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Meeting
“Stochastic Models in Biomathematics and Applications”

SMOD 2026

BOOK OF ABSTRACTS

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Dipartimento di Matematica – Università degli Studi di Salerno
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FOREWORD

The Meeting "Stochastic Models in Biomathematics and Applications" (SMOD 2026) is a program of lectures for a group of specialists in various fields of Probability and Mathematical Statistics, with special focus on Stochastic Models, Biomathematics and Applications. We aim to have a scientifically interesting and stimulating opportunity to exchange information and to promote fruitful interactions.

Main topics of the Meeting include Stochastic models and applications, Stochastic processes, Stochastic orderings and information measures, Spread of infectious diseases, Finite-velocity random motions, Diffusion processes and first exit times, Compound counting processes, Random lifetimes in additive hazards models, Mathematical models and statistical analysis of mixed shock models, Fractional stochastic processes for population dynamics, Variational inequalities and applications to network equilibrium problems, Variational problems in information processing, Inference in diffusion processes.

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Testing heteroskedasticity in diffusion processes

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Diffusion processes derived from deterministic growth equations are widely employed in modeling population dynamics and related socio–economic phenomena. While classical deterministic models capture the average trajectory of the system, stochastic extensions provide a more realistic description of the observed dynamics. In particular, when the variance of the stochastic component depends on the state of the process or evolves over time, the system exhibits heteroskedasticity. Traditional heteroskedasticity tests are typically based on regression residuals and assume a fixed discrete–time model structure; however, such approaches are not directly applicable in the context of continuous–time diffusion processes.

We propose a heteroskedasticity test for diffusion processes arising from stochastic versions of growth equations. The test is formulated as a distributional specification test and relies on the Jensen–Shannon divergence to measure discrepancies between the empirical distribution of standardized diffusion increments and the theoretical normal distribution implied by a homoskedastic diffusion model. Since the finite–sample distribution of the test statistic is not available in closed form and depends on parameter estimation and discrete observation schemes, critical values are obtained via Monte Carlo simulation under the null hypothesis of homoskedasticity. The Monte Carlo calibration explicitly accounts for estimation uncertainty and discretization effects by replicating the entire testing procedure on simulated paths generated under the null model.

A comprehensive Monte Carlo simulation study is conducted to assess the finite–sample performance of the proposed test. The results show that the Monte Carlo calibrated procedure achieves accurate size control under the homoskedastic null hypothesis and exhibits good power against a broad class of heteroskedastic alternatives, including state–dependent, multiplicative, and time–varying diffusion coefficients.

References

1. Chen, Q., Hu, M., and Song, X. (2017) A nonparametric specification test for the volatility functions of diffusion processes. *Econometric Reviews*, **38**(5), 557–576.

2. Dette, H. and Podolskij, M. (2012) Testing the parametric form of the volatility in continuous time diffusion models. *Journal of Econometrics*, **168**(1), 122–144.

3. Kristensen, D. (2010) Nonparametric filtering of the realized spot volatility. *Econometric Theory*, **26**(4), 960–989.

Advanced survival modeling approaches for prognostic analysis via multi-omic data integration

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High-throughput omics technologies have significantly advanced biomedical research by enabling comprehensive molecular profiling. While single omics layers provide limited information, their integration offers a multidimensional view of disease biology, improving prognostic modeling and supporting personalized medicine, particularly in oncology.
Survival analysis based on the Accelerated Failure Time (AFT) model is a powerful framework for linking time-to-event outcomes with molecular predictors. Integrating multi-omics data within this model allows the investigation of how molecular alterations across different data views jointly affect patient survival and recurrence, facilitating biomarker discovery and improving survival prediction.
In this talk, we propose a novel cooperative survival analysis approach, termed CoopAFT, which extends the AFT model through a penalized likelihood framework for joint estimation and variable selection. The log-linear AFT model is defined as

$$\log T_i = \boldsymbol{u}_i^T \boldsymbol{\beta}_{\boldsymbol{u}} + \boldsymbol{z}_i^T \boldsymbol{\beta}_{\boldsymbol{z}} + \sigma \varepsilon_i, \quad i = 1, \ldots, n,$$

where $\varepsilon_i \in \mathbb{R}$ is a random error independent from the two omics data views $\boldsymbol{u}_i$ and $\boldsymbol{z}_i$, $\boldsymbol{\beta}_{\boldsymbol{u}}$ and $\boldsymbol{\beta}_{\boldsymbol{z}}$ are the corresponding regression coefficients and σ is a scale parameter.
Model parameters $\boldsymbol{\theta} = ({\boldsymbol{\beta}_{\boldsymbol{u}}}^T, {\boldsymbol{\beta}_{\boldsymbol{z}}}^T, \sigma)^T \in \mathbb{R}^p \times \mathbb{R}^+$, with $p = p_u + p_z$, are estimated by minimizing a penalized negative AFT log-likelihood, combining a cooperative penalty that enforces agreement between the two data views and an ℓ_1-penalty promoting sparsity, i.e.,

