

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 of Statistics and Operations Research

Welcome address

Dear participant,

It is our pleasure to welcome you to the first edition of the International Workshop on Stochastic Processes and their Applications (IWSPA 2020), to be held virtually and online on November 24th and 26th, and December 1st, 3rd and 9th using video conferencing tools.

The workshop is organized by the Working Group on "Stochastic Processes and their Applications" of the Spanish Society of 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: Frank Ball, Antonio Di Crescenzo, Nikolai Leonenko and Martín López-García. Furthermore, 26 thirty-minute talks will be presented in five 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 2020!

November 2020

Antonio Gómez-Corral and Miguel González Velasco

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Javier Villarroel Rodríguez, Universidad de Salamanca, Spain

Program at a glance

Tuesday, November 24th, 2020. Chair: Antonio Gómez-Corral

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

15:00-15:45 (GMT+1) Keynote talk 1: Some results and applications of geometric counting processes, Antonio Di Crescenzo

15:45-16:15 (GMT+1) Contributed talk 1: Space-time Pareto processes to generate scenarios for natural disasters, Fátima Palacios Rodríguez

16:15-16:45 (GMT+1) Contributed talk 2: Quantifying infection transmission in a stochastic SIV model with imperfect vaccine, María Jesús López-Herrero

17:00-17:30 (GMT+1) Contributed talk 3: A diffusion process for modelling HyperGompertz-type behaviour, María A. Baamonde Seoane

17:30-18:00 (GMT+1) Contributed talk 4: Likelihood approximation in logistic-type diffusions by means of Hermite polynomials, Antonio Barrera

18:00-18:30 (GMT+1) Contributed talk 5: Speed, accuracy and persistence impact on the immune response: A stochastic approach, Mario Castro

Thursday, November 26th, 2020. Chair: Javier Villarroel

15:00-15:45 (GMT+1) Keynote talk 2: Exact approaches for the analysis of stochastic epidemic processes on networks, Martín López García

15:45-16:15 (GMT+1) Contributed talk 6: A semilinear functional approach for space-time bivariate processes, Antoni Torres

16:15-16:45 (GMT+1) Contributed talk 7: Inference for two-sex branching processes for X-linked recessive disorders: ABC methodology, Alicia León Naranjo

17:00-17:30 (GMT+1) Contributed talk 8: Markovian discrete-time study of the distribution of the number of infected during the active phase of a non-immunizing communicable disease, Diana Taipe

17:30-18:00 (GMT+1) Contributed talk 9: On multitype random forests with a given degree sequence, the total population of branching forests and enumerations of multitype forests, Osvaldo Angtuncio Hernández

18:00-18:30 (GMT+1) Contributed talk 10: On the covariance function for Markovian arrival processes, Marcos González Bernal

Tuesday, December 1st, 2020. Chair: Miguel González Velasco

15:00-15:45 (GMT+1) Keynote talk 3: Epidemics on networks with preventive rewiring, Frank Ball

15:45-16:15 (GMT+1) Contributed talk 11: A stochastic model of the cash-flow in a service station or company, Javier Villarroel

16:15-16:45 (GMT+1) Contributed talk 12: Maximum likelihood estimation in population-size-dependent branching processes with almost sure extinction, Carmen Minuesa

17:00-17:30 (GMT+1) Contributed talk 13: On the number of inspections of the population that find an active process: A first approach to estimate the contact rate of a disease, María Gamboa

17:30-18:00 (GMT+1) Contributed talk 14: δ -records in the linear drift model, Miguel Lafuente

18:00-18:30 (GMT+1) Contributed talk 15: Towards renewable-dominated electric energy systems: planning and operation under uncertainty, María Ruth Domínguez Martín

Tuesday, December 3rd, 2020. Chair: María Dolores Ruiz Medina

15:00-15:45 (GMT+1) Keynote talk 4: Limit theorems, scaling of moments and intermittency for integrated finite variance supOU processes, Nikolai Leonenko

15:45-16:15 (GMT+1) Contributed talk 16: Itô vs Stratonovich in the Langevin model of brownian motion, Carlos Escudero Liébana

16:15-16:45 (GMT+1) Contributed talk 17: Spatiotemporal central and non-central limit results for a class of gaussian and chi-square subordinated fields, María Dolores Ruiz-Medina

17:00-17:30 (GMT+1) Contributed talk 18: ABC SMC estimation in controlled branching processes without knowledge of the maximum reproduction capacity, Inés María del Puerto

17:30-18:00 (GMT+1) Contributed talk 19: Escape and first arrival times in the Sparre Andersen risk model with a non renovation initial time, Juan Antonio Vega Coso

18:00-18:30 (GMT+1) Contributed talk 20: On some fractionally integrated Gauss-Markov processes and applications in neuronal modeling, Enrica Pirozzi

Wednesday, December 9th, 2020. Chair: Gerardo Sanz

15:00-15:30 (GMT+1) Contributed talk 21: Non-local Pearson diffusions, Giacomo Ascione

15:30-16:00 (GMT+1) Contributed talk 22: Diffusion limits at small times for coalescent processes with mutation and selection, Phil Hanson

16:00-16:30 (GMT+1) Contributed talk 23: Stochastic optimal control problems and related Kolmogorov equations, Ștefana-Lucia Anița

16:45-17:15 (GMT+1) Contributed talk 24: Multitype branching models for systems of communicating populations, Manuel Mota

17:15-17:45 (GMT+1) Contributed talk 25: Tests for non-stationarity based on theory of records: An application to climate change, Jorge Castillo-Mateo

17:45-18:15 (GMT+1) Contributed talk 26: Birth death swap population in random environment and aggregation with two timescales, Sarah Kaakäi

