Workshop

Junior Female Researchers in Probability 2026

Berlin, June 24–26, 2026

Berlin-Oxford IRTG 2544 · TRR 388 · Freie Universität Berlin · Humboldt-Universität zu Berlin · Technische Universität Berlin · WIAS

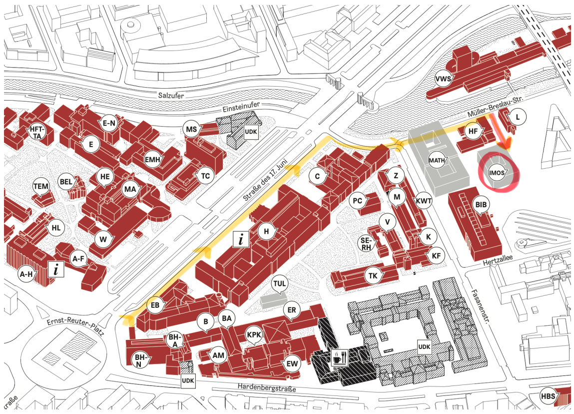
Contents

Introduction

It is our great pleasure to welcome you to the workshop **Junior female researchers in probability**. We hope you enjoy illustrative talks and an interactive and inspiring exchange and networking.

Venue

The workshop will take place in presence at TU Berlin (IMoS building) at Fasanenstraße 89, 10623 Berlin. The building can be accessed only from Mueller-Breslau-Straße, via a path between the HF and L building.



Presentations

The talks of the keynote and invited speakers each last one hour, and the contributed talks each last 20 minutes including questions.

Website

You can find further information on the web page of the workshop: https://wias-berlin.de/workshops/JFRP26/.

Organisers

Peter Bank, Franziska Bielert, Dörte Kreher, Helena Kremp, Gemma Sedrakjan, Janine Steck, Thomas Wagenhofer, Maite Wilke Berenguer, Alexander Zass.

Timetable

Registration Wednesday 8:30–8:50
Welcome Wednesday 8:50–9:00

	WEDNESDAY 24	THURSDAY 25	FRIDAY 26
9:00	Etheridge	Alonso Ruiz	Ling
10:00	coffee break		
10:40	Brunet Guasch	Kuzgun	Heinrich
11:00	Kołodziejska	Stavrianidi	Portillo del Valle
11:20	Krasnowska	Tao	Laurence
11:40	Fernández Baranda	Thierbach	Ongarato
12:00	lunch break		
13:30	Crucianelli	Khatun	Alvarenga
13:50	Zorzi	Mulay	Gernholt
14:10	Ceylan	Peñaloza Velasco	Gonçalves
14:30	Kwossek	Voß	15:10 closing
14:50	coffee break		
15:30	Engström	Morozova	
15:50	Bonesini	Avalos-Pacheco	
17:00	Q&A (to 18:30)		
		18:00 dinner	

Keynote speakers

Brownian motion and the isoperimetric inequality: A way for fractals?

Patricia Alonso Ruiz

University of Jena

An inequality with a long history, the isoperimetric one! Among its practical applications, think of being able to decide the shape of a given amount of material which maximizes the volume you can wrap with it. If the material shows fractal features, like being highly porous and symmetric, you may need to pause, go back to the isoperimetric inequality, and reexamine its formulation: Which volume measure do you use? Which perimeter measure? And what kind of relationship (!) between them can you expect?

... and where is Brownian motion, by the way?

This talk will address the questions above, revisiting a beautiful connection between Brownian motion, functions of bounded variation and the isoperimetric inequality originally due to Ledoux. We will see how these ideas may provide a fruitful approach to study isoperimetric problems on fractal spaces, and in particular on some, whose micro- and macrostructure present different scaling.

The talk is based on joint work with Fabrice Baudoin (Aarhus University).

The Forwards and Backwards of Population Models

Alison Etheridge

University of Oxford

What can we infer about the history of a population from the patterns of genetic variation that we observe today? There is a long history of mathematical modelling of the demographic dynamics of a population and their effect on the genetic relationships between individuals sampled from that population, but the assumptions imposed to ensure analytic tractability are often very strict. Here we lay out a broad class of models that might describe how spatially heterogeneous populations live, die and reproduce. This class is particularly well suited to modelling plant populations. In particular, a novelty of our approach is that we explicitly model a juvenile phase, which, as we illustrate with a toy example, could have important implications for quantities that we might try to infer from genetic data.

