4TH TOULOUSE ECONOMICS AND BIOLOGY WORKSHOP

EVOLUTION : TRANSMISSION MECHANISMS & POPULATION STRUCTURE

PROGRAM

30 & 31

MAY 2016

Organizers:

Ingela ALGER &
Jörgen WEIBULL

Co-organizers:

Jeanne BOVET &
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Toulouse School of Economics

Manufacture des Tabacs
S Building - Room MS001

1 rue des
Amidonniers
31000 Toulouse

MONDAY 30 MAY, 2016

09:00-09:30	**Welcome Coffee and Opening**	
09:30-10:30	**Paul Seabright** *(IAST & TSE),* David R. Pugh & Mark Schaffer Sexual selection, exogamy and the evolution of social behavior	
10:30-11:00	**Coffee Break**	MS002
11:00-12:00	**David C. Queller** *(Washington University, St Louis)* The social gene: the elements of selection, transmission, and evolution	
12:00-13:00	**Gabriella Conti** *(University College London)* Before Birth: Prenatal Shocks, Investments, and Development	
13:00-14:00	**Lunch**	MS002
14:00-15:00	**Poster Session I** **Paul Acker** *(EDB UMR 5174, University Paul Sabatier, Toulouse, France)* The cues to quit in kittiwakes: social information in sequential habitat selection across spatial scales **Pim Edelaar** *(University Pablo de Olavide – Spain)* A novel framework to integrate all mechanisms of adaptation to local environments, and its relevance to evolution and population structure **Cesar Fortes-Lima** *(AMIS UMR-5288, University Paul Sabatier, Toulouse, France)* Genetic model-based methods to unravel complex admixture histories in the Atlantic world **Sylvain Gibaud** (*Mathematics Institute - University Paul Sabatier, Toulouse, France*) A demographic prisoner's dilemma **Pradiptajati Kusuma** *(AMIS UMR-5288, University Paul Sabatier, Toulouse, France)* The Austronesian dispersal over the Indo-Pacific region **Claire Morandin** *(University of Helsinki, Finland)* Comparative transcriptomics reveals the conserved building blocks involved in parallel evolution of diverse phenotypic traits in ants **Aïda Nitsch** *(IAST, Toulouse, France)* Is dispersal a good strategy? Sibling competition, dispersal and fitness outcomes in humans **Harilanto Razafindrazaka** *(AMIS UMR-5288, University Paul Sabatier, Toulouse, France)* Global study of the influence of genetics on the preference for specific flavors between populations	MS003
15:00-16:00	**Hisashi Ohtsuki** *(The Graduate University for Advanced Studies, Hayama)* Evolution of cumulative culture	
16:00-16:30	**Coffee Break**	MS002
16:30-17:30	**Sarah Mathew** (*Arizona State University, Tempe)* Altruistic Warriors and Moral Citizens: Conflict and Cooperation In A Pastoral Society Shows That Cultural Transmission Enabled The Evolution Of Human Prosociality	
19:30	**Dinner** (by invitation only)	

TUESDAY 31 MAY, 2016

09:00-09:30	**Coffee**	MS002
09:30-10:30	**Jean Clobert** (*Station d'Ecologie Théorique et Expérimentale du CNRS, Moulis)* Information and the spatial repartition of animals	
10:30-11:30	**Joan E. Strassmann** *(Washington University, St Louis)* The impact of population structure on kin selection and symbiosis in microbial interactions	
11:30-12:00	**Coffee Break**	MS002
12:00-13:00	**Poster Session II** **Jeanne Bovet** *(IAST, Toulouse, France)* Preferred Women's Waist-to-Hip Ratio Variation over the Last 2,500 Years **Florence Debarre** *(CIRB, Collège de France, Paris, France)* Mutation and the evolution of social behaviour in structured population **Mark Dyble** *(University College London, United Kingdom)* Sex equality explains the low relatedness of hunter-gatherer bands **Roberta Fisher** *(Vrije University, Amsterdam, Netherlands)* What drives the evolution of symbiosis? **Andrea B. Migliano** *(University College London, United Kingdom)* Hunter-gatherer social networks are optimized for cultural exchange **Noble Robert** *(ISEM, University of Montpellier, France)* Cooperation increases stress resistance in social cheats **Jorge Peña** *(Max Planck Institute for Evolutionary Biology, Plön, Germany)* Endogenous group size and the evolution of cooperation **Arnaud Tognetti** *(IAST, Toulouse, France)* Are cooperative men showing off? Contributions to a public good are larger under sexual competition	MS003
13:00-14:00	**Lunch**	MS002
14:00-15:00	**Mats Gyllenberg** *(University of Helsinki)* Optimisation in evolution and utility in economics	
15:00-16:00	**Ingela Alger** *(TSE-CNRS-IAST)* or **Jörgen Weibull** *(Stockholm School of Economics and IAST)* Does evolution lead to maximizing behavior?	
16:00-16:30	**Coffee Break**	MS002
16:30-17:00	**General Discussion & Conclusion**	MS001
20:00	**Dinner** (by invitation only)	

