Ecodep Conference 2021,
September 15-17, 2021

`http://doukhan.u-cergy.fr/ecodep.html`

Paul Doukhan

Paris Seine University, AGM UMR 8088, CYU site Saint-Martin, 95000 Cergy-Pontoise, France
`http://doukhan.u-cergy.fr/conference2021.html`

The conference will be totally free but **registration** is mandatory. Indeed the specific point is that both online and physical presence are possible entails to be precise about registrations.

Please register as soon as possible, other informations about AGM may be consulted online https://cyagm.cyu.fr/ecodep-activities.

Since the conference is not only online we suggest the link https://www.traveldoc.aero/ to determine wether you are allowed to travel to the conference place.

After/During all this pandemic time our idea was to propose a real physical conference so that the organisation committee will do his very best to welcome you in the best conditions if your institution allows for it.

Six sessions of around 3 hours will aim at organising adequate orientations of the project ECODEP. One of the session will be include posters, each poster may be presented with a few slides in the conference room.

The conference will be online and physical: one may attend the talk through a link to be found on the ecodep calendar in the homepage `https://doukhan.u-cergy.fr/conference2021.html` of the conference.

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1 Schedule

Paris Time is indicated and the duration of talks does include questions.
The online abstracts book version will be updated and will include the correct information.

- September 15

  - Morning
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    * 10:00-10:40 **Hansjoerg Albrecher** (online).
      Asymptotic analysis of the Greenwood statistic and extensions for very heavy tails.
    * 10:40-11:20 **Félix Cheysson**.
      Evolution of groups at high risk of death from Covid-19 using hospital data.
    * 11:20-12:00 **Xiequan Fan** (online).
      Self-normalized Cramer moderate deviations for a supercritical Galton-Watson process.
    * 12:00-12:50 **Gennady Samorodnitsky** (online).
      Scaling and Taylor's law for heavy tailed observations (jointly with Joel Cohen and Richard Davis).

  - Afternoon
    * 15:00-15:40 **Tran Chi**.
      Time reversal of the spin alprocess for a population model with competition and environmental change.
    * 15:40-16:20 **Julien Randon Furling**.
      On the convex hull of certain stochastic processes.
    * 16:20-17:00 **Isidora Avila** (online).
      Alteration of coastal productivity and artisanal fisheries interact to affect a marine food web.
    * 17:00-18:00 **Poster session**:
      · Nawel Aries (CDER & University Boumédienne, Algiers)
      · Natalia Bahamonde (PUCV, Valparaiso)
      · Hugo Bernard (ENSAI),
      · Guillaume Franchi (ENSAI).
      · Branda Goncalves (LPTM, CYU, Cergy).
      · Louis Lebecq & Jean-Baptiste Roux (UBS, Vannes)
      · Frederico Maddanu (University of Rome Tor Vergata)
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    * 18:00-20:00 **Welcome cocktail**.

- September 16

  - Morning
    * 9:30-10:00 **Coffee**.
    * 10:00-10:40 **Pierre Alquier** (online).
      Tight Risk Bound for High Dimensional Time Series Completion (jointly with Nicolas Marie, Amélie Rosier).
    * 10:40-11:20 **Benjamin Poignard** (online).
      Sparse Factor Models: Asymptotic Properties (jointly with Yoshikazu Terada).
    * 11:20-12:00 **Denys Pommeret**.
      K-sample test of copulas.

* 12:00-12:40 **Julien Chiquet**.
  The Poisson-Lognormal Model as a Versatile Framework for the Joint Analysis of Species Abundances (jointly with Mahendra Mariadassou, Stéphane Robin).

– Afternoon

* 15:00-15:40 **Victor de la Pena** (online).
  Unbiased estimation of the Gini index.
* 15:40-16:20 **Imma Valentina Curato** (online).
  Inheritance of strong mixing and weak dependence under renewal sampling.
* 16:20-17:00 **Jüri Lember** (online).
  Viterbi path and training with (Bayesian) HMM.
* 17:00-17:40 **Chris Watkins** (online).
  Making Sex Tractable: an evolutionary model with detailed balance (jointly with Jüri Lember and Jenny Poulton).
* 20:00 **Conference dinner:** L'Entracte des Gobelins (please register).

