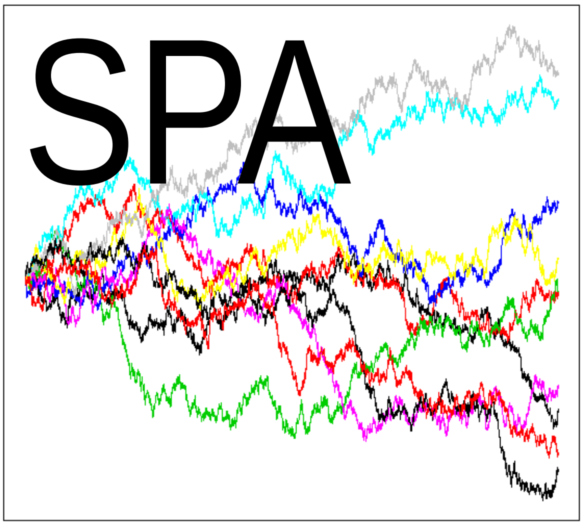
2nd International Workshop on Stochastic Processes and their Applications

Program and Abstracts

A virtual workshop organized by the Working Group on ”Stochastic Processes and their Applications” of the Spanish Society for Statistics and Operations Research



Welcome address

Dear participant,

It is our pleasure to welcome you to the second edition of the International Workshop on Stochastic Processes and their Applications (IWSPA 2021), to be held virtually and online on November 23^{rd}, 25^{th} and 30^{th}, and December 2^{nd} using video conferencing tools.

The workshop is organized by the Working Group on "Stochastic Processes and their Applications" of the Spanish Society for Statistics and Operations Research in an attempt to give visibility to the research carried out on the field by different research groups in Spain and to encourage their interaction with foreign researchers.

We are very pleased that the following researchers, leaders in our field, have agreed to give keynote talks: Mogens Bladt, Thomas Opitz, Anand N. Vidyashankar and Cristina Zucca. Furthermore, 24 thirty-minute talks will be presented in four sessions. The keynote and contributed talks are related to areas of stochastic processes such as birth and death processes, branching processes, Markov processes, diffusion processes, Markovian arrival processes, matrix-analytic methods, random walks in continuous time, renewal theory, space-time processes, and others, as well as their applications in population dynamics, genetics, epidemiology, cancer, cell kinetics, economics, finance, reliability, geophysics and environment.

We wish you a profitable stay in the virtual room of IWSPA 2021!

November 2021
Antonio Gómez-Corral and Miguel González Velasco
Coordinators of the Working Group and co-chairs of IWSPA 2021

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Yarovaya, Elena, Lomonosov Moscow State University, Russia
Ye, Yinna, Xi'an Jiaotong-Liverpool University, China
Zucca, Cristina, Università degli Studi di Torino, Italy

Program at a glance

Tuesday, November 23rd, 2021. Chair: Pepa Ramírez-Cobo

14:55-15:00 (GMT+1) Opening words: Antonio Gómez-Corral, Miguel González Velasco

15:00-15:45 (GMT+1) Keynote talk 1: Inhomogeneous phase-type distributions, by Mogens Bladt, University of Copenhagen, Denmark

15:45-16:15 (GMT+1) Contributed talk 1: Study of the exact reproductive number for SIS models with vertical and horizontal transmissions, by Fátima Palacios-Rodríguez, Universidad de Sevilla, Spain

16:15-16:45 (GMT+1) Contributed talk 2: A multi-stage model of cell proliferation and death: tracking cell divisions with Erlang distributions, by Giulia Belluccini, University of Leeds, UK

17:00-17:30 (GMT+1) Contributed talk 3: Penalty functions for a class of insurance risk processes with two-sided jumps, by Ekaterina T. Kolkovska, CIMAT, Mexico

17:30-18:00 (GMT+1) Contributed talk 4: A cumulant approach for the first-passage-time problem of diffusion processes, by Giuseppe D'Onofrio, Università degli Studi di Torino, Italy

18:00-18:30 (GMT+1) Contributed talk 5: Multi-sigmoidal stochastic growth models for the description of COVID-19 waves, by Antonio Barrera, Universidad de Málaga, Spain

18:30-19:00 (GMT+1) Contributed talk 6: Solving Poisson's equation for birth–death chains: Structure, instability, and accurate approximation, by José Niño Mora, Universidad Carlos III de Madrid, Spain

Thursday, November 25th, 2021. Chair: José Miguel Angulo Ibáñez

15:00-15:45 (GMT+1) Keynote talk 2: First passage time for diffusion processes: direct and inverse problem, numerical and simulative approach, by Cristina Zucca, Università degli Studi di Torino, Italy

15:45-16:15 (GMT+1) Contributed talk 7: Gaussian simply markovian processes over topological versions of graphs, by Juan Baz González, Universidad de Oviedo, Spain

16:15-16:45 (GMT+1) Contributed talk 8: The two barrier escape problem for compound renewal processes with two sided-jumps, by Javier Villarroel, Universidad de Salamanca, Spain

17:00-17:30 (GMT+1) Contributed talk 9: The method of moments and its applications in the theory of branching random walks, by Elena Yarovaya, Lomonosov Moscow State University, Russia

17:30-18:00 (GMT+1) Contributed talk 10: Profit optimization for a stochastic model of cattle growth and variable price categories, by Carlos A. Braumann, Universidade de Évora, Portugal

18:00-18:30 (GMT+1) Contributed talk 11: Studying signals with scale-free dynamics using multi-fractal analysis, by Tahmineh Azizi, Florida State University, USA

18:30-19:00 (GMT+1) Contributed talk 12: Critical controlled branching processes: a Feller diffusion approximation, by Pedro Martín-Chávez, Universidad de Extremadura, Spain

Tuesday, November 30th, 2021. Chair: Fátima Palacios-Rodríguez

15:00-15:45 (GMT+1) Keynote talk 3: Modeling extreme-value dependence in spatial processes: a comparative overview from max-stability to conditional extremes, by Thomas Opitz, Biostatistics and Spatial Processes Lab of INRAE, Avignon, France

15:45-16:15 (GMT+1) Contributed talk 13: Central limit theorem and its convergence rate on counting measures for a branching random walk with immigration in a random environment, by Yinna Ye, Xi'an Jiaotong-Liverpool University, China