ABSTRACTS TALKS

Ingela Alger or **Jörgen Weibull**

Does evolution lead to maximizing behavior?

A long-standing question in biology and economics is whether individual organisms evolve to behave as if they were striving to maximize some goal function. We here formalize this "as if" question in a patch-structured population in which individuals obtain material payoffs from (perhaps very complex multimove) social interactions. These material payoffs determine personal fitness and, ultimately, invasion fitness. We ask whether individuals in uninvadable population states will appear to be maxi- mizing conventional goal functions (with population-structure coefficients exogenous to the individual's behavior), when what is really being maximized is invasion fitness at the genetic level. We reach two broad conclusions. First, no simple and general individual-centered goal function emerges from the analysis. This stems from the fact that invasion fitness is a gene-centered multigenerational measure of evolutionary success. Second, when selection is weak, all multigenerational effects of selection can be summarized in a neutral type-distribution quantifying identity-by-descent between individuals within patches. Individuals then behave as if they were striving to maximize a weighted sum of material payoffs (own and others). At an uninvadable state it is as if individuals would freely choose their actions and play a Nash equilibrium of a game with a goal function that combines self-interest (own material payoff), group interest (group material payoff if everyone does the same), and local rivalry (material payoff differences).

Jean Clobert

Information and the spatial repartition of animals

We will review the mechanisms of information by which animals take a decision to move. We will mainly focus on dispersal decisions and we will review the interdependence between the dispersal causes, the type/timing of information acquired, and the location to which disperse. We will end-up by sketching the way by which the vision of the meta-population functioning can be ameliorated.

Gabriella Conti

Before Birth: Prenatal Shocks, Investments, and Development

The fetal origins of several phenotypic traits are now recognized in a vast, interdisciplinary literature. The observation that early life influences can alter later disease risk is based on the idea that organisms enact adaptive processes to allow genotypic variation to be preserved during transient environmental changes. Cues for such "developmental plasticity" operate particularly during early development, and might involve epigenetic mechanisms. In this talk I will first review some key challenges which are tackled in the economic analysis of "fetal origins". I will then open the "black box" of what happens in utero by presenting novel insights on pre- and post-natal development based on unique data from fetal ultrasounds scans. I will start by revealing that inequalities in socioeconomic status and gender emerge since the early stages of conception. I will then show that birthweight - the most widely used measure of health at birth in economics - is a proxy for specific aspects of prenatal development, and that other neonatal measures are more informative about different dimensions of fetal health capital. I will further show that alternative measures of perinatal health capital are differentially predictive of child development, above and beyond birthweight - and that not accounting for them might overstate the significance of birthweight, and underestimate the importance of perinatal health. Lastly, I will investigate how prenatal shocks affect early development, through gender-specific biological and behavioural pathways. I will conclude by showing some implications of this research for the intergenerational transmission of inequality and the role of interventions starting in the prenatal period.

Mats Gyllenberg

Optimisation in evolution and utility in economics

It is a wide spread misconception that evolution optimises some quantity like "fitness" or reproductive success. In this talk I give a brief introduction to adaptive dynamics, which is a mathematical theory that explicitly takes into account the interaction between population dynamics (ecology) and evolution by natural selection. Using the well-known rock-scissors-paper-game as a metaphor, I give necessary and sufficient conditions for when there is a function which is optimised by natural selection. It turns out that evolutionary optimisation is extremely rare and hardly can happen in nature. The existence of an optimisation principle in the theory of evolution by natural selection is from a mathematical point of view closely related to the existence of a utility function in economics. I show how our results can be reformulated as necessary and sufficient conditions for the existence of a utility function.

