Conference Schedule

Day 1: Monday 28 oct. 2024

Plenary Session

Title: Random Projections: on sub-Gaussianity and sparsity
Speaker: Aurélien Garivier
Abstract:
Random projections are a simple and computationally efficient dimensionality reduction technique in unsupervised machine learning. They are based on the existence low-distortion embeddings of points from high-dimensional into low-dimensional Euclidean space. We will discuss in this talk how to construct such projections, and in particular the possibility to use simple and sparse matrices.

Parallel Sessions

Track 1:MACHINE LEARNING / APPRENTISSAGE Statistique

- **Session** 1: Theoretical guarantees in KL for Diffusion Flow Matching (**M. Gentiloni**)
  - Flow Matching (FM) (also referred to as stochastic interpolants or rectified flows) stands out as a class of generative models that aims to bridge in finite time the target distribution $\nu^\star$ with an auxiliary distribution μ leveraging a fixed coupling π and a bridge which can either be deterministic or stochastic. These two ingredients define a path measure which can then be approximated by learning the drift of its Markovian projection. The main aim of this talk is to provide relatively mild assumption on $\nu^\star$, μ and π to obtain non-asymptotics guarantees for Diffusion Flow Matching (DFM) models using as bridge the conditional distribution associated with the Brownian motion. More precisely, I will present bounds on

the Kullback-Leibler divergence between the target distribution and the one generated by such DFM models that hold true under moment conditions on the score of $\nu^\star$, μ and π, and a standard L^2-drift-approximation error assumption.

- **Session** 2: Decorrelation of deformation models via shape representation by varifolds (**R. Mouhli**)

  – In computational anatomy, registration tasks are performed by applying diffeomorphic deformations to the data. These deformations can range from simple ones such as translations, rotations and scalings, to more complex transformations such as the Large Deformation Diffeomorphic Metric Mapping (LDDMM) model. Coupling these different models makes it possible to decompose a deformation into several deformations, enabling better interpretability of the studied deformation by analyzing each model's contributions. To ensure that the more complex models do not replicate the deformations already created by the simpler models, we introduce a quantification of the correlation between different models. In this talk, I will first introduce the LDDMM model and its application for matching tasks, then I will present our first results on the decorrelation of the actions of two deformations on a shape represented as actions in a space of varifolds.

- **Session** 3: Particle Gradient Descent for Kernel logistic Regression via Sparse regularization on measures (**A. Simoes**)

  – We are interested in supervised learning kernel methods for binary classification. In the case of kernel-based regularization, kernel logistic RIDGE (KRR) regression is the one of the most widely used method. It relies on the representer theorem (Fan and Zou (2020)), which shows a simple form of KRR: a sum of kernels centered on the data points, with weights being solution to a quadratic program. This resolution implies two main issues, the dependency of the estimator on the observation locations and the number of parameters needed, as large as the sample size. In this work, we address these issues using ideas of sparsity that appeared in high dimensional statistics. More pre- cisely, we work under the assumption that the regression function can expressed as a weighted sum of few kernels located at points. This assumption is the cornerstone of continuous sparse regression on measures,

which represents the target regression function by a discrete measure. The main objective of this work is to delimit the benefits and limitations of both methods, KRR and continuous sparse regression methods. Continuous sparse regression for logistic regression has been overlooked in the literature and this work, for the first time, gives a comprehensive comparison of this method, referred to as Beurling logistic (Blogistic) with KRR. In this article, we consider a different regular- ization norm of that used in KRR as could do Beurling LASSO in high dimensional problems. An impli- cation of this modification is the non-verification of the representer theorem's hypothesis, which need a Tikhonov regularization. The underlying idea is to estimate and look directly for the target Dirac masses, forcing the sparsity of the estimator thanks to an 1 norm. We mainly study this estimator through a Conic Particle Gradient Descent introduced by Chizat (2019) in the case of a two layer Neural Network. This algorithm works as throwing some particles, that corresponds to the kernels describing the estimator and move them with respect to some Gradient Descent, the result is the appearance of aggregation around the Dirac. The limits of KRR and Blogistic are presented through various aspects such as the support, the parameters, the score and the fairness.

- **Session** 4: An adaptive method for nonlinear model order reduction using sparse polynomials(**S. Joel**)

  - Model order reduction methods are used to approximate a manifold of functions from a high-dimensional space by a low-dimensional space or manifold. We here propose a new approach that aims at building a low-dimensional nonlinear manifold Mn, given a desired target precision. The description of the manifold is similar to (1) or (2), with $M_n = \{L(a) + N(a) : a \in R_n\}$, where L is a linear map onto a n-dimensional space Vn and N is a nonlinear map onto a complementary space. Here, we propose an adaptive strategy for the construction of the maps L and N , the latter using compositions of sparse polynomials. The manifold Mn is estimated "offline" from a set of training samples and then used "online" to approximate the solution of parameter-dependent equations, using a Galerkin-type projection method. We investigate through numerical experiments the performance of our method on several parameter-dependent problems. The results reveal the advantage of our approach compared to linear approximation, and its

competitive performance against state of the art nonlinear methods. This is a joint work with Antoine Bensalah and Anthony Nouy. References (1) J. L. Barnett, C. Farhat, and Y. Maday. Neural-network-augmented projection-based model order reduction for mitigating the kolmogorov barrier to reducibility of cfd models, 2022. (2) R. Geelen, L. Balzano, S. Wright, and K. Willcox. Learning physics-based reduced-order models from data using nonlinear manifolds, 2024.

Track 2: Methodes Numeriques pour les EDP

- **Session** 1: Finite volume method for Cahn-Hilliard equations with surfactants (**M. Castellano**)
  - This work focuses on the numerical analysis of a phase field model with surfactants, originally introduced by Laradji et al . The model describes the phase separation dynamics between water and air in the presence of surfactants, and has numerous applications in pharmacology, biology, and physics, among others. We represent this dynamics using two coupled Cahn-Hilliard equations. Cahn-Hilliard equations model the phase separation process of two non-miscible fluids, for which the fluids spontaneously separate forming sub-domains of pure phases . We therefore use a first Cahn-Hilliard equation to describe the phase separation dynamics between water and air. We assume that the two fluids occupy the entire domain of interest . It is then sufficient to study the evolution of a single concentration (called order parameter and taking values in (–1, 1), where –1 corresponds to air and 1 corresponds to water). Surfactants (diminutive form of Surface Active Agents) are molecules soluble in water, having a molecular structure composed by both a hydrophilic part and a hydrophobic part, which drives them to aggregate at the surface of water . We model this behavior through a second Cahn-Hilliard equation, representing surfactants as a fluid separating from water. One of the crucial aspects of this model lies in the choice of a coupling potential in a manner that ensures the well-posedness of the problem and the stability of the numerical system, all while maintaining physical validity . We propose a finite volume method associated with this model, and perform the numerical analysis of this scheme (energy estimation, existence, convergence, etc.). Numerical simulations will be provided to validate the model.

