers (University of Bath, UK)	Fluctuation spectra reveal hidden structures of ecological networks
14:50	Prerna Singh (University of Sheffield, UK)	A trade-off between two tolerance strategies of the host leads to evolutionary branching

15:10	Robert John Noble (Department of Biosystems Science and Engineering, ETH Zurich, Basel, Switzerland; Department of Mathematics, City, University of London, UK)	Robust, Universal Tree Balance Indices
15:30	Freya Bull (University of Edinburgh, UK)	A model for the infection dynamics of a urinary catheter
15:50	Luigi Esercito (Bielefeld University, Germany)	Lines of descent in a Moran model with frequency-dependent selection and mutation
BioQuant SR42		
14:30	Cinzia Soresina (University of Graz, Austria)	Multistability and time-periodic spatial pattern in the cross-diffusion SKT model
14:50	Toyo Valentina Vignal (Maxwell Institute Graduate School, UK)	Impact of different destocking strategies on the resilience of dry rangelands
15:10	Maria Rosaria Mattei (University of Naples Federico II, Italy)	Modelling the effect of ionic strength on bacterial adhesion in biofilm formation
15:30	Konstantinos Alexiou (University of St Andrews, UK)	A stochastic multiscale modelling framework for the evolution of phenotype-structured cell populations
15:50	Léonard Dekens (Univeristé Claude Bernard Lyon 1, France)	Evolution of dispersal during range expansion: explicit long-time approximation of sexual species' spatial trait distribution
BioQuant SR44		
14:30	Prakrati Dangarh (Imperial College London, UK)	Mechanistic modelling of pre-school wheezing and progression to school-age asthma
14:50	Punya Alahakoon (The University of Melbourne, Australia)	An estimation framework to study epidemic fade-out using multiple outbreak data
15:10	Kamil Wołos (Nalecz Institute of Biocybernetics and Biomedical Engineering of the Polish Academy of Sciences, Poland)	Cardiac function assessment in patients with chronic kidney disease using subject-specific cardiovascular modeling
15:30	Vaclav Klika (Czech Technical University in Prague, Czech Republic)	Replacing Donnan theory: Upscaled Poisson-Nernst-Planck equations in mildly heterogeneous charged porous media
15:50	Jessica Crawshaw (The University of Oxford, UK)	The role of Hierarchical Bayesian inference in understanding Macular degeneration treatment strategies

Mathematikon Hörsaal		
14:30	Dimitris I. Kalogiros, (Bristol Population Health Science Institute, Bristol Medical School, University of Bristol, UK)	A model-based analysis of the transmission dynamics and control of hepatitis B virus in Punjab (India)
14:50	Zhang, Dongni (Stockholm University, Sweden)	Epidemic models with digital and manual contact tracing
15:10	Augustine Okolie (Technical University of Munich, Germany)	Phylogenetic methods for infectious models
15:30	Andreas Ott (Karlsruhe Institute of Technology, Germany)	A topological data analysis approach for the surveillance of emerging adaptive mutations in the evolution of SARS-CoV-2
15:50	Marcel Fang (Sorbonne Université, France; Inria, France)	Modelling, Analysis, Observability and Identifiability of Epidemic Dynamics with Reinfections
Mathematikon A		
14:30	Adriana Zanca (The University of Melbourne, Australia)	Push or pull? Cell proliferation and migration during wound healing
14:50	Kieran Boniface (University of Surrey, UK)	The roles of different modes of force generation in tissue engineering problems
15:10	Tessa M. Vergroesen (Institute of Biology, Leiden University, The Netherlands)	Falsifying computational models of angiogenesis through quantitative comparison of in vitro to in silico endothelial cell networks
15:30	Ross Carter (Sainsbury Laboratory, Cambridge University, UK)	The Mechanical Control of Differential Growth in Plants
15:50	Cato Hastings (Department of Cell and Developmental Biology, University College London, UK)	"Neighbourhood watch" model: embryonic epiblast cells assess positional information in relation to their neighbours
Mathematikon B		
14:30	Gesa Grüning (Carl von Ossietzky Universität Oldenburg, Germany)	The influence of dynamical degrees of freedom on compass sensitivity: A comparison between plant and migratory bird cryptochrome
14:50	Pedro Jaramillo (Bordeaux University, IMB, France)	Mean field model of single cell electroporation
15:10	Aida Hashtroud (Max Planck Institute for the Physics of Complex Systems, Germany)	A biophysical model of DNA methylation ageing
15:30	Andrea De Gaetano (CNR - Consiglio Nazionale delle Ricerche, Italy)	Fractional stochastic differential models of glucose control