Sarah Mathew

Altruistic Warriors and Moral Citizens: Conflict and Cooperation In A Pastoral Society Shows That Cultural Transmission Enabled The Evolution Of Human Prosociality

Unlike other animals, humans cooperate extensively in large groups comprised of genetically unrelated individuals. This unique form of cooperation could have evolved through cultural group selection, i.e. selection among populations having different culturally transmitted norms. I will present findings from the Turkana, a politically uncentralized population of pastoralists in Kenya which indicate that: 1) the Turkana maintain costly large-scale cooperation in warfare through peer punishment of free riders; 2) Turkana norms regulating punishment help solve the second-order free rider problem and promote group-beneficial punitive behavior; and 3) Turkana norms regulating warfare benefit the cultural group, not smaller or larger social units. The nature and scale of cooperation and conflict is consistent with selection acting on the level of cultural groups, suggesting that cultural group selection has played a key role in the evolution of human pro-sociality.

Hisashi Ohtsuki

Evolution of cumulative culture

Culture can grow cumulatively if socially learnt behaviors are improved by individual learning before being passed on to the next generation. Previous studies showed that this kind of learning strategy is unlikely to be evolutionarily stable in the presence of a trade-off between learning and reproduction. This is because culture is a public good that is freely exploited by any member of the population in their model (cultural social dilemma). Here I investigate the effect of vertical transmission (transmission from parents to offspring), which decreases the publicness of culture, on the evolution of cumulative culture in both infinite and finite population models. In the infinite population model, I confirm that culture accumulates largely as long as transmission is purely vertical. It turns out, however, that introduction of even slight oblique transmission drastically reduces the equilibrium level of culture. Even more surprisingly, if the population size is finite, culture hardly accumulates even under purely vertical transmission. This occurs because stochastic extinction due to random genetic drift prevents a learning strategy from accumulating enough culture. Overall, those theoretical results suggest that introducing vertical transmission alone does not really help solve the cultural social dilemma problem. If time allows I will also talk about a learning model in a spatially structured population.

David C. Queller

The social gene: the elements of selection, transmission, and evolution

Biologists and philosophers have long debated the units of selection. Richard Dawkins gave priority to the gene because of its immortality. Others like, like Ernst Mayr, have instead emphasized the unity of the selected individual. David Hull suggested that these are both important, calling the first replicators and the second interactors. Here I show that it the relationship between these two kinds of units that is the key to the evolutionary response to selection and what that relationship is. There are sufficient differences in my approach that I will refer not to the *units* of selection but to the *elements* of selection, transmission, and evolution. Instead of assuming a vertical or hierarchical structure, I will use a horizontal one. I adopt Dawkins' view of taking a focal gene and viewing everything else, including other genes, as part of its environment. I then apply Alan Templeton's suggestion that units/elements of selection ought to involve identifying only the causal components that are necessary to predict or describe selective change. Using parallel models from adaptive dynamics and the Price equation, I show that elements of genic evolution can be defined as the product or *intersection* of elements of selection and elements of co-transmission or genetic structure. An element of evolution needs to be added whenever it has both distinct effects on fitness and distinct patterns of structure. I show how this logic applies to all kinds of interactions with the focal gene: with other alleles at its locus, with other loci, with other individuals of the same species, and with individuals of other species. Because this formalization of Dawkins's gene-centered view does not assume hierarchical levels of selection, it may be well suited to explaining the emergence of such levels.

Paul Seabright, David R. Pugh & Mark Schaffer

Sexual selection, exogamy and the evolution of social behavior

This paper models the co-evolution by natural selection of an individually costly social behavior trait together with a preference for mating partners who bear that trait. It is well known that costly cooperative behavior can be favored by natural selection if cooperators are likely to associate preferentially with other cooperators; but the mechanisms by which such preferential association may come about have typically been considered as exogenously determined. In this paper we use insights from the theory of sexual selection to endogenize the presence of mechanisms of preferential association, as well as generalizing the argument from cooperative behavior to other kinds of individually costly social behavior. We show that the existence of equilibria with individually costly social behavior depends on general properties of the matching functions that determine probabilities of association given preferences as a function of the relative frequencies of behavioral traits in the population. We derive conditions for the existence of multiple stable monomorphic equilibria and also for balanced polymorphic equilibria in which different behavioral traits coexist.