18:15-18:25 (GMT+1) Closing words: Antonio Gómez-Corral, Miguel González Velasco, María Dolores Ruiz Medina

Abstracts

Tuesday, November 24th, 2020

15:00-15:45 (GMT+1) Keynote talk 1: **Some results and applications of geometric counting processes**

Author: Antonio Di Crescenzo

Within the most known counting processes, wide interest is addressed to the Poisson process and its generalizations such as the compound Poisson processes. Among these processes, we focus on the so-called geometric counting process. This is characterized by a marginal distribution of geometric type, arrival times with Pareto distribution, positively correlated increments, overdispersion property, and asymptotic behavior different from the Poisson process. This makes the geometric process suitable for describing the dynamics of certain phenomena of interest in seismology and in software reliability. As example, we examine applications to sequences of earthquakes, and to the occurrence of errors in telephony systems. We also analyze first-crossing-time problems, shock models and compound counting models whose shocks and claims occur according to the geometric counting process.

15:45-16:15 (GMT+1) Contributed talk 1: **Space-time Pareto processes to generate scenarios for natural disasters**

Authors: Fátima Palacios Rodríguez, G. Toulemonde, J. Carreau, T. Opitz

Extreme events of natural phenomena not only can entail material damages but also devastating consequences for human societies and ecosystems. To better manage the risks of destructive natural disasters, impact models can be fed with simulations of extreme scenarios to study sensitivity to temporal and spatial variability. However, since extreme events are rare by definition, it is not easy to find a wide catalogue of extreme scenarios as inputs to impact models that allow us to densely study the phenomena. The main aim of this work is to simulate these extreme scenarios. Firstly, we set up a general framework for space-time generalized Pareto process. It allows developing a methodology to stochastically simulate realistic spatio-temporal extreme fields. To this end, we use a moderate number of observed extreme space-time episodes to generate an unlimited number of extreme scenarios of any magnitude. The extremal dependence structure is fully data-driven, and we require parametric assumptions only for the univariate tails, based on asymptotic theory. In order to quantify the magnitude of extreme behavior of events, a crucial component in our methodology is the definition of the cost functionals over a sliding space-time window. These functionals characterize extreme episodes as episodes whose return period, appropriately aggregated over space and time, exceeds a high threshold. Our framework draws sound theoretical justification from extreme value theory, building on generalized Pareto limit processes. Particularly, we exploit asymptotic stability properties by decomposing extreme event episodes into a scalar magnitude variable (that is resampled), and an empirical profile process representing space-time variability. To illustrate our approach, we consider hourly gridded precipitation data in Mediterranean France. It illustrates how spatio-temporal cost functionals can be defined, how they affect the selection of extreme episodes, and how the magnitude of the newly sampled scale variables impacts the magnitude of the lifted extreme episodes on the original marginal scale.

16:15-16:45 (GMT+1) Contributed talk 2: **Quantifying infection transmission in a stochastic SIV model with imperfect vaccine**

Author: María Jesús López-Herrero

In this communication we quantify the spread of an infectious disease that does not confer immunity, within a population that is partially protected against the disease by a vaccine. We consider a homogeneous and uniformly mixed population. The disease is transmitted by direct contact with an infected individual. The population is not isolated, so we assume an additional source of infection due to external contacts. Some individuals in the population have been protected against the disease with an available

vaccine that confers immunity, but it is not a perfect vaccine and some contacts between vaccinated and infectious individuals produce an effective contagion. Once a vaccinated individual gets the infection, he no longer belongs to the class of individuals that have been vaccinated and he belongs to the infective class while he is infectious. After being recovered, individuals become susceptible to the disease, no matter if they were previously vaccinated or not.

The underlying mathematical model involves a stochastic SIVS model, where individuals evolve among Susceptible, S, Vaccinated, V, and Infected, I; compartments. Assuming constant population size during outbreaks, a continuous time Markov chain (CTMC) model represents changes in the composition of infected and vaccinated classes.

Two random variables will quantify the transmission of the epidemic process with reintroduction: R_{e0} , the number of infectious cases caused directly by the first infected individual, and R_p , which is the number of infectious cases caused by any infectious spreader until the first recovering occurs. These random variables act as stochastic counterparts to the basic reproduction number, R_0 , and more specifically the control reproduction number, R_c , when there is an available vaccine.

The talk is based on the paper: Gamboa & Lopez-Herrero Measuring Infection Transmission in a Stochastic SIV Model with Infection Reintroduction and Imperfect Vaccine. *Acta Biotheoretica* <https://doi.org/10.1007/s10441-019-09373-9>.

17:00-17:30 (GMT+1) Contributed talk 3: **A diffusion process for modelling HyperGompertz-type behaviour**

Authors: María A. Baamonde Seoane, P. Román Román, F.A. Torres Ruiz

The modelling and study of dynamic systems, particularly growth systems, has been subject of analysis in recent decades. Traditionally, the deterministic models are been used for this purpose. Despite the good results obtained by applying these deterministic models, it is necessary to introduce into the models certain elements capable of describing the influence of factors which can have a significant effect on the evolution of the process. In this way, deterministic models are extended to stochastic models while taking into account the random influences affecting the dynamics of the phenomenon. Some of these diffusion models emerge as solutions to a stochastic differential equation after modifying a deterministic one by introducing in it a term of white noise. Other diffusion processes are constructed in such a way that their mean function is a certain growth curve.