• September 17

– Morning

* 9:30-10:00 **Coffee.**
* 10:00-10:40 **Lionel Truquet**.
  Multivariate binary time series models for absence/presence data in ecology.
* 10:40-11:20 **Michael Neumann** (online).
  Bootstrap for integer-valued GARCH(p, q) processes.
* 11:20-11:30 Pause.
* 11:30-12:10 **Catherine Aaron**.
  Local Convex Hull density, support and level set estimation (jointly with Ricardo Fraiman).
* 12:10-13:00 **Adam Jakubowski**.
  Phantom distribution functions for maxima on random trees.

– Afternoon

* 14:40-15:20 **Leonardo Videla** (online).
  Stochastic persistence of ecological communities driven by Lévy noise.
* 15:20-16:10 **Enrique Cabana** (online).
  Discrete random SIR models for the Covid-19 pandemic in Uruguay.
* 16:10-17:00 **Joël E. Cohen** (online).
  COVID-19 cases and deaths in the United States, Taylor's law of fluctuation scaling, and heavy tails.

2 Abstracts

- **Catherine Aaron** (University of Clermont Auvergne).
  Local Convex Hull density, support and level set estimation.

  In "A local nearest-neighbor convex-hull construction of home ranges and utilization distribution", Getz and Wilmer proposed an algorithm for home range and utilization distribution (core area) estimation. We aim to theoretically study this method. With Olivier Bodart, in 2016 we proved that the home range (support) estimator is consistent (and minimax when regularity conditions are satisfied). More recently, we proved, with Ricardo Fraiman, that the core area (level set) estimator has to be slightly modified to achieve minimax rates. In the talk we will present the initial algorithm, the proposed modifications, why they are expected to improve the initial method and the associated asymptotic results.

- **Hansjoerg Albrecher** (HEC, Lausanne).
  Asymptotic analysis of the Greenwood statistic and extensions for very heavy tails.

  We revisit and unify the asymptotic analysis of the classical Greenwood statistic comprising the ratio of the sum of squares and the sum squared of independent and identically distributed random variables with regularly varying tails. We discuss some of its application areas and extend the analysis to the situation of arbitrary powers. Finally, we study the robustness of the asymptotic expressions when some of the terms in the statistic are dropped.

- **Pierre Alquier** (Riken AIP, Tokyo), Nicolas Marie, Amélie Rosier.
  Tight Risk Bound for High Dimensional Time Series Completion.

  Initially designed for independent datas, low-rank matrix completion was successfully applied in many domains to the reconstruction of partially observed high-dimensional time series. However, there is a lack of theory to support the application of these methods to dependent datas. In this paper, we propose a general model for multivariate, partially observed time series. We show that the least-square method with a rank penalty leads to reconstruction error of the same order as for independent datas. Moreover, when the time series has some additional properties such as periodicity or smoothness, the rate can actually be faster than in the independent case.

- **Isidora Avila** (Advanced Conservation Strategies, Santiago).
  Alteration of coastal productivity and artisanal fisheries interact to affect a marine food web.

  Top-down and bottom-up forces determine ecosystem function and dynamics. Fisheries as a top-down force can shorten and destabilize food webs, while effects driven by climate change can alter the bottom-up forces of primary productivity. We assessed the response of a highly-resolved intertidal food web to these two global change drivers, using network analysis and bioenergetic modelling. We quantified the relative importance of artisanal fisheries as another predator species, and evaluated the independent and combined effects of fisheries and changes in plankton productivity on food web dynamics. The food web was robust to the loss of all harvested species but sensitive to the decline in plankton productivity. Interestingly, fisheries dampened the negative impacts of decreasing plankton productivity on non-harvested species by reducing the predation pressure of harvested consumers on non-harvested resources, and reducing the interspecific competition between harvested and non-harvested basal species. In contrast, the decline in plankton productivity increased the sensitivity of harvested species to fishing by reducing the total productivity of the food web. Our results show that strategies for new scenarios caused by climate change are needed to protect marine ecosystems and the wellbeing of local communities dependent on their resources.

  This is a joint work with Derek Corcoran, Alejandro Pérez-Matus, Evie A. Wieters, Sergio A. Navarrete, Pablo A. Marquet & Fernanda S. Valdovinos.

- **Enrique Cabana** (Udelar, Montevideo).
  Discrete random SIR models for the Covid-19 pandemic in Uruguay.