16:15-16:45 (GMT+1) Contributed talk 14: On first-passage times and sojourn times in finite QBD processes: An application to varicella-zoster infections, by Diana Taipe Hidalgo, Universidad Complutense de Madrid, Spain

17:00-17:30 (GMT+1) Contributed talk 15: A fractional generalization of some stochastic Gompertz-type models, by Enrica Pirozzi, Università degli Studi di Napoli Federico II, Italy

17:30-18:00 (GMT+1) Contributed talk 16: Why are cell populations replenished via multiple intermediate compartments?, by Flavia Feliciangeli, University of Leeds, UK

18:00-18:30 (GMT+1) Contributed talk 17: The curve-crossing problem for the delayed Brownian motion, by Giacomo Ascione, Università degli Studi di Napoli Federico II, Italy

18:30-19:00 (GMT+1) Contributed talk 18: Near-record values in discrete random sequences, by Miguel Lafuente, Universidad de Zaragoza, Spain

Thursday, December 2nd, 2021. Chair: Miguel González Velasco

15:00-15:45 (GMT+1) Keynote talk 4: Sharp large deviation estimates for functionals of stochastic fixed point equations, by Anand N. Vidyashankar, George Mason University, USA

15:45-16:15 (GMT+1) Contributed talk 19: Portfolio optimization for differente anticipating integrals, by Carlos Escudero, Universidad Nacional de Educación a Distancia, Spain

16:15-16:45 (GMT+1) Contributed talk 20: Regenerative controlled branching processes with continuous time, by Inés María del Puerto, Universidad de Extremadura, Spain

17:00-17:30 (GMT+1) Contributed talk 21: Gaussian processes in the sphere, by Antoni Torres-Signes, Universidad de Málaga, Spain

17:30-18:00 (GMT+1) Contributed talk 22: New insights on the MAP counting process, by Marcos González Bernal, Universidad Carlos III de Madrid, Spain

18:00-18:30 (GMT+1) Contributed talk 23: A stochastic SVIR model with imperfect vaccine and external source of infection, by María Gamboa Pérez, Universidad Complutense de Madrid, Spain

18:30-19:00 (GMT+1) Contributed talk 24: Weighted least square estimation in branching processes with carrying capacity, by Carmen Minuesa, Universidad de Extremadura, Spain

Abstracts

Tuesday, November 23rd, 2021

15:00-15:45 (GMT+1) Keynote talk 1: **Inhomogeneous phase-type distributions**

Author: Mogens Bladt
Affiliation: Department of Mathematical Sciences, University of Copenhagen, Denmark

An inhomogeneous Phase-type distribution (IPH) is the distribution of the time until absorption of an, in general, time–inhomogeneous Markov process on a finite state–space. If the Markov process happens to be time–homogeneous, then we obtain a distribution which is a classical phase–type distribution (PH).

The IPH distributions form a dense class of distributions on the positive reals, which enables them to approximate any positive distribution arbitrarily well and with different kinds of tail behaviour. As opposed to classical PH distributions, which can only posses an exponential tail, we are able to define and deal with distributions with heavy tails (like e.g. Weibull or Pareto) or light tails (like e.g. Gompertz). This is important for applications where tail behaviour is an issue like in insurance risk.

In this talk we provide an overview of the basic construction, properties and estimation of the IPH distributions.

15:45-16:15 (GMT+1) Contributed talk 1: **Study of the exact reproductive number for SIS models with vertical and horizontal transmissions**

Authors: Fátima Palacios-Rodríguez
Affiliation: Departamento de Estadística e Investigación Operativa, Universidad de Sevilla, Spain

Although in real life there are diseases that can be transmitted vertically and horizontally, there is not a large number of works on epidemic models that take into account both transmissions. In this talk, we deal with a SIS model with vertical and horizontal transmissions. We assume that individuals can be recovered by treatment or by themselves. In addition, we describe the number of infected and of susceptible individuals as a finite two-dimensional quasi birth-death process. We focus on the study of the exact reproductive number. Particularly, we decompose the exact reproductive number as the sum of two random variables that represent: the vertical exact reproductive number and the horizontal exact reproductive number. Different numerical experiments are presented and discussed.
This is a joint work with A. Gómez-Corral and M.T. Rodríguez-Bernal.

16:15-16:45 (GMT+1) Contributed talk 2: **A multi-stage model of cell proliferation and death: tracking cell divisions with Erlang distributions**

Authors: Giulia Belluccini[1], Martín López-García[1], Grant Lythe[1], Carmen Molina-París[1,2]
Affiliations: [1]Department of Applied Mathematics, University of Leeds, LS2 9JT Leeds, UK
[2]Theoretical Biology and Biophysics, Theoretical Division, Los Alamos National Laboratory, Los Alamos, NM, USA

Lymphocyte populations, stimulated *in vitro* or *in vivo*, grow as cells divide. Stochastic models are appropriate because some cells undergo multiple rounds of division, some die, and others of the same type in the same conditions do not divide at all. If individual cells behave independently, each can be imagined as sampling from a probability density of times to division. The most convenient choice of density in mathematical and computational work, the exponential density, overestimates the probability of short division times. We consider a multi-stage model that produces an Erlang distribution of times to division, and an exponential distribution of times to death. The resulting dynamics of competing fates is a type of cyton model. The underlying idea is to divide the cell cycle into a given number of stages, and the cell is required to sequentially visit each stage in order to divide. At each stage, each cell may either proceed to the next one or die. Cells can be classified across generations depending on the number of times that they have undergone cell division, and the interest is in estimating the number of cells in each generation over time, which can be then compared to appropriate experimental data. Using Ap-

proximate Bayesian Computation based on Sequential Monte Carlo (ABC-SMC) methods, we compare our model to published cell counts, obtained after CFSE-labelled OT-I and F5 T cells were transferred to lymphopenic mice. The death rate is assumed to scale linearly with the generation and the number of stages of undivided cells (generation 0) is allowed to differ from that of cells that have divided at least once (generation greater than zero). Multiple stages are preferred in posterior distributions, and the mean time to first division is longer than the mean time to subsequent divisions. Our multi-stage model is able to account for competition between cellular fates (cell death vs division) while incorporating a non-exponential division time probability distribution, and allows us to find closed expressions for the mean number of cells in each generation.