- **Session** 3: Discrete hypocoercivity for a nonlinear kinetic reaction model (**T. Laidin**)

  – I will present a work in collaboration with M. Bessemoulin-Chatard and T. Rey, in which we consider a non-linear kinetic model describing a two-species generation-recombination reaction that can be considered as a simplified version of models describing the generation and recombination of electron-hole pairs in semiconductors. I will introduce a finite volume discretization of this model for which we can prove an exponential decay towards the steady state using discrete hypocoercivity methods. After presenting the ideas of the proof in the continuous framework, I will highlight the main difficulties induced by the discretization process. The properties of the method will then be illustrated by several numerical examples.

- **Session** 3: Schémas uniformément précis pour les systémes hyperboliques de relaxation (**Mahmoud**)

  – Notre objectif est d'examiner des systèmes hyperboliques de relaxation et d'en proposer une approximation numérique à l'aide de méthodes volumes finis. Ces systèmes incluent des termes convectifs et des termes sources de relaxation non linéaires. Nous nous concentrons ici sur le modèle proposé par Jin et Xin [4] :

$$\partial_t u + \partial_x v = 0 \tag{1}$$

$$\partial_t v + \lambda^2 \partial_x u = \frac{1}{\varepsilon} \left(f(u) - v \right), \tag{2}$$

  où $f(u)$ est une fonction non linéaire satisfaisant la condition sous-caractéristique $\lambda \geq |f'(u)|$.

  Nous étudions deux régimes limites lorsque le temps de relaxation ε tend vers 0 et ∞, ainsi que des régimes intermédiaires. Lorsque ε tend vers zéro, l'équilibre satisfait l'équation $\partial_t u + \partial_x f(u) = 0$, et lorsque ε tend vers l'infini, nous retrouvons les solutions du système hyperbolique 2×2 homogène avec les vitesses caractéristiques λ et $-\lambda$.

  Notre objectif est de développer et d'analyser des schémas numériques garantissant une précision uniforme dans ces différents régimes. Pour ce faire, nous introduisons deux schémas : une adaptation du schéma implicite de Béreux et Sainsaulieu [1] avec une

approximation HLL, et un solveur de Riemann dans l'esprit du schéma préservant l'asymptotique proposé dans [2]. Le caractère uniformément précis des schémas est étudié comme dans [3] et des comparaisons sont faites par rapport à un schéma à pas fractionnaire implicite standard. Les résultats numériques mettent en évidence la bonne précision uniforme des schémas.

References

[1] F. Bereux and L. Sainsaulieu, "A Roe-type Riemann solver for hyperbolic systems with relaxation based on time-dependent wave decomposition," *Numerische Mathematik*, 1997.

[2] C. Berthon, A. Crestetto, and F. Foucher, "A well-balanced finite volume scheme for a mixed hyperbolic/parabolic system to model chemotaxis," *Journal of Scientific Computing*, 2016.

[3] F. Filbet and A. Rambaud, "Analysis of an asymptotic preserving scheme for relaxation systems," *ESAIM: Mathematical Modelling and Numerical Analysis*, 2013.

[4] S. Jin and Z. Xin, "The relaxation schemes for systems of conservation laws in arbitrary space dimensions," *Communications on Pure and Applied Mathematics*, 1995.

- **Session** 4 : Une stratégie de sous-cyclage pour des méthodes de Volumes-Finis Lagrangiennes, appliquée à l'interaction fluide-structure (**A. Gangloff**)

  – Nous nous intéressons aux effets d'une onde de souffle sur une structure déformable. La simulation numérique de ce problème soulève de nombreuses difficultés, dues en particulier à son caractère multi-échelle en espace et en temps. La méthode monolithique consiste à résoudre le problème sur un seul domaine avec une méthode numérique unique. Le pas de temps est alors contraint par la plus grande vitesse d'onde dans l'ensemble du domaine. La méthode partitionnée consiste à découper la zone de simulation en plusieurs morceaux afin d'adapter la stratégie de résolution à la physique locale. Cette approche permet de choisir les méthodes numériques utilisées pour résoudre chaque problème. Nous utilisons les équations d'Euler pour modéliser le fluide et un modèle hyperélastique pour le solide. Les méthodes numériques sont basées sur les schémas Lagrangiens colocalisés GLACE ou

EUCCLHYD dans le domaine fluide et dans le domaine solide. Ces méthodes sont conservatives et entropiques. Nous proposons une méthode partitionnée couplant ces méthodes et supportant un pas de temps local à chaque domaine. Nous utilisons des méthodes Arbitraire-Lagrange-Euler dans chacun des domaines de résolution, ce qui permet de conserver une interface lagrangienne entre les zones fluides et structures. Nous montrons comment résoudre le problème à la frontière de manière à conserver les propriétés des méthodes numériques. Une attention particulière est portée à la conservation (masse, quantité de mouvement, énergie totale). Nous illustrons sur des exemples d'interaction fluide-structure, l'intérêt de la méthode.

Track 3: Control

- **Session** 1: Computer-assisted proofs of non-reachability for the heat equation control system (**I. Hasenohr**)

  - It is customary to design a control system in such a way that, whatever the chosen control satisfying the constraints, the system does not enter so-called unsafe regions. This work introduces a general computer-assisted methodology to prove that a given linear parabolic control system with compact constraints avoids a chosen unsafe set. Relying on support hyperplanes, we devise a functional such that the property of interest is equivalent to finding a point at which the functional is negative. Actually evaluating the functional first requires time- and space-discretisation. We thus provide explicit, fine estimates for finite elements discretisation. Second, computations lead to roundoff errors, which are dealt with by means of interval arithmetic. The control of both error types then leads to rigorous, computer-assisted proofs of non-reachability of the unsafe set.