  Two models for Covid are discussed: both are discrete, based on Markov chains with random thinnings. The simpler one adds the effect of vaccination and explores the use of Google mobility records for short-term predictions. The other one exploits the availability of data including the individual histories of Covid-19 patients, during a short initial period of the epidemic. Both models can be run in an interactive internet platform, with automatic access to data taken from the epidemic evolution and the vaccination process in Uruguay, `https://emcabana.shinyapps.io/Rvac/`.

- **Joel E. Cohen** (Lab of populations - Rockefeller University & Columbia, NY).
  COVID-19 cases and deaths in the United States, Taylor's law of fluctuation scaling, and heavy tails.

  COVID-19 cases and deaths are reported by primary administrative subdivisions of the US (called "states") and by secondary administrative subdivisions within each state (called "counties"), cumulatively, day by day, since the pandemic began in the US in January 2020. We show that, on day 1 of each of the 15 months from April 2020 through June 2021, the relationship between the variance and the mean of cumulative cases and of cumulative deaths over counties within each state is well approximated by a power-law variance function known in ecology as Taylor's law or Taylor's power law of fluctuation scaling. The upper tails of the empirical distributions of cases and deaths by state suggest the possibility of a heavy-tailed distribution with infinite variance. These observations have practical consequences and may be theoretically interpretable.

- **Imma Valentina Curato** (Lab of Finance, ULM).
  Inheritance of strong mixing and weak dependence under renewal sampling.

  Let X be a continuous-time strongly mixing or weakly dependent process and T a renewal process independent of X with inter-arrival times (τ_i). We show general conditions under which the sampled process (X_{τ_i}, τ_i) is strongly mixing or weakly dependent. Moreover, we explicitly compute the strong mixing or weak dependence coefficients of the renewal sampled process and show that exponential or power decay of the coefficients of X is preserved (at least asymptotically). Our results imply that essentially all central limit theorems available in the literature for strongly mixing or weakly dependent processes can be applied when renewal sampled observations of the process X are at disposal.

- **Julien Chiquet** (MIA-Paris, Université Paris-Saclay, AgroParisTech, INRAE, Paris, France).
  The Poisson-Lognormal Model as a Versatile Framework for the Joint Analysis of Species Abundances.

  Joint Species Distribution Models (JSDM) provide a general multivariate framework to study the joint abundances of all species from a community. JSDM account for both structuring factors (environmental characteristics or gradients, such as habitat type or nutrient availability) and potential interactions between the species (competition, mutualism, parasitism, etc.), which is instrumental in disentangling meaningful ecological interactions from mere statistical associations. Modeling the dependency between the species is challenging because of the count-valued nature of abundance data and most JSDM rely on Gaussian latent layer to encode the dependencies between species in a covariance matrix. The multivariate Poisson-lognormal (PLN) model is one such model, which can be viewed as a multivariate mixed Poisson regression model. Inferring such models raises both statistical and computational issues, many of which were solved in recent contributions using variational techniques and convex optimization tools. The PLN model turns out to be a versatile framework, within which a variety of analyses can be performed, including multivariate sample comparison, clustering of sites or samples, dimension reduction (ordination) for visualization purposes,

or inferring interaction networks. This paper presents the general PLN framework and illustrates its use on a series a typical experimental datasets. All the models and methods are implemented in the `R`-package PLNmodels, available from `cran.r-project.org`.

This is a joint work with Mahendra Mariadassou (MaIAGE, Université Paris-Saclay, INRAE, Jouy-en-Josas, France) and Stéphane Robin (MIA-Paris, Université Paris-Saclay, AgroParis-Tech, INRAE, Paris & CESCO, UMR 7204, MNHN, CNRS, UPMC, Paris, France),

- **Félix Cheysson** (Sorbonne University, Paris).
  Evolution of groups at high risk of death from Covid-19 using hospital data.

  In France, death rates due to Covid-19 halved between the beginning and the end of the first wave of the pandemic. While this diminution can be explained by better knowledge of the disease, better care for the patients, and a slight increase in the proportion of young patients during the second half of the wave, it is not clear whether it is homogeneous for all age groups. In this talk, we focus on the estimation of death rates for groups at risk from Covid-19. Rather than arbitrarily building the groups at risk from patients' demographic data, they are estimated using classification trees (CART). To study the temporal evolution of groups at risk from Covid-19, we introduce statistical tools for the comparison of CART trees derived from the theory of robust estimation. This allows us to propose a statistical test to determine changes through time in the death rates for each demographic group. Finally, we illustrate this method on the first wave of the pandemic.