Joan E. Strassmann

The impact of population structure on kin selection and symbiosis in microbial interactions

A challenge for understanding interactions is accurately assessing the population structure under which they evolved. Field studies can reveal the relative frequency of interactions with relatives and non-relatives and encounters with other species. The soil-dwelling social amoeba *Dictyostelium discoideum* has a social stage in which individuals aggregate and then some die, forming a sturdy stalk that helps others disperse. Does kin selection explain this altruism? Population structure, relatedness, and costs and benefits are important issues. In addition to these, it turns out that the amoebae also interact with bacteria in ways that extend from infection to farming. Some bacteria help their bearers prevail over non-relatives in stalk/spore competition. Others are crops carried by amoeba farmers. Analogies with human interactions can point to fruitful directions for investigation, but the answers are surprising.

Paul Acker, Aurélien Besnard, Jean-Yves Monnat & Emmanuelle Cam

The cues to quit in kittiwakes: social information in sequential habitat selection across spatial scales

Many studies have shown that animals use conspecific reproductive success (i.e. public information) to select their breeding habitat, in order to optimize their fitness prospects. Such mechanism of habitat copying has been suggested to promote breeding aggregations and hence the evolution of sociality. Public information is available at several spatial scales but might not be consistent across scales. The scale at which individuals use the information is thus crucial to understand the habitat selection process, but to date it has very seldom been considered. We explored how a colonial gull, the kittiwake (Rissa tridactyla) adjusts its use of public information for departure decisions across nested scales. The study population consists of a set of colonies subdivided into social groups composed of several cliffs containing nest sites. We assessed how the local breeding success, apparent individual state (i.e. sex, previous breeding experience, status and own performance) and latent spatial, individual and annual contexts influence dispersal probability at each spatial scale (i.e. that of the nest, cliff, social group and colony), conditionally on departure at the lower scales. We modeled 10702 observations of individual location in two successive breeding seasons, involving 2558 banded birds over 32 years of intensive monitoring. We used mixed sequential binary regressions and performed robust Bayesian estimation and variable selection with shrinkage priors. Our results show that individuals decide whether to quit their previous location at a specific scale according to the local breeding success evaluated at this scale, disregarding information available at upper scales. Further, the wider the scale considered, the stronger this negative effect of the local success on dispersal probability becomes. Moreover, the influence of the individual state rapidly vanishes across scales. Sex and experience only have an effect on the probability to leave the nest site. The individual status (i.e. breeder or non-breeder) and performance (i.e. breeding failure or success) modulate the use of local success only for the decision to leave the nest site and subsequent decision to leave the cliff. Additionally, the latent individual heterogeneity in dispersal probability was substantial solely at the social-group scale. These results demonstrate that the balance between personal and public information use for dispersal decisions varies according to the individual state and spatial scale considered. This brings out that the study of (dispersal) decisions has to integrate the (spatial) scales across which the information is available to encompass the whole (habitat) choice process. On the light of complementary theoretical work, we discuss the efficiency and evolution of social information use in metapopulations where individual repartition follows a spatial or social structuration.

Jeanne Bovet & Michel Raymond

Preferred Women's Waist-to-Hip Ratio Variation over the Last 2,500 Years

The ratio between the body circumference at the waist and the hips (or WHR) is a secondary sexual trait that is unique to humans and is well known to influence men's mate preferences. Because a woman's WHR also provides information about her age, health and fertility, men's preference concerning this physical feature may possibly be a cognitive adaptation selected in the human lineage. However, it is unclear whether the preferred WHR in western countries reflects a universal ideal, as geographic variation in non-western areas has been found, and discordances about its temporal consistency remain in the literature. We analyzed the WHR of women considered as ideally beautiful who were depicted in western artworks from 500 BCE to the present. These vestiges of the past feminine ideal were then compared to more recent symbols of beauty: Playboy models and winners of several Miss pageants from 1920 to 2014. We found that the ideal WHR has changed over time in western societies: it was constant during almost a millennium in antiquity (from 500 BCE to 400 CE) and has decreased from the 15th century to the present. Then, based on Playboy models and Miss pageants winners, this decrease appears to slow down or even reverse during the second half of the 20th century. The universality of an ideal WHR is thus challenged, and historical changes in western societies could have caused these variations in men's preferences. The potential adaptive explanations for these results are discussed.