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tba

Patrícia Gonçalves
IST Lisbon

tba.

Invited talks

An almost infinite sites model

Alejandra Avalos-Pacheco

JKU Linz

A main challenge in molecular evolution is to find computationally efficient mutation models with flexible assumptions that properly reflect genetic variation. The infinite sites model assumes that each mutation event occurs at a site never previously mutant, i.e. it does not allow recurrent mutations. This is reasonable for low mutation rates and makes statistical inference much more tractable. However, recurrent mutations are common enough to be observable from genetic variation data, even in species with low per-site mutation rates such as humans. The finite sites model on the other hand allows for recurrent mutations but is computationally unfeasible to work with in most cases. In this work, we bridge these two approaches by developing a novel molecular evolution model, the almost infinite sites model, that both admits recurrent mutations and is tractable. We provide a recursive characterization of the likelihood of our proposed model under complete linkage and outline a parsimonious approximation scheme for computing it. We show the usefulness of our model in simulated and human mitochondrial data. Our results show that the AISM, in combination with a constraint on the total number of mutation events, can recover accurate approximations to the maximum likelihood estimator of the mutation rate. An implementation of our model is freely available along with code for reproducing our computational experiments at https://github.com/Cronjaeger/almost-infinite-sites-recursions.

A mean-field model for pollution abatement via cap and trade mechanism

Ofelia Bonesini

LSE London

We consider a Mean Field Game (MFG) model of competitive firms operating under an AK production technology, where output is proportional to capital and production generates emissions. In this setting, we introduce a regulator whose objective is the reduction of cumulative emissions, in the spirit of Emission Trading Systems (ETS), where firms must hold and trade permits to cover their emissions in a regulated market. The regulator acts as a central planner and controls the supply of permits, balancing emission reduction and aggregate output. Permits are allocated through a dynamic auction mechanism that adjusts supply in real time to achieve both market efficiency and the regulators long-term objectives. The regulator and the firms interact through the endogenous permit price, which is determined by the regulators policy and affects firms optimal strategies via the market clearing condition. The regulators optimal policy is derived within a Mean Field Control (MFC) framework. Exploiting the linear-quadratic structure and the presence of common noise, we characterise the equilibrium via a system of coupled FBSDEs and associated Riccati equations. Our results provide a tractable characterisation of optimal permit allocation policies in large economies and offer insights into the design of efficient emission trading mechanisms.

This is a joint work in progress with Giacomo Lanaro.

Regularization by noise: from singular SDEs to singular Young SDEs

Chengcheng Ling

University of Augsburg

Regularization By Noise refers to the phenomenon that stochastic perturbations can improve the behavior of singular dynamical systems. In particular, noise may compensate for irregular features such as low-regularity coefficients, degenerate structures, or memory effects, and thereby lead to better-posed and more stable equations. Since its origins in foundational works of the 1970s, this topic has developed into a broad and active area of modern stochastic analysis.

In this talk, I will discuss several aspects of regularization by noise for singular stochastic differential equations (SDEs), with particular emphasis on both the classical Brownian setting and more singular models driven by fractional noise. The focus will be on questions of well-posedness, qualitative dynamical behavior, and approximation. I will also discuss how these ideas can be implemented in equations with singular drift driven simultaneously by Brownian and fractional Brownian noises.

Contributed talks

The Rightmost Particle of the Contact Process in Dynamic Random Environments

Isabella Alvarenga
Université d'Orléans

This talk studies the contact process with inherited sterility, a probabilistic model inspired by population control strategies based on partial sterility transmitted across generations. For comparison, we also introduce the Spont process, another contact process in a dynamic random environment. We define both models on the one-dimensional integer lattice and prove a central limit theorem for the position of the rightmost occupied site. The main difficulties arise because the Spont process lacks self-duality and the inherited sterility model is non-attractive. Our approach uses renewal times and an analysis of active infection paths to obtain an embedded i.i.d. structure.

Joint work with Aurélia Deshayes.

Funding: This work was carried out while the speaker was a PhD student at the University of Warwick and was funded by the EPSRC.