17:00-17:30 (GMT+1) Contributed talk 3: **Penalty functions for a class of insurance risk processes with two-sided jumps**

Author: Ekaterina T. Kolkovska
Affiliation: Centro de Investigación en Matemáticas (CIMAT), Guanajuato, México

We investigate Gerber-Shiu penalty functions for two-sided jumps risk processes perturbed by a spectrally negative Lévy process. We consider a class of gain distributions which includes the phase type distributions, mixtures of exponential distributions, and more general rational distributions. For the claim size distributions we work with several types of light- and heavy-tailed distributions. We provide formulas for the penalty functions of the risk processes and obtain the asymptotic behaviors of the ruin probability and the joint tail of the surplus and the severity at ruin. We also show that our asymptotic results are sharp.
Keywords: Two-sided risk process, Lévy process, ruin probability, severity of ruin, surplus before ruin, asymptotic ruin probability.

17:30-18:00 (GMT+1) Contributed talk 4: **A cumulant approach for the first-passage-time problem of diffusion processes**

Authors: Giuseppe D'Onofrio
Affiliation: Dipartimento di Matematica 'G. Peano', Università degli Studi di Torino, Torino, Italy

I will focus on an approximation of the first passage time probability density function of a square-root stochastic process (CIR) by using cumulants and a Laguerre-Gamma polynomial approximation. The feasibility of the method relies on closed form expressions for cumulants and moments of any order recovered from the Laplace transform of the probability density function and using the algebra of formal power series. To improve the approximation, sufficient conditions on cumulants are stated. The resulting procedure is made easier to implement by the symbolic calculus and a rational choice of the polynomial degree depending on skewness, kurtosis and hyperskewness. Finally I will present some case-studies coming from neuronal and financial modeling to show the goodness of the proposed approximation even for a low number of terms of the approximating series.
The talk is based on a joint work with *Elvira Di Nardo.*

18:00-18:30 (GMT+1) Contributed talk 5: **Multi-sigmoidal stochastic growth models for the description of COVID-19 waves**

Authors: Antonio Barrera[1], Patricia Román-Román[2,3], Juan-José Serrano-Pérez[3], Francisco Torres-Ruiz[2,3]
Affiliations: [1]Departamento de Análisis Matemático, Estadística e Investigación Operativa, y Matemática Aplicada, Facultad de Ciencias, Universidad de Málaga, Spain.
[2]Instituto de Matemáticas de la Universidad de Granada (IMAG), Granada, Spain.
[3]Departamento de Estadística e Investigación Operativa, Facultad de Ciencias, Universidad de Granada, Granada, Spain.

One of the main applications of stochastic processes is the development of models for the description of certain dynamics concerning random effects. Following recent SARS-CoV-2 virus pandemic, multiple models have arisen in order to help to understand infection behavior. Particular cases are those related with stochastic models involving growth curves. In addition to their capabilities to describe growth phenomena, they may also be employed to determine useful characteristics of the dynamics, such as the peaks of infections or deaths in a disease context.

In this work, two stochastic models are proposed to describe the evolution of the first two infection waves of the SARS-CoV-2 virus pandemic in different regions in Spain. Such two models are derived from the classic Gompertz and Weibull growth curves, respectively; both showing multi-sigmoidal behavior as a result of the introduction of polynomials in the original models. Multi-sigmoidal models have shown good flexibility and reasonable possibilities for the application of inference procedures (see [1, 2, 3]).

The estimation of the parameters is addressed here by maximum likelihood. Procedures to deal with issues derived from such approach are proposed. In particular, we focus on the normalization of the observation interval, the search of initial solutions for numerical methods aiming to solve the likelihood equations, and the estimation of the degrees of the polynomials involved in the models. This last issue is addressed by considering Bayesian procedures of variables selection in normal regression models (see [4] and references therein).

In addition to the comparison between Gompertz and Weibull multi-sigmoidal stochastic models, the application of these models to COVID-19 pandemic data suggests a way to determine the peaks of infection and deaths, which can be associated with inflection times of the models. In order to deal with this information, point estimations and first-passage times are also considered.

References:

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2. Di Crescenzo, A.; Paraggio, P.; Román-Román, P.; Torres-Ruiz, F. Applications of the multi-sigmoidal deterministic and stochastic logistic models for plant dynamics. *Appl. Math. Model.* 92, 884–904, 2021.
3. Barrera, A.; Román-Román, P.; Serrano-Pérez, J.J.; Torres-Ruiz, F. Two multi-sigmoidal diffusion models for the study of the evolution of the covid-19 pandemic. *Mathematics* 9, 2409, 2021.
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18:30-19:00 (GMT+1) Contributed talk 6: **Solving Poisson's equation for birth–death chains: Structure, instability, and accurate approximation**

Author: José Niño Mora
Affiliation: Departamento de Estadística, Universidad Carlos III de Madrid, Spain

Poisson's equation plays a fundamental role as a tool for performance evaluation and optimization of Markov chains. For continuous-time birth–death chains with possibly unbounded transition and cost rates as addressed herein, when analytical solutions are unavailable its numerical solution can in theory be obtained by a simple forward recurrence. Yet, this may suffer from numerical instability, which can hide the structure of exact solutions. This paper presents three main contributions: (1) it establishes a structural result (convexity of the relative cost function) under mild conditions on transition and cost rates, which is relevant for proving structural properties of optimal policies in Markov decision models; (2) it elucidates the root cause, extent and prevalence of instability in numerical solutions by standard forward recurrence; and (3) it presents a novel forward–backward recurrence scheme to compute accurate numerical solutions. The results are applied to the accurate evaluation of the bias and the asymptotic variance, and are illustrated in an example.

Thursday, November 25th, 2021

15:00-15:45 (GMT+1) Keynote talk 2: **First passage time for diffusion processes: direct and inverse problem, numerical and simulative approach**

Author: Cristina Zucca
Affiliation: Department of Mathematics "G. Peano", University of Torino, Italy

In several applications the dynamics of the variables of interest is described via suitable stochastic processes constrained by boundaries. Often the focus is on the first passage time (FPT) of diffusion processes through constant or time varying boundaries. Generally the dynamics of the involved variables are described via a suitable diffusion process $\{X_t, t \geq 0\}$ constrained by an assigned boundary $b : (0, \infty) \to \mathbb{R}$ and the distribution features of the FPT

$$\tau_b = \inf \{ t > 0 \mid W_t \geq b(t) \} \tag{1}$$

of X_t over b are investigated. This is the direct FPT problem. However there are also instances when the underlying stochastic process is assigned, one knows or estimates the FPT distribution F_b and wishes to determine the corresponding boundary shape. This is the inverse first passage time problem. Unfortunately, explicit solutions of the direct or inverse first-passage problems are known only in a limited number of special cases. Hence, simulations and numerical methods become necessary tools for the study.

