Poster identifiants - RAW March 5th, 2020
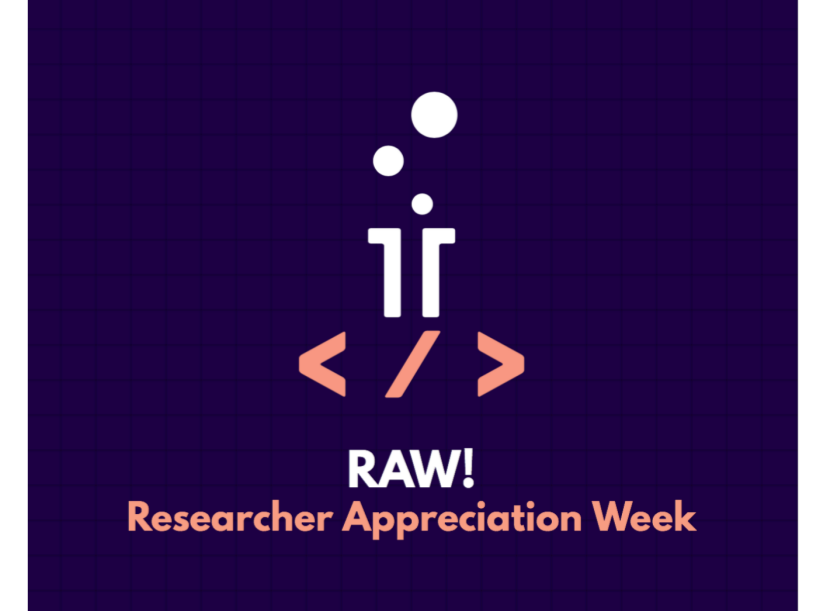
Poster identifiant	Name	Abstract	Field of research	Best poster award candidate
1	Nurit Eliash	While ectoparasitic Varroa mites cause minimal damage to their co-evolved ancestral host, the eastern honey bee (Apis cerana), they devastate their novel host, the western honey bee (Apis mellifera). The host switch caused worldwide population collapses, threatening global food security. Varroa management strategies have focused on breeding for bees tolerance. But, can Varroa overcome these counter-adaptations in a classic coevolutionary arms race? Despite increasing evidence for Varroa genetic diversity and evolvability, this eventuality has largely been neglected. We therefore suggest a more holistic paradigm for studying this host-parasite interaction, in which 'Varroa-tolerant' bee traits should be viewed as a shared phenotype resulting from Varroa and honey bee interaction. Understanding Varroa genetic architecture and quantifying its possible contribution to 'Varroa-tolerant' traits should improve breeding programs and Varroa management. Regular genetic monitoring of the mite-bee population will enable predicting eruptions of mite infestation, or resistance events for novel pesticides before they occur. Still, studies evaluating the relative contribution of mite and bee phenotypes to the infestation dynamics and colony mortality are necessary.	Environmental & Ecological Sciences	X
2	Saacnicteh Toledo Patino	Protein (r)evolution. Mimicking Nature to engineer artificial enzymes Only in the past two decades, enzymes have gained greater attention as complementary or even substitution to conventional chemistry protocols. They do not only offer mild, sustainable and selective chemistry but also a wide repertoire of reactions. Nearly 50% of these catalysts require the assistance of organic molecules, so-called coenzymes, to drive their otherwise unattainable reactions. Hence, a better understanding on how these nanomachines have evolved to efficiently employ these molecules not only provides valuable information about their sophisticated chemistry, but also reveals mechanistic constrains for enzyme design. Only recently, the first case of naturally occurring coenzyme promiscuity was reported, in which the reaction outcome is different (reduction and oxidation). Inspired by this natural event, the present work aims to switch the coenzyme specificity of natural enzymes as alternative approach to design novel biosynthetic tools. As proof of principle, we target the conversion of an oxidoreductase into a methyl transferase.	Molecular, Cellular, and Developmental Biology	X
3	Bianca Sieveritz	The ventromedial thalamic nucleus plays a prominent role in Parkinsonian disease. In addition to impaired motor control, Parkinson patients also demonstrate impairments in decision-making. The ventral motor thalamic nuclei (MT) send projections to prelimbic cortical layer 1 that target dendrites of deeper layer pyramidal neurons, corticostriatal neurons and layer 1 inhibitory interneurons. Optogenetic inhibition of prelimbic corticostriatal neurons on a cost-benefit decision-making paradigm biases rats towards a high benefit-high cost as compared to a low benefit-low cost option, even though animals' perception of benefit and cost value does not change. Furthermore, MT has been implicated in coding choice behavior, indicating that MT input to prelimbic cortex may be involved in cost-benefit decision-making. Optogenetic inhibition of corticostriatal neurons on the cost-benefit decision-making further disinhibited high-frequency neurons in striosomes that in turn inhibit striatal projection neurons, implying that thalamostriatal input may also be involved in cost-benefit decision-making. To determine if MT input to prelimbic cortical layer 1 or to striatum is involved in cost-benefit decision-making, we trained five-week-old Sprague-Dawley rats to perform a benefit-benefit, cost-cost and cost-benefit decision-making task that offered animals a choice between: i- a high reward and a low reward ii- a high cost and a low cost, and iii- a high cost-high reward and low cost-low reward option. Optogenetic inhibition of MT terminals in prelimbic cortical layer 1 significantly increased the percentage of high cost-high benefit choices, even though animals' perception of benefit and cost value remained unchanged. In-vivo electrophysiology in anesthetized animals suggests that this change in choice behavior is due to a down-regulation of deeper layer pyramidal neurons in prelimbic cortex upon inhibition of MT terminals. In contrast, chemogenetic inactivation of MT thalamostriatal projections did not bias choice choice behavior on any of the three tasks.	Neuroscience	X