A multi-type birth-death model of the evolution of metastatic competence reveals distinct metastatic trajectories across cancer types

Meritxell Brunet Guasch
University of Edinburgh

Metastasis is the leading cause of cancer mortality, yet its evolutionary origin remains unresolved. Classical models posit either that metastatic competence is intrinsic to all tumor cells (single-stage) or that it arises through rare evolutionary transitions along specific lineages (multistage). To investigate this, we develop a multitype birthdeath process in which primary tumor cells divide and die stochastically and acquire metastatic competence at rate μ, after which they can seed metastases. We introduce an efficient simulation framework to reconstruct phylogenies relating sampled primary tumor cells to detectable metastases, mimicking available patient sequencing data. We show that the phylogenetic diversity of metastasesquantified by the frequency with which metastatic samples form monophyletic cladesdepends strongly on μ. By integrating epidemiological data on metastatic prevalence with phylogenetic diversity statistics, we demonstrate that joint analysis enables identification of μ, thereby providing a quantitative strategy to measure the evolutionary accessibility of metastatic competence in human tumors. Application to breast, colorectal, and pancreatic cancer data reveals order-of-magnitude differences in inferred μ that correlate with differences in cancer lethality.

This work connects branching-process theory, phylogenetic statistics, and population-level data, providing a probabilistic framework for comparing metastatic potential across cancer types.

Work by Meritxell Brunet Guasch, supervised by Tibor Antal (Edinburgh School of Mathematics) and Kamila Naxerova (Harvard Medical School).

Global universal approximation with Brownian signatures

Mihriban Ceylan
University of Mannheim

In recent years, signature based methods have been very successfully applied in mathematical finance. At the very heart of these methods are universal approximation theorems, establishing that continuous functionals can be approximated arbitrary well on compact sets by linear maps acting on signatures. However, in the context of mathematical finance, the restriction to compact sets causes a lack of theoretical justification for the use of signature based methods.

In this talk, we provide various global universal approximation theorems in the L^p-sense with respect to the Wiener measure. In particular, we demonstrate that functionals on rough path space can be approximated globally in the L^p-sense w.r.t. the Wiener measure. This allows, for instance, to approximate solutions to stochastic differential equations driven by Brownian motions by signature based models, leading to a certain universality of signature based models for financial markets.

Non-linear Graphon Mean Field Games

Carla Crucianelli
Princeton University

When studying a non-cooperative stochastic differential game, it is classical to use the mean-field game framework. However, this approach has its limitations when the particles interact through a random graph. This is because we expect the heterogeneity of the system to be retained in the large population limit. In this talk, we consider a non-cooperative stochastic differential game with player interactions modeled through a sequence of graphs converging to a graphon. We show that under standard regularity conditions and dissipativity of the drift of the state process, when the numer of players goes to infinity, the game converges to a general graphon game. The limit is quantitative and based on a new form of propagation of chaos for interacting FBSDEs on graphs. Further, when the cost function satisfies the Lasry-Lions monotonicity condition, we propose an existence and uniqueness result for graphon games. Our proof relies on investigating a system of uncountably many McKean-Vlasov type BSDEs driven by a continuum of Brownian motions. We study this BSDE in a specific probability framework called a Fubini extension and discuss its well-posedness, characterize the graphon mean-field equilibrium and show its existence and uniqueness. The existence proof is based on a new application of the continuation method.

Joint work with Dylan Possamaï and Ludovic Tangpi.

Low-dimensional adapted optimal transport and its Schrödinger equations

Linn Engström

KTH Royal Institute of Technology

During the last decade there has been a rapid development of methods for computationally addressing optimal transport problems; motivated by applications within robust finance and machine learning, effort has also been made to generalize these techniques to problems equipped with additional causality constraints. Solving such adapted optimal transport (AOT) problems computationally remains a challenging task though for problems formulated over many periods. In this talk we will present an efficient framework for solving a class of AOT problems computationally. Our method leverages on sparse structures inherent in the problems and allows for deriving a low-dimensional version of the adapted Schrödinger equations.

Joint work with Sigrid Källblad.

