Recherche avancée

Affichage des résultats 41 à 60 sur 7049 au total

AGENDA

Pertinence: 100%

Evolution of evolvability under fluctuating selection

Empirical evidence suggests that fluctuating selection is a major evolutionary mechanism. The most straightforward consequence of rapid changes of the fitness function is the induced response of the mean phenotype in the population. Yet, repeated back-and-forth evolutionary trajectories are also suspected to affect the genetic architecture underlying the phenotypic characters subject to continuous adaptation. In order to better understand the long-term consequences of fluctuating selection, we modeled the response of complex, multilocus genetic architectures to various natural selection regimes — stabilizing, directional, and fluctuating. This model accounts for gene-gene interactions (through multilinear epistasis), and thus allows to investigate the dynamics of evolutionary potential at two distinct levels: (i) the standing genetic variation, i.e. the capacity for the population to respond immediately to directional selection, and (ii) the level of canalization (measured as the average effect of new mutations),which reflects the capacity for the population to replenish genetic variation. Both analytical results and individual-based simulations show that fast fluctuations (white noise change in the phenotypic optimum every generation) are essentially similar to stabilizing selection, promoting a degree of genetic canalization and low evolvability. In contrast, when large fluctuations of the phenotypic optimum (beyond the phenotypic range of the population) occur every 10 to 100 generations, equilibrium mutational effects and genetic variance are higher and the population is more evolvable. However, there was no evidence that decanalization and increased evolvability were adaptive, and fluctuating selection remains intrinsically more constraining than genetic drift.

06/11/2020

AGENDA

Pertinence: 100%

Identification of long non-coding RNAs (lncRNAs) in dogs using RNASeq

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Pertinence: 100%

Estimation of macroevolutionary rates from the fossil record

Understanding the processes of speciation and extinction is a major challenge in evolutionary biology and methodological advances have been improving our ability to infer the dynamics of species diversification from dated phylogenies of extant taxa and from the fossil record. The interpretation of diversity trajectories through time, however, goes beyond the estimation of rates of speciation and extinction, and may involve complex processes of niche filling, correlated trait evolution, and biotic interactions. Here I present a new Bayesian framework to analyze fossil occurrence data and jointly estimate times of origin and disappearance of taxa and rates of speciation and extinction. Speciation and extinction rates can vary through time and their temporal dynamics can be decoupled. Simulations show that model selection and parameter estimation are robust in the presence of incomplete taxon sampling. The statistical framework is extended to allow hypothesis testing with a particular focus on exploring the effect of diversity dependent processes, trait-correlated diversification, and competition among clades. The method is tested on fossil data sets of three mammal clades (the Rhinocerotidae, Ursidae, and Canidae) investigating different aspects of their Cenozoic diversification.

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Pertinence: 100%

Probabilistic approaches for detecting and locating whole genome duplications.

Whole Genome Duplications (WGDs) can be difficult to detect when they are old and when synteny has been disrupted by genome rearrangements. To test the presence of WGDs on a species phylogeny, I will present two methods which do not require synteny information and build strength from the phylogenetic framework. They rely on a probability model for the evolution of gene families on a species tree with WGDs. Both methods use multiple gene families across multiple species. One method relies on aligned molecular sequences and the other simply uses information on gene counts. We assessed their performance with simulations and on a benchmark yeast dataset, where we recover strong evidence for a well-established WGD and a low retention rate of duplicated genes after this WGD.

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AGENDA

Pertinence: 100%

Negotiation for resources in sibling barn owls: a model of animal communication dynamics

Animal conflict is usually seen as static, where each competitor has a definite underlying quality (i.e. condition, good genes) that determines its signal level. However, although many morphological signals are fixed during early development, some signals remain flexible through life (e.g. vocalisation, most behavioural traits). The level of signals of an individual can thus often fluctuate to avoid interferences, to adapt to both the presence of an audience or the resource holding potential and motivation of opponents. These fluctuations raise the question of how individuals decide at each moment their level of investment in signalling to claim a resource. Animals are indeed expected to constantly modulate their investment in a contest according to the payoff. Because of the inherent difficulty to study the temporal dynamics of communication between several individuals, how animals decide to enter or leave the contest and to what level invest in signalling has received mainly theoretical developments. Using the barn owl (Tyto alba) as a model species, I will present recent advances in the understanding of the role of cognition (individual recognition, memory) and social interactions in the dynamics of a communication process.

06/11/2020

AGENDA

Pertinence: 100%

The evolution of genetic architectures underlying quantitative traits (and its consequences)

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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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Pertinence: 100%

Evidence de sélection dans le génome humain: adaptation polygénique et fardeau d'expansion

Les populations humaines ont connu une expansion hors d'Afrique dans les 50,000 dernières années qui a certainement nécessité des adaptations au niveau génétiques, mais qui ont aussi pu avoir des conséquences sur leur fitness. Dans cette conférence, je présenterai nos travaux récents sur l'identification de sélection polygénique au niveau de voies métaboliques chez l'homme, ainsi que sur l'accumulation potentielle de mutations délétères lors d'expansions spatiales.