4	Margaret A Mars Brisbin	Microbial eukaryotes (protists) are important contributors to marine biogeochemistry and play essential roles as both producers and consumers in marine ecosystems. Among protists, mixotrophs—those that use both heterotrophy and autotrophy to meet their energy requirements—are especially important to primary production in low-nutrient regions. Acantharian protists (clades E & F) accomplish mixotrophy by hosting Phaeocystis spp. as algal endosymbionts and are extremely abundant in subtropical low-nutrient regions where they form productivity hotspots. Despite their ecological importance, acantharians remain understudied due to their structural fragility and inability to survive in culture. In order to overcome these challenges and illuminate key aspects of acantharian biology and ecology—including distribution, abundance, and specificity and specialization of symbioses—single-cell RNA sequencing methods were developed for acantharians and used alongside environmental metabarcode sequencing and high-throughput, in-situ imaging. Major findings from this thesis were that i) acantharian cell (> 250 µm) concentrations decrease with depth, which correlates to patterns in relative sequence abundances for acantharian clades with known morphologies but not for those lacking known morphology, and that ii) while individual acantharians simultaneously harbor multiple symbiont species, intra-host symbiont communities do not match environmental communities, providing evidence for multiple uptake events but against continuous symbiont turnover, and that iii) photosynthesis genes are upregulated in symbiotic Phaeocystis, reflecting enhanced productivity in symbiosis, but DNA replication and cell-cycle genes are downregulated, demonstrating that hosts suppress symbiont cell division. Moreover, storage carbohydrate and lipid biosynthesis and metabolism genes are downregulated in symbiotic Phaeocystis, suggesting fixed carbon is relinquished to acantharian hosts. Gene expression patterns indicate that symbiotic Phaeocystis is not nutrient limited and likely benefits from host-supplied ammonium and urea, thus providing evidence for nutrient transfer between hosts and symbionts. Importantly, genes associated with protein kinase signaling pathways that promote cell proliferation are downregulated in symbiotic Phaeocystis. Deactivation of these genes may prevent symbionts from overgrowing hosts and therefore represents a key component of maintaining the symbiosis. This research contributes new insights into the ecologically relevant photosymbioses between Acantharea and Phaeocystis and illustrates the benefits of combining single-cell sequencing and imaging technologies to illuminate important microbial relationships in marine ecosystems.	Marine Science	X
5	Aleksandra Bliznina	Oikopleura dioica is a globally distributed, tunicate plankton that is commonly used for developmental studies due to its short life cycle (5 days), high fecundity and small (70 Mb) genome. As the closest relative of vertebrates, it occupies a key phylogenetic position within the chordate phylum and is of great evolutionary interest. The sequencing of the North Atlantic strain reveled that O. dioica exhibits remarkable genome plasticity compared with other metazoans. Its genome has undergone extreme compaction possibly arising from the loss of multiple DNA repair pathways. Indeed, a lot of genes appear to have been lost or scrambled throughout the genome, including normally conserved cluster of Hox genes. Despite such dramatic changes, O. dioica retains over 18,000 genes, maintains a simplified chordate body plan and shares common developmental trajectories. Here, we provide a chromosome-scale comparative sequence analysis among the O. dioica individuals found from geographically distant locations: Pacific (Osaka and Okinawa, Japan) and North Atlantic (Norway) Oceans, and Mediterranean Sea (Spain). Nanopore sequencing data for the Okinawan and Spanish individuals were assembled into megabase-sized scaffolds. Analysis of four genomes reveals a high divergence among morphologically identical individuals that have been so far classed as the same species. I will discuss how analysis of molecular signature of the breakpoints will allow to uncover a possible molecular mechanism behind the genome reshuffling in this species. We expect that the insights obtained from this analysis will form the basis for understanding whether the larvacean O. dioica contains cryptic species.	Marine Science	X