- **Tran Chi** (Université Gustave Eiffel, Champs sur Marne).
  Time reversal of the spinal process for a population model with competition and with environmental change.

  We consider a stochastic individual-based population model with interaction and trait-structure. The traits evolve through mutations, and the evolution can be approximated in large population by a non-linear PDE that admits a non-trivial stationary solution. We can approximate the stochastic population process by a linear process where the interactions are frozen, when the population is close to this stationary measure. This allows us to derive, when the population is large, the equation satisfied by the ancestral lineage of a uniformly sampled individual at a fixed time T, which is the path constituted of the traits of the ancestors of this individual in past times $t < T$. We show that the time reversal of this process solves a simple SDE, that we derive explicitly in two important cases: for traits driven by drifted Brownian motions or drifted jump processes.

- **Xiequan Fan** (Tianjin University). *Self-normalized Cramer moderate deviations for a supercritical Galton-Watson process.*

  Let $(Z_n)_{n\geq 0}$ be a supercritical Galton-Watson process. Consider the Lotka-Nagaev estimator for the offspring mean. In this paper, we establish self-normalized Cramer type moderate deviations and Berry-Esseen's bounds for the Lotka-Nagaev estimator. The results are believed to be optimal or near optimal.

- **Oleg Klesov** (KPI, Kiev).
  Uniform Strong Law of Large Numbers

  Let L be a collection of indices and $X(l)$ be independent identically distributed random variables. Given a family $\{A\}$ of finite subsets of L, consider the sums $S(A)$ of $X(l)$ with indices belonging to A. Then we search the conditions imposed on random variables and the family of subsets such that $S(A)/|A|$ has a limit almost surely as $|A|$ grows where $|A|$ means the number of indices in A. The case of convergence in probability does not create difficulties in this setting in contrast to the almost sure convergence.

  This work is jointly with Yu.V.Bogdanskii.

- **Adam Jakubowski** (Mikolai Kopernikus University, Torùn).
  Phantom distribution functions for maxima on random trees.

  Let $(Q, N, C_1, C_2, \ldots)$ be a random vector, where $N \in \{0, 1, 2, \ldots, \infty\}$ and $\{C_i\}$ is an i.i.d. sequence of non-negative weights. Consider the following distributional equation

  $$R =_d \Big(\bigvee_{i=1}^{N} C_i R_i \Big) \vee Q,, \tag{$*$}$$

  with random variables $\{R_i\}$ independent, identically distributed as R and independent of $(Q, N, C_1, C_2, \ldots)$. This equation is similar to the higher-order Lindley equation [6].

  In [5] a minimal/endogenous solution to $(*)$ is constructed on a weighted branching tree and it is shown that R has a power law, i.e. $P(|R| > x) \sim H x^{-\alpha}$ for some $\alpha > 0$ and $H > 0$.

  In [1], under slightly stronger assumptions, the power law property is derived by constructing a *leading branch* along which the maxima contribute to the tail probabilities. This provides a tool for simulations of the constant H.

  The idea of [1] motivates the present work. Using methods developed in [3] and [2] , we investigate the existence of a phantom distribution function along a particular branch of a rooted tree (like in the case of integer-valued lattices in [4]) and aim at extending this result to weighted branching trees.

  This is *a work in progress*, joint with Paul Doukhan.

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  [4] A. Jakubowski, I. Rodionov and N. Soja-Kukieła, Directional phantom distribution functions for stationary random fields, *Bernoulli*, **27 (2021)**, 1028–1056.
  [5] P.R. Jelenković and M. Olvera-Cravioto, Maximums on trees, *Stochastic Process. Appl.*, **125 (2015)**, 217–232.
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- **Jüri Lember** (University of Tartu).
  Viterbi path and training with (Bayesian) HMM.

  Viterbi training (VT) is a computationally cheap parameter learning algorithm in many latent variable models such as hidden Markov models (HMM), mixture models and many others. At every step of iteration of VT, given a a set of parameters, the most likely outcome of latent/nuisance variable is found (Viterbi path in HMM case), and then the parameters are re-estimated. As such, VT can be considered as Maximization-Maximization (MM) algorithm, opposed to Expectation-Maximization (EM) algorithm, where at every step of iteration, the nuisance parameters are integrated out. As a parameter estimation method, VT is often (typically) notoriously wrong. There are several reasons for giving a biased estimate, one of them is lack of so-called asymptotic fixed point property. This leads to an idea of adjusted VT, where the asymptotic bias is taken into consideration.