Hematopoiesis as a continuum: from stochastic compartmental model to hydrodynamic limit

Ana Fernández Baranda

CMAP, Ecole Polytechnique, CNRS, Institut polytechnique de Paris, Inria, Palaiseau, France

We consider a multiscale stochastic compartmental model with three types of cells (stem cells, immature cells and mature cells) which combines cell proliferation and cell differentiation. We derive a hydrodynamic limit when the number of immature compartments goes to infinity obtaining a partial differential equations system with boundary conditions, modelling hematopoiesis as a continuum. We assume that proliferation and differentiation are regulated and let the corresponding rates depend on the number of mature cells. This leads us to model the dynamics of the population by a Markov process in continuous time and discrete space, which does not satisfy the branching property. We prove the convergence in law of the stem and mature cells population size processes and of the empirical measures of the immature cells dynamics, conveniently rescaled, to the unique triplet involving coupled functions and a measure, which are solutions of a deterministic measure valued equation with boundary dynamics. The cell differentiation induces a transport term in space and the main difficulty comes from the boundary effects coming from stem and mature cells. We also prove that the limiting measure admits at each time a density with respect to Lebesgue measure and can be characterized as solution of a partial differential equation.

Joint work with Vincent Bansaye (CMAP), Stéphane Giraudier (Université Paris Cité), and Sylvie Méléard (CMAP).

Decoupling and decay of two-point functions in a two-species TASEP

Sabrina Gernholt

University of Bonn

We study the two-species totally asymmetric simple exclusion process (TASEP) on the integers, a prototypical example of a multi-component model in the KPZ universality class. Under stationary initial conditions, we establish the asymptotic decoupling of the marginal height profiles along characteristic lines and prove the decay of two-point functions in the large-time limit. Both results confirm predictions of the nonlinear fluctuating hydrodynamics theory.

The talk is based on joint work with Patrik Ferrari, available at arXiv:2504.00765.

On Siegmund duality and time reversal of solutions to Lévy-driven SDEs

Henriette Heinrich

TU Dresden

We study Siegmund duality in the setting of Lévy-driven SDEs and derive explicit representations of the Siegmund dual and the inverse flow, whenever they exist, in the class of generalized Ornstein-Uhlenbeck processes. Siegmund duality is of particular interest as the stationary distribution of the dual process provides information about the hitting time of zero of the original process. We show that both the dual and the process corresponding to the inverse stochastic flow are again generalized Ornstein-Uhlenbeck processes. This yields a connection to pathwise time reversal of solutions to Lévy-driven SDEs.

The Diameter of Random Uniform Hypergraphs in the dense regime

Asrafunnesa Khatun

Indian Institute of Science Education and Research Bhopal

Random graphs are widely utilized to model real-world networks such as social, information, and biological networks. Structural parameters, in particular the diameter, enhance our understanding of the connectivity and behavior of random networks. However, real networks often differ from Erdős-Rényi models. The Erdős-Rényi $\mathscr{G}(n,p)$ random graph model is defined on the vertex set $[n] = \{1, 2, \ldots, n\}$ and each possible edge is included independently with probability p, $0 < p < 1$. Bollobás showed that the diameter of $\mathscr{G}(n,p)$ concentrates only on two points using the moments method. A natural generalization of the Erdős-Rényi $\mathscr{G}(n,p)$ random graph is the random uniform hypergraph model $\mathscr{H}(n,t,p)$, defined on the set of vertices $[n] = \{1, 2, \ldots, n\}$ and each possible hyperedge of size t is included independently with probability p. Random hypergraphs capture higher-order interactions in the real-world such as epidemic spreading, information dissemination, protein complexes, and chemical reactions, more accurately than random graphs.

In this talk, I will present recent work with Kartick Adhikari on the diameter of random uniform hypergraphs. We showed that in the dense regime, the diameter of $\mathscr{H}(n, t, p)$ concentrates only on two points. As a corollary, we obtained the Bollobás result. To overcome the strong path dependencies in hypergraphs, we used the Stein-Chen method, in particular size-biased distribution, FKG inequality, and coupling technique.

Asymptotic fluctuations of multi-type Crump–Mode–Jagers processes

Alicja Kołodziejska

JLU Gießen

In the talk, I will present a central limit theorem for the general (C-M-J) branching processes with finitely many types. The result covers a wide range of branching processes, both Markovian and non-Markovian, and unifies and extends limit theorems for specific processes existing in the literature. I will describe the connection between the asymptotic behaviour of the multi-type C-M-J process and certain intrinsic martingales. The talk is based on ongoing joint work with Konrad Kolesko and Matthias Meiners.