06/11/2020

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Pertinence: 100%

Reconciliation-based detection of co-evolving gene families

Genes located in the same chromosome region share common evolutionary events more often than other genes (e.g. a segmental duplication of this region). Their evolution may also be related if they are involved in the same protein complex or biological process. Identifying co-evolving genes can thus shed light on ancestral genome structures and functional gene interactions.We devised a simple, fast and accurate probability method based on species tree-gene tree reconciliations to detect when two gene families have co-evolved. Our method observes the number and location of predicted macro-evolutionary events, and estimates the probability of having the observed number of common events by chance. Simulation studies confirm that our method effectively identifies co-evolving families. This opens numerous perspectives on genome-scale analysis where this method could be used to pinpoint co-evolving gene families and thus help to unravel ancestral genome arrangements or undocumented gene interactions.(Work in collaboration with Vincent Ranwez et Yao-ban Chan.)————————————————————FRENCH————————————————————
Detection de co-évolution basée sur la réconciliation d'arbres phylogénétiquesEn comparaison avec des gènes situés sur des chromosomes distincts, les gènes situés dans une même région chromosomique prennent part à des évènements évolutifs communs (par exemple dans le cas d'une duplication en tandem de cette région). Leur évolution peut également être liée s'ils sont impliqués dans le même complexe de protéines ou dans le même processus biologique. Identifier des gènes qui ont co-évolué peut donc aider à mieux comprendre les structures génomiques ancestrales et les interactions fonctionnelles des gènes étudiés. Dans cette presentation nous allons decrire une méthode probabiliste basée sur la réconciliation d'arbres phylogénétiques: les macro-évènements évolutifs sont estimés avec une méthode de réconciliation; ensuite nous estimons la probabilité d'avoir le nombre d'évènements communs observés par hasard, faisant l'hypothèse forte que tous les macro-évènements évolutifs sont indépendants les uns des autres. Les simulations réalisées montrent que cette approche est prometteuse. Ce projet est issu de la collaboration avec Vincent Ranwez et Yao-ban Chan.

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Pertinence: 100%

Genome wide quantification of RNA transcripts

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AGENDA

Pertinence: 100%

A Diversity of Conservation Dilemmas with Demographic Solutions

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Pertinence: 100%

Non-random inbreeding with respect to phenotype biases estimates of inbreeding depression

Animals often show substantial variation in dispersal behaviour and resident individuals are more likely to inbreed. At least part of the variation in dispersal behaviour may be phenotype-dependent, potentially leading to non-random inbreeding with respect to a particular phenotype. Here we show that non-random inbreeding in structured populations can have important implications for estimates of the effect of inbreeding (inbreeding depression). We do this using a long-term individual-based data set for a population of Eurasian dippers (Cinclus cinclus), a bird species living exclusively along streams and rivers. Extensive pedigree data show that close inbreeding is relatively common in this species. However, inbreeding birds are not a random subsample of the population but are smaller on average. Given the significant heritability of body size, inbred individuals are smaller due to both additive genetic and inbreeding effects. Importantly, the effects of inbreeding are overestimated if additive genetic effects are not accounted for. We show how estimating the effects of inbreeding within an animal model framework removes this bias, highlighting the importance of integrating quantitative genetics and animal behaviour when measuring the effects of inbreeding in the wild.

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Dating phylogenies with incompletely preserved fossils

In recent years, evolutionary biologists have become increasingly interested in dating phylogenies. This is usually accomplished by calibrating interior nodes in the tree against the fossil record, an ad hoc approach with a considerable risk of mirepresenting the fossil information. I discuss an alternative approach, in which fossils are included along with extant taxa in a Bayesian total-evidence analysis. By coding morphological characters for both extant and extinct taxa, it is possible to explicitly integrate over the uncertainty in the placement of individual fossils, while using their ages to date the tree. In such a total-evidence analysis of the early radiation of the Hymenoptera (wasps, ants and bees), we showed that fossils contributed significantly to the estimation of divergence times, despite considerable uncertainty in their placement. The posterior distributions on divergence times were less sensitive to prior assumptions and tended to be more precise than in standard node dating. The total-evidence analysis also showed that four of the seven Hymenoptera calibration points used in node dating were based on erroneous or doubtful assumptions about fossil placement. One of the most important advantages of total-evidence dating over node dating is that it provides a better platform for further modeling of important aspects, such as the fossilization process and the sampling of extinct and extant taxa. We are currently exploring such extensions of the basic model.

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Pertinence: 100%

Heteroplasmy in human mitochondrial DNA: characteristics, transmission, and tissue-specificity.

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Pertinence: 100%

Choanoflagellates, animal evolution, and the role of microbial eukaryotes in global ocean ecology

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Network-based approaches for the spatial spreading of communicable diseases

Mathematical and computational approaches based on network theory and complex system dynamics are increasingly showing their potential to address open problems on the spreading of communicable diseases on a spatially structured and heterogeneous human population. I will review my recent research work in this direction presenting studies on both fundamental problems and specific epidemic events. On the theoretical side, I will show how the mathematical formalism of reaction-diffusion processes and metapopulation networks can shed light on the impact of the complex features characterising individuals' mobility patterns on the propagation of emerging infections. How do traveling flows, journey duration and difference in travel frequency impact local mixing and transmission of influenza-like diseases? How do the mobility of individuals and their distribution in space determine dominance/co-dominance regimes in case of multiple interacting strains of the same pathogen? Besides these fundamental research questions, the same formalism can form the basis of data-driven computational models for the spatial spreading of real infection events. In case of an epidemic emergency, such models represent valuable tools for estimating in real time the transmission potential of the disease, providing assessment of the epidemic situation and projections of possible unfolding scenarios. I will discuss the two paradigmatic examples of the 2009 H1N1 pandemic and of the MERS-CoV outbreak.

06/11/2020

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