$$\widehat{\boldsymbol{\theta}} = \underset{\boldsymbol{\theta} \in \mathbb{R}^p \times \mathbb{R}^+}{\operatorname{argmin}} \left\{ -\frac{1}{n} \ell(\boldsymbol{\theta}) + \mathcal{P}_{\lambda,\rho}(\boldsymbol{\theta}) \right\},$$

where the penalty term $\mathcal{P}_{\lambda,\rho}(\cdot)$ is given by

$$\mathcal{P}_{\lambda,\rho}(\boldsymbol{\theta}) = (1-\rho)\lambda \|\mathbf{U}\boldsymbol{\beta}_{\boldsymbol{u}} - \mathbf{Z}\boldsymbol{\beta}_{\boldsymbol{z}}\|^2 + \rho\lambda(||\boldsymbol{\beta}_{\boldsymbol{u}}||_1 + ||\boldsymbol{\beta}_{\boldsymbol{z}}||_1).$$

Parameter $\lambda > 0$ is the regularization parameter tuned by some data-driven criterion, while $\rho \in [0, 1]$, is a user-defined parameter representing the trade-off between the two penalties. The optimization problem is efficiently solved using a proximal gradient descent algorithm. We establish theoretical consistency of the proposed estimator and assess its performance through simulation studies and real cancer survival data analyses.
Overall, the CoopAFT framework enhances survival prediction by integrating complementary multi-omics information, supporting robust biomarker identification and personalized

treatment strategies in cancer research.

References

1. Angelini, C., De Canditiis, D., De Feis, I., and Iuliano, A. (2024). A Network-Constrain Weibull AFT Model for Biomarkers Discovery. *Biometrical Journal*, **66(7)**, e202300272.

2. Ding, D. Y., Li, S., Narasimhan, B., & Tibshirani, R. (2022). Cooperative learning for multiview analysis. *Proceedings of the National Academy of Sciences*, **119(38)**, e2202113119.

The time-nonlocal harmonic oscillator and the time-nonlocal Ornstein-Uhlenbeck process

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While in recent years, time-nonlocal Kolmogorov equations have been used to describe several physical models, in particular anomalous diffusions, there are not so many results concerning time-nonlocal Schrödinger-type equations. Time-fractional Schrödinger equations were first considered in [1], where the author already noticed the loss of several fundamental properties of the solutions, that implied the non-coherence with the classical quantum mechanics. Nevertheless, these equations have been shown to be of particular interest in quantum information theory in [2]. In this talks, we will consider a time-nonlocal Schrödinger equation, both in the imaginary and the real time axis, with the quantum harmonic oscillator potential. In particular, we will exhibit both strong and distributional solutions in negative order Hermite-Sobolev spaces and we will provide a Mehler-type formula for the integral kernel of the time-changed semigroup. Furthermore, in the fractional setting, we will also consider the equation coming from the application of a Wick rotation, as in [1], proving that solutions of such an equation converge towards a non-constant steady state. All these results are obtained by means of an intertwining relation between the Hermitian with the quadratic potential and the generator of an Ornstein-Uhlenbeck process. This is part of an ongoing joint work with Nikolai Leonenko.

References

1. Naber M. (2004) Time fractional Schrödinger equation *J. Math. Phys.* **45.8**, 3339–3352
2. Zu C., Gao Y. and Yu X. (2021) Time fractional evolution of a single quantum state and entangled state *Chaos, Solitons & Fractals* **147**, 110930

Are all distributions distorted?

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Distortion functions were introduced by Yaari [5] within the theory of choice under risk, aiming to perform a "distortion" on the initial risk distribution. Specifically, an increasing continuous function $q : [0, 1] \to [0, 1]$ such that $q(0) = 0$ and $q(1) = 1$ is named distortion function. Then, given a cumulative distribution function (CDF) F, the distorted CDF from F through q is $F_q = q(F)$. Similarly for the survival function (SF) $\overline{F} = 1 - F$ by considering the dual distortion function with respect to q, namely $\tilde{q}(u) = 1 - q(1 - u)$, for $u \in [0, 1]$. Indeed, $\overline{F}_q = \tilde{q}(\overline{F})$ is the distorted SF of F_q. Nowadays distorted distributions are employed in several fields, such as Order Statistics, Reliability Theory and Survival Analysis, to name a few (see Navarro [2] and references therein). In this talk, we define and study new distortion functions based on the well-known Receiver Operating Characteristic (ROC) curve. They can be used to provide the distortion function which connects two CDFs (or two SFs) when distortion-based model assumptions are unknown. We also consider new distortions which are related with the concept of partial area under the ROC curve through recent univariate skewed models (see Navarro and Arevalillo [3]). Note that, any distortion function is a CDF with support included in $[0, 1]$. In this sense, various stochastic orders and aging classes (cf. Shaked and Shanthikumar [4]) are characterized by using the interpretation of ROC-based distortions as CDFs of suitable relative random variables. Some connections with equilibrium distribution, Lorenz curve and Gini's index are provided too. A real data application of the distortion-based results allows us to evaluate the performance of some Machine Learning classifiers by using semiparametric estimations of the ROC. The talk is based on Capaldo et al. [1].