Coalescence in Multi-type Branching Processes

Janique Krasnowska

University of Warwick

Branching processes constitute a broad class of stochastic models with applications across many problems in biology. Understanding the ancestry of a sample of individuals is a fundamental question in evolutionary biology and helps describe phenomena such as genetic drift and speciation. The genealogy of branching processes has been studied extensively in the setting where all individuals in a population share a common offspring distribution. A natural generalisation is to consider populations consisting of multiple types of individuals with distinct offspring distributions, representing features such as genetic types, mutations, or dormant and active states.

In this work, we study a supercritical multi-type GaltonWatson process with a possibly countably infinite number of types. We derive an expression for the distribution function of the generation of the most recent common ancestor for a sample of k individuals drawn from a large generation. Under moment conditions on the offspring distributions, we also establish upper and lower bounds, with explicit constants, for this distribution function in terms of moments of the inverse population size. Finally, through simulation studies, we demonstrate that our approach is computationally more efficient than direct simulation of the genealogy of a sample.

This is joint work with Paul Jenkins and Adam Johansen.

Two-point function of KPZ fixed point with Gaussian initial data

Sefika Kuzgun
MPI MiS

In this talk we consider KPZ fixed point starting from a Gaussian process with stationary increments. Using Malliavin integration by parts, we establish a formula for the two-point correlation of the spatial derivative of the KPZ fixed point in terms of the second derivative of its variance.

This talk is based on an ongoing joint work with Arjun Krishnan.

Pathwise stochastic integration and invariance with respect to the choice of the partition sequence

Anna Kwossek
University of Vienna

In this talk, we present a pathwise approach to stochastic integration: Using the concepts of quadratic variation and Lévy area of a continuous path along a sequence of time partitions, we construct a pathwise integral as a limit of general Riemann sums. In a probabilistic framework, when the underlying process is a semimartingale, this notion of integration is consistent with stochastic integration. Furthermore, we give necessary and sufficient conditions for the quadratic variation and Lévy area of a continuous path to be invariant with respect to the choice of the partition sequence.

This talk is based on joint work with Purba Das and David Prömel.

Noise induced stabilization in stochastic chemical reaction network

Lucie Laurence
University of Bern

Chemical reaction networks (CRNs) are commonly analyzed through deterministic or stochastic models that track molecular populations over time. In regimes with large molecule counts, stochastic dynamics are typically approximated by deterministic mass-action kinetics. We present a CRN that defies this expectation: while the deterministic system is unstable, exhibiting finite-time blow-up of trajectories within the interior of the state space, its stochastic counterpart is positive recurrent.

References

[1] Agazzi, A. and Laurence, L.: Noise-induced stabilization in a chemical reaction network without boundary effects. (2025) arXiv:2506.12163

Statistical inference for Nemytskii-type McKean-Vlasov SDEs via DNN

Ekaterina Morozova

Universität Duisburg-Essen

The current talk is based on the joint research with Denis Belomestny, which is devoted to the statistical inference for a nonlinear drift coefficient and invariant distribution of the McKean-Vlasov SDEs of Nemytskii-type. The key feature of this type of equations is that their coefficients — in our case the drift — depend on the law of the solution through its density. This leads to certain theoretical challenges, as this dependence implies that the coefficients lack continuity in their measure component, which makes most of the results available for McKean-Vlasov SDEs inapplicable (see, e.g., [2]).

In this research, we are considering a particular form of such equations, which can be viewed as a nonlinear perturbation of the Ornstein-Uhlenbeck process. We study its analytical properties, comparing them to those of the classical Ornstein-Uhlenbeck process, and, in particular, establish the chi-squared convergence to the stationary distribution. On the statistical side, we propose an MLE-type approach allowing for a nonparametric estimation of the invariant density of this nonlinear process and the drift function using classes of deep neural networks, which develops the ideas of [1].

References

[1] Belomestny, D. and Orlova, T. (2025). Statistical Inference for Conservation Law McKean-Vlasov SDEs via Deep Neural Networks. SIAM/ASA Journal on Uncertainty Quantification, 13(2), 425–448.

[2] Grube, S. (2023). Strong solutions to McKean-Vlasov SDEs with coefficients of Nemytskii-type. Electronic Communications in Probability, 28, 1–13.