A stochastic diffusion model related to a reformulation of the HyperGompertz growth curve is proposed. This curve is a generalization of the classic Gompertz curve and it can be obtained from the general growth curve studied by Turner et al. (1976). To this end, the lognormal diffusion process with exogenous factor is considered. The process verifies that its mean function is HyperGompertz curve. This indicates that the process can be considered as a valid tool for studying data showing HyperGompertz-type behaviour. The main features of the process are studied, and the maximum likelihood estimation for the parameters is considered. There exist explicit expressions for the estimates of the parameters of the initial distribution of the process, but the estimations of the rest of parameters yields a complex system of equations, whose explicit solution cannot be guarantee and it is necessary to implement numerical methods, such as Newton-Raphson, for which an initial solution is required. A strategy to achieve such solution is presented, based on the information provided by the sample data and using some basic characteristics of the HyperGompertz curve, such as the limit value (if any) and the inflection points. In order to validate the procedures described, we carry out some studies based on simulated data. This simulation study focuses on the strategies related to the estimation of the parameters of the model.

Acknowledgements

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17:30-18:00 (GMT+1) Contributed talk 4: **Likelihood approximation in logistic-type diffusions**

by means of Hermite polynomials

Authors: Antonio Barrera, P. Román Román, F. Torres Ruiz

It is well-known that dynamics with logistic behaviour are widely used in modelling in different research areas. Logistic-type, (continuous) time-inhomogeneous diffusion processes can be built from the classic ordinary differential equation by including a time-dependent growth rate and a regulation function with noise perturbation. Usually, the corresponding probability transition density functions are not known explicitly, so are the likelihood functions. Therefore, inference procedures such as the maximum likelihood estimation may not be applicable. In order to deal with this issue, one may consider approximations of the unknown transition density. Limit theorems guarantee convergence to true densities, as well as to true likelihood functions.

One successful approach, used mainly in Finance, is based on the Hermite expansion of the density around the standard normal distribution. Nevertheless, in many applications, assumptions about Gaussian distributions may not be met. Hence, a modified approach (see [1]) consists on the transformation of the diffusion into another process with transition density close to that of the normal distribution. Such transformations are reversible, thus the approximated transformed density may lead to approximations of the original unknown probability transition density function. Subject to some assumptions, the sequence of partial sums is proved to converge to the true density, and the same result applies to corresponding likelihood functions. The extension of these works to time-inhomogeneous processes was carried out in [2], by considering certain modifications.

In this work, the aforementioned procedure is revised and adapted to the case of logistic-type, time-inhomogeneous diffusion processes. Some results are then established in terms of the time-dependent growth rate function. Remarks about the influence of the sole growth rate function are discussed.

References

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2. Egorov, A.V., Haitao, L., Yuewu, X. (2003). Maximum likelihood estimation of time-inhomogeneous diffusions. *Journal of Econometrics*, 114, 107-139.

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18:00-18:30 (GMT+1) Contributed talk 5: **Speed, accuracy and persistence impact on the immune response: A stochastic approach**

Authors: Mario Castro

Many biological problems rely on the ability of the receptors to discriminate between agonist and antagonist proteins. This is especially critical in immunology where a virus infection can be detected by a T-cell even when the number of infected cells is counted by the numbers. In this talk I will expose different stochastic observables (from speed to accuracy) and how to compute them using matrix analytic methods and generating functions even if the times between events are semi-Markovian.

Thursday, November 26th, 2020

15:00-15:45 (GMT+1) Keynote talk 2: **Exact approaches for the analysis of stochastic epidemic processes on networks**

Author: Martín López García

This research work is framed within the area of modelling hospital-acquired infections. I will introduce a number of existing compartmental-based approaches for modelling the spread of (typically antibiotic resistant) bacteria in hospital settings. Mathematical models with a relatively small number of compartments can be used for representing the spread of bacteria across patients and healthcare workers (HCWs), including relevant factors such as environmental contamination. However, more complex approaches (i.e.,

models with a large number of compartments, or network-based representations) are needed for example when introducing spatial considerations or HCW-patient contact network structures. When looking at network-based approaches, I will show some recent work on analysing exactly these epidemic dynamics on small networks. When considering an SIR epidemic process on a network, this analytic and computational approach amounts to the analysis of the exact 3^N -states continuous-time Markov chain (CTMC), and makes special focus on algorithmic aspects and the organisation of the space of states $S = \{S, I, R\}^N$. Finally, I will present some recent results on the applicability of graph-automorphism lumping techniques in these systems.

15:45-16:15 (GMT+1) Contributed talk 6: **A semilinear functional approach for space-time bivariate processes**

Authors: Antoni Torres, M.P. Frías, M.D. Ruiz Medina

Functional Data Analysis (FDA) techniques are applied in a multivariate framework, for spatiotemporal prediction of infection disease incidence and mortality. Specifically, spatial heterogeneous nonlinear parametric functional regression trend model fitting is first achieved. Log-Gaussian linear residual correlation analysis is then performed in a Classical and Bayesian framework. The combined plug-in predictor is computed for space-time prediction of the bivariate process, describing the temporal evolution of infection disease incidence and mortality maps (see [1] for the Hilbert-valued Ornstein-Uhlenbeck log-intensity case, and [2] for the cyclical non-linear univariate infinite-dimensional process context). The results are applied to space-time prediction of COVID-19 incidence and mortality in the Spanish Communities. A comparative study with Machine Learning (ML) regression model is also performed in a FDA framework. The results could be extrapolated to other countries.