  We then turn to the seemingly unrelated problem of HMM segmentation in Bayesian setup. With priors in parameters in HMM, the model is not any more an HMM, in fact it has much longer memory and different properties. In particular, Markov property fails and Viterbi algorithm does not work any more and several iterative algorithms should be used instead.

We develop EM analogue and also apply above-mentioned MM algorithm. Surprisingly enough, in this setting MM algorithm works very well. This relates the VT to Bayesian setup and gives one more explanation to the bad behavior in parameter estimation.

- **Michael Neumann** (Lab of Mathematics, Jena).
  Bootstrap for integer-valued GARCH(p,q) processes.

  We consider integer-valued processes with a GARCH structure and prove existence and uniqueness of a stationary distribution as well as absolute regularity with exponentially decaying coefficients. As our main result, we construct a coupling of the original process and its bootstrap counterpart which implies bootstrap consistency for different types of statistics.

- **Victor de la Pena** (Lab of Statistics, Columbia, New-York).
  Unbiased estimation of the Gini index.

  In this talk, I will present an approach to calculate the moments of the bias of the Gini index.

- **Benjamin Poignard** (Riken-AIP, Osaka).
  Sparse Factor Models: Asymptotic Properties.

  We consider the problem of estimating a factor model based variance covariance matrix when the factor loading matrix is assumed sparse. We develop a penalised Z-estimation framework to handle the identifiability issue of the factor loading matrix while fostering sparsity in potentially all its entries. We prove the oracle property of the penalised Z-estimator for the factor model, that is the penalisation procedure can recover the true sparse support and the estimator is asymptotically normally distributed. The non-penalised loss functions are deduced from the class of Bregman divergence losses, providing new estimators for factor modelling. These theoretical results are supported by empirical studies.

  This is a work with Yoshikazu Terada (Osaka University).

- **Denys Pommeret** (ISFA Lyon and Marseille).
  K-sample test of copulas.

  Copulas are still extensively studied and used to model the dependence of multivariate observations. Many applications can be found in fields such as energy, environment or ecology. Several authors believe that copula approaches are among the tools all ecologists should be considering for analysis of their data in the 21st century." In a one-sample case, there are many tests to compare an observed copula to a target copula.
  In the two-sample case, Rémillard and Scaillet (2009) proposed a test to compare two nonparametric copulas, that is to test H0: $C_1 = C_2$, where C_1 and C_2 are two copulas observed on two iid samples, which may be paired.
  To our knowledge, there is no extension to the K-sample case ($K > 2$). However, the increasing amount of data requires sometimes more comprehensive analyzes. It is in this sense that we propose an equality test of K copulas simultaneously, when K populations are observed. We want to test the following hypothesis: H0: $C_1 = C_2 = \cdots = C_K$ from K iid samples, possibly paired. We obtain the exact asymptotic null distribution of the test statistic and we prove the convergence of the test. The idea of the test is to transform the observations to uniform laws, then to use the decomposition of the density of the copula in an orthogonal Legendre polynomials basis. Returning to the copula function we obtain what are called copula coefficients which characterize each copula. The test then amounts to simultaneously comparing these coefficients. We provide some illustrations of this method, in particular we suggest a clustering algorithm to classify populations with similar forms of dependence.
  Reference.
  Y I Ngounou B, D Pommeret (2020) Nonparametric estimation of copulas and copula densities by orthogonal projections, *Arxiv-2010.15351.*

- **Julien Randon Furling** (University Paris 1, Panthéon-Sorbonne).
  On the convex hull of certain stochastic processes.

  Lévy processes are often used to model animal movement, and the convex hull of such processes is then often taken as a proxy for the so-called home range of the animal (or group of animals). In this talk I will review a range of results on the convex hulls of random walks and Lévy processes, both in the plane and in higher dimensions, in particular the expected perimeter length in the planar case, or the expected number of faces on the boundary, expected d-dimensional volume, and other geometric properties of these random convex polytopes.

- **Gennady Samorodnitsky** (Cornell University, Ithaca).
  Scaling and Taylor's law for heavy tailed observations (jointly with Joel Cohen and Richard Davis).

  Very scaling laws have been observed in physical and biological applications. One of the best known such laws is the Taylor law, relating the sample mean and the sample variance of observed data. We present a theory explain a number of such scaling laws for heavy tailed observations using both weak limit theorems and large deviations.