15:50	Dariusz Wrzosek (University of Warsaw, Poland)	Direct/indirect taxis and pattern formation in predator-prey models.
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CT4 - Friday, 23.09.2022, 11:00–12:40

DKFZ big		
11:00	Richard J. Beck (Moffitt Cancer Center, USA)	Modelling the evolutionary landscape of aneuploidy
11:20	Monica Salvioli (TU Delft, The Netherlands)	Game theory to improve treatment of Non-Small Cell Lung Cancer
11:40	Chandler D. Gatenbee (Moffitt Cancer Center, USA)	Immunosuppressive niche engineering at the onset of human colorectal cancer
12:00	Adam L. MacLean (University of Southern California, USA)	Modeling the stochastic dynamics of metastatic breast cancer in complex tumor microenvironments
DKFZ small		
11:00	Maximilian Strobl (H Lee Moffitt Cancer Center & Research Institute, USA)	Mathematical model-informed adaptive cancer therapy
11:20	Ambika Bhatt (Moffitt Cancer Center and Research Institute, USA)	Using Patient-Reported Outcome Dynamics to Predict Response to Immunotherapy in Non-Small Cell Lung Cancer
11:40	Jill A. Gallaher (Moffitt Cancer Center, USA)	Coupling PSA and testosterone dynamics to better classify tumor resistance in prostate cancer
12:00	Johnny T. Ottesen (Roskilde University, Denmark)	Mathematical modeling of inflammation and blood cancers
Mathematikon Hörsaal		
11:00	Yang Han (University of Manchester, UK)	Statistical Design and Analysis of Diagnostic Tests for Mutating Viruses

11:20	Jonathan Hamley (Department of Visceral Surgery and Medicine, Bern University Hospital, University of Bern, Switzerland; Department of Biomedical Research, University of Bern, Switzerland; Bern Center for Precision Medicine, Switzerland)	Infectious disease in the workplace: Quantifying uncertainty in outbreak size
11:40	Antonio Gómez-Corral (Complutense University of Madrid, Spain)	On the use of time-discretized models as approximations to continuous-time epidemic models
12:00	James Daniel Munday (Centre for Mathematical Modelling of Infectious Disease, London School of Hygiene and Tropical Medicine, UK; Department of Infectious Disease Epidemiology, London School of Hygiene and Tropical Medicine, UK)	Evaluating the use of cross-sectional infection and antibody positivity with social contact data to produce age-specific forecasts of SARS-CoV-2 incidence
Mathematikon A		
11:00	Thomas Hodgson (Heriot-Watt University, UK)	Collective Navigation in Flowing Environments
11:20	Frederic Alberti (Bielefeld University, Germany)	The general labelled partitioning process in action: recombination, selection, mutation, and more
11:40	Sarah Anne MacQueen (University College Dublin, Ireland)	Bumblebee pollination service predictions from an individual based model depend on foraging site selection method
12:00	Enrico Di Gaspero (Bielefeld University, Germany)	The Moran Model of population genetics: a new link between forward-time and backward-time perspectives
Mathematikon B		
11:00	Maya Mincheva (1: Northern Illinois University, USA)	Identifying parameter regions for oscillations in reaction networks models
11:20	Johannes Gabriel Borgqvist (Wolfson Centre for Mathematical Biology, University of Oxford, UK)	Occam's razor gets a new edge: the use of symmetries in model selection
11:40	Laura Cifuentes Fontanals (Freie Universität Berlin, Germany; Max Planck Institute for Molecular Genetics, Germany)	Control strategy identification in Boolean networks
12:00	Leo P.M. Diaz (The University of Melbourne, Australia)	Practical applications of hypergraphs to modelling biochemical systems

12:20	Erika Tsingos (Mathematical Institute, Leiden University, The Netherlands)	Modelling mechanical interactions with a fibrous extracellular matrix using a hybrid cellular Potts model and molecular dynamics framework.
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