- **Session** 2: Boundary bilinear optimal control of linear nonlocal parabolic problems involving an intergral kernel (**J. Larrouy**)

  - In this talk, we consider a linear nonlocal heat equation in a bounded domain with a nonlocal space term (accounted by a spatial convolution kernel) involving a boundary multiplicative control contained in Neumann boundary conditions. After securing the well- posedness of the problem, we derive several properties from the control-to-state mapping. We then prove the existence

of at least one optimal control for the problem under study, and establish first and second order optimality conditions leading to local uniqueness of an optimal control. Finally, we demonstrate that we are able to reach global uniqueness of optimal control by means of additional assumptions.

- **Session** 3: Contrôle en temps minimal d'un oscillateur à fréquence variable (**K. Lutz**)

  – Motivé par une analogie avec les transferts entre états stationnaires de la mécanique quantique, cet exposé porte sur le contrôle non-linéaire (affine) de l'oscillateur harmonique "classique", éventuellement amorti. L'état instantané du système, décrit par sa position et sa vitesse, est solution d'une équation différentielle ordinaire linéaire. Dans cette équation, le contrôle se manifeste en modifiant au cours du temps la raideur du puits de potentiel quadratique dans lequel le système évolue. L'objectif est de décrire qualitativement la structure des contrôles admissibles (contraintes) qui permettent de transférer le système entre deux états prescrits de vitesse nulle et ce en temps minimal, c'est-à-dire le plus rapidement possible. En proposant une réinterprétation spectrale fructueuse du temps minimal de contrôle et des trajectoires associées, des résultats qualitatifs précis sont obtenus. Dans le cas non-amorti, on montre notamment (i) une minoration a priori du temps minimal en fonction des données du problème, et (ii) que tout contrôle optimal est nécessairement constant par morceaux avec au plus trois temps de transition entre les valeurs minimales et maximales autorisées.

- **Session** 4: On an optimal control of an ill-posed advection-diffusion model with nonlocal diffusion (**E. Rinaldo**)

  – In this presentation, we investigate the optimal control of a convection-diffusion model for an incompressible fluid, incorporating both a classical gradient operator and a Laplace fractional operator of order $0 < s < 1$. We begin by approximating the ill-posed problem with a family of well-posed problems that possess appropriate regularity. We demonstrate that the solutions of these well-posed problems converge to the solutions of the original ill-posed problem.Subsequently, we examine the minimization problem associated with the perturbed model. This approach enables us to characterize the optimal ill-posed model as the limit of the optimal solutions of the family of well-posed problems.

Track 4: Branchement/Modèle stochastique pour la biologie et la santé

- **Session** 1: An individual-based stochastic model reveals strong constraints on allometric relationships with minimal metabolic and ecological assumptions (**V. Brodu**)

  – Across the whole range of organisms, from unicellulars to macrovertebrates, observations suggest the existence of general allometric relationships. It is of the form $B \propto M^{\alpha}$, where B and M are biological parameters, M being typically a mass, and α is called the allometric coefficient. Moreover, this allometric structure is very precise and often presented as

  $$\beta = \delta = \gamma - 1 = \alpha - 1, (1)$$

  with β, δ, γ being allometric coefficients related to, respectively, the birth, death, growth and metabolic rates in the population. During this talk, our goal is to determine in a bottom-up approach what are the possible allometric coefficients under elementary –and ecologically relevant-constraints. We design a stochastic individual-based model structured in energy, for single species interacting with an external resource. Populations are characterized by a typical energy at birth, ranging from small to high values, so that our model is valid for the whole spectrum of possible body sizes. We show in particular that assuming an allometric coefficient α related to metabolism strongly constrains the range of possible values for β, δ, γ, and we recover Equation (1). We further identify and discuss the precise and minimal ecological mechanisms that are involved in these strong constraints on allometric relationships. Mathematically, this gives rise to a Piecewise Deterministic Markov Process (PDMP). The study of this process allows us to identify various behaviors for our population, depending on the allometric coefficients. Among the main tech- niques used, we highlight the notion of asymptotic pseudotrajectory, several couplings and a Lyapunov argument.

- **Session** 2: Inference of cell differentiation trajectories using a modified optimal transport method based on a probabilistic model of gene dynamics (**C. Fournié**)

  – While two cells may possess the same genome, they can express their genes differently, leading to distinct cellular outcomes. Cel-

lular differentiation is the biological process that leads a cell to opt for a particular cellular identity. Recently, single-cell RNA-sequencing has allowed to provide gene expression levels at specific times for a large number of individual cells and a large number of genes simultaneously during such a process. Repeating such measurements at different timepoints gives then access to the temporal variation, or transport, of a distribution on a gene expression space. The full temporal trajectory of the distribution characterizes the differentiation process. The optimal transport theory has been used to infer cellular differentiation trajectories from single-cell RNA-seq data (Schiebinger et al. 2019). However, this theory assumes that cells move, in the gene expression space, by diffusion, when real gene dynamics are much more complex. Our work aims to study the interest, for inferring cell differentiation trajectories, of using a modified optimal transport method based on more realistic gene dynamics. To reach this goal, we will compare the solutions of the Schrodinger problem (Shrödinger, 1932), which is equivalent to the solution of the optimal transport problem (Ripani, 2017), when the underlying gene model is either assumed to be diffusive or driven by a piecewise deterministic Markov process (PDMP) representing the 2-states model of gene expression (Herbach et al., 2017). This model has been shown to reproduce realistic mRNA and protein dynamics at the single cell level. We will present some results based on a toy gene regulatory model and simulated data to do so. By studying the entropy between the solutions of the two Schrodinger problems (diffusive or PDMP-based) under different conditions (on the size of the network, on its dynamics, but also the data: number of cells, etc.), we will show that using the PDMP formalism provides a better approximation of the differentiation process than the standard diffusive process. This work has been performed in collaboration with Elias VENTRE (Univesity of British Columbia), Aymeric BARADAT (ICJ, Université de Lyon), Olivier GANDRILLON (LBMC, ENS de Lyon) and Fabien CRAUSTE (MAP5, Université Paris Cité).

- **Session** 3: Modèle dynamique pour la représentation de données d'expression des gènes en cellules uniques (**M. Gaillard**)
  - A first simplification of the gene expression mechanism considers that a gene is transcribed into messenger RNA, which in turn is translated into protein. Single-cell data have revealed the pres-

ence of biological variability between cells of identical genome and environment, highlighting not only epigenetic aspects but also the stochastic nature of gene expression. This stochasticity raises two issues from a statistical perspective. First, we need to be able to estimate the variability between cells (or between genes) using, for example, the Shannon entropy (Gandrillon et al., 2021). On the other hand, in the context of regulatory networks underlying cell states and types, we need to build a model that takes into account both stochasticity and the interaction of genes with each other. Here we focus on a dynamical model of gene expression, formulated as a piecewise-deterministic Markov process (PDMP) and describing an arbitrary number of interacting genes (Herbach et al., 2017). This stochastic model is able to reproduce the biological variability measured experimen- tally (Ventre et al., 2023), while being compatible with the observation of a transient peak in Shannon entropy during differentiation processes such as hematopoiesis (Dussiau et al., 2022). We first justify the existence and uniqueness of an invariant distribution for this model, and estimate the rate of convergence to it. This distribution then admits an analytical expression for a wide class of parameters and can be interpreted as a probabilistic graphical model of the hidden Markov field type, with good properties for the inference of interactions.