Here we study the direct FPT problem by means of simulations. We present an efficient method for simulating directly the first-passage time without building the whole paths of the diffusion process and without any approximation error. We introduce a rejection sampling algorithm which permits to perform an exact simulation of the first-passage time for general one-dimensional diffusion processes.

The inverse FPT problem is studied with a numerical approach. We proposed an algorithm to determine the unknown time dependent boundary when the distribution of the FPT is assigned for a multivariate Gauss-Markov process.

References:

1. S. Herrmann and C. Zucca (2020) Exact simulation of first exit times for one-dimensional diffusion processes (with S. Herrmann) *ESAIM: Mathematical Modelling and Numerical Analysis* 54(3), pp. 811–844
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15:45-16:15 (GMT+1) Contributed talk 7: **Gaussian simply markovian processes over topological versions of graphs**

Authors: Juan Baz González
Affiliation: Departamento de Estadística e Investigación Operativa y Didáctica de la Matemática, Universidad de Oviedo, Spain

The study of Gaussian Markov Random Fields (GMRFs) has attracted the attention of a large number of scientific areas due to its increasing usage in several fields of application, mainly because the sparseness of its precision matrix. In this type of models, the conditional dependence-independence structure is determined with a simple undirected graph. For some of the easiest cases, the path graph and the cycle graph, Gaussian Simply Markovian processes defined over the topological versions of such graphs, the real line and the circle, have been widely studied in the literature. This topological versions of graphs are known in topology as 1-dimensional CW-complex. In this direction, the following questions arise: there exist Gaussian Simply Markovian processes over the topological version of any graph? If so, how can be constructed? Unfortunately, the classical methods for constructing GMRFs, such that definition thought clique potentials, the approach of Speed and Kiiveri or the walk construction, cannot be extended successfully to this type of stochastic processes. Thus, a new construction method for GMRFs, the forward walk construction, which can be easily extended to Gaussian Simply Markovian processes defined over topological versions of graphs, is proposed. The main advantage of this method is the possibility of expanding a edge in the graph leaving the rest of the distribution invariant, which allow us to extend easily this construction to Gaussian Simply Markovian processes using forward topological paths. On the other hand, the amount of GMRFs that can be constructed with this method is limited. The continuity of the resulting process sample paths, the relationship to Algebraic Topology and the discussion of a possible field of application are also discussed.

16:15-16:45 (GMT+1) Contributed talk 8: **The two barrier escape problem for compound renewal processes with two-sided jumps**

Author: Javier Villarroel, José A. Vega
Affiliation: Instit. Univ. Física y Matemáticas and Dept. Estadística, University of Salamanca, Spain

We consider the problem of determining two-sided exit probabilities for a compound renewal process with drift and two sided jumps. In certain cases the problem can be reduced to determining the distribution of a random sum of i.i.d. random variables. In a general situation this problem is reduced to solving a certain integral equation. We obtain explicit expressions for the escape probability for certain classes of jump times and sizes.
Keywords: Two sided exit probabilities, Compound renewal process, Laplace transforms.

17:00-17:30 (GMT+1) Contributed talk 9: **The method of moments and its applications in the theory of branching random walks**

Author: Elena Yarovaya
Affiliation: Department of Probability Theory, Lomonosov Moscow State University, Russia.

The method of moments for proving of limit theorems in the modern sections of stochastic processes, such as, e.g., branching random walks, which are described in terms of the generation and transport of particles, is widely used. In such processes, depending on the structure of the branching environment, the properties of a random walk, and the dimension of a space in which the process is considered, the asymptotic behavior in time of the moments for the number of particles and the rate of their growth have significant differences. It is shown how the growth of the limiting moments of the number of particles at each point of the multidimensional lattice corresponds to the limiting structure of the particle field under various assumptions on intensities of generation and transport of particles. The key question is in which cases the normalized limiting (in time) moments of the number of particles guarantees the uniqueness of the probability distribution and, as a consequence, convergence in distribution to a certain limiting random variable. Limit theorems on the behavior of branching random walks in an inhomogeneous medium for sources of different intensities proved using Carleman's condition are presented without any assumptions on the variance of the random walk jumps. The question about the explicit form of the distribution of the limiting random variable remains open. We show that in some cases it can be answered.

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17:30-18:00 (GMT+1) Contributed talk 10: **Profit optimization for a stochastic model of cattle growth and variable price categories**

Author: Carlos A. Braumann[1,2], Gonçalo Jacinto[1,2] and Patrícia A. Filipe[1,3]
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A general deterministic growth model of individual animals is the ODE $dY(t) = \beta(\alpha - Y(t))dt$, where $Y(t) = h(X(t))$ is a transformed size obtained by applying a strictly increasing C^1 function h to the actual size $X(t)$ of the animal at age t, α is the average transformed size at maturity, and β is a growth parameter. The growth curves most commonly used are solutions of the ODE for particular choices of h and are taken as mean curves for the classical regression models used. These do not take into account the dynamics of the growth process and the effect on such dynamics of random fluctuations in the internal and external environment. Therefore, we use the general stochastic differential equation model $dY(t) = \beta(\alpha - Y(t))dt + \sigma dW(t)$, where σ measures the intensity of environmental fluctuations and $W(t)$ is a standard Wiener process. Applications using real weight data of Mertolengo cattle breed males are presented.

The use of these more realistic models can help farmers optimize their profit. To this end we obtain the probability distribution, the mean, the standard deviation, and other quantities of interest of the profit obtained by raising and selling an animal under the more general, and more realistic, situation where the price paid per kg to the farmers depends on the animal's age and weight category. We conclude that farmers are selling the animals a little earlier than the optimal selling age, which results in a lower profit.

We also present sensitivity results for small changes on the estimates of the model parameters and conclude that they have a small effect on the optimal expected profit and a negligible effect on the optimal selling age.