References

1. Capaldo M., Arevalillo J M., & Navarro J. (2025). Distorted distributions and ROC curves. *Scandinavian Journal of Statistics* **52**, 1786–1815.
2. Navarro J. (2022). *Introduction to System Reliability Theory.* Springer.
3. Navarro J., Arevalillo J.M. (2023). On connections between skewed, weighted and distorted distributions: applications to model extreme value distributions. *Test* **32**, 1307–1335.
4. Shaked M., Shanthikumar J.G. (2007). *Stochastic Orders.* Springer, New York.

5. Yaari M.E. (1987). The dual theory of choice under risk. *Econometrica: Journal of the Econometric Society* **55**, 95–115.

A brief summary of the main aspects of the long range voter model and the p−voter model

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Statistical mechanics was born to provide a powerful theoretical framework to describe equilibrium collective phenomena emerging from the interaction of many degrees of freedom in thermodynamical or chemical systems. In non-equilibrium settings there is no comprehensive theory yet, but we can study each system individually by investigating its time evolution (dynamics) by means of stochastic equations that involve, in some way, the time evolution of the degrees of freedom of the system. We focus on ordering processes, one of the simplest yet most paradigmatic classes of non-equilibrium dynamics. These processes are relevant not only in physics, where they model the relaxation toward ordered equilibrium phases, but also in interdisciplinary contexts such as social and biological [5,6] dynamics.

We first study analytically the ordering kinetics of the long-range voter model in arbitrary dimensions [2,3,4]. The model consists of N agents (or spins) described by binary variables $S_i = \pm 1$, where at each time step an agent copies the state of another chosen at distance r with probability $P(r) \propto r^{-\alpha}$, with $\alpha > 0$. The long-range voter model is exactly solvable and exhibits nontrivial ordering behavior depending on the interaction exponent α.

Although similar in spirit to the Ising model − the physical model used to describe ordering in ferromagnets − the dynamics of voter model turns out to be different from the Ising one. We then introduce and investigate a generalization of the voter dynamics, the long-range p−voter model [1]. In this model, each agent adopts the state of the majority of p other agents selected at distances distributed according to the same algebraic probability $P(r)$. For $p = 2$, the dynamics can be exactly mapped onto the standard long-range voter model. For $p \geq 3$ the equations for correlation functions do not close and we employ numerical simulations to characterize the ordering kinetics. We find that the system crosses over to the dynamical universality class of the Ising model with long-range coupling $J(r) \propto r^{-\alpha}$.

Our results highlight the emergence of a transition in dynamical universality controlled by the parameter p, underscoring the role of simple, analytically tractable models as building blocks for understanding more complex non-equilibrium phenomena. Owing to universality, insights gained from these minimal models are expected to be relevant across a wide range of physical, biological, and social systems.

References

1. Corberi, F., dello Russo, S., and Smaldone, L., “Ordering kinetics with long-range interactions: interpolating between voter and Ising models,” *J. Stat. Mech.: Theory Exp.* **2024**, 093206 (2024).

2. Corberi, F., and Castellano, C., “Kinetics of the one-dimensional voter model with long-range interactions,” *J. Phys.: Complexity* **5**, 025021 (2024).

3. Corberi, F., and Smaldone, L., “Ordering kinetics of the two-dimensional voter model with long-range interactions,” *Phys. Rev. E* **109**, 034133 (2024).

4. Corberi, F., dello Russo, S., and Smaldone, L., “Coarsening and metastability of the long-range voter model in three dimensions,” *Phys. Rev. E* **110**, 024143 (2024).

5. Kimura, M., and Weiss, G. H., “The stepping stone model of population structure and the decrease of genetic correlation with distance,” *Genetics* **49**, 561–576 (1964).

6. Malécot, G., Yermanos, D., and K. M. R. Collection, *The Mathematics of Heredity*, W. H. Freeman, New York (1970).

A stochastic growth model with random catastrophes applied to population dynamics

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Stochastic growth models and sigmoidal dynamics play a fundamental role in capturing patterns frequently encountered in natural systems. They are widely employed in biology and ecology to describe processes such as population evolution, disease transmission, and adaptive responses to environmental variability. In this work, we investigate a lognormal diffusion process subject to random catastrophic events, modeled as sudden jumps that reset the system to a new random state. The novelty of the model lies in the assumption that the post-catastrophe restart level follows a binomial distribution. As a consequence, after each catastrophic event the population does not simply revert to its initial size, but instead to a random level reflecting the survival probability of individual members.
The proposed framework is applied to the dynamics of a wolf population subject to external disturbances. The results indicate that the model is able to realistically reproduce complex population trajectories, characterized by phases of gradual growth alternated with sudden declines driven by random external events.

