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Emergence of global patterns in bacterial growth: from single cells to communities

Understanding how phenomenological behaviors observed in biological systems emerge from molecular interactions of many individual unit and how these interactions shape the response of living systems to a changing environment are challenging questions which lie at the interface between multiple disciplines. In this talk I will draw an example from the human gut microbiome, the full consortium of microbes living in association with the human gut. Recent developments in DNA sequencing have made it possible to monitor how the compositions of microbial species change in time. Analysis of healthy adults under antibiotic treatment showed that the gut microbiota could take several weeks to recover after treatment cessation. This suggests that the combination of inter-species and host-microbe interactions and external perturbations could lead to hysteresis phenomena. We investigate this possibility and propose an out of equilibrium stochastic model able to explain this phenomenon. Our study reveals the importance of noise-activated dynamics in the recovery from antibiotic-perturbed states.

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Apport des modèles mécanistes pour l'évaluation des interventions dans l'infection par le virus de l'immunodéficience humaine (VIH)

Les modèles mathématiques basés sur des systèmes d'équations différentielles ont permis des avancées majeures dans l'infection par le VIH au milieu des années 1990 notamment en quantifiant la production et la disparition du virus et des cellules infectées. Depuis des progrès ont été réalisés dans l'estimation des paramètres de ce type de modèle. Concomitamment, la prise en charge des patients infectés par le VIH avec des traitements antirétroviraux et des immuno-interventions est en constante amélioration. Nous présenterons les nouveaux développements et les applications en cours notamment pour l'optimisation des traitements antirétroviraux et le développement clinique des immuno-interventions dont l'interleukine 7.

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Inférence causale dans les études observationnelles

L'évaluation de l'efficacité d'une intervention repose principalement sur des essais contrôlés randomisés (ECR), dont le plan d'expérience permet d'inférer la causalité. A l'inverse, les études observationnelles sont généralement considérées comme permettant d'étudier une association mais pas de relation causale entre une exposition et le devenir des sujets. Cet exposé présente deux différentes méthodes permettant une inférence causale dans les études observationnelles (scores de propensity et variables instrumentales), et illustre leur utilisation à l'aide d'exemples.

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Nouvelle formule de séminaires internes

Deux équipes présentent des résultats ou des questions qui leurs sont propres afin de favoriser de nouvelles discussions au sein du laboratoire.

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Using empirical estimates of spontaneous mutation rates and their phenotypic effects for evolutionary and ecological inference

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Are old ages useless? Shedding light on the allelic spectrum of late-onset diseases

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Le séminaire interne : Bioinformatique et Génomique Évolutive / Écologie Évolutive des Populations se déroulera le mardi 25 novembre 2014 de 13 h à 14 h - amphithéâtre 1 Déambulatoire (la Doua)

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Adaptation to viruses in the proteome of mammals.

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On bias of measures of explained variation in survival analysis

Papers evaluating measures of explained variation, or similar indices, invariably use independence from censoring as the most important criterion. And they invariably end up suggesting that some measures meet this criterion, and some don't, leading to a conclusion that the first are better than the second. As a consequence, users are offered measures that cannot be used with time-dependant covariates and effects, not to mention extensions to repeated events or multi state models. We explain in this paper that the above mentioned criterion is of no use in studying such measures, since it simply favours those that make an implicit assumption of a model being valid everywhere. Measures not making such an assumption are disqualified, even though they are better in every other respect. We show that if these, allegedly inferior, measures are allowed to make the same assumption, they are easily corrected to satisfy the 'independent-from-censoring' criterion. Even better, it is enough to make such an assumption only for the times greater than the last observed failure time τ . Which, in contrast with the 'preferred' measures, makes it possible to use all the modelling flexibility up-to τ , and assume whatever one wants after τ . As a consequence, we claim that measures being proffered as better in the existing reviews, are exactly those that are inferior

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A mouse tale of a World invasion

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Structural organization of human replication timing domains

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Reconstructing the history of speciation from NGS data and the evolution of introgression rates between two diverging lineages

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Modélisation de l'exposition aux maladies infectieuses

Le succès de transmission d'une maladie infectieuse repose entre autres sur les interactions entre des individus susceptibles et des personnes contagieuses. L'acquisition d'une infection par un patient dans un établissement de santé n'échappe pas à ce schéma. En effet, les autres patients, les professionnels de santé, les visiteurs sont des sources potentielles d'infection pour les patients. La quantification de la contribution de ces différentes expositions sur le risque d'infection donnerait des informations utiles pour la prévention et le contrôle des épidémies hospitalières. Dans une première partie, à travers différents modèles statistiques, nous étudierons comment l'exposition à différentes sources modifie le risque d'acquisition d'une infection grippale parmi les patients. Dans une seconde partie, nous discuterons de la mesure de l'exposition à l'aide d'une mesure électronique des contacts, et du niveau de détails utile à introduire dans les modèles mathématiques de prédiction. Les résultats ont des retombées en termes d'épidémiologie hospitalière et de modélisation.

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Parasitisme, spéciation et adaptation : la pyrale du maïs sous (presque) toutes ses coutures.

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Long-term consequences of maternal and sibling effects

The early developmental period of an organism is a sensitive period where organisational and activational effects occur and thus, small disturbances have important and long-lasting consequences. Parents can modify, to some extent, the abiotic and biotic conditions experienced by their offspring, during both the prenatal and postnatal stages through differential behavioural and/or physiological input. In this seminar, I will focus on prenatal effects, such as litter-sex composition and maternal programming for the future environment in yellow-bellied marmots (*Marmota flaviventris*), a ground-dwelling sciurid rodent.

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Joint estimation of K related regression models with simple L1-norm penalties

We propose a new approach, along with refinements, based on L1 penalties and aimed at jointly estimating several related regression models. It is especially useful in epidemiology and clinical research when data come from several strata of a population. The main interest of our approach is that it can be rewritten as a weighted lasso on a simple transformation of the original data set. In particular, it does not need new dedicated algorithms and is ready to implement under a variety of regression models, e.g. linear or logistic models using standard R packages. Moreover, asymptotic oracle properties are derived along with preliminary non-asymptotic results, suggesting good theoretical properties. Our approach is further compared with state-of-the-art competitors under various settings on synthetic data: these empirical results confirm that our approach performs at least similarly to its competitors. As a final illustration, an analysis of road safety data is provided.

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