- **Session** 4 : Modélisation de la croissance de champignons filamenteux (**L. Kuwata**)

  – On modélise la croissance du réseau mycélien d'un champignon filamenteux par un processus de branchement spatial. Chaque filament est représenté par la position de son extrémité, dont la trajectoire est solution d'une équation différentielle stochastique avec un terme de drift dépendant de toutes les autres trajectoires. Le branchement peut s'effectuer soit au niveau de l'extrémité soit le long d'un filament à des taux dépendant de la position, et les filaments peuvent s'arrêter de croître à un taux dépendant en outre de la position des autres extrémités. On étudie la limite en grande population du processus et on caractérise le processus limite comme la solution faible d'une certaine équation aux dérivées partielles.

Day 2: Tuesday 29 oct. 2024

Plenary Session

Title: Dynamic regulation of motility in structured environments drives spatial organisation of bacterial crowds: insights from experimental data and mathematical modeling
Speaker: Michèle Romanos
Abstract:
Myxococcus xanthus, a social bacterium, exhibits fascinating collective behaviors such as rippling and swarming, where cells self-organize into complex patterns. This talk presents new biological data on these behaviors, featuring high-resolution analyses of cell movements and reversals. Based on these observations, we derive a kinetic model that identifies a key factor that facilitates the emergence of rippling patterns. Additionally, we introduce a 2D agent-based model that links bacterial reversals to congestion through dynamic motility regulation. This model provides a framework that accurately captures the two patterns observed in the data. The model also highlights the role of background anisotropy in pattern formation. This work is a collaboration with Vincent Calvez (Laboratoire de Mathématiques de Bretagne Atlantique), Tâm Mignot and Jean-Baptiste Saulnier (Laboratoire de Chimie Bactérienne - Marseille).

Parallel Sessions

Track 1: EDP pour la biologie et la santé

- **Session** 1: A weighted finite volume scheme for growth-fragmentation models (**J. Granet**)
    - We are interested in the numerical discretization of the growth-fragmentation equation. This type of models typically describes the time evolution of a mass-structured population from the growth and division of its individuals. Integral properties of said population provide macroscopic quantities that may help calibrating the model on experimental data. More precisely, we are interested in the 0th and 1st moments of the solution, corresponding respectively to the total population density or of the total population mass. However, the numerical resolution of such models may often encounters consistency issues with respect to one or several of its integral properties. In this talk, I will introduce a new finite

volume scheme corrected with weights, which allows to simultaneously retrieve the model's solution and its two first moments. The expression of such weights will first be discussed depending on the type of discretization used. Then, the method will be extended to compartmented growth-fragmentation equations arising in the mathematical modeling of a yeast cells population.

- **Session** 2: A model of oocyte population dynamics for fish oogenesis (**L. Fostier**)
  - We introduce and analyze a PDE size-structured population model, with nonlocal non- linearities on recruitment and growth rates to take into account interactions between cells. We pay special attention to the recruitment term, and its influence on the long-time be- havior of the population. This model is well-suited for representing fish oocyte population dynamics within the ovary.Using data on the size distribution of oocytes in the ovaries of fish of different ages, we will present preliminary studies on the inverse problem and parameter estimation. These results are based on a biologically-informed neural network (BINN).
- **Session** 3: On the Fundamental Equation of a mutation equation (**G. Garnier**)
  - Mutations are an essential mechanism that plays a key role in the history of life; in particular, they explain the appearance of new hereditary traits within a population. These new traits can modify the selective or fitness value of an individual. In evolutionary biology, biologists are interested in distribution of fitness effects (DFE) of new mutations since it is a key element to understanding the evolutionary trajectory of a population. In this talk, we present a PDEs model based on the Growth-Fragmentation Equation that describes the evolution of the fitness of a cell line over the time . We study the fundamental solution of this equation and we describe some asymptotic properties. For this study, we rely and the Laplace transform, the Mellin transform and the Wiener-Hopf method. This work is done with Marie Doumic and Miguel Escobedo.
- **Session** 4: Mathematical model of the circadian rhythm in a population of hepatocytes (**Maréchal Anastasia**)

– The circadian clock influences behavioral and physiological processes over a period of around 24 hours. Within an organism, circadian oscillations occur at different scales. The suprachiasmatic nucleus (SCN) acts as the central clock, propagating the rhythm to peripheral clocks (tissues, organs) down to individual cells. Cellular clocks are characterized by theoscillation of key compounds, governed by a regulatory network. Recent studies have shown that, even in the absence of a functional SCN, neighboring liver cells in mice may still exhibit synchronized oscillations, indicating some synchronization at the level of a population of cells. Mathematical models have already been developed for the dynamics of the intracellular regulatory network, centered on feedback loops based on transcription-translation of some proteins. Although this type of system makes it possible to examine the coordination of clocks of a small number of cells, it is inadequate for studying the synchronization in an entire population. To address this gap, an age-structured population model is constructed here to represent cells and their progression through the circadian cycle. Numerical simulations are conducted to explore the dynamics of the model. Simulations with some parameter sets result in a completely synchronized cell population after several cycles, while other parameter sets lead to a desynchronized population.

Track 2: Optimisation

- **Session** 1: Inertial Methods with Viscous and Hessian driven Damping for Non-Convex Optimization (**R. Maulen-Soto**)

  – In this paper, we aim to study non-convex minimization problems via second-order (in- time) dynamics, including a non-vanishing viscous damping and a geometric Hessian-driven damping. Second-order systems that only rely on a viscous damping may suffer from oscillation problems towards the minima, while the inclusion of a Hessian-driven damping term is known to reduce this effect without explicit construction of the Hessian in practice. There are essentially two ways to introduce the Hessian-driven damping term: explicitly or implicitly. For each setting, we provide conditions on the damping coefficients to ensure convergence of the gradient towards zero. Moreover, if the objective function is definable, we show global convergence of the trajectory towards a critical point as well as convergence rates. Besides, in the autonomous case, if the objective function is Morse, we conclude that the trajectory

converges to a local minimum of the objective for almost all initializations. We also study algorithmic schemes for both dynamics and prove all the previous properties in the discrete setting under proper choice of the stepsize.