References

1. Di Crescenzo A., Musto S., Paraggio P., Torres-Ruiz F. (2025) Special lognormal diffusion processes with binomial random catastrophes and applications to economic data. *Applied Mathematical Modelling* **145**, 116146. https://doi.org/10.1016/j.apm.2025.116146

2. Giorno V., Spina S. (2017) A note on diffusion processes with jumps. In: *Computer Aided Systems Theory – EUROCAST 2017* (Eds. Moreno-Díaz R., Pichler F., Quesada-Arencibia A.), pp. 64–71. Springer. https://doi.org/10.1007/978-3-319-74727-9_8

A variance-based approach to study the importance of components and subgroups in a coherent system: the regression importance signature

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The regression importance index of a coherent system evaluates a component's importance, taking into account the system's conditional mean lifetime when the component's failure time is known (see Arriaza et al. [1]). The aim is to extend such importance measure to subgroups of components, introducing the "regression importance signature". This is a tool designed to identify, for any fixed number k of components, the subgroup of size k whose joint state most significantly influences system lifetime variability. Unlike traditional single-component indices, the importance signature captures heterogeneity and interactions, reducing them to intuitive behaviours in series or parallel systems and revealing subsystems or dependencies that cannot be detected by individual measures. In addition, we investigate new properties of the importance index that enhance understanding of how component reliability and structural role jointly affect the system. General results for dependent components are provided, as well as conditions for comparing individual components and subgroups, with a particular attention on system modules. The talk is based on a recent work with A. Di Crescenzo and A. Suárez-Llorens, cf. [2].

References

1. Arriaza A., Navarro J., Sordo M.A., Suárez-Llorens, A. (2023) A variance-based importance index for systems with dependent components. *Fuzzy Sets Syst.* **467**, 108482. https://doi.org/10.1016/j.fss.2023.02.003.

2. Di Crescenzo A., Pisano G., Suárez-Llorens, A. (2025) Analysis of systems with dependent components through a variance-based index and regression importance signature. *Currently under revision.*

Stochastic dynamics with self-exciting factor for Monkeypox transmission

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We develop a stochastic human-rodent compartment model for Mpox transmission that combines diffusion noise with Hawkes self-exciting jumps in the human infection dynamics. Including Hawkes processes allows, for instance, to model the short but significant spikes in transmission happening after crowded events. For the coupled human-rodent system, we prove global existence, uniqueness and positivity of solutions, derive a basic reproduction number R_0 that guarantees almost sure extinction when $R_0 < 1$, and obtain explicit persistence-in-the-mean conditions for both infected rodents and humans, which define persistence thresholds for the joint dynamics. Numerical experiments show how clustered human transmission events, environmental variability and control measures shift these thresholds and shape the frequency and size of Mpox outbreaks.

References

1. Applebaum D. (2009) *Lévy Processes and Stochastic Calculus.* Cambridge: Cambridge University Press, 2nd edition.
2. Arnold L. (1972) *Stochastic, Differential Equations: Theory and Applications.* Wiley, New York.
3. Hawkes A.G. (1971) Spectra of Some Self-Exciting and Mutually Exciting Point Processes. *Biometrika* , **58**, 83-90.
4. Kunita H. (2019) *Stochastic Flows and Jump-Diffusions.* Springer, Singapore.
5. Mao X. (1997). *Stochastic Differential Equations and Applications.* Horwood Publishing Chichester, UK.
6. Rahman G., Tymoshenko O., Di Nunno G. (2025). Insights on stochastic dynamics for transmission of monkeypox: biological and probabilistic behavior, *Mathematical Methods in the Applied Sciences* **48**(15), 14316-14333.

Fractional Pearson diffusions and continuous time random walks

Nikolai Leonenko

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We define fractional Pearson diffusions [4,5,6] by non-Markovian time change in the corresponding Pearson diffusions [1,2,3]. They are governed by the time-fractional diffusion equations with polynomial coefficients depending on the parameters of the corresponding Pearson distribution. We present the spectral representation of transition densities of fractional Pearson diffusions, which depend heavily on the structure of the spectrum of the infinitesimal generator of the corresponding non-fractional Pearson diffusions (fPDs). Also, we present the strong solutions of the Cauchy problems associated with fractional Pearson diffusions and the correlation structure of these diffusions. Continuous time random walks (CTRW) have random waiting times between particle jumps. We define the correlated CTRWs that converge to fPDs [4,5,6]. The jumps in these CTRWs are obtained from Markov chains through the Bernoulli urn-scheme model, Wright-Fisher model and Ehrenfest-Brillouin-type models. The jumps are correlated so that the limiting processes are not Levy but diffusion processes with non-independent increments. This is a joint work with M. Meerschaert (Michigan State University, USA), I. Papic (University of Osijek, Croatia), N. Suvak (University of Osijek, Croatia) and A. Sikorskii (Michigan State University, USA).

We also briefly discussed the related problems for Stretched non-local Pearson diffusions (based on the joint paper [7] with L.Beghin (La Sapienza University, Rome, Italy), I. Papic (University of Osijek, Croatia) and J. Vaz (UNICAMP. Campinas, Brazil).

