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Vibrio diversity and oyster mortality: the hypothesis of a new polymicrobial disease

Vibrios have been associated with successive mortality outbreaks ofCrassostrea gigas) in France that have resulted in losses up to 100% of production. Given the near monoculture of C. gigas in Europe, there is an urgent need to understand the epidemiology of these outbreaks, particularly the role of Vibrio in the diseases.The study of the Vibrios distribution on fine phylogenetic and spatial scales has demonstrated that vibrios coexisting in the water column can be divided into closely related populations, which pursue different lifestyles i.e. ecological population (Hunt et al., 2008). However, a link between ecological populations and pathogenicity has not been demonstrated, and it is unclear whether pathogenicity is a trait primarily linked to clones or to populations comprising a large number of distinct genotypes.In the presentVibrio populations in an intensive oyster cultivation area. We demonstrate that Vibrio populations do not assemble neutrally in oysters from water column populations i.e. specific genotypes colonize the oysters. Combining experimental ecology, high throughput infection assay and genome sequencing, we showed that the onset of disease in oysters is associated with progressive replacement of diverse, benign colonizers by members of a phylogenetically coherent virulent population together with quorum sensing pheromone producers. Analyses of oyster mortality following experimental infection suggest that disease onset can be facilitated by the presence of non-virulent strains. Oyster disease may thus represent a new form of polymicrobial disease, in which non-pathogenic strains contribute to increased mortality.Hunt DE, et al. (2008) Resource partitioning and sympatric differentiation among closely related bacterioplankton. Science 320(5879):1081-1085.Lemire A, Goudenège D, Versigny T, Petton B, Calteau A, Labreuche Y, Le Roux F. (2014) Populations, not clones, are the unit of vibrio pathogenesis in naturally infected oysters. ISME J. Dec 9. doi: 10.1038/ismej.2014.233

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Lessons from 30 years of natural disturbances in the Bavarian Forest National Park

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Transposable element evolution in Drosophila

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Similarities and differences between evolutionary processes in linguistics and biology

Among biologist as well as linguists, it is now widely accepted that there are many striking parallels between the evolution of life forms and the history of languages. Starting from the rise of language studies as a scientific discipline in the early 19th century, up to today's recent "quantitative turn" in historical linguistics, scholars from both disciplines have repeatedly pointed to similarities between the respective research objects in biology and linguistics. During the last two decades, this has lead to a new school of "quantitative historical linguistics". Based on the key assumption that the characteristic processes of language change and biological evolution are so similar that the methods designed for one discipline may also be used in the other one, methods which were originally designed to study biological evolution (methods for phylogenetic reconstruction, sequence alignment, or biological network analysis) have now repeatedly been applied to linguistic data.Unfortunately, not all analogies which have been made between evolutionary processes in linguistics and biology reflect true similarities in the processes. Striking differences between the research objects of both disciplines are often ignored. In the talk, I will review proposed similarities between evolutionary processes in the two disciplines and discuss their methodological implications.

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Bad luck of cancer - or misinterpreted statistics?

A recent paper in Science (January 2015) claimed that the majority, 64% to be precise, of cancers is due to bad luck, so non-preventable. The message was spread quickly through media, including serious ones like BBC (and also radio Slovenia, if I may add). And while the paper has been criticized by many, the authors seem to stick to the original message.In this talk I'll give my view of the paper and try to defend a counter message that their analysis gives them absolutely no grounds to make such a claim. The arguments that I'll present have, to my knowledge, not appeared in published reactions to the paper. Obviously, if I am right, they are wrong, and vice versa. If I was Bayesian, I would, at present, give a 0.99 prior probability to the first option. Either way, it should be fun.

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Human sex differences in height : A costly evolution due to gender hierarchy.

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Titre à venir

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Understanding molecular evolution: insights from animals and plants

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Dispersion des vers de terre en Agroécosytèmes : résultats du projet Edisp

La dispersion est un processus central pour le maintien de la biodiversité dans les paysages. Cependant les patterns de dispersion et leurs déterminants sont encore mal documentés, en particulier chez les organismes du sol. En conséquence, une grande partie des déterminants de la biodiversité des sols n'est toujours pas comprise.Nous exposons les résultats d'un projet ANR de quatre ans sur la dispersion des vers de terre, un organisme clé dans le maintien de nombreux services écosystémiques. Avec une combinaison d'approches (1) de terrain multi-échelle, (2) de (méta) communauté, (3) de génétique du paysage, et (4) d'expérience en laboratoire, nous avons identifié des mécanismes centraux qui permettent aux vers de terre de disperser dans un agro-écosystème de manière adaptée, et nous montrons l'importance de la dispersion pour le maintien de la diversité spécifique et génétique.Nos résultats suggèrent également que la dispersion passive joue un rôle sous estimé dans la dynamique spatiale de ces organismes.