Scaling Limits of Barely Supercritical Random Trees

Vinita Mukund Mulay

University of Duisburg-Essen

Consider a sequence of supercritical branching processes conditioned on survival such that their extinction probability $q_n \uparrow 1$. Such a sequence is called a sequence of barely supercritical branching processes, since the processes become more ‘critical’. In this talk we study the scaling limit of the family trees of such a sequence. Using contour based arguments over supercritical random trees with geometric distribution we describe the limiting object, which can be characterized by a branching Brownian motion with a negative drift and state dependent branching.

Based on joint ongoing work with Anita Winter (University of Duisburg-Essen).

Stable measure transformations for affine jump-diffusions

Beatrice Ongarato
TU Dresden

Affine processes are Markov processes whose characteristic functions admit an exponentially affine dependence on the initial state. This structural property underlies their widespread use in applications, as it ensures a balance between model flexibility and analytical tractability. This naturally raises the question of whether the affine property is stable under changes to equivalent probability measures. In this work, we provide a full characterization of the class of locally equivalent probability measures that preserve the affine structure in a general affine jump-diffusion setting. Building on the methodological framework developed for general Markov processes, we exploit the additional affine structure to derive necessary and sufficient conditions on admissible transformations. Our results yield an explicit and verifiable criterion, enhancing the applicability of our work across multiple areas.

Joint work with Claudio Fontana (University of Padova).

The time to the most recent common ancestor (TMRCA) of genealogies in populations of varying size

Lizbeth Peñaloza Velasco
Universidad Iberoamericana

In population genetics, coalescent theory models how the ancestors of samples trace back through time, forming genealogical trees. Once we have a suitable coalescent model for the genealogy of a population, we can employ mathematical tools to address biological questions, such as determining the time required to reach the most recent common ancestor (TMRCA) of a sample.

In this talk, I will present results on the density and moments of the TMRCA for time-inhomogeneous coalescent processes, which describe the genealogies of populations evolving under deterministically varying population sizes, using recent results on inhomogeneous phase-type random variables.

This work is with Alejandro H. Wences (UNAM), Matthias Steinrücken (University of Chicago), and Arno Siri-Jégousse (UNAM).

References

[1] H. Wences A., L. Peñaloza, M. Steinrücken and A. Siri-Jégousse. The TMRCA of general genealogies in populations with deterministically varying size. Theoretical Population Biology, 165: 1-9, 2025.

Random walks with echoed steps

Daniela Portillo del Valle

University of Zürich

A random walk with echoed steps (RWES) is a process $\{\tilde{S}_n\}_{n\geq 1} = \{\tilde{X}_1 + \cdots + \tilde{X}_n\}_{n\geq 1}$ that inserts memory and echo into an ordinary random walk (ORW) with i.i.d. steps, $X_1 + \cdots + X_n$. The RWES is defined recursively as follows. Let $\tilde{S}_1 = X_1$. With probability $1-p$, the n-th increment of the RWES follows that of the ORW, $\tilde{X}_n = X_n$. Otherwise, $\tilde{X}_n$ is set as a random echo of a uniform sample of the past steps $\tilde{X}_1, \ldots, \tilde{X}_{n-1}$ determined by a random factor ξ_n. Namely, $\tilde{X}_n = \xi_n \tilde{X}_{\mathcal{U}[n]}$ with probability p, where $\mathcal{U}[n] \sim \text{Uniform}\{1, \ldots, n-1\}$. The RWES is a broad generalization of the elephant random walk and of the positively/negatively/unbalanced step-reinforced random walks. We determine strong convergences of $\tilde{S}$ when the echo law ξ is non-negative. The rates of convergence are determined by the product $p\mathbb{E}\xi$ and exhibit a phase transition with critical value at $p\mathbb{E}\xi = 1$. Highlight that in its super-critical regime, the RWES has super-linear scaling exponentsobserved for the first time in this type of random walks with memory. We provide Laws of Large Numbers, conditions for the convergence of $\tilde{S}$ around its mean towards random series and provide some distributional properties of the limits. Our approach relies on the interpretation of the model in terms of continuous time branching random walks, random recursive trees, Pólya urns, and associated martingales.