References

1. Avram, F., Leonenko, N.N and Suvak, N., (2013) Spectral representation of transition density of Fisher-Snedecor diffusion, Stochastics, 85, no. 2, 346-369
2. Bourguin, S., Campese, S., Leonenko, N. and Taqqu, M.S. (2019) Four moments theorems on Markov chaos, Annals of Probability, vol. 47 , no. 3, 1417-1446
3. Kulik, A.M. and Leonenko, N.N. (2013) Ergodicity and mixing bounds for the Fisher-Snedecor diffusion, Bernoulli, Vol. 19, No. 5B, 2294-2329
4. Leonenko, N.N., Meerschaert, M.M and Sikorskii, A. (2013) Fractional Pearson diffusions, Journal of Mathematical Analysis and Applications, vol. 403, 532-546
5. Leonenko, N.N., Papic, I., Sikorskii, A., Suvak, N. (2017) Heavy-tailed fractional Pearson diffusions, Stochastic Processes and their Applications, 127(11): 3512-3535
6. Leonenko, N.N., Papic, I., Sikorskii, A., Suvak, N. (2018) Correlated continuous time random walks and fractional Pearson diffusions, Bernoulli, 24(4B): 3603-3627

7. Beghin, L., Leonenko, N., Papic, I. and Vaz, J. (2026) Stretched non-local Pearson diffusions, Stochastic Processes and Applications, published on line 30/12/2025, https://authors.elsevier.com/c/1mMJO15DqVU1Ze

On some basic boundary value problems in thermoelasticity with microtemperatures

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This contribution is devoted to the analytical study of two boundary value problems for the thermoelasticity system with microtemperatures, which is a generalised model that accounts for thermal effects at the microscale through additional temperature fields. Our focus is on two classical boundary value problems: the Dirichlet problem and the second boundary value problem (Neumann-type). Our analysis relies on potential theory and the theory of reducible operators and differential forms. Unlike in the classical framework, the Dirichlet problem is represented by an elastic single-layer thermoelastic potential, while the second problem is formulated using a double-layer thermoelastic potential. This formulation enables us to reduce the resulting singular integral equations to Fredholm systems and establish representability and solvability results under suitable compatibility conditions on the boundary data.
This is a joint work with Vita Leonessa (see 1. and 2.).

References

1. V. Leonessa, A. Malaspina (2025) On the Dirichlet problem for the system of thermoelasticity with microtemperatures. *Mediterranean Journal of Mathematics* **22**, 1–19.
2. V. Leonessa, A. Malaspina (2025) On the second boundary value problem for the system of thermoelasticity with microtemperatures. *Constructive Mathematical Analysis* **8**(Special Issue: ICCMA), 57–67.

Cox-Ingersoll-Ross and Bessel diffusion processes: interaction, estimation, applications

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In a certain sense, the squared Bessel process can be considered the result of a phase transition in the Cox-Ingersoll-Ross process. We underline their common and distinct properties. More precisely, we begin by presenting several results that provide upper and lower bounds for the time-asymptotic growth rates of both processes. These bounds exhibit notable similarities between the two models. We explore the approximation of CIR and squared Bessel processes by a sequence of CIR processes. We prove the convergence of this sequence in integral norms, assuming that the corresponding coefficients converge. Additionally, we establish upper bounds on the rate of convergence. It turns out that the CIR and squared Bessel processes are closely related, as the squared Bessel process can be represented as the limit of a sequence of CIR processes. However, as anticipated, the upper bounds involve coefficients that depend on the length of the time interval and tend to infinity as the interval length increases. In this sense, the processes diverge, or, in other words, they move apart. We apply this approximation to the problem of parameter estimation for the squared Bessel process using the maximum likelihood method. To establish the strong consistency of the constructed drift parameter estimator, we approximate the squared Bessel process by a sequence of CIR processes, for which the necessary convergence can be derived from their ergodic properties. Furthermore, we show how to estimate the diffusion coefficient of the process based on the realized quadratic variations. Finally, we investigate both processes using the concept of stochastic instability. From this perspective, the properties of the squared Bessel and CIR processes are fundamentally different. We demonstrate that the squared Bessel process exhibits stochastic instability, whereas the CIR process is ergodic and, in this sense, stochastically stable. The talk is mostly based on the paper Y. Mishura, K. Ralchenko and S. Kushnirenko "Driven by Brownian motion Cox-Ingersoll-Ross and squared Bessel processes: Interaction and phase transition". Physics of Fluids, Vol.37, Iss.1 pp. 1 - 15, - 2025

Parameter sensitivity analysis in a stochastic birth-death model for B-cells dynamics