Acknowledgements: The authors belong to the research centre CIMA (Centro de Investigação em Matemática e Aplicações), supported by FCT (Fundação para a Ciência e a Tecnologia, Portugal), project UID/04674/2020. This work was developed within the Operational Group PDR2020-1.0.1-FEADER-031130 - Go BovMais (Productivity improvement in the system of bovine raising for meat), funded by PDR 2020. We are grateful to the Associação de Criadores de Bovinos Mertolengos and to his head engineer José Pais for having provided the data and for continuous support.

18:00-18:30 (GMT+1) Contributed talk 11: **Studying signals with scale-free dynamics using multifractal analysis**

Authors: Tahmineh Azizi
Affiliation: Department of Mathematics, Florida State University, USA

Sometimes when we study signal regularity, we may see some phenomena that do not have characteristic scale. These scale free signals have been observed in biomedical signal processing, geophysics, finance, and internet traffic. To clarify more, when data is translation invariant, we may need to estimate autocorrelation or power spectral density (PSD) means that signal statistics like mean and variance do not change over time. In another hand, those signals that do not have characteristic scale, called scale-invariant signals that means the signal statistics do not change if we stretch or shrink the time axis. When we study translation invariant or scale invariant signals, or the signals with different scaling behaviour, we are not able to use the classical signal processing and we need to perform fractal analysis. When we study real world signals in biology, finance and so on, depending on scale and higher order moments, we may confront with signals that display nonlinear power-law behaviours. For these type signals, we need to apply multifractal analysis. In multifractal analysis we discover whether some type of power-law scaling exists for various statistical moments at different scales. A process called monofractal, if it can be characterized using a single scaling exponent, or this process is a linear function of the moments. Likewise, a process called multi-fractal, if we see the scaling behaviour follows a function which is non-linear in the moments. In this study, we will review these type processes and will provide some examples to compare the multifractal spectra of two financial time series along with the brown noise.

18:30-19:00 (GMT+1) Contributed talk 12: **Critical controlled branching processes: A Feller diffusion approximation**

Authors: M. González, P. Martín-Chávez, I. del Puerto

Affiliation: Departamento de Matemáticas, Universidad de Extremadura, Spain

Controlled branching processes are stochastic processes appropriated to model generation sizes in population dynamics studies where a control on the growth of population size is necessary at each generation. The main aim of this paper is to provide a Feller diffusion approximation for critical controlled branching processes. Previously, González and del Puerto - Methodol Comput Appl Probab (2012) 14:843–861, have proved the result by using operator semigroup convergence theorems. An alternative proof is now provided making use of limit theorems for martingale differences. From inference viewpoint, the interest of developing this result stems from the usefulness of it in determining the asymptotic distributions of estimators of the main parameters of a controlled branching process.
Acknowledgements: This research has been supported by grant
PID2019-108211GB-I00 funded by MCIN/AEI/10.13039/501100011033, by "ERDF A way of making Europe".
Keywords: Controlled branching processes:controlled branching processes, weak convergence theorem; martingale differences.

Tuesday, November 30th, 2021

15:00-15:45 (GMT+1) Keynote talk 3: **Modeling extreme-value dependence in spatial processes: a comparative overview from max-stability to conditional extremes**

Author: Thomas Opitz
Affiliation: Biostatistics and Spatial Processes, INRAE, Avignon, France

The asymptotic representations of extreme-value theory are the foundation for the statistical models developed for extreme values arising in phenomena such as windstorms, extreme precipitation or heatwaves. When there is dependence among extreme events, the classical limit theory suggests using max-stable processes for observations of maxima, and generalized Pareto processes for observations of exceedances above a high threshold. Both of the aforementioned types of processes are characterized by an asymptotic stability property of the dependence structure. However, this asymptotic stability often cannot be found empirically at observed quantile levels when studying real data. For example, the spatial area of exceedances of a temperature threshold during heatwaves may tend to become smaller on average when higher thresholds are considered. Another drawback of max-stable processes is that they have a very complex probabilistic structure, making statistical inference intricate.

Over the last years, more flexible "subasymptotic" modeling approaches have been developed for dependent extremes. Specifically, we here focus on the conditional extremes framework which provides high flexibility, preserves an asymptotic motivation and has recently been extended to spatial and spatiotemporal processes. After normalizing marginal distributions, certain nonstationary Gaussian processes can be used to model the behavior of the original process given that it exceeds a fixed threshold at a fixed location. This trans-Gaussian modeling approach establishes interesting links between classical geostatistics and extreme-value theory. In this talk, the construction of such models will be explained, and Bayesian estimation using the INLA-SPDE approach will be illustrated for Sea Surface temperatures of the Red Sea.

15:45-16:15 (GMT+1) Contributed talk 13: **Central limit theorem and its convergence rate on counting measures for a branching random walk with immigration in a random environment**

Authors: Chunmao Huang[1], Yinna Ye[2]
Affiliations: [1]Department of Mathematics. Harbin Institute of Technology, Weihai, China
[2]Department of Applied Mathematics, School of Science. Xi'an Jiaotong-Liverpool University, Suzhou, China

In the classical model of branching random walk, Asmussen and Kaplan (1976) and Kaplan and Asmussen (1976) made investigation on the central limit analogues for the associated counting measure $Z_n(\cdot)$. Let N be the offspring number of an individual in a branching process (BP). Then under the assumption

$\mathbb{E}N(\log N)^{1+\lambda} < \infty$, for some $\lambda > 0$; they proved the following central limit theorem holds, when the BP is supercritical: $\forall y \in \mathbb{R}$,

$$m^{-n} Z_n((-\infty, \sqrt{n}y]) \overset{n\to\infty}{\longrightarrow} W\Phi(y), \quad \text{a.s.} \tag{2}$$

where $m = \mathbb{E}(N) \in (1, \infty)$, W is the a.s. limit of $Z_n(\mathbb{R})/m^n$, as $n \to \infty$, and Φ is the cumulative distribution function of standard normal.

Gao et al. (2014, 2016) established an analogue of (2) under two types of conditions and found its convergence rate for a BRW in i.i.d random environment (cf. Thm 2.2, Thm 2.3 in Gao et al. (2014), Thm 2.3 in Gao and Liu (2016), resp.).