- **Session** 2: Sur la dualité entre les algorithmes de Frank-Wolfe et les méthodes de plans coupants (**T. Moquet**)

  – L'algorithme de Frank-Wolfe (2), ou algorithme du gradient conditionnel, est un algorithme classique d'optimisation convexe. Il permet d'approximer un minimiseur d'une fonction convexe f de classe C^1 sur un sous-ensemble convexe fermé borné K d'un espace de Hilbert H, ne nécessitant que d'être capable de minimiser des produits scalaires de la forme $\langle \mu, x \rangle$ pour x dans K, et ce pour n'importe quel μ dans H. L'algorithme de plans coupants permet quant à lui de minimiser une fonction convexe et différentiable g sur un sous-ensemble convexe fermé borné D de H, ne nécessitant que de construire et minimiser une approximation par en-dessous de g qui soit convexe et affine par morceaux. Je vais vous présenter un résultat obtenu pendant mes deux premières années de thèse établissant la dualité, au sens de Fenchel-Rockafellar, entre une extension d'une variante plus robuste de l'algorithme de plans coupants, la Level Method (3), et un algorithme pouvant être vu comme une extension de l'algorithme de Frank-Wolfe permettant d'étudier des fonctions s'écrivant comme une somme d'une fonction de classe C^1 et d'un terme non lisse. Je précise également les garanties théoriques obtenues pour ces méthodes, ainsi qu'un résultat sur leur vitesse de convergence.

- **Session** 3: Existence of Monge maps for the Gromov-Wasserstein problem (**T. Dumont**)

  – The Gromov-Wasserstein problem is an optimal transport (OT)-like optimization prob- lem over the set of transport plans between two probability measures, possibly supported on different spaces. It induces a distance over the set of probability measures that is invariant by isometries. Just like in the OT case, it is natural to ask for conditions guaranteeing some structure on the optimal transport plans, for instance if these are induced by a (Monge) map, i.e. if every point of the source measure is sent on one point of the target measure (there is no splitting of mass). In (1), we study this question in Euclidean spaces when the cost functions

are either given by (i) inner products or (ii) squared distances, two standard choices in the literature. We establish the existence of an optimal map in case (i) and of an optimal 2-map (the union of the graphs of two maps) in case (ii), both under an absolute continuity condition on the source measure. After a short introduction to OT theory with a focus on the existence of optimal maps, I will go over the results of (1). Depending on time, I may also talk about some numerics for (ii), in the simplest case, dimension one, where there is still much to be understood.

- **Session** 4: Abstract Cutting Plane Method applied to Sparse Optimization (**S. Rakotomandimby**)

  – In usual convexity, a function is closed convex if and only if it is the supremum of its affine minorants. In abstract convexity, affine functions are replaced by other elementary functions belonging to some set H. By definition, a function is abstract H-convex if it is the supremum of its H-minorants. Few abstract H-convex minimization algorithms have been studied, such as the abstract cutting plane method and the abstract branch-and-bound method. Recent work, on the 0 pseudonorm has highlighted elementary functions that makes the 0 pseudonorm abstract H-convex – the so-called E-CAPRA affine functions. As explicit formulas for the E-CAPRA subdifferential of the 0 pseudonorm have been calculated, it has been made possible to implement abstract H-convex minimization algorithms to the special case of the 0 pseudonorm. We present our numerical tests on the E-CAPRA cutting plane method applied to the following sparse optimization problems: the minimization of the 0 pseudonorm in a blunt closed cone, and the computation of the spark of a matrix (known to be a NP-hard problem).

Track 3: STATISTIQUES

- **Session** 1: Variations régulières cachées de processus ponctuels de cluster (**F. Baeriswyl**)

  – Dans cet exposé, on s'intéresse aux variations régulières cachées de certains processus ponctuels marqués de cluster de Poisson. Les variations régulières cachées de ces processus s'expriment comme les convergences successives, sur un espace de mesures ponctuelles dont on recoupe successivement des cônes de plus en plus larges

de mesures ponctuelles, des distributions de versions renormalisées desdits processus. Plus particulièrement, à chaque étape $k+1$, on retire de l'espace des mesures considérées les mesures ponctuelles avec au plus k points et on établit une convergence avec une vitesse d'exposant $k+1$. On souligne que ces principes de variations régulières cachées successives sont équivalentes à des principes classiques de déviations larges et on établit la fonction de taux à l'aide de ces outils. On déduit de ces résultats, qui portent sur les processus ponctuels, des résultats (sur l'espace de Skorokhod) de variations régulières cachées pour certaines fonctionnelles. Ce travail est une collaboration avec Olivier Wintenberger.

- **Session** 2: Modélisation de la communication entre les lymphocytes T et les cellules dendritiques (**L. Brolon**)

  – Lorsqu'un agent infectieux pénètre notre organisme, il est repéré par des cellules dendritiques (DC) qui émettent alors des signaux biochimiques afin de déclencher une réaction immunitaire, induisant la différenciation des lymphocytes T (LT), qui vont à leur tour émettre des signaux pour agir contre l'agent infectieux.

  Modéliser le lien entre les signaux émis par les DC (input) suite à la rencontre avec un pathogène et ceux émis par les LT en réaction (output) présente plusieurs difficultés : les DC peuvent émettre des signaux de nature différente, plusieurs DC peuvent émettre plusieurs signaux identiques ou différents en même temps, et les LT intègrent des combinaisons de ces signaux. Un signal de DC peut donc avoir différents effets sur les signaux des LT en fonction des autres signaux émis simultanément par les DC, nous appellerons cela un contexte. Chaque signal doit être analysé dans son contexte.

  Un premier modèle multivarié a été établi en 2019(1) permettant de prendre en compte les effets simultanés de la communication DC-LT. Ce travail a étudié l'effet des signaux de DC sur les LT dans certains contextes très simples (présence d'un autre signal), mais n'est pas directement généralisable.

  Afin de répondre à la problématique, nous avons dans un premier temps utilisé des modèles d'arbres de décision (MOB(2)), de forêt aléatoire (SIRUS(3)) et de régression spline (MARS(4)).

  Lors de cet exposé, je présenterai une étude permettant de comparer ces différents modèles et d'en établir les limites.