On the density of the supremum of nonlinear SPDEs

Alexandra Stavrianidi

University of Münster

The existence and regularity of densities for the supremum of stochastic processes is a classical problem in probability theory. While such questions are well understood for several Gaussian processes, much less is known for nonlinear stochastic partial differential equations. In this talk, I will present joint work with G. Karali, K. Tzirakis, and P. Zoubouloglou establishing the existence of a density for the supremum of solutions to a class of nonlinear SPDEs in one spatial dimension driven by space-time white noise. The class includes the nonlinear stochastic heat equation on a bounded domain with Dirichlet or Neumann boundary conditions. The proof relies on Malliavin calculus and a Bouleau-Hirsch type criterion adapted to suprema of random fields.

An SPDE-based proof on jointly invariant measures for KPZ/Burgers

Ran Tao

Max Planck Institute for Mathematics in the Sciences

We develop an SPDE-based proof of the jointly invariant measures for the KPZ/Burgers equation in the periodic and full-space settings. In contrast to prior proofs that rely on the ColeHopf transform and integrable semi-discrete approximations to the coupled system (Groathouse-Rassoul-Agha-Seppäläinen-Sorensen; Corwin-Gu-Sorensen), our method works directly at the level of the coupled SPDEs, utilizing the established one-point invariant measures and time-reversal of energy solutions of KPZ equation.

This is ongoing joint work with Alex Dunlap, Nicolas Perkowski, and Hendrik Weber.

A Variational Approach to the Aviles-Giga Gibbs Measure

Clara Thierbach

HU Berlin

The Aviles-Giga functional is one of the most prominent models arising in the variational modelling of pattern formation in materials. It has applications ranging, e.g., from blistering phenomena in thin films to liquid crystals. In this talk, we will discuss a characterization of the associated Gibbs measure in the sense of statistical mechanics. For that, we build on ideas that were developed by N. Barashkov and M. Gubinelli in their work on the Φ^4_d model.

Joined work with Jean-Dominique Deuschel (TU Berlin) and Barbara Zwicknagl (HU Berlin).

References

[1] N. Barashkov and M. Gubinelli. A variational method for Φ^4_3. Duke Mathematical Journal, 169(17), November 2020.

Data-Driven Optimal Stopping of Multidimensional Diffusions via Nonparametric Estimation

Laura Voß

Kiel University

We study optimal stopping for multivariate diffusion processes from a statistical perspective. Our approach is based on a structural representation of the value function as the minimum of a linear potential operator acting on non-negative drivers. This representation separates stochastic dynamics, payoff structure, and stopping geometry, and enables a direct statistical analysis of stopping rules via estimation of the value operator.

The analysis proceeds in two steps. First, under full information, we establish a potential representation of the value function in terms of the martingale generator and an occupation measure formulation of optimal stopping. Second, in the data-driven setting, we construct nonparametric

estimators of the value operator by estimating transition densities. A key feature of the analysis is that the resulting operator error bounds are *uniform* over a class of diffusion models and *uniform* over (t, x) in a prescribed domain, yielding genuinely nonparametric learning guarantees beyond a fixed-model setting.

Trembling-Hand Refinements in Mean Field Games

Lucrezia Zorzi
University of Verona

We introduce trembling-hand refinements for Mean Field Games (MFGs) aimed at selecting equilibria that are robust to small perturbations in the population behaviour. The idea is inspired by Selten's trembling-hand perfection in finite games and adapts it to the mean field setting, where perturbations naturally act at the level of controls and propagate through the dynamics to induce perturbed population flows. Within this framework, we model population trembles through relaxed controls with full support, which represent small random deviations from the equilibrium strategy. This leads to two notions of refinement, depending on whether robustness is required along at least one sequence of perturbations or uniformly across all admissible perturbations. The proposed refinements provide a principled equilibrium selection mechanism in Mean Field Games with multiple equilibria. We illustrate their effectiveness through several examples, including linear-quadratic models and models with saturated terminal interactions, where trembling-hand perfection selects the equilibria that remain stable under small behavioural errors. Finally, we discuss a sufficient condition for uniform trembling-hand perfection based on a uniform strict gap property of the Hamiltonian, ensuring that the equilibrium control remains locally optimal under perturbations of the population flow.

This is joint work with Luca Di Persio (University of Verona) and Luciano Campi (University of Milan).

Speaker Index