Florence Debarre

Mutation and the evolution of social behaviour in structured population

Models on the evolution of social behaviour in structured populations classically assume that mutation is weak or absent -- as illustrated by the focus in the literature on fixation probabilities to define evolutionary success, or the use of identity by descent in computations of the "r" term ("relatedness") in Hamilton's famous inequality $r b > c$. Here, we investigate the evolution of social behaviour in structured populations under arbitrary mutation. Considering populations of fixed size, where, in the absence of selection, all individuals have identical probabilities of reproducing and identical probabilities of surviving to the next time step, we provide conditions for the success of one strategy against another in arbitrary two-player games. We thereby extend Hamilton's inequality and provide a formula for relatedness that holds for arbitrary mutation rates, and is valid for any life-cycle.

Mark Dyble

Sex equality explains the low relatedness of hunter-gatherer bands

The social organisation of mobile hunter-gatherers has several derived features, including low within-camp relatedness and fluid meta-groups. Although these features have been proposed to have provided the selective context for the evolution of human hypercooperation and cumulative culture, how such a distinctive social system may have emerged remains unclear. We present an agent-based model suggesting that, even if all individuals in a community seek to live with as many kin as possible, within-camp relatedness is reduced if men and women have equal influence in selecting camp members. Our model closely approximates observed patterns of co-residence among Agta and Mbendjele BaYaka hunter-gatherers. Our results suggest that pair-bonding and increased sex egalitarianism in human evolutionary history may have had a transformative effect on human social organisation.

Pim Edelaar

A novel framework to integrate all mechanisms of adaptation to local environments, and its relevance to evolution and population structure

Evolutionary theory emphasizes the centrality of natural selection as the cause of genetic adaptation. Other evolutionary forces (mutation, recombination and random gene flow) generate mostly-deleterious genetic variation, which natural selection then acts upon. Specifically, gene flow is typically thought to homogenise genotypes across populations and thereby act as an antagonist of natural selection, and as an inhibitor of adaptation. Here we show conceptually and empirically that gene flow as caused by "selection of the environment" is a driver of adaptation that is distinct from natural selection. This is supported by a novel framework to understand the mechanisms of adaptation, acknowledging that individuals as well as environments can be changed. Applying this in nature, we found that ground-perching grasshoppers colonising street pavements surprisingly maintain their camouflage, because individuals select those pavements that are similar to their own colouration. Habitat use changes after individual colouration is experimentally altered. This behaviour of selecting the environment results in a marked adaptive, genetic population structure, and enhanced scope for assortative mating. Our results demonstrate that evolutionary theory needs to incorporate that individuals are not only targets of selection (by the environment), but also agents of selection (of the environment). We foresee that the application of our insights could bring significant advances in any field (including technical and human sciences) addressing adaptation.

Roberta Fisher

What drives the evolution of symbiosis?

The formation of symbiotic partnerships between unrelated species has been instrumental in shaping the evolution of biological complexity and diversity. Cooperative partnerships between different species are found everywhere, and in most cases provide clear benefits and new functions to both parties. However, the degree to which symbionts benefit their hosts can vary dramatically (both within- and between- species). For example, Rhizobia vary in how efficiently they fix nitrogen, and under many conditions plants are able to grow and reproduce relatively well without them. On the other end of the spectrum, aphids cannot survive without their intracellular Buchnera symbionts, which provide them with essential amino acids. Evolutionary theory makes the unambiguous prediction that vertical transmission should lead to more beneficial symbionts and hosts that are dependent on them for survival and reproduction. Here, we test this hypothesis using data from the literature in phylogenetically controlled comparative analyses of bacterial symbionts and their diverse hosts. We use data from experiments where host fitness was measured with and without their symbiont, allowing us to calculate quantitatively the effect of symbionts on their host's fitness. Our results provide the first quantitive confirmation of the long-held prediction that vertically transmitted symbionts have larger fitness effects on their hosts than horizontally transmitted symbionts, using the largest and most general test to date. Furthermore, we show that a potential consequence of this is that vertically transmitted symbionts have significantly smaller genomes, and that this is correlated with their fitness effect of the host: smaller genomes produce larger fitness effects.