- **Session** 3: Nonparametric Regression for Conditional Density Estimation (**A. Reisach**)

  - We propose a procedure that makes the problem of conditional density estimation amenable to nonparametric regression and thus allows the use of flexible function approximators such as neural networks or random forests that work well even in high dimensions. We prove and characterize the convergence of our method to the true conditional density in the data limit and provide preliminary empirical results comparing our method to the state of the art on common regression datasets.

- **Session** 4: Variance of Mann-Kendall tau for ARMA process (**N Thibeau Sutre**)

  - The modified non-parametric Mann-Kendall test is a classical test to detect trends in time series when auto-correlation is present, based on the assumption of asymptotic normality of the Mann-Kendall statistic. In this presentation, we give a closed-form expression for the asymptotic variance of the Mann-Kendall tau in the case of renormalized ARMA process and deduce non-asymptotic normality for renormalized AR and MA process. Thus, we prove that the assumption of asymptotic normality of the test does not hold for every structure of auto- correlation. We illustrate these results in the context of trend testing for early warning signals detection. Furthermore, these asymptotic results have more far-reaching consequences given that the departure from the normal approximation is already visible for small time series lengths.

Track 4: Mechanique des Fluides et des Structures

- **Session 1**: Stability of partially congested travelling wave solutions of the presureless Navier-Stokes equations with singular diffusion (**E. Deléage**)

  - We prove the non-linear stability of a class of travelling-wave solutions to the extended Aw-Rascle system with a singular offset function, which is formally equivalent to the com- pressible pressureless Navier-Stokes system with a singular viscosity. These solutions encode the effect of congestion by connecting a congested left state to an uncongested right state, and may also be viewed as approximations of solutions to the 'hard-congestion model'. By

using carefully weighted energy estimates we are able to prove the non-linear stability of viscous shock waves to the Aw-Rascle system under a small zero integral perturbation, which in particular extends previous results that do not handle the case where the viscosity is singular.

- **Session 2**: Modélisation de la dynamique des membranes à courbure variable sous l'effet des fluctuations thermiques. (**M. Adel Djibaoui**)

  – Du fait de leur organisation et des fonctions multiples qui leur sont conférées par leur structure complexe, les membranes cellulaires présentent un intérêt à la fois fondamental et applicatif, mais leur approche nécessite souvent une approche interdisciplinaire combinant outils mathématiques et physiques et connaissances biologiques. Reflet de cette complexité, l'élucidation de la relation entre leurs structures et leurs fonctions multiples se heurte à des obstacles majeurs. D'origine structurale et fonctionnelle, la complexité des membranes biologiques résulte d'un vaste ensemble d'interactions moléculaires s'exprimant dans les processus biologiques mais aussi de l'exploitation de couplages naturels entre divers mécanismes physico-chimiques. De nombreux modèles relevant de la Biophysique visent une description mécanique et thermodynamique de ces membranes s'appuyant sur la fameuse fonctionnelle (énergie) de Canham-Helfrich (3, 2), prenant en compte la forme, c'est-à-dire la géométrie et la topologie des membranes et permettant la détermination des configurations d'équilibre des membranes. Du point de vue mécanique, ces membranes présentent les caractéristiques combinées de solides et de fluides (écoulement interne à la membrane comme évoqué dans le vieux modèle de la mosaïque fluide (5)). L'étude présentée ici concerne un modèle mécanique simple de membranes cellulaires planes ou courbées et permettant de décrire les interactions induites entre protéines incluses dans celle-ci (1). Basé sur une extension simple de la fonctionnelle de Helfrich, le modèle décrit d'abord la dynamique déterministe des déplacements normaux de membranes élastiques homogènes et isotropes. Le spectre des excitations de basse énergie (ondes de courbure) est discuté dans le cas de membranes de haute symétrie telles les vésicules sphériques ainsi que la forme générale de la compliance de celles-ci. Dans une seconde étape, la théorie générale des fluctuations thermiques (4) de la membrane est présentée ainsi que ses effets sur les interactions résiduelles en-

tre protéines incluses, de nature entropique. La forme du potentiel d'interaction correspondant est calculée numériquement dans le cas de membranes planes. Le rôle potentiel de ces interactions sur l'organisation des protéines au sein de la membrane est discuté. Leurs réorganisations au sein de la membrane pourraient être approchées efficacement comme transitions de phases de la membrane 'habillée' par une analogie intéressante de notre modèle avec le gaz de Coulomb 2D.

- **Session 3:** Partial regularity and L3 -norm concentration effects around possible blow-up points for the micropolar fluid equations (**H. Llerena**)

  – The micropolar fluid equations constitute a coupled system composed of three variables: velocity, pressure, and microrotation velocity, which allow modeling certain fluids with an internal microstructure, such as blood, polymers, or liquid crystals.

  In this presentation, we will first demonstrate that if the velocity belongs to $L_t^\infty L^3(Q_r(t,x))$, where $Q_r(t,x)$ is a time-space ball centered at a point (t,x), it is possible to deduce a gain of regularity for the solution within the interior of this ball. This type of result allows us, in turn, to observe a dominating effect of the velocity over the other variables, which is a novel aspect of our work.

  Finally, we will present some results on the behavior of the spatial L^3 norm of the velocity as we approach a possible blow-up time.

- **Session 5:** Solutions des équations de Navier-Stokes avec décroissance spatiale rapide forcée (**M. Pageard**)

  – Je présenterai un résultat de décroissance spatiale récemment obtenu pour les équations de Navier-Stokes incompressibles dans $\mathbb{R}^n$. En général, les solutions mild de ces équations ne peuvent pas décroître plus rapidement, en variable d'espace, que $x^{-(n+1)}$. C'est une conséquence des propriétés de décroissance du noyau d'Oseen. On propose ici une approche permettant de construire des solutions mild avec une meilleure vitesse de décroissance. L'idée est d'introduire une force extérieure au système, qui permet d'éliminer le terme lentement décroissant dans un profil asymptotique précédemment obtenu par Brandolese et Vigneron. La preuve est basée sur une construction algorithmique de forces extérieures, inspirée par un travail récent de Brandolese et Okabe.

Day 3: Wednesday 30 oct. 2024

Plenary Session

Title: The facilitated exclusion process and a Stefan problem
Speaker: Oriane Blondel
Abstract:
Abstract: We study an interacting particle system in one dimension that presents an absorbing phase transition. We will walk through some consequences of this phase transition for the large scale limit of the process, and notably the emergence of a free boundary problem in the hydrodynamic limit.