The objective of our study is to introduce firstly a more generalised model, branching random walk with immigration in random environment, where a random number of immigrants are taken into consideration in each generation. Secondly, we try to establish the central limit theorem for $Z_n(\cdot)$ and find the convergence rate. Thirdly, we attempt to extend the results from i.i.d environment to stationary and ergodic one. It turns out that the central limit theorem holds in our new model and the similar convergence rate is found under weaker conditions of type $\mathbb{E}N(\log N)^{1+\lambda} < \infty$, compared to those in Gao and Liu (2016).

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Keywords: Branching random walk with immigration, counting measure, random environment, central limit theorem, convergence rate

16:15-16:45 (GMT+1) Contributed talk 14: **On first-passage times and sojourn times in finite QBD processes: An application to varicella-zoster infections**

Authors: Diana Taipe Hidalgo
Affiliation: Facultad de Estudios Estadísticos. Universidad Complutense de Madrid, Spain

In this communication, we revisited level-dependent quasi-birth-death processes with finitely many possible values of the level and phase variables by complementing the work of Gaver, Jacobs and Latouche [1]. We have extended their theory by studying a random descriptors of interest which are defined inspired in their application to epidemic models; namely, first-passage times and hitting probabilities to higher levels, number of upcrossings and sojourn times. Our algorithmic solution is based on Gaussian elimination, which is applicable in all proposed descriptors since the underlying rate matrices have a block-structured form. Using the results obtained, we illustrate the applicability of our methodology though a numerical study of an epidemic model for the transmission of varicella-zoster virus within a nursing home for elderly people, subjected to repeated outbreaks.

This talk is based on the paper: Gómez-Corral A, López-García M, Lopez-Herrero MJ, Taipe D. On First-Passage Times and Sojourn Times in Finite QBD Processes and Their Applications in Epidemics. Mathematics. 2020; 8(10):1718. https://doi.org/10.3390/math8101718

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17:00-17:30 (GMT+1) Contributed talk 15: **A fractional generalization of some stochastic Gompertz type models**

Author: Enrica Pirozzi
Affiliation: Dipartimento di Matematica e Applicazioni, Università di Napoli FEDERICO II, Italy

Inspired by two fractional Gompertz curves previously introduced in Bolton et al. (2014) and Frunzo et al. (2019), we involved in the construction of stochastic versions in Ascione and Pirozzi (2020). Specifically, we studied a class of linear fractional-integral stochastic equations, for which an existence and uniqueness result of a Gaussian solution was proved. Such kind of equations were then used to construct fractional stochastic Gompertz models. In addition, a new fractional Gompertz model, based on the previous two, was introduced and its stochastic version was also provided. Now, in Ascione and Pirozzi (2021), we focus on the construction of deterministic and stochastic extensions of the Gompertz curve by means of generalized fractional derivatives induced by complete Bernstein functions. Precisely, we first introduce a class of linear stochastic equations involving a generalized fractional integral and we study the properties of its solutions. Deterministic generalized fractional Gompertz curves are introduced by means of Caputo-type generalized fractional derivatives, possibly with respect to other functions. Their stochastic counterparts are then constructed by using the previously considered integral equations to define a rate process and a generalization of lognormal distributions to ensure that the median of the newly constructed process coincides with the deterministic curve.
This is a joint work with Giacomo Ascione.

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Acknowledgement: The authors are partially supported by MIUR–PRIN 2017, project Stochastic Models for Complex Systems, no. 2017JFFHSH.

17:30-18:00 (GMT+1) Contributed talk 16: **Why are cell populations replenished via multiple intermediate compartments?**

Authors: Flavia Feliciangeli[1,2], Martin López García[1], Carmen Molina-París[1,4], Mario Castro Ponce[3], Hanan Dreiwi[1], Grant Lythe[1]
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Populations of cells are efficiently maintained in our body through mechanisms that still need to be completely unraveled. Novel experimental techniques allow us to start tracking individual cells and their progeny. We think about “product cells” as mature and fully differentiated cells, and “progenitor cells” as cells which are able to “self-renew” and generate product cells. Then, a commonly observed pattern in experiments is that a small population of progenitor cells maintains, via a sequence of intermediate states, a larger population of product cells.

In this work, we model cells sharing the same attributes (or phenotype) as belonging to the same mathematical state (or compartment). Our compartmental model consists of a sequence of C compartments, each of them containing cells which can either die, divide or change phenotype (entering the next compartment). This model represents the dynamics of the progeny of a single progenitor cell as a stochastic process. Moreover, we identify cells by their generation: the progenitor cell is said to be in generation zero and daughter cells of a given cell in generation n are considered to be in generation $n+1$. Since we are interested in the ultimate fate of the system, we proceed as in the theory of discrete-time branching processes, by defining relationships between random variables making use of probability generating functions.
Firstly, we define the random variable $\mathbf{R}$ as the number of product cells that are descended from one progenitor cell and analyse its probability generating function. Secondly, we consider the relationship between D, the mean generation number of cells exiting from the last compartment of the sequence, and $N = \mathbb{E}[\mathbf{R}]$, the mean number of such cells produced from a single progenitor. We study the dependence of $\mathbf{R}$ and D on the number of intermediate states C. We find that the production of a large number, N, of product cells via a long sequence of compartments (*i.e., C* large) is associated with a low "division load" (*i.e.,* the number of rounds of division, D). Since every round of division brings with it a risk of mutation, the maintenance of a population of function-specific product cells via a low value of D can, in principle, decrease the risk of cancerous mutations.

18:00-18:30 (GMT+1) Contributed talk 17: **The curve-crossing problem for the delayed Brownian motion**

Authors: Giacomo Ascione
Affiliation: Scuola Superiore Meridionale, Univertà degli Studi di Napoli Federico II, Italy

Nowadays, the link between diffusion processes and partial differential equations has been widely exploited. In particular, the densities of diffusion processes killed upon exiting a specific open set are known to solve a initial/boundary-value partial differential problem and such result can be extended to the moving boundary case. On the other hand, one can obtain stochastic representations of the solutions of some time-nonlocal parabolic equations by exploiting the properties of a certain class of semi-Markov processes, obtained by means of an independent time-change from a strong Markov process. The main tool in this approach is a subordination principle, that, however, does not hold in the moving boundary problem. Here, we want to address the problem of the first crossing time between a time-changed Brownian motion and a moving boundary described via an increasing continuous function. Precisely, we prove, that the Dynkin-Hunt formula still holds time-changed Brownian motion killed upon crossing the boundary and the obtained function is the fundamental solution of the time-nonlocal heat equation with a zero exterior condition with respect to the moving boundary. This is part of an ongoing joint work with Prof. Pierre Patie from Cornell University and Prof. Bruno Toaldo from University of Turin.