Cesar Fortes-Lima, Hannes Schroeder, Andres Ruiz-Linares, Maria-Catira Bortolini, Tom Gilbert, Martin Sikora & Jean-Michel Dugoujon

Genetic model-based methods to unravel complex admixture histories in the Atlantic world

The transatlantic slave trade enacted as the most traumatic long-distance migration in human history. Current diversity in the Americas is the result of complex episodes of admixture between the early inhabitants, European colonists, and enslaved Africans that have arrived in the American continent over the last five centuries. To obtain a fine-scale genetic perspective and uncover admixture patterns in African descendants, we analysed whole mitochondrial genomes (mtDNA), Y chromosome markers (47 Y-STRs and 96 Y-SNPs), and genome-wide data for the Illumina HumanOmni5 BeadChip (4.5 million variants) from six African-American communities from South America (French Guiana, Brazil, and Colombia), six putative West-African ancestors, and continental reference population included in the 1000 Genomes Project Phase 3. Both, the Afro-Brazilian and the Afro-Colombian population present different demographic migration models and admixture timing associated to their different colonial pasts. MtDNA genome, Y chromosome and X chromosome uncovered sexual asymmetric admixture patterns in admixed African-American populations, consistent with an excess of European male contribution and elevate African female ancestry. Besides, all genetic systems revealed strong African ancestry (above 98%) in Noir Marron communities. We also applied a historical framework to provide new insight into haplotype sharing between African-Americans and African geographic groups across the continent. In Noir Marron, both global and local ancestry inferences highlighted remarkably genome-wide ancestry linked to the populations residing today in the historical Bight of Benin region. Therefore, this study reveals new light on complex admixture dynamics in the Atlantic world, and reconstruct broken African ancestral roots throughout African descendants.

Sylvain Gibaud

A demographic prisoner's dilemma

I will present an evolutionnary game model based on a multi-agent system. In it the evolution will not be managed by a generation system whereby after play a new population is drawn but instead by the fact that agents who perform poorly will die. Our model represents a spatialized prisoner's dilemma where the players move on a torus and play against other players only if they are at the same location. As it is usually done in evolutionnary games, the action of the players will be fixed. A player will be either a cooperative player (who always cooperates) or a defecting player who always defects). This system has been explored using simulations (or approximations). The poster will show a probabilistic framework in which we can prove theoretical results.

Pradiptajati Kusuma, Nicolas Brucato, Murray P. Cox, Denis Pierron, Herawati Sudoyo, Thierry Letellier & François-Xavier Ricaut

The Austronesian dispersal over the Indo-Pacific region

The Austronesian expansion was a major human migration in Southeast Asia, triggered by the spread of agricultural populations approximately 5,000 years ago. Thought to have originated in Taiwan, its influence spread through Philippines and Indonesian archipelago, ultimately impacting a wide geographical area ranging from Remote Oceania in the east, to Madagascar and the eastern coast of Africa in the west. This expansion had outsized cultural and genetic impact on these territories, but the populations caught up in the dispersal were regionally different and diverse across the Indo-Pacific region. This created a diverse modern range of Austronesian populations with their own cultural traits and genetic heritage. The farming-language dispersal hypothesis, drawn on linguistic and archaeological evidences, has been for three decades the main model to explain the Austronesian expansion, supporting an agriculturally driven demic expansion of Austronesian speakers from Taiwan. Recent population genetics studies have challenged this model, and a more complex picture is emerging where language shift and gene-flow are dependant of the landscape (coastal/highland, size of the islands, distance between islands) and human population structure (population density, populated/unpopulated land). To better understand the differential Austronesian genetic impact on populations from the vast Indo-Pacific region, we have started a project to reconstruct the population history, using genetic, epigenetic and epidemiological markers, on more than 2,000 individuals from the three main regions impacted by the Austronesian speakers: the East African coast, the Indonesian archipelago and the Papua New Guinea regions. We will present in this paper the first results and perspectives of this project based on genetic data (mitochondrial DNA, Y-chromosome DNA, genome-wide SNPs) and molecular epidemiology (viral DNA and host resistance mechanisms to diseases).