#	Name	Abstract	Field	
6	Audrey Denizot	According to the concept of the 'tripartite synapse', information processing in the brain results from dynamic communication between neurons and astrocytes. Astrocytes are a type of glial cells in the brain that, contrary to neurons, do not exhibit electrical signals. Their excitability results from transient elevations of their intracellular Ca^{2+} concentration. Those signals occur in response to neuronal activity and can trigger the modulation of neuronal communication by astrocytes. 80% of Ca^{2+} signals observed in astrocytes occur in fine cellular ramifications that are too fine to be resolved spatially with conventional light microscopy. Little is currently known about the mechanisms of Ca^{2+} signaling in those fine structures, which can only be assessed by super-resolution microscopy and computational modeling. In this study, we investigate the roles of the spatial properties of astrocytic ramifications on Ca^{2+} dynamics. Because of the low volumes and low number of molecules at stake, we use a stochastic spatially-explicit voxel-based model of Ca^{2+} signals that we have developed in 3D, implemented with STEPS software. The model is validated by reproducing key parameters of Ca^{2+} signals that were recorded with high-resolution Ca^{2+} imaging in organotypic brain slices. Our simulations reveal the importance of the spatial organization of the implicated molecular actors for Ca^{2+} dynamics. Particularly, we predict that different spatial organizations can lead to very different types of Ca^{2+} signals, even for two processes displaying the exact same densities of Ca^{2+} channels. We perform simulations in different process geometries and propose potential effects of cellular geometry on the speed and probability of signal propagation. By modeling realistic astrocyte geometry at the nanoscale, this study provides a better understanding of information processing during neuron-astrocyte communication and overall of information processing in the brain.	Neuroscience	X
7	Hemanta Sarmah	The multi-subunit eukaryotic CCR4-NOT complex, imparts gene expression control primarily via messenger RNA (mRNA) decay. Here, we present the role of subunit CNOT9 in target mRNA decay during embryonic development. CNOT9 null mice appear normal during onset of gastrulation yet exhibit growth and differentiation defects accompanied by extensive cell death by embryonic day 9.5. Sox-2 Cre conditional knockout mice show marginal rescue and brief delay in phenotype emergence suggesting defects to be epiblast-dominant. Among various identified targets, we show that Lefty2 mRNA expression is post-transcriptionally regulated by CNOT9. Lefty2 3'-UTR containing mRNA has significantly higher stability in cells expressing CNOT1-binding-mutant form of CNOT9, relative to cells expressing wild-type form of CNOT9. In addition, CNOT9 primarily localizes within cytoplasm and bridges interactions between the CCR4-NOT complex and miRNA-RISC complex in gastrulating embryos.	Molecular, Cellular, and Developmental Biology	X
8	Julian Katzke	Lineages diversify into different ecological niches with phenotypes that are different in form and function. However, evolutionary patterns, tradeoffs and constraints shaping differences in functional traits are not well understood. Ants evolved a wide range of lifestyles, behaviors, and ecologies. One of the most notable features of the ant radiation is the striking diversity of mandible shapes and sizes, relative to the diversity in other insects. Mandibles are the primary tools that ants use to interact with the world, and they have both social and ecological functions, but we still lack an understanding of the factors that shaped and promoted their diversification. To address these gaps, I aim to perform a broad comparative analysis of the ant mandible evolution. First, I am mapping morphological variation, infer tempo and mode in evolution and ask whether mandibles fall into distinct types or vary in a continuous morphospace. Second, I create a model to approximate function and performance from anatomical data. Third, as mandibles and the attaching muscles vary greatly within ant heads and as it is an open question how these systems evolve, I will investigate mandibles and muscles considering the whole head with a focus on brain and head capsule. I will identify functional tradeoffs, and physical and ecological constraints to explain patterns of convergence, generalization and specialization. To approach these projects, I comparatively analyze functional anatomy using high-resolution x-ray tomography of genera mapped onto an ant-wide phylogeny and factor in ecological data and other functional traits. I quantify morphology with geometric morphometric methods and function and performance by measuring biomechanical aspects of the system. Investigating the evolutionary history of ant mandibles will potentially open a new model system for analyses of ecomorphological diversification.	Environmental & Ecological Sciences	X