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The aim of this talk is to present a stochastic model, based on a two-dimensional birth-death process, to represent the dynamics of antigen processing in B cells, a fundamental component of the adaptive immune system. Such cells display protein receptors on their membrane, which bind with foreign antigens and process them. Within this framework, we introduce the process $\mathcal{X}(t) := \{(X(t), Y(t)),\ t \geq 0\}$, where $X(t)$ and $Y(t)$ represent the number of free and occupied receptors, respectively. After deriving the partial differential equation satisfied by the probability generating function of the process, we obtain closed and tractable expressions for the main moments and analyze both their transient and long-term behavior. Particular interest is given to the role of the model parameters in the system dynamics from a biological perspective. To this aim, we conduct a sensitivity analysis to assess how variations in the model parameters affect the first-order moments. Specifically, we combine global variance-based sensitivity analysis, through the computation of Sobol' indices, with a local analysis based on small perturbations around fixed points in the parameter space, carried out using elasticity functions. This twofold approach allows us to quantify the individual and joint contributions of the parameters to the output variability, as well as to assess the system's responsiveness to localized changes. The results highlight that even minimal variations in parameters associated with antigen–receptor binding, especially at early stages of the process, can lead to significant changes in the expected number of occupied receptors.

The results presented in this talk are based on a joint work with V. Casolaro and A. Di Crescenzo, currently in press in the Journal of Theoretical Biology.

References

1. Mustaro V., Casolaro V. and Di Crescenzo A. (2026). On the dynamics of antigen receptors on the B-cell membrane through a two-dimensional stochastic process. *Journal of Theoretical Biology*, accepted for publication.

Mittag-Leffler functions and convex ordering

Thomas Simon

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The convex order is a classical stochastic order that compares the dispersion of real random variables. In this talk we wish to apply this notion to study the monotonicity of the classical Mittag-Leffler function E_α with respect to its fractional parameter α, in various contexts. We also show how this notion is helpful for characterizing the log-convexity and the log-concavity of the two-parameter Mittag-Leffler function $E_{\alpha,\beta}$ on the positive half-line. This is based on joint works with Rui Ferreira (Porto), Roberto Garrappa (Bari), Stefan Gerhold (Vienna) and Marina Popolizio (Bari).

A tail-sensitive generalization of Spearman's coefficient for upper-tail dependence analysis

Miguel Angel Sordo Díaz

Dpto. Estadística e Investigación Operativa, Universidad de Cádiz, Spain

Quantifying dependence during extreme events is of paramount importance in fields such as finance, insurance, and environmental sciences. Classical correlation measures often fail to capture co-movements in the tails of distributions. Tail dependence measures — particularly those derived from copula theory — provide a natural framework for modeling such behavior. In this paper, we introduce two classes of copula-based dependence measures designed to assess tail dependence at sub-asymptotic levels. The first class includes, as special cases, Spearman's coefficient and Blest's index, while the second arises as a limiting case of the first. Our approach generalizes Spearman's coefficient to focus explicitly on tail behavior, offering a flexible and interpretable tool for evaluating co-movements in extreme, yet non-asymptotic, regions of the distribution. For both classes, we establish theoretical properties, propose rank-based estimators, derive their asymptotic distributions, and demonstrate their performance through simulation studies and an empirical application.

An easily verifiable dispersion order for discrete distributions

Alfonso Suárez Llorens

Dpto. Estadística e Investigación Operativa, Universidad de Cádiz, Spain

Dispersion is a fundamental concept in statistics, but classical measures — particularly stochastic orders — face important limitations in the discrete setting. We propose a new weak dispersive order for discrete distributions that relaxes restrictive support conditions while preserving key properties. In addition, we introduce variability measures based on probability concentration that satisfy classical axioms and are easy to interpret. Empirical examples illustrate the usefulness of the proposed approach.

Some results for fractional stochastic modeling in biomathematics

Enrica Pirozzi

Dipartimento di Matematica e Fisica, Università degli Studi della Campania "Luigi Vanvitelli", Caserta, Italy

Recently the fractional calculus approach in the construction of non-Markov processes for models with memory revealed a powerful mathematical tool. Time-changed processes and fractionally integrated process have been proposed for modelling the interaction between the myosin head and the actin filament, the physio-chemical mechanism triggering the muscle contraction and now not completely understood. Each of these two models includes memory effects in different way. We describe such features from a theoretical point of view and with simulations of sample paths. Mean functions and covariances are provided considering constant and time-dependent tilting forces by which effects of external loads are included. The investigation of the dwell time of such phenomenon is carried out by means of density estimations of the first exit time (FET) of the processes from a strip: this mimics the times of the steps of the myosin head during the sliding movement outside a potential well due to the interaction with the actin. For the case of the time changed diffusion process we specify an equation for the probability density function of the FET from a strip. The schemes of two simulation algorithms are provided and performed. Some numerical and simulation results are given and discussed.

These results are based on a joint work with Nikolai Leonenko and they can be found in [1].

References

1. Leonenko, N., Pirozzi, E. (2025) The time-changed stochastic approach and fractionally integrated processes to model the actin-myosin interaction and dwell times. *Mathematical Biosciences and Engineering* **22(4)**, 1019–1054.