Andrea B. Migliano, A. Page, J. Gómez-Gardeñes, S. Viguier, M. Dyble, J. Thompson, N. Chaudhary, G. D. Salali, D. Smith, J. Strods, R. Mace, M. G. Thomas, V. Latora & L. Vinicius
Hunter-gatherer social networks are optimized for cultural exchange

Unlike non-human primates, humans typically have extensive social interactions with non-kin. In modern societies this is expected since increased population size increases the proportion of non-kin individuals available for social interaction. However, the extent to which this behavior is a feature of ancestral humans and the potential adaptive value of non-kin interaction is not known. We employ a new portable wireless sensing technology (motes) to characterize social networks in Agta and BaYaka hunter-gatherers – as a model of pre-agricultural societies – in unprecedented detail. We show that strong non-kin friendships are extensive, optimize global cultural information exchange efficiency, and appear early in development. We argue that a predisposition to form strong non-kin ties may facilitate the evolution of some distinctive human characteristics such as cumulative culture, hypersociality and hypercooperation.

Claire Morandin, Liselotte Sundström, Heikki Helanterä & Alexander S. Mikheyev
Comparative transcriptomics reveals the conserved building blocks involved in parallel evolution of diverse phenotypic traits in ants

Reproductive division of labor in eusocial insects is a striking example of a shared genetic background giving rise to alternative phenotypes, namely queen and worker castes. Queen and worker phenotypes play major roles in the evolution of eusocial insects. Their behavior, morphology and physiology underpin many ecologically relevant colony-level traits, which evolved in parallel in multiple species. Using queen and worker transcriptomic data from 16 ant species we tested the hypothesis that conserved sets of genes are involved in ant eproductive division of labor. We further hypothesized that such sets of genes should also be involved in the parallel evolution of other key traits. We applied weighted gene co-expression network analysis, which clusters co-expressed genes into modules, whose expression levels can be summarized by their ‘eigengenes’. Eigengenes of most modules were correlated with phenotypic differentiation between queens and workers. Furthermore, eigengenes of some modules were correlated with repeated evolution of key phenotypes such as complete worker sterility, the number of queens per colony, and even invasiveness. Finally, connectivity and expression levels of genes within the co-expressed network were strongly associated with the strength of selection. Although caste-associated sets of genes evolve faster than non caste-associated, we found no evidence for queen or worker associated co-expressed genes evolving faster than one another. These results identify conserved functionally important genomic units that likely serve as building blocks of phenotypic innovation, and allow the remarkable breadth of parallel evolution seen in ants, and possibly other eusocial insects as well.

Aïda Nitsch, Virpi Lummaa & Charlotte Faurie

Is dispersal a good strategy? Sibling competition, dispersal and fitness outcomes in humans

Determining the fitness consequences of dispersal and its interplay with sibling interactions is pivotal for understanding the evolution of family living. On the one hand, dispersal could be a strategy to avoid sibling competition, thereby increasing the access to competing resources. On the other hand, dispersal could mainly benefit philopatric individuals through a decrease of the intra-familial competition in the natal territory. These two explanations of dispersal imply different drivers of dispersal and relative fitness between philopatric and dispersing siblings. Moreover, sibling dominance and the intensity of intra-familial competition are likely to influence the fitness outcomes of each strategy. However, studies investigating the fitness outcomes of dispersal according to the intensity of sibling competition are scarce. Using a large demographic dataset on humans from preindustrial Finland (n=4,000), we investigated the fitness consequences of dispersal on different indicators of lifetime reproductive success according to sex-specific birth rank. Contrary to our predictions, the negative effect of same-sex elder siblings on reproductive success was similar between philopatric and dispersing individuals for both males and females. This study is one of the first investigating the fitness consequences of dispersal according to the intra-familial competition and has important implications for the evolution of family dynamics, dispersal and sibling interactions in humans and in other species.