References

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16:15-16:45 (GMT+1) Contributed talk 7: **Inference for two-sex branching processes for X-linked recessive disorders: ABC methodology**

Author: Alicia León Naranjo

The evolution of the number of individuals carrying the alleles, R and r, of a gene linked to X chromosome has been described using a multitype two-sex branching process in [1]. The R allele is considered dominant and the r allele is supposed to be recessive and defective, responsible of a disorder. Hemophilia, red-green color blindness or the Duchenne and Becker's muscular dystrophies are examples of this kind of diseases. For this model we investigate the estimation of its main parameters from a Bayesian standpoint. Concretely, we apply the Approximate Bayesian Computation (ABC) methodology to approximate its posterior distributions. The accuracy of the procedure is illustrated and discussed by way of a simulated example developed with R.

This is a joint work with Miguel González, Cristina Gutiérrez and Rodrigo Martínez.

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1. González, M., Gutiérrez, C., Martínez, R., and Mota, M. (2016). Extinction probability of some recessive alleles of X-linked genes in the context of two-sex branching processes. In *Branching Processes and their Applications, Lecture Notes in Statistics – Proceedings* (del Puerto, I.M. et al., Eds), vol. 219, chapter 17. Springer-Verlag. DOI: 10.1007/978-3-319-31641-3.

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17:00-17:30 (GMT+1) Contributed talk 8: **Markovian discrete-time study of the distribution of the number of infected during the active phase of a non-immunizing communicable disease**

Author: Diana Taipe Hidalgo

The RE-distribution (ratio of expectations distribution) characterizes the behavior of the number of infected individuals of a small community during the active process of a non-immunizing communicable disease. Due that infected individuals return to the susceptible state after infection, we propose an SIS (susceptible- infectious-susceptible) stochastic model to describe the infective process by a discrete-time Markov chain. In particular, we remark the appropriate choice of the inspection time interval to observe the population to guarantee an event, either infection or recovery.

As we treat with an isolated and finite population, it is sure that there are no infective individuals in the long-term, although extinction may take a very long time. In this work, we focus on RE-distribution as a measure to understand the behavior before an outbreak ends. Thus, its applicability permits us to calculate the number of infectives at each inspection interval during an active epidemic. To determine the values, we use the relation between the one-step transition probabilities and one-step first passage time probabilities, which leads to a system of equations whose coefficient matrix is tridiagonal. Our solution for dealing with this numerical problem appeals to a recursive algorithm based on Gaussian elimination.

According to this process, given an initial number of infected individuals is possible to represent the RE- probability mass function and the average duration of the active epidemic. For illustrative propose, we present numerical experiments that show different scenarios in which varying model parameters as population size, transmission and recovery rates, and the length between inspections. Our results demonstrate that it is essential to fix the value of the population size and the initial number of infected individuals because they condition the shape of RE-distribution. Furthermore, the factors involved in the transmission dynamics characterize an outbreak and quantify the need to inspect individuals more or less frequently.

17:30-18:00 (GMT+1) Contributed talk 9: **On multitype random forests with a given degree sequence, the total population of branching forests and enumerations of multitype forests**

Author: Oswaldo Angtuncio Hernández

In this talk, we introduce the model of uniform multitype forests with a given degree sequence (MFGDS). The construction is done using the results of Chaumont and Liu 2016, and a novel path transformation on multidimensional discrete exchangeable increment processes, which is a generalization of the Vervaat transform. By mixing the laws of MFGDS, one obtains multitype Galton-Watson (MGW) forests conditioned with the number of individuals of each type (CMGW). We also obtain the joint law of the number of individuals by types in a MGW forest, generalizing the Otter-Dwass formula. This allows us to get enumerations of multitype forests with a combinatorial structure (plane, labeled and binary forest), having a prescribed number of roots and individuals by types. Finally, under certain hypotheses, we give an easy algorithm to simulate CMGW forests, generalizing the unitype case given by Devroye in 2012. The previous results can be considered as the first step to obtain the profile of the multitype Lévy forest.

18:00-18:30 (GMT+1) Contributed talk 10: **On the covariance function for Markovian arrival processes**

Authors: Marcos González Bernal, R.E. Lillo, P. Ramírez-Cobo

Markovian arrival processes (MAPs) [2], are known to constitute a versatile class of point processes that allow for dependent inter-arrival times. In this work, we aim to exploit such property for modeling modern call centers which are characterized by non-negligible dependence patterns, see [1]. However, instead of focusing on the inter-arrival times distribution which has been the most considered perspective in the literature, we center on the associated counting process. In this setting, the covariance function for the

MAP is examined in depth, from both a theoretical and applied viewpoints. Some findings in regards its properties and numerical evaluation are discussed.

References

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2. Neuts, M.F. (1979). A versatile Markovian point process. *Journal of Applied Probability*, 16, 764-779.

Tuesday, December 1st, 2020

15:00-15:45 (GMT+1) Keynote talk 3: **Epidemics on networks with preventive rewiring**

Author: Frank Ball

A stochastic SIR (susceptible \rightarrow infective \rightarrow recovered) epidemic model defined on a social network is analysed. The underlying social network is described by an Erdős-Rényi random graph but, during the course of the epidemic, susceptible individuals connected to infectious neighbours may drop or rewire such connections. Large population limits of the model are derived giving both convergence results for the early branching process-like behaviour, and, assuming a major outbreak, the main phase of the epidemic process which converges to a deterministic model that is equivalent to a certain pair approximation model. Law of large numbers results are also obtained for the final size (i.e. total number of individuals infected) of a major outbreak. The limiting final fraction infected may be discontinuous in the infection rate λ at its threshold λ_c , thus making a discrete jump from 0 to a strictly positive number.

Joint work with Tom Britton (Stockholm University).