9	Yazmin Zurita	Interactions between species are one of the main drivers of community dynamics and stability, as well as biodiversity support. However, how these ecological networks are modified under disturbance is not yet clear. For my doctoral research, I will a) analyse the spatial and seasonal dynamics of the ant food web across a strong gradient of human disturbance to gain a better understanding of how these factors affect ant trophic interactions, including key network parameters such as connectance, modularity, and nestedness, and b) compare the roles of native and invasive ants on different islands to understand how direct biotic factors (invasive species) affect the interactions in different communities. With this work I will contribute to the understanding of how ecological networks change spatially and temporally when subjected to disturbance.	Environmental & Ecological Sciences	X

10	Kamila Mustafina	Self-cleaving ribozymes engineered to be activated or inhibited by a small molecule binding to an RNA aptamer inserted within a ribozyme (aptazymes) have proven to be useful for controlling gene expression in living cells. In mammalian cells, an aptazyme embedded in the 5′ or 3′ untranslated region of an mRNA functions as a synthetic riboswitch to chemically regulate gene expression. However, the variety of aptazyme architectures and the ribozyme scaffolds that have been used for mammalian riboswitches has been limited. In particular, fewer synthetic riboswitches that activate gene expression in response to a small molecule (ON-switches) in mammalian cells have been reported compared to OFF-switches. In this work, we developed mammalian riboswitches that function as guanine-activated ON-switches based on a novel aptazyme architecture in which an aptamer and a ribozyme are fused in tandem. The riboswitch performance was optimized by fine-tuning the stability of a critical stem that controls the ribozyme structure and function, yielding switches with ON/OFF ratios greater than 6.0. Our new aptazyme architecture expands the RNA device toolbox for controlling gene expression in mammalian cells	Molecular, Cellular, and Developmental Biology	X
11	Bogna Ignatowska-Jankowska	Distinct behavioral effects of cannabinoids in 3D motion capture of freely moving mice Bogna M Ignatowska-Jankowska1, Aysen Gurkan Ozer1, Alexander Kuck1, Micah Niphakis2, Daisuke Ogasawara 2, Benjamin F Cravatt2, Marylka Yoe Uusisaari1 1Neuronal Rhythms in Movement Unit, Okinawa Institute of Science and Technology, Japan 2Department of Chemical Physiology, Scripps Research Institute, La Jolla, CA 92037, USA One of behavioral effects of cannabinoid CB1 receptor activation is inhibition of locomotor activity. However, effects of endogenous cannabinoids on behavior have not been extensively studied. Here we aimed to assess whether enhancing endocannabinoid signaling produces effects similar to exogenous cannabinoid agonists. To elevate signaling of endocannabinoids 2-Arachidonoylglycerol and Anandamide we used selective inhibitors (MJN110 and PF3845, respectively) of Monoacylglycerol lipase and Fatty Acid Amide Hydrolase, enzymes responsible for their degradation. High-speed, high-resolution 3D motion capture system (Qualisys) was used to track movement (3D trajectories and velocity of markers) during voluntary locomotor tasks: open field exploration, vertical and horizontal climbing, beam walking, aerial righting reflex. The results revealed distinct behavioral phenotypes induced by different cannabinoids. Low doses of synthetic cannabinoid agonist CP55,940 (0.03, 0.1, 0.3 mg/kg) produced significant bidirectional, task-dependent effects: a decrease of activity and widened stance in the open field, but increased activity in the climbing task (n=10). MJN110 (1.25, 2.5 mg/kg) significantly increased the activity both in the open field and climbing tasks (n=10) and preliminary data indicate this increase is CB1-mediated (n=6). PF3845 did not have a significant effect on activity or gait at the moderate dose (10 mg/kg) and significantly decreased activity at high dose (30 mg/kg). The results suggest that selective elevation of 2-AG and AEA signaling results in distinct, bidirectional effects on behavior that are different from exogenous cannabinoid agonists. Furthermore, the work highlights the strength of 3D motion capture as precise and sensitive tool to evaluate wide range of behaviors in rodents.	Neuroscience	-
12	Yuko Hasegawa	To characterize morphological features of two Japanese bobtail squid species, E. berryi and E. morsei, images were acquired over the course of their development. Their relatively small size, short life span, lack of cannibalistic nature, and ability to live in high densities make them suitable for laboratory culture and cephalopod models. Both squid species were captured in Mie, Japan, in spring 2018 and then cultured in laboratory. F1 animals were used for micro-CT and light microscopy-based observation. The imaging-based approaches used here enabled visualization of both external and internal morphological features that can provide essential information for future experiments using these emerging cephalopod models.	Marine Science	-