Paraller Sessions

Track 1: Probabilité mécanique statistique et EDS

- **Session** 1: Pénalisation d'arbres de Galton-Watson marqués (**S. Boulal**)
  - Dans cet exposé, on s'intéresse à des arbres de Galton-Watson dont la particularité est que chaque nœud peut être marqué avec une probabilité dépendant de son nombre d'enfants, cela, indépendamment des autres nœuds. Par la suite, à l'aide d'une méthode appelée pénalisation nous favorisons les arbres avec un grand nombre de marques. Plus précisément, cette méthode permet d'obtenir des martingales qui sont dans notre cas des fonctions de M_n, le nombre de marques jusqu'à la génération n–1. Ces martingales étant positives et de moyenne 1, nous pouvons alors définir de nouvelles probabilités sous lesquelles nous étudions les lois des arbres marqués.
- **Session** 2: Hydrodynamic limit of a Facilitated Exclusion Process with slow and fast boundaries (**Da Cunha**)
  - The one-dimensional Facilitated Exclusion Process (FEP) is a model of interacting particle system whose microscopic dynamics is purely stochastic and which belongs to the class of Kinetically Constrained Lattice Gases. Due to the dynamical constraints, this model displays a phase transition at the critical density 1/2, below which the system is completely frozen. In recent years, the FEP has been extensively studied on the periodic setting, but in this

talk I will consider it with boundary conditions. We put the system in contact with reservoirs that can inject and remove particles at both ends, regulating the speed of those exchanges thanks to a parameter $\theta \in \mathbb{R}$. I will describe the hydrodynamic limit of this model in the diffusive timescale, when it starts from its supercritical phase. Namely, the macroscopic density of particles evolves according to a fast diffusion equation with different boundary conditions, such as Dirichlet, Robin or Neumann, depending on the value of the parameter θ. FEP's behavior is quite peculiar as, contrary to other exclusion models, there is a distinction between two types of particles (active and frozen), and macroscopically the reservoirs act on the density of active particles. This is a joint work with Clément Erignoux and Marielle Simon.

- **Session** 3: ndes stationnaires pour l'équation de Gross-Pitaevskii avec bruit blanc en espace. (**Mackowiak**)

  – L'équation de Gross-Pitaevskii est un modèle physique pour décrire les condensats de Bose-Einstein. Il s'agit d'une équation de Schrödinger non-linéaire, qui apparaît comme limite en champ moyen de l'équation de Schrödinger linéaire à N particules dans un potentiel confinant. Ajouter un potentiel aléatoire à cette équation est une façon simple de modéliser les inhomogénéités spatiales. En ce sens, un potentiel bruit blanc peut être vu comme un modèle jouet de potentiel aléatoire à faible longueur de corrélation. Comprendre les solutions stationnaires d'une telle équation est une bonne façon de comprendre le comportement en temps long des solutions du problème d'évolution. Dans cet exposé, je présenterai la construction et les propriétés connues des ondes stationnaires en présence d'un potentiel bruit blanc. On verra que la présence d'un bruit blanc impose une régularité maximale aux solutions stationnaires. Les questions de localisation et de stabilité seront également abordées.

- **Session** 4: Percolation de premier passage avec dépendance(**Marivain**)

  – On étudie un modèle de percolation de premier passage où les temps de passage ne sont plus supposés iid. En effet, on associe un même temps de passage à toutes les arêtes d'une même droite de $\mathbb{Z}^d$. Les temps de passage associés à deux droites distinctes ont en revanche même loi et sont indépendants. On démontre la

croissance linéaire des temps de passage à direction fixée où la limite est, contrairement au modèle classique, identifiée.

Track 2: Reaction Diffusion

- **Session** 1: Une équation de Fisher-KPP avec une dimension spatiale et une dimension phénotypique : persistance et propagation (**Boutillon**)
  - We consider a nonlocal reaction-diffusion equation which models a population structured
    in space and in phenotype. We assume that the population lives in a heterogeneous environment, so that the same individual may be more or less fit according to its spatial position. We give a criterion for the persistence of the population, we prove that (on persistence) the population spreads and give a formula for the spreading speed. The arguments are based on principal eigenvalues of elliptic operators.
- **Session** 2: A class of fractional parabolic reaction-diffusion systems with control of total mass: theory and numerics (**Daoud**)
  - In this talk, we present some new results about global-in-time existence of strong solutions to a class of fractional parabolic reaction–diffusion systems posed in a bounded domain of RN . The nonlinear reactive terms are assumed to satisfy natural structure conditions which provide nonnegativity of the solutions and uniform control of the total mass. Global existence of strong solutions is proved under the assumption that the reactive terms are at most of polynomial growth. Also, we present some numerical simulations in order to examine the global existence of solutions to systems with exponentially growing right-hand sides, which remains so far an open theoretical question even in the case where the diffusion is driven by the classical Laplacian.
- **Session** 3: Regimes and mechanisms of inflammation described by reaction-diffusion systems (**El Hajj**)
  - Inflammation is considered as a fundamental defense mechanism of our organisms to various external stimuli. It plays a major role in several diseases including cardiovascular diseases, cancer, and neurodegenerative diseases. This work presents some generic inflammation models based on reaction-diffusion equations that describe the concentrations of unin-

flamed cells, inflamed cells, pro-inflammatory mediators of inflammation (classically activated macrophages and pro-inflammatory cytokines) and anti-inflammatory mediators of inflammation (alternatively activated macrophages and anti- inflammatory cytokines). First, we examine a reduced system that describes the pro-inflammatory aspect in a cell culture. We distinguish several regimes of inflammation progression namely a non-inflammatory state, the set-up of a normal inflammation, a chronic inflammation and hyper-inflammation correlated with cytokines storm. Furthermore, we deduce two mechanisms of propagation determined by positive feedback between inflammation and immune response which provides a qualitative understanding of various inflammatory reactions. The first mechanism is lead by the interaction between the activation of uninflamed cells and inflammatory cytokines whereas the second mechanism depends on the positive feedback loop between the immune cells and inflammatory cytokines, possibly leading to cytokine storm. We show that in- flammation spreads in the tissue as a reaction-diffusion wave and we determine its speed of propagation through analytical and numerical methods. Finally, we extend our study to the complete model that was initially proposed, perform numerical simulations and suggest more biological interpretations of the results. We consider how the anti-inflammatory mechanism process affects the behavior of the system.