15:45-16:15 (GMT+1) Contributed talk 11: **A stochastic model of the cash-flow in a service station or company**

Authors: Javier Villarroel, J.A. Vega

Assuming that customers arrive at a certain company or service station according to a Poisson or a general renewal process we construct a related point process that can be used to describe the cash flow given that the company charges a fixed amount x per service. We analyze how different competing effects, like the price of the basic service, the number of services and the operational costs, determine the process $(X_t)_{t \geq 0}$ which records the company's profit. We study how to fix an adequate price that optimizes different statistics of the profit process $(X_t)_{t \geq 0}$ like mean and typical deviation.

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16:15-16:45 (GMT+1) Contributed talk 12: **Maximum likelihood estimation in population-size-dependent branching processes with almost sure extinction**

Authors: P. Braunsteins, S. Hautphenne, Carmen Minuesa

Population-size-dependent branching processes (PSDBPs) are models which describe the evolution of populations where individuals in the same generation produce their offspring independently according to a probability law which depends on the current population size. An interesting family of PSDBPs are branching processes with a carrying capacity. These enable us to model populations which show a logistic growth, where the population size tends to oscillate, for a long period of time, around a threshold value known as the carrying capacity. This value is interpreted as the maximum number of individuals that the ecosystem can support in view of its resources.

In this work, we consider discrete-time PSDBPs. First, we determine the maximum likelihood estimators (MLEs) of the main parameters of the model when we observe the entire family tree. Next, we focus on the case where we only observe the total population size at every generation up to some generation. We show that the MLEs of the offspring means based on the family tree correspond to the MLEs based on the population sizes and we derive its limiting properties. Given that the extinction of these processes is certain, the study of the asymptotic properties is more complex. Precisely, this requires us to condition on the survival of the process in a distant future and to analyse the corresponding estimator in the Q -process associated with the original branching process. Thus, we introduce a new type of consistency, which we call Q -consistency. We prove that our estimators are Q -consistent and that their conditional limit is close to the true value of the parameter. We also establish their asymptotic normality. Finally, we illustrate our results with a simulated example developed with the statistical software R.

17:00-17:30 (GMT+1) Contributed talk 13: **On the number of inspections of the population that find an active process: A first approach to estimate the contact rate of a disease**

Author: María Gamboa Pérez

This communication is framed within the area of epidemic modelling and studies infectious disease dynamics in a stochastic markovian approach. In this area, most of the research works deal with continuous-time models.

However, the current work involves a discrete-time SIS model to represent the spread of a disease within a closed population of moderate size N that is inspected periodically. The evolution of the disease can be represented by a one-dimensional Markov chain: $\{I_n; n \geq 0\}$, where I_n is a random variable giving the number of infective individuals in the population at the n -th inspection. In this case, the Markov chain describing I_n has a finite state space with only one absorbing state in 0 infective individuals thus, the eradication of the epidemic is certain with probability one.

The main objective of this research is to analyze the number of inspections that find an active epidemic. This variable is denoted by $T = \min\{n \geq 0 : I_n = 0\}$, and is the discrete-time analogous of the extinction time that describes the length of the epidemic process. I describe its probabilistic behavior in terms of distribution functions based on the conditional first-passage times T_i , for $1 \leq i \leq N$, defined as the number of inspections that take place during an outbreak, given that at present population contains $I_0 = i$ infected. Expected values m_i , for $1 \leq i \leq N$, provide the long-run average value of inspections prior to the epidemic end, given that the outbreak started with i infected and came from explicit expressions based on a first-step argument. I will compare mass functions T_i and expected values m_i on different scenarios to investigate the influence of the model parameters in the probabilistic behavior of these random variables.

The estimation of the parameters in mathematical models is a habitual problem in statistics, I propose for the variables T_i , for $1 \leq i \leq N$, a procedure to estimate the contact rate of a disease. This methodology is based on statistical techniques and numerical methods as Nelder-Mead and simulation.

The talk is based on the paper: Gamboa M. and López-Herrero M.J. (2018). On the number of periodic inspections during outbreaks of discrete-time stochastic SIS epidemic models. Mathematics 6, article 128.DOI: 10.1007/s11538-013-9836-3.

17:30-18:00 (GMT+1) Contributed talk 14: **δ -records in the linear drift model**

Authors: R. Gouet, Miguel Lafuente, J. López, G. Sanz

The concept of δ -record has been proposed in the literature as a natural extension of records. Given a sequence of random variables $\{X_i\}_{i \in \mathbb{N}}$, the n -th observation is a δ -record if

$$X_n > \max(X_1, X_2, \dots, X_{n-1}) + \delta,$$

where $\delta \in \mathbb{R}$ is a fixed parameter. Under this definition, δ -records are more frequent than records if $\delta < 0$, increasing the potential number of applications.

Recently, there has been a rising interest in the study of records and extremes in the field of Statistical Physics for modeling phenomena such as global warming or analyzing stocks-prices, among others. As a consequence, properties about models with drift, such as drifted random walks and the Linear Drift

Model (LDM), have been profusely studied in the last decade. In this contribution we will consider δ -records from observations following a LDM, that is, where observations are drawn from time-series of the form $Y_n = X_n + cn$, $n \geq 1$, where c is a slope parameter and $\{X_i\}_{i \in \mathbb{N}}$ is a sequence of i.i.d. continuous random variables.

In this setting, we prove the continuity in the trend parameter c and δ of the probability of δ -record. We characterize its asymptotic positivity and its behaviour as well as giving exact computations in some examples. In the case of positive trend we find that the asymptotic probability of δ -record observations converges to a positive value if and only if $\mathbb{E}[X_i^+] < \infty$. We also analyze in detail some examples of heavy-tailed distributions, with $\mathbb{E}[X_i^+] = \infty$, and assess the role of δ in the speed of convergence of the probability to 0. An interesting measure is the correlation between δ -record events, which indicates whether δ -record observations attract or repel each other. We derive a formula for the correlation and analyze its value in several families of distributions.