- **Lionel Truquet** (ENSAI, Rennes).
  Multivariate binary time series models for absence/presence data in ecology.

  To understand the dynamic of vectors with binary coordinates, we develop a mulitvariate probit/logistic time series models. To fit such models to absence/presence data involving multiple species observed at various observation sites, we consider the situation of panel type data and consider both time-varying and fixed covariates that can be included in the dynamic. We then consider statistical inference of the parameters of the model using composite and pseudo-likelihood estimator, when both the horizon time and the number of sites grow to infinity. Asymptotic properties of the estimators are based on some multiparameter versions of ergodic theorems.

- **Leonardo Videla** (Instituto de Ingeniería Matemática, Universidad de Valparaíso, Chile).
  Stochastic persistence of ecological communities driven by Lévy noise.

  In this talk we present the basic notion of strong stochastic persistence (SSP) of ecological communities, as developed during the last years by Hening, Nguyen, Benaïm, Schreiber and other researchers. We illustrate some new results in the case of Lévy-driven Lotka-Volterra SDE, and show a simple application to food-chains with intraspecific competition.

- **Chris Watkins** (RHUL, London).
  Making Sex Tractable: an evolutionary model with detailed balance.

  We introduce a new model of sexual evolution with mutation and selection, a variant of the Moran process, and we discuss its properties. In this (abstract) model, the stationary (mutation-selection equilibrium) distribution has a simple closed form for multi-locus genomes and arbitrary fitness landscapes. We give examples of exact calculations of statistics of the stationary distribution - and of other properties of the evolutionary process - for various fitness landscapes, for both finite and infinite populations. As far as we are aware, these calculations can be done differently and more simply for this model than for previous models: we use exact recursions to analyse finite-population stationary distributions, and an argument using the de Finetti representation of an exchangeable breeding process to obtain the limit distribution for infinite populations.

  We also consider the informational properties of the evolutionary process, and we demonstrate that Hamming codes can be used to increase the amount of information maintained by selection for given mutation-rate and intensity of selection. We give examples of extensions

of the model in which genomes are represented as sets (using a Beta process) and as networks (using node-exchangeable graphs), and show that these more complex models have similar analytical tractability.

This is a joint work with Jüri Lember (University of Tartu) and Jenny Poulton (RHUL)

3   Social Program

Beginning such a program let us realise two things,

- first I should apologise because it is so restrictive but it is necessarily biased;

- the second point it to think about the importance of keeping all those incredibly beautiful places which justify thousands times the existence of projects in analogous lines.

The forthcoming text is full of links: click on locations to safely travel during this complicate period.

The social program ([1]) will be free:

- Brazil: Iguazu falls, Rio-Corcovado, Amazonia Forests,

- Chile: Patagonia, Paranal, Atacama desert, Valparaiso, Caleta Portales,

- China: The great wall, Peking-Forbidden city, Hong-Kong,

- France: Lyon ([2]), Nantes-Machines de l'Ile, Paris-Plage, Paris-Tara Expedition, Vannes, Luminy,

- Germany: Aachen, Berlin, Heidelberg, Munich-Hofbraeuhaus, Oberwolfach,

- Mexico: Mexico-Frida Khalo Museum, Mexico-Coyoacan,

- New Caledonia: Nouméa,

- Poland: Torun, Varsaw-Jewish Museum,

- Spain: Barcelona-La Pedrera, Figueras-Dali Museum, Granada,

- USA : Colorado, New York City,

- Venezuela: Delta del Orinoco, Salto Angel.

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[1]Don't hesitate to help for improving this important feature of the conference.

[2]Sorry for reducing the attraction of this beautiful city to food but a social program should include a conference dinner and Lyon is the capital of Gastronomy...

Let us hope that we can meet physically in this city for a physical event!

The Welcome Cocktail on September 15 is for physically present colleagues.

4   Participants

Participants come from all over the world and to turn this conference in a link between researcher we thought that an easy access to all of them may be a successful tool for further contacts; people attending this conference are located in Belgium, Brazil, Canada, Chile, China, Cyprus, Denmark, Germany, France, Hong-Kong, Hungary, Indonesia, Ivory Coast, Japan, Mauritius, New Caledonia, Pakistan, Peru, Poland, Portugal, Russia, Singapore, South Korea, Spain, Switzerland, Ukraine, United Kingdom, United States of America, Uruguay and Vietnam.

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