ABP estimates and first exit time in cylindrical domains

Antonio Vitolo

Dipartimento di Matematica, Università di Salerno, Via Giovanni Paolo II 132, 84084 Fisciano (SA), Italy

In a recent paper we proved existence and uniqueness results of second-order fully nonlinear uniformly elliptic equations with Dirichlet boundary conditions, including the mean first exit time for a stochastic process, in domains of cylindrical type. In this talk, based on the improved Alexandroff-Bakelman-Pucci estimate, we show that this result can be used to estimate higher moments of the first exit time, as well as how it can be extended to more general operators, playing a role in geometric problems of mean partial curvature and stochastic differential games.

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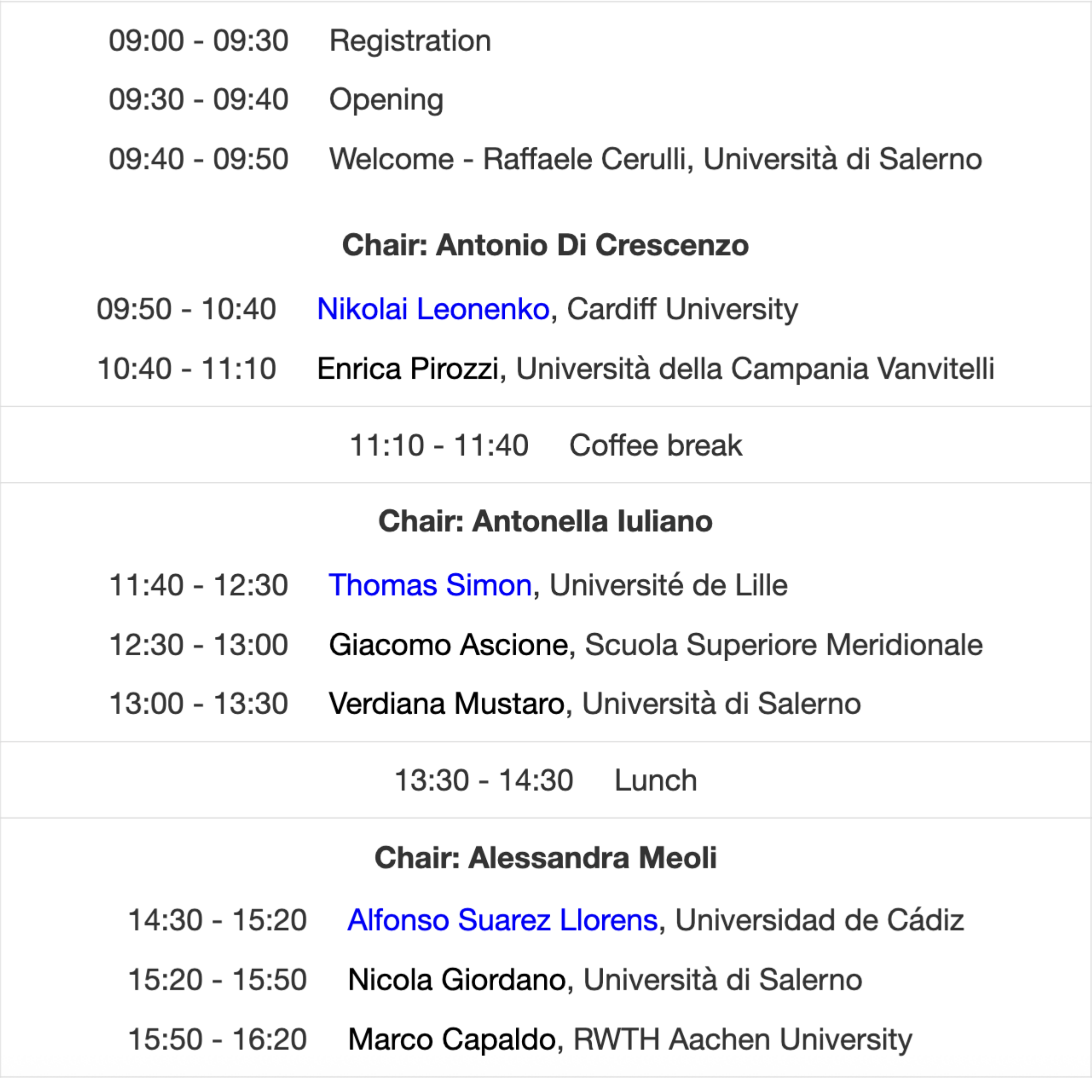
Program – Tuesday, January 20



09:00 - 09:30	Registration
09:30 - 09:40	Opening
09:40 - 09:50	Welcome - Raffaele Cerulli, Università di Salerno
	Chair: Antonio Di Crescenzo
09:50 - 10:40	Nikolai Leonenko, Cardiff University
10:40 - 11:10	Enrica Pirozzi, Università della Campania Vanvitelli
11:10 - 11:40	Coffee break
	Chair: Antonella Iuliano
11:40 - 12:30	Thomas Simon, Université de Lille
12:30 - 13:00	Giacomo Ascione, Scuola Superiore Meridionale
13:00 - 13:30	Verdiana Mustaro, Università di Salerno
13:30 - 14:30	Lunch
	Chair: Alessandra Meoli
14:30 - 15:20	Alfonso Suarez Llorens, Universidad de Cádiz
15:20 - 15:50	Nicola Giordano, Università di Salerno
15:50 - 16:20	Marco Capaldo, RWTH Aachen University