Vasse M., **Noble R.**, Akhmetzhanov A., Torres-Barceló C., Gurney J., Benateau S., Gougat-Barbera C., Kaltz O. & Hochberg M.E.

Cooperation increases stress resistance in social cheats

Ecological antagonisms play key roles in shaping population biology, in particular by inducing stress responses and selecting for tolerant or resistant phenotypes. Little is known, however, about their impact on social traits, such as the production of public goods. Evolutionary trade-off theory predicts that adaptation to stresses should lessen investments in costly helping behaviours, but support for this prediction is scarce. We employed theory and experiments to investigate how ecological antagonism influences social dynamics and resistance evolution in the bacterium Pseudomonas aeruginosa. We found that producers of costly iron chelating molecules (siderophores) most rapidly declined in frequency under intermediate antibiotic pressure. Moreover, the dominance of non-producers in mixed cultures was associated with higher survival and resistance to antibiotics than in either producer or non-producer monocultures. Mathematical models explain this counterintuitive result, and show how these qualitative patterns are predicted to generalise to many other systems.

Jorge Peña, Georg Nöldeke & Arne Traulsen

Endogenous group size and the evolution of cooperation

Game-theoretic models of the evolution of cooperation often assume that group size is constant or that its distribution is fixed. However, in many natural systems group formation can be endogenous in a way that the group size distribution depends on the level of cooperation in the population. Examples include social microbes producing adhesive proteins, bark beetles attacking host trees, burying beetles preparing and burying carcasses, and social carnivores participating in collective hunting or confrontational scavenging. Here, we explore the evolutionary consequences of endogenous group formation in a volunteer's dilemma. In our model, individuals are sequentially recruited by focal groups until the critical number of cooperators needed to provide the collective good is reached. Our rule of group formation generates predictions that are in stark contrast to those resulting from standard group formation processes. In particular, protected polymorphisms are impossible and the invasion barrier for cooperator mutants is less severe at sufficiently low cost-to-benefit ratios. Our results highlight the importance of explicitly accounting for endogenous processes of group formation in models of social evolution.

Harilanto Razafindrazaka, Veronica Pereda-Campos, Camille Ferdenzi, Thierry Talou, Margit Heiske, Francois Ricaut, Thierry Letellier, Moustafa Bensafi & Denis Pierron

Global study of the influence of genetics on the preference for specific flavors between populations

The great diversity of genes encoding the olfactory receptors has open new research challenges. Indeed it has been demonstrated on European individuals that polymorphisms located on these receptor influence (i) perception of aroma and odor experience (ii) food selection. However there is no comparison yet between populations and then it is not possible yet to determine how the observed genetic diversity influence food practices around the world. This is why we have designed a study, which will allow to measure and compare odor perception by a standardized way across populations. Here we present first results on Malagasy populations. During this session poster, we also invite you to participate in smelling some specific flavor and see what could be your genetic profile. Like a game this test is easy and fun for the participants.

Arnaud Tognetti, Dimitri Dubois, Charlotte Faurie & Marc Willinger

Are cooperative men showing off? Contributions to a public good are larger under sexual competition

Why humans cooperate in large groups and with non-kin remains a puzzle for researchers across the natural and social sciences. Despite a large amount of theoretical and experimental investigations of cooperation, the potential role of sexual selection has been overlooked. Yet, competition for access to mates could induce positive selection for cooperation. Using controlled laboratory experiments, we analyse whether and how the sex composition of a social environment, testosterone level, and relationship status affect contributions to a public good. The results show that variation in sex composition alters the amount of money that men (but not women) contribute to a public good. Notably, in line with the competitive helping hypothesis, awareness of the presence of a woman leads to larger contributions by men, most likely by inducing competition between them. Furthermore, this tendency is exacerbated in single men compared to men in a couple.

However, we find no link between basal testosterone level and cooperativeness. We argue that men adopt cooperative behaviours as a signalling strategy in the context of mate choice and hence that cooperation is partly sexually selected. Our findings highlight the need to consider sexual selection as an additional mechanism for cooperation.