18:30-19:00 (GMT+1) Contributed talk 18: **Near-record values in discrete random sequences**

Authors: Miguel Lafuente[1], Raúl Gouet[2], F. Javier López[1] and Gerardo Sanz[1]
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[2]Departamento Ingeniería Matemática y Centro de Modelamiento Matemático, Universidad de Chile, Chile

Outstanding achievements and world records in athletics such as, for instance, the 100-meter dash, always hit the headlines and provoke public admiration. However, bad and more frequently seen record values from the economy, the climate or the healthcare systems, also receive a lot of attention in the media and contribute to general anxiety. Crucial social questions emerge as we face a steady flow of records, which appear to be ominous signs of dramatic underlying phenomena.

The mathematical theory of records is well developed, especially for data generated by independent and identically distributed (iid) random variables, with continuous underlying distribution function. As it is well-known, in this setting one can only expect about $\log n$ record values among n observations and so, records are really exceptional. However, the real world shows a different picture in terms of higher frequency of record observations, and this has lead to the study of more realistic non-stationary models to fit such data and make inferences. The concept of "almost-record" emerged as a natural extension of record and has proven to be worthy from a mathematical as well as an applied perspective. The general idea of values that fail but are close to being a record has been translated into a variety of definitions that have been theoretically analyzed and applied in widely different contexts.

The main object of interest in this work are the so-called near-records, introduced by Balakrishnan et al (2005). In particular, we focus on the analysis, exact as well as asymptotic, of the different stochastic processed related to near records obtained from an underlying sequence of discrete (integer-valued) random variables. We consider the structure of the process of near-record values when the underlying variables are discrete, also in "time axis". Analogously to what happens in the continuous case, the near-records process turn out to be a discrete cluster point process that we characterize through its probability generating functional. We derive from this characterization different properties and we obtain expressions for the moments of the process.

Defining the hazard function as $r_i = p_i/y_{i-1}$, where $p_i = P(X = i)$ and $y_i = P(X > i)$, we prove that the number of near-records is finite when $\sum_{i=0}^{\infty} r_i^2 < \infty$.

On the other hand, in the other case $\sum_{i=0}^{\infty} r_i^2 = \infty$, and some mild additional conditions, we prove that he number of near-record satisfy a strong law of large number . Moreover, under the same conditions, a Central Limit Theorem for the process of near-record is also obtained.

In short, the condition $\sum_{i=0}^{\infty} r_i^2 < \infty$ is a necessary and sufficient condition for the finiteness of the number of near-records and in the case that the condition is not met, a law of large numbers and asymptotic normality is fulfilled.

Thursday, December 2nd, 2021

15:00-15:45 (GMT+1) Keynote talk 4: **Sharp large deviation estimates for functionals of stochastic fixed point equations**

Author: Anand N. Vidyashankar

Affiliation: Department of Statistics, George Mason University, USA

Stochastic fixed point equations (SFPE) arise in a variety of theoretical and applied problems in branching processes, branching random walk, GARCH and ARCH models in finance, and other population growth models. In this presentation, we will describe the non-logarithmic large deviation behavior of functionals of the SFPE and show that for a large class of functionals the rate functions exhibit a phase transition over regimes that govern large and small exceedances. We use these results to derive the conditional large deviations and related central limit theorems. (Joint work with Jeffrey Collamore).

15:45-16:15 (GMT+1) Contributed talk 19: **Portfolio optimization for different anticipating integrals**

Author: Carlos Escudero Liébana

Affiliation: Universidad Nacional de Educación a Distancia, Spain

We consider a simple setting for portfolio optimization in a financial market in which an insider trader is present. We model it using anticipating stochastic calculus and compare the results that follow from the use of the Russo-Vallois forward, the Ayed-Kuo, and the Hitsuda-Skorokhod integrals. The optimal portfolio in each of these cases is found, and a comparison between these three different investment strategies is established. This result give some indication that the forward integral provide a better description of the problem.

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Keywords: insider trading, optimal portfolios, anticipating stochastic integrals, Malliavin calculus, mathematical modeling of information.

16:15-16:45 (GMT+1) Contributed talk 20: **Regenerative controlled branching processes with continuous time**

Authors: M. González[1], M. Molina[1], I. del Puerto[1], G.P. Yanev[2,3], N.M. Yanev[3]
Affiliations: [1]Department of Mathematics. University of Extremadura, Spain
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[3]Department of Operations Research, Probability and Statistics, Institute of Mathematics and Informatics, Bulgarian Academy of Sciences, Bulgaria

Controlled branching processes in continuous time are considered in this talk. Given a discrete-time controlled branching process, $\{Z_n,\ n = 0, 1, 2 \ldots\}$, and a renewal process, $\{N_t,\ t \geq 0\}$, the process $\{Y(t),\ t \geq 0\}$, with $Y(t) = Z_{N(t)}$ is referred to as CBP *subordinated by a renewal process* or as *randomly indexed* CBP. If $N(t) = n$ then, at time t, the population size is $Y(t) = Z_n$. We assume that the renewal period is the common lifespan of all individuals. The process $\{Y(t),\ t \geq 0\}$ is a Markov chain with exponentially distributed individual lifespans in the particular case when the renewal period is a homogeneous Poisson process. We establish two limit theorems when the mean of the renewal periods is either finite or infinite with zero being an absorbing state. Then we will focus our attention in studying such processes allowing an immigration component at zero. We propose an extension of the process $\{Y(t),\ t \geq 0\}$, namely, the regenerative process $\{U(t),\ t \geq 0\}$. It coincides with $\{Y(t),\ t \geq 0\}$ until it hits zero, then upon staying at zero for a random time period, the process regenerates. We will provide the asymptotic behaviour of $\{U(t),\ t \geq 0\}$. The results provided in this talk have been recently published in González et al (2021a,b).