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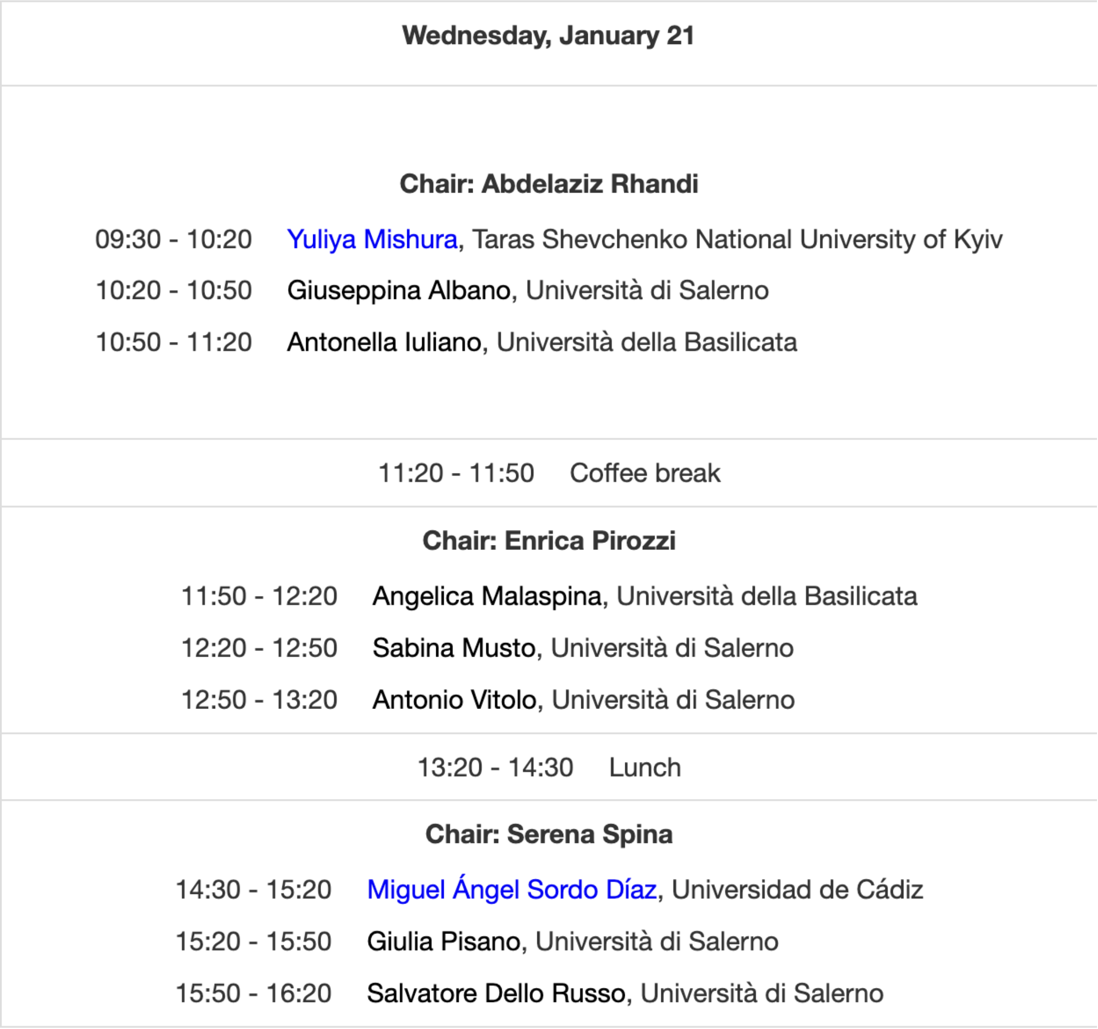
Program – Wednesday, January 21



Wednesday, January 21

Chair: Abdelaziz Rhandi

09:30 - 10:20	Yuliya Mishura, Taras Shevchenko National University of Kyiv
10:20 - 10:50	Giuseppina Albano, Università di Salerno
10:50 - 11:20	Antonella Iuliano, Università della Basilicata
11:20 - 11:50	Coffee break

Chair: Enrica Pirozzi

11:50 - 12:20	Angelica Malaspina, Università della Basilicata
12:20 - 12:50	Sabina Musto, Università di Salerno
12:50 - 13:20	Antonio Vitolo, Università di Salerno
13:20 - 14:30	Lunch

Chair: Serena Spina

14:30 - 15:20	Miguel Ángel Sordo Díaz, Universidad de Cádiz
15:20 - 15:50	Giulia Pisano, Università di Salerno
15:50 - 16:20	Salvatore Dello Russo, Università di Salerno

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