Also, the asymptotic behaviour of the random variable indicating the number of δ -records among the first n observations, $N_{n,\delta}$, is studied. We completely characterize its asymptotic finiteness depending on the sign of the trend parameter c and the tails of the distribution, and give moment conditions and normalizing sequences for the convergence (almost sure and in distribution) of this random variable to the asymptotic δ -record probability. Finally, we illustrate our results with a real temperature dataset, where even for relatively short time-series ($n = 69$), the asymptotic theoretical results seems to be in good agreement with the observed data.

18:00-18:30 (GMT+1) Contributed talk 15: **Towards renewable-dominated electric energy systems: planning and operation under uncertainty**

Authors: María Ruth Domínguez Martín, M. Carrión

The integration of renewable energies in power systems represents a key point to achieve the environmental goals of the European Commission for 2050. However, the electricity production from wind and solar technologies depends on resources which are variable and, in general, difficult to predict. Hence, a high penetration of stochastic resources in power systems introduces high levels of uncertainty in planning and operations. On the other hand, renewable technologies are still under maturing stage and their investment costs are subject to high uncertainty. In this session, two works will be presented. The first work consists on solving a multi-stage investment model in generating capacity using four different formulations, namely: a multi-stage stochastic programming problem, a linear-decision-rule approach, a two-stage stochastic programming problem solved under a rolling window framework, and the deterministic problem. The outcomes obtained by each formulation are compared. In the second work, we tackle the planning of the European power system for 2050. First, we use a multi-stage investment model to determine the optimal generating and storage capacity decisions, and second, we analyse the daily operation of the resulting problem.

Tuesday, December 3rd, 2020

15:00-15:45 (GMT+1) Keynote talk 4: **Limit theorems, scaling of moments and intermittency for integrated finite variance supOU processes**

Author: Nikolai Leonenko

Superpositions of Ornstein-Uhlenbeck type (supOU) processes provide a rich class of stationary stochastic processes for which the marginal distribution and the dependence structure may be modeled independently [1,2]. In this paper we investigate the limiting behavior of integrated supOU processes with finite variance [3,4,5] (see also [7] for multifaced behaviour of supOU processes in the case the infinite variance).

We show that after suitable normalization four different limiting processes may arise. The type of limit depends on the decay of the correlation function as well as on the characteristic triplet of the marginal distribution. supOU processes, moreover, may exhibit intermittency, a phenomenon affecting the rate of growth of moments [3,4,5,6]. We establish this rate for each of the four limiting scenarios. The rate changes at some point indicating that there is a change-point in the asymptotic behavior of absolute moments. For such a behavior to be possible, the moments in the limit theorem do not converge beyond

some critical point. We show that this point is related to the dependence structure of the supOU process. The intermittency phenomenon appears also in some other models, for example, in the subclass of ambit processes [2] known as trawl processes [5].

Joint work with D. Grahovac (Osijek University, Croatia) and M. Taqqu (Boston University, USA)

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15:45-16:15 (GMT+1) Contributed talk 16: **Itô vs Stratonovich in the Langevin model of brownian motion**

Author: Carlos Escudero Liébana

The Langevin stochastic differential equation describes the velocity of a Brownian particle. Thus, the Langevin model for Brownian motion can be regarded as a physically refined version of the Wiener process, for which the velocity is not well-defined, at least as a function-valued stochastic process. One of the advantages of the Langevin model is that it permits to compute the kinetic energy of the Brownian particle. Moreover, the computation of this quantity has been used as a model problem for the comparison between the Itô and Stratonovich stochastic integrals and their use in physics. While the traditional conclusion is that the Stratonovich integral should be preferred in this context, we show that it leads to an infinite multiplicity of solutions. In contrast, the uniqueness of the solution to the Itô stochastic differential equation and its physical meaningfulness make its use simpler. We discuss the implications that this fact may have on the general discussion about the Itô vs Stratonovich dilemma.

16:15-16:45 (GMT+1) Contributed talk 17: **Spatiotemporal central and non-central limit results for a class of gaussian and chi-square subordinated fields**

Authors: N. Leonenko, María Dolores Ruiz-Medina

Sojourn measures have play a crucial role in the description of geometric characteristics of random surfaces, providing information on level crossing and possible extreme values. An extensive literature can be found in the field of stochastic processes, and statistics. Particularly, the asymptotic behavior, when the window size grows, of the volume of excursion sets has been widely investigated. The present work addresses this problem in the spatiotemporal process context, considering the case of long range dependence (LRD) Gaussian and chi-square random fields. Specifically, a reduction theorem is derived. Some central and non-central limit results can then be established for LRD spatiotemporal random fields constructed by subordination from Gaussian and chi-square random fields.

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17:00-17:30 (GMT+1) Contributed talk 18: **ABC SMC estimation in controlled branching processes without knowledge of the maximum reproduction capacity**

Authors: M. González, C. Minuesa, Inés María del Puerto

The purpose of this work is to approximate the posterior distribution of the parameters of interest of controlled branching processes without explicit likelihood calculations nor any knowledge of the maximum number of offspring that an individual can produce. We consider that only the population sizes at every generation and at least the number of progenitors of the last generation are observed, but the number of offspring that every individual gives birth to is unknown at any generation. The method proposed is two-fold. We firstly make use of an Approximate Bayesian Computation based on sequential Monte Carlo (SMC ABC) model choice algorithm to estimate the posterior distribution of the maximum reproductive capacity. Secondly, to estimate the posterior distribution of the parameters of interest, we run the rejection ABC algorithm and the post-processing on the output of the previous method by considering an appropriated summary statistic. The accuracy of the proposed method is illustrated by means of a simulated example developed with the statistical software R.