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17:00-17:30 (GMT+1) Contributed talk 21: **Gaussian processes in the sphere**

Authors: A. Torres-Signes[1], M.P. Frías[2] and M.D. Ruiz-Medina[3]
Affiliations: [1]Departamento de Estadística e Investigación Operativa, Universidad de Málaga, Spain
[2]Departamento de Estadística e Investigación Operativa, Universidad de Jaén, Spain
[3]Departamento de Estadística e Investigación Operativa,Universidad de Granada, Spain

Let $\mathcal{C}(\mathcal{T})$ be the random almost surely continuous functions from an interval $\mathcal{T}$ into a Riemannian d–dimensional manifold $\mathcal{M}$ of $\mathbb{R}^{d_0}$ $(d \leq d_0)$. We consider the supremum norm induced by the geodesic distance $d_{\mathcal{M}}$

$$\|x(t) - y(t)\|_{\mathcal{C}(\mathcal{T})} = \sup_{t \in \mathcal{T}} d_{\mathcal{M}}(x(t), y(t)).$$

We apply the methodology, based on Rigged-Hilbert-Spaces, and Kuelb's lemma, to define the continuous embeddings

$$\left(\mathcal{C}(\mathcal{T}), \|\cdot\|_{\mathcal{C}(\mathcal{T})}\right) \hookrightarrow \left(\widetilde{H}, \langle\cdot,\cdot\rangle_{\widetilde{H}}\right) \hookrightarrow \left(\mathbb{H}, \langle\cdot,\cdot\rangle_{\mathbb{H}}\right).$$

Here, $(\mathbb{H}, \langle \cdot, \cdot \rangle_{\mathbb{H}}) = \left\{ v : \mathcal{T} \to \mathbb{R}^{d_0}, \sum_{i=1}^{d_0} \int_{\mathcal{T}} |v_i(t)|^2 dt < \infty \right\}$ defines the ambient Hilbert space with $\langle u, v \rangle_{\mathbb{H}} = \sum_{i=1}^{d_0} \int_{\mathcal{T}} v_i(t) u_i(t) dt$. Space $\widetilde{H}$ has inner product $\langle v, u \rangle_{\widetilde{H}} = \sum_{i=1}^{d_0} \int_{\mathcal{T}} k(t,s) v_i(t) u_i(s) dt ds$, with, according to Kuelb's lemma, $\int_{\mathcal{T}} k(t,s) \phi_n(s) ds = t_n \phi_n(t)$, and $\sum_{n=1}^{\infty} t_n = 1$, such that, for $v \in \widetilde{H}$, $\|v\|_{\mathbb{H}} \leq \|v\|_{\widetilde{H}}$. We restrict our attention to the d–dimensional sphere with the geodesic distance $\|x(t) - y(t)\|_{\mathcal{C}(\mathcal{T})} = \sup_{t \in \mathcal{T}} \ \arccos(x(t)^T y(t))$, for every $t \in \mathcal{T}$. The methodology presented allows us to define an infinite-dimensional version of Von Mises-Fisher probability distribution (see Bhattacharya and Bhattacharya, 2012), and the implementation of functional prediction techniques based on spherical ARH(1) processes (see, e.g., Ruiz-Medina and Álvarez, 2019, in the Euclidean context).

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17:30-18:00 (GMT+1) Contributed talk 22: **New insights on the MAP counting process**

Author: Marcos González Bernal[1], Rosa E. Lillo[1,2] and Pepa Ramírez-Cobo[3]
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[3]Departamento de Estadística e Investigación Operativa, Universidad de Cádiz, Spain

Markovian arrival processes (MAPs) are known to constitute a versatile class of point processes that allow for dependent inter-arrival times. In this work, our goal is to exploit such property for modeling modern call center data, which are characterized by non-negligible dependence patterns and overdispersion. Most of previous statistical approaches for MAPs are based on the distribution of the inter-arrival times. In this work, however, a different perspective is adopted, being the inference focused on the properties of the associated counting process. We propose an optimization problem that not only adjusts the quantities that characterize the inter-arrival times, but also takes into account some counting process' descriptors. In addition, new properties concerning the correlation patterns and the monotonicity of the covariance function of the counting process will be illustrated.

18:00-18:30 (GMT+1) Contributed talk 23: **A stochastic SVIR model with imperfect vaccine and external source of infection**

Author: María Gamboa Pérez
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In this talk we deal with a compartmental stochastic SIR (Susceptible-Infected-Recovered) type-model with an additional compartment of vaccinated individuals. We assume a constant-sized, homogeneous, and uniformly-mixed population suffering from a contagious disease. The infectious disease confers immunity and is transmitted by direct contact with an infected individual. Population is not isolated thus an additional source of infection it is assumed due to external contacts. The vaccine is not perfect at all and some individuals that previously have been vaccinated can be infected by an infective individual. Vaccine protection lasts for at least the length of an outbreak, hence further vaccination during the outbreak is not considered.

We describe the evolution of an epidemic process in terms of an absorbing three-dimensional continuous-time Markov chain (CMTC) where individuals evolve among Susceptible, S, Vaccinated, V, Infected, I and Recovered, R; compartments. We show how a particular organization of states in this CTMC leads to the study of a level-dependent quasi birth-and-death process (LD-QBD).

We quantify the evolution of an epidemic process analysing the random variable, W_M that measures the time a threshold number of individuals to become infected and provide an efficient algorithm to compute any of its moments. Then we illustrate our methodology with a sensitivity
analysis to assess the influence of varying model parameters on some numerical characteristics of this random variable.

18:30-19:00 (GMT+1) Contributed talk 24: **Weighted least square estimation in branching processes with carrying capacity**

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The purpose of this work is to propose estimators of the parameters of branching processes with a logistic growth. Our target parameter is the carrying capacity, which represents the maximum number of individuals of the species that an environment can sustain given the available resources.

To tackle this problem, we focus on discrete-time population-size-dependent branching processes. These processes are characterised by the fact that individuals give birth independently and with a reproduction law that depends on the current population size. In a parametric context for these reproduction probability laws, we provide some weighted least square estimators based on the observation of the population sizes up to some generation. We illustrate their asymptotic properties, such as consistency and asymptotic normality, by means of several examples. We also apply our methodology to estimate the carrying capacity of an endangered population of birds.