- **Session** 4: Etude numérique de modèles non-locaux et leurs applications en biologie (**Marguet**)
  - Nous nous intéressons ici à de nouveaux modèles mathématiques non-locaux, les modèles type "aggregation-diffusion". Après avoir présenté l'intérêt biologique de l'équation d'aggregation-diffusion puis exposé quelques simulations numériques de cette équation, nous nous intéresserons à un modèle non-local plus compliqué représentant la dynamique des cellules dans le cas d'une co-invasion macrophage-tumeur. Nous discuterons de la modélisation mathématique de ce phénomène, ainsi que des simulations numériques obtenues pour ce modèle.

Track 3: Methodes Numeriques pour les EDP

- **Session** 1: Serendipity pour les complexes discrets avec régularité supplémentaire (**Salah**)

- Nous abordons le problème de la recherche de versions de sérendipité de complexes de de Rham approximatifs avec une régularité améliorée. Le point de départ est une nouvelle construction abstraite de portée générale qui, étant donnée trois complexes liées par des applications d'extension et de réduction, génère un quatrième complexe dont la cohomologie est isomorphe aux premiers. Cette construction est utilisée pour concevoir de nouvelles versions de sérendipité des complexes de rot-rot et de Stokes dérivées dans l'esprit de de Rham discret.

- **Session** 2: Theoretical and numerical analysis of a diffusion problem on a moving domain (**Dupouy**)

  - This presentation delves into the theoretical and numerical study of a diffusion problem on a moving domain. This problem, considered as a simplified model for corrosion phenomenons, is set in one dimension, and has three unknowns: the concentration inside the domain u, and the moving boundaries whose evolutions depend on the concentration u. The objective is to demonstrate that the continuous system possesses a solution and that this solution converges to a travelling wave profile. After establishing the existence of this travelling wave, I perform free energy calculations to derive a priori bounds on the solution, which are useful to prove its existence. On the numerical side, a finite volume method is employed for the spatial discretization, coupled with an implicit Euler scheme for the time discretization. The monotonicity of the scheme gives a priori $L^\infty-$bounds on the solution which, coupled with a Brouwer's topological degree argument, give the existence of a solution to the numerical scheme. Implementing it and plotting solutions illustrates the convergence of any solution towards the travelling wave profile. Moreover, by analysing the convergence of this scheme, I ultimately demonstrate the existence of a solution to the continuous system.

- **Session** 3: A fully explicit numerical method for waves in quasi-incompressible media (**Ramiche**)

  - In this work, we present a fully explicit high-order space-time discretization approach for the computation of elastic field propagation in quasi- incompressible media. For space discretization, our approach relies on, first, the use of high- order continuous finite elements with mass-lumping, and, second, the use of an

explicit Chebyshev Leap-frog scheme to deal with time discretization. The Chebyshev Leap-frog scheme is used to overcome the stability constraint (CFL condition) caused by the nearly incompressibility while still maintaining the explicitness. We present an approach that is valid for full hexahedral meshes (where the elastic field is sought in Q k and the pressure in Q k–2) or fully tetrahedral meshes. For tetrahedral meshes, new enriched, using higher-degree bubble functions, P_3^* and P_2^* elements are presented (the pressure is sought respectively in P 2 or in P 1). Furthermore, through the application of the so-called macro-element technique, we provide proof of the stability of the finite element discretization. This allows us to carry out error estimates for the semi-discrete problem in space (accounting in particular for quadrature errors). Numerical results will be presented including some 3D medical applications cases.

- **Session** 4: Approximation numérique du problème de continuation unique enrichi par une base de données pour les équations de Stokes (**C. James**)

  – Ce papier étudie le problème de la continuation unique pour les équations de Stokes étant donné une base de données de mesures de population. Ce problème est posé comme problème de minimisation sous la contrainte d'une EDP et discrétisé par la méthode des éléments finis. Il est régularisé par les données de population, en imposant que la solution vive proche d'un sous-espace de dimension fini généré par la base de données. Cette étude examine dans quelle mesure l'inclusion des données de population dans la résolution améliore les résultats théoriques et numériques. La méthode proposée permet l'obtention des estimations d'erreur globales pour la vitesse et la pression, à une vitesse de convergence améliorée. L'inclusion des données de population a aussi un impact très avantageux sur les tests numériques, en 2D comme en 3D, et surtout quand les mesures sont peu abondantes.

Track 4: THEORIE DES JEUX

- **Session** 1: No-Regret Learning in Strategic Games: Geometry and Dynamics (Davide Legacci) – Time

  – A fundamental question in multi-agent learning theory is whether players eventually learn to emulate rational behavior through repeated interactions, while minimizing their incurred regret. This

question finds a positive answer in the class of potential games, where players have common interests. By contrast, in harmonic games - the strategic counterpart of potential games, where players have conflicting interests - very little is known outside the narrow subclass of 2-player zero-sum games with a fully-mixed equilibrium. In this work we examine the convergence properties of standard learning schemes in harmonic games: we show that the continuous time dynamics exhibit recurrent behavior, whereas discrete-time dynamics - augmented with a suitable extrapolation step - converge to a Nash equilibrium from any initial condition, guaranteeing at most O(1) regret to all players. In terms of methods, we leverage tools from differential - and in particular Riemannian - geometry, and dynamical systems theory.

- **Session** 2: Escape Rate Games and Competitive Spectral Radii (Loïc Marchesini) – Time

  – We consider a new class of repeated zero-sum games in which the payoff of one player

  is the escape rate of a dynamical system which evolves according to a nonexpansive nonlin- ear operator depending on the actions of both players. Considering order preserving finite

  dimensional linear operators over the positive cone endowed with Hilbert's projective (hemi-)metric, we recover the matrix multiplication games, introduced by Asarin et al., which

  generalize the joint spectral radius of sets of nonnegative matrices and arise in some popula- tion dynamics problems (growth maximization and minimization). We establish a two-player

  Mañe's lemma characterizing the value of the game in terms of a nonlinear eigenproblem. This generalizes to the two-player case the characterization of joint spectral radii in terms of extremals norms. This also allows us to show the existence of optimal strategies of both players.

- **Session** 3: A Brouwer-Tarski fixed-point theorem (Yu) – Time

  – New n-dimensional fixed-point theorems for possibly discontinuous functions are established, extending Brouwer's fixed-point theorem and encompassing interesting cases of Tarski's fixed-point theorem. The main idea is to require that at any discontinuity point where the graph of the function "crosses the diagonal",

the function satisfies a specific as- sumption (similar to upward jumps). For this purpose, we classify some types of discontinuities, and use them to prove our new fixed-point theorems, with some applications in game theory.