Acknowledgements

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17:30-18:00 (GMT+1) Contributed talk 19: **Escape and first arrival times in the Sparre Andersen risk model with a non renovation initial time**

Author: Juan Antonio Vega Coso

The present work studies the first arrival time to the upper boundary and the escape time in the $[0, b]$ region in the Sparre Andersen risk model, with random initial time, which is not mandatory a renovation time. First, the basic definitions of the first arrival and escape times are presented, distinguishing the case of the initial time being a renovation time or not. Finally, expressions for these characteristic times are provided as well as the integral equations that satisfy both, first arrival and escape mean times.

18:00-18:30 (GMT+1) Contributed talk 20: **On some fractionally integrated Gauss-Markov processes and applications in neuronal modeling**

Author: Enrica Pirozzi

New stochastic processes are obtained as the fractional Riemann-Liouville integral of order $\alpha \in (0, 1)$ of Gauss-Markov (GM) processes. The general expressions of the mean, variance and covariance functions are given. Due to the central rule, for the fractional integral of standard Brownian motion and of the non-stationary/stationary Ornstein-Uhlenbeck processes, the covariance functions are carried out in closed-form. In order to clarify how the fractional order parameter α affects these functions, their numerical evaluations are shown and compared also with those of the corresponding processes obtained by ordinary Riemann integral. The simulation of these fractional integrated processes can be performed starting from the obtained covariance functions. We also investigate the entropy of such new processes. On simulated sample paths of such processes, the entropy is specifically estimated by computing its approximation ApEn. The results are useful for fractional neuronal models with long range memory dynamics and involving correlated input processes. The stochastic Leaky Integrate-and-Fire (LIF) model

is revisited adopting a fractional derivative instead of the classical one and a correlated input in place of the usual white noise. In such a context, the fractionally integrated GM processes can be fruitfully used to obtain new neuronal models. Specific examples are provided. Graphical comparisons are provided and discussed.

This is a joint work with Mario Abundo (Dipartimento di Matematica, Università di Roma Tor Vergata, Italy).

Wednesday, December 9th, 2020

15:00-15:30 (GMT+1) Contributed talk 21: **Non-local Pearson diffusions**

Author: Giacomo Ascione

In this talk we consider a class of time-changed processes obtained by composing a Pearson diffusion with the inverse of a subordinator, as done in [1]. Such time-changed processes provide stochastic representations of solutions of some Cauchy problems with a non-local derivative in time induced by a suitable Bernstein function, defined for instance in [3,2]. In particular we show the existence of strong solutions for these equations via spectral methods, by using different approaches depending on the spectral category of the generator of the parent Pearson diffusion. Then we use the spectral decomposition results to deduce first order stationary and limit distributions of the introduced processes. As already mentioned, the talk is based on the work [1], which is a joint work with Nikolai Leonenko from Cardiff University and Enrica Pirozzi from Università degli Studi di Napoli Federico II.

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15:30-16:00 (GMT+1) Contributed talk 22: **Diffusion limits at small times for coalescent processes with mutation and selection**

Author: Phil Hanson

The Kingman coalescent is a fundamental model in the study of population genetics that models lines of ancestry into the past. The number of lineages t units of time into the past - denoted $N_t^{0,0}$ - is a Markovian death chain on \mathbb{N} where, since any two lineages coalesce independently at rate 1, the death rate is $n(n-1)/2$ when $N_t = n$. One of the interesting phenomena exhibited by $N_t^{0,0}$ is “coming down from infinity” (CDI) whereby the process can be started with an infinite number of lineages and then becomes finite instantaneously almost surely. The speed at which this happens is characterised by a function ν_t such that

$$\frac{N_t^{0,0}}{\nu_t} \rightarrow 1,$$

as $t \rightarrow 0$, almost surely. For the Kingman coalescent, the appropriate function is $\nu_t = 2/t$.

The genetic mechanisms of mutation and selection can independently be incorporated into this framework. For mutation, as well as having lineages coalesce, we now attach an exponential clock of rate $\theta/2 \geq 0$ to each lineage. When this clock rings the lineage mutates and is lost.

When selection is present in a population model, one genetic type has an advantage over another. This means that forward in time, the type of an offspring cannot be determined unless the types of both parents are known. When considering an ancestry backwards in time this uncertainty is modelled by lineages splitting into two at rate $\sigma/2$. The resulting model is known as the Ancestral Selection Graph (ASG); first introduced by Krone and Neuhauser in 1997. The number of lineages - denoted $N_t^{\sigma,\theta}$ - is now a birth/death process with rates $n \mapsto n-1$ at rate $n(n-1+\theta)/2$ and $n \mapsto n+1$ at rate $n\sigma/2$.

As $n \rightarrow \infty$, these linear alterations are small compared to the original coalescent effect. Through an analysis of hitting times we show that these processes - with and without selection - both have the same speed of CDI as the original coalescent. These asymptotics are then used to prove the following:

$$\lim_{t \rightarrow 0} \mathbb{E} \left[\sup_{s \leq t} \left(\frac{s N_s^{\sigma, \theta}}{2} - 1 \right)^k \right] = 0, \quad \sigma, \theta \geq 0.$$

This control near zero, along with a coupling of the ASG and Kingman coalescent via a Poisson random measure characterisation, allows us to prove the convergence of

$$\epsilon^{-\frac{1}{2}} \left(\frac{\epsilon t N_{\epsilon t}^{\sigma, \theta}}{2} - 1 \right) \rightarrow Z_t := \frac{1}{\sqrt{2t}} \int_0^t u dW_u$$

in distribution in $D([0, \infty), \mathbb{R})$ as $\epsilon \rightarrow 0$, where W is a standard Brownian motion.