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Baiting for phylogenetic fishing

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Phylogenetic Fate Mapping

We are exploring techniques using single cell genomic sequencing in human beings for the purpose of defining phylogenetic trees to explain the relationship of cells within defined human tissues. I will discuss how we used single cell exome and whole genome sequencing to identify patient and donor adipocytes in human white adipose tissue biopsies taken from bone marrow recipients and discuss future projects using similar methods to explore cellular identities in human tissue samples.

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Beyond Jarman-Bell: how principles of digestive physiology can and cannot inform on ecological diversification.

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Evaluation quantitative et qualitative d'un dispositif de surveillance basé sur le principe de la déclaration obligatoire : l'exemple de la surveillance de la brucellose chez les bovins en France

La surveillance de la brucellose chez les bovins, maladie pour laquelle la France est indemne depuis 2005, a pour objectif principal d'assurer la détection de tout nouveau foyer qui surviendrait sur le territoire. Cette surveillance repose principalement sur la surveillance évènementielle (clinique) : celle-ci impose aux éleveurs et aux vétérinaires la déclaration de tout avortement chez les bovins, suivi du dépistage de la femelle ayant avorté vis- à-vis de la brucellose. Toutefois, en amont de ce travail, il était admis par l'ensemble des acteurs, sans que cela ait été rigoureusement évalué, que cette surveillance souffrait d'une forte sous-déclaration et nécessitait d'être améliorée.Les objectifs de l'évaluation de ce dispositif étaient : 1) de quantifier le niveau de sous-déclaration et estimer l'effet de différents facteurs sur le processus de déclaration ; 2) d'analyser le processus de décision conduisant les éleveurs et les vétérinaires à participer ou non au dispositif.Afin de répondre au premier objectif, le principe des méthodes de capture-recapture unilistes a été retenu. L'ensemble des observations a pu être modélisé à l'aide des méthodes MCMC et de deux modèles multi-réponses, le modèle de Poisson enflé en zéro (ZIP) et le modèle hurdle. La deuxième étude a consisté à mener des entretiens semi-directifs auprès de 12 éleveurs et de leurs 8 vétérinaires.

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Host phylogeny and diet drive the structure of mammalian microbial communities at different phylogenetic scales

Bacterial communities (microbiota) living in Mammal guts are composed of thousands of bacterial species that are essential for host physiology, immunity and diet. It has been shown that host phylogeny (genetics and immune system of the host) and diet are the two major factors driving the composition of gut microbiota. However, major questions remain: (i) the relative contribution of host phylogeny and diet at short and long time scales is highly debated and the two processes are not well characterized, (ii) host phylogeny may drive the composition through co-evolution with bacterial lineages or through niche selection, with closely-related hosts retaining similar bacteria from the environment. Here, we show that host phylogeny and diet are for the most part independent processes and do not drive the bacterial composition at the same taxonomic scale. Diet determines what lineage is present or not at deep bacterial phylogenetic levels through gain or loss of lineages creating nested communities. Host phylogeny, however, selects the lineages at finer scales through true turnover of lineages, consistent with a more stringent selection of tolerated antigens. Finally, it appears that co-speciation between hosts and bacterial lineages plays a minor role in driving the correlation between community composition and host phylogeny, suggesting that environmental filtering by host genetics is the dominant process at selecting bacterial lineages. Our results shed light on the long-timescale evolutionary dynamic of gut bacterial communities, which are multi-layered phylogenetic structures shaped very differently by host phylogeny and diet.

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Gathering, updating, and calibrating phylogenies for The Open Tree of Life

The Open Tree of Life project is a collaborative effort to synthesize, share, and update a comprehensive phylogeny of all 2.3 million named species. We have completed a draft synthesis of a single tree from hundreds of phylogenetic estimates using taxonomy as a scaffold. This synthesis is not static but rather will be continually revised as new data become available. This undertaking requires development of both novel infrastructure and analysis tools. I will discuss three components of this project: Phylesystem, an open database and web application for community curation of phylogenies using a git-based datastore, PhyScraper, a pipeline to continually update phylogenetic estimates as new data is generated, and FastDate, an algorithm to rapidly generate maximum a posteriori estimates of time-calibrated trees, even for phylogenies with hundreds or thousands of tips. Together, these developments reduce impediments to accessing, analyzing and reusing the phylogenetic information which is essential to biological research today.