This is joint work with Dario Spanò, Paul Jenkins and Jere Koskela.

16:00-16:30 (GMT+1) Contributed talk 23: **Stochastic optimal control problems and related Kolmogorov equations**

Author: Stefana-Lucia Anița

Our talk concerns the optimal control of the following stochastic differential equation with feedback inputs:

$$\text{Minimize}_{u \in \mathcal{M}_c^u} \mathbb{E} \left[\int_0^T \int_{\mathbb{R}^d} \{g(X^u(t, x)) + h(u(X^u(t, x)))\} d\nu(x) dt \right],$$

where X^u is the solution to

$$\begin{cases} dX(t) = f(X(t), u(X(t)))dt + \sigma(X(t))dW(t), & t \in [0, T] \\ X(0) = x \in \mathbb{R}^d. \end{cases}$$

The problem is reduced to the deterministic optimal control problem:

$$\text{Minimize}_{u \in \mathcal{M}_c^u} \{I(u) = \int_0^T \int_{\mathbb{R}^d} \varphi^u(t, x) d\nu(x) dt\}$$

where φ^u is a solution of the Kolmogorov equation (where the controls are of open-loop type):

$$\begin{cases} \frac{\partial \varphi}{\partial t}(t, x) = f(x, u(x)) \cdot \nabla \varphi(t, x) + \frac{1}{2} q_{ij}(x) \frac{\partial^2 \varphi}{\partial x_i \partial x_j}(t, x), & x \in \mathbb{R}^d, t \in (0, T] \\ \varphi(0, x) = g(x) + h(u(x)) = \varphi_0^u(x), & x \in \mathbb{R}^d. \end{cases}$$

We discuss the relationship between the stochastic optimal control problem and the deterministic optimal control problem. The existence of an optimal control is proved for the deterministic control problem in a particular case and necessary optimality conditions are derived. Some comments and further extensions are discussed. The presentation is based on the results in [Anița, Ș.-L. (2020, <https://doi.org/10.1080/00207179.2020.1806360>). A stochastic optimal control problem with feedback inputs. *International Journal of Control*].

16:45-17:15 (GMT+1) Contributed talk 24: **Multitype branching models for systems of communicating populations**

Authors: Manuel Mota, M. Molina

Branching processes provide a powerful tool for studies on population dynamics, including the modeling of migrations events. In this work, we propose a new branching model to describe the simultaneous evolution of several populations which present migration flows among them. We show that the new model can be viewed as a modification of a multitype Galton-Watson branching process. Some asymptotic results

that extend Kesten Stigum theory are also provided.

17:15-17:45 (GMT+1) Contributed talk 25: **Tests for non-stationarity based on theory of records: An application to climate change**

Author: Jorge Castillo-Mateo

Most of the works on climate change focus their research on the analysis of the mean trend in location, whereas another important aspect to consider are the changes in variability and the tails of the distribution. Although there are numerous tests based on signs and ranks to detect trend in location, there is not a generalised test to perform an equivalent analysis in the extremes. A field that will be useful in this context and causes a great interest in the population is the theory of records, which is part of the extreme value theory. Thus, our general aim is to review and develop powerful statistical tests based on theory of records, together with other exploratory tools, in order to analyse the existence of non-stationary behaviour in climate extremes.

Given a sequence (X_t) of independent and identically distributed (IID) random variables, an observation X_i is called a record if $X_i > \max_{t < i} \{X_t\}$. Under this setup, the binary variables (I_t) that indicate the record occurrence at time t are independent and have a Bernoulli distribution with probability $p_t = 1/t$. This implies that the distribution of the statistics relative to the record occurrence does not depend on the distribution of X_t . The underlying idea to build distribution-free tests is to use the distribution of the record occurrence in an IID series, and to study if the observed records are compatible with that behaviour. More precisely, we suggest different statistics based on the binary variables I_t and the probability of record p_t . For non-stationarity to be the only possible alternative against the hypothesis of randomness in time dependent and seasonal data, a processing methodology of the series is applied. Although using only upper records is interesting in itself, gathering the information from the upper and lower records of the forward and backward series significantly increases the power of the tests.

Finally, we show a study of size and power, followed by an application of the tests to assess the effect of global warming in the extremes of daily maximum temperature time series in a Spanish region. The processing, exploratory data analysis and inference tools implemented and presented are available in the R package **RecordTest** that is available from CRAN.

17:45-18:15 (GMT+1) Contributed talk 26: **Birth death swap population in random environment and aggregation with two timescales**

Author: Sarah Kaakai

In this talk, I will present some recent results on stochastic heterogeneous population dynamics in random environment, in which individuals can change of characteristics (<https://arxiv.org/abs/1803.00790>).

I will first present some comparison and construction results for counting processes, based on their pathwise representation as solutions of stochastic differential equation driven by Poisson measures.

Then, I will introduce a class of heterogeneous population dynamics structured by discrete subgroups, including changes of characteristics. The variability of the environment is also taken into account in a general way, leading us to rely heavily on results obtained in the first part.

In the presence of two timescales, we prove an averaging result for aggregated “macro” population, extending classical averaging results obtained in the Markov case. In particular, we illustrate the emergence of density dependence for demographic rates in the presence of heterogeneity.

Joint work with Nicole El Karoui.