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Transitions between combined and separate sexes in plants

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Characterisation of the bacterial replicons

The genome of bacteria is classically separated into essential, stable and slow evolving replicons (chromosomes) and accessory, mobile and rapidly evolving replicons (plasmids). This paradigm is being questioned since the discovery of genomic elements that possess both chromosomal and plasmidic features. These Extra-Chromosomal Essential Replicons (ECERs), be they called "megaplasmids", "secondary chromosomes" or "chromids", are found in diverse lineages across the bacterial phylogeny and are generally believed to be modified plasmids. However, their true nature and the mechanisms permitting their integration within the sable genome are yet to be formally determined. The relationships between replicons, with reference to their Genetic Information Inheritance Systems (GIIS), were explored under the assumption that the inheritance of ECERs is integrated to the cell cycle and highly constrained in contrast to that of standard plasmids. A global comparative genomics analysis including all available complete bacterial genome sequences, was performed using GIIS functional homologues as parameters and applying several analytical procedures. GIIS proved appropriate in characterizing the level of integration within the stable genome, as well as the origins, of the replicons. The study of ECERs thus provides clues to the genetic mechanisms and evolutionary processes involved in the replicon stabilization into the essential genome and to the continuity of the genomic material.

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A turtle view of the evolution of genomes and sex determination

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Dynamics of slow cell renewal in humans

Human tissues constantly replace dying cells with newborn cells. The pace at which they are replaced, however, varies by orders of magnitudes between blood cells, which are renewed every day and neurons, for which renewal is non-existent or limited to specific regions of the brain. Between those extreme are many tissues that turnover on a time scale of years, although no direct measurements have been done. We present here a mathematical method to estimate cell turnover in slowly renewing biological systems. Age distribution of DNA can be estimated from the integration of radiocarbon derived from nuclear bomb-testing during the cold war (1955-1963). For slowly renewing tissues, this method provides a better estimate of the average age of the tissue than direct estimates from the bomb-curve. Moreover, death, birth and turnover rates can be estimated. We highlight this method with data from hippocampal neurons and cardiomyocytes.

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Relevance: 100%

Recherche de biomarqueurs de la récupération motrice dans l'AVC en imagerie multimodale

L'accident vasculaire cérébral est une cause majeure de handicap acquis chez l'adulte. Les biothérapies ont montré un effet bénéfique sur la plasticité neuronale (synaptogénèse, angiogenèse, repousse dendritique et immunomodulation) et la récupération neurologique en ischémie expérimentale. D'après les critères du consortium STEP sur les biothérapie dans l'AVC, la démonstration de l'effet des CSM requiert plusieurs étapes: 1) Un nombre plus important de patients dans les études ; 2) Une meilleure compréhension des mécanismes de régénération cellulaire et de réorganisation neuronale chez l'homme afin de déterminer les patients susceptibles de répondre au traitement ; 3) Une évaluation quantitative de l'effet des CSM par l'introduction de biomarqueurs de neuroimagerie, en particulier de l'imagerie fonctionnelle et de la mesure de l'intégrité de la substance blanche en imagerie de diffusion. Le projet HERMES a tenté d'identifier des biomarqueurs d'IRM dans le cadre d'un essai clinique ISIS (PHRC2007 CHU de Grenoble) incluant 31 patients ayant présenté un AVC de moins de 2semaines. Le protocole d'imagerie cérébrale a permis de modéliser la récupération motrice en fonction de l'étude en IRM fonctionnelle de l'activation ces réseaux moteurs par une tâche motrice (IRMf), de la connectivité structurale par l'étude du tenseur de diffusion (DTI), et de la connectivité fonctionnelle de repos (rs-IRMf), en ajoutant l'étude de la perfusion cérébrale et de la réserve cérébro-vasculaire au CO2. L'intérêt de ces biomarqueurs d'imagerie est également d'évaluer l'effet du traitement sur la récupération motrice à 6 mois. La validation de des biomarqueurs de neuroimagerie, permettra de tester leur utilisation dans le cadre de l'essai clinique multicentrique européen (RESSTORE) testant l'effet des cellules souches allogéniques dans l'AVC subaigu incluant 400 patients. Contact : Mme Mariethé CHAUMEIL Inscription gratuite mais obligatoire avant LUNDI 05 OCTOBRE 2015 Courriel : mariethe.chaumeil@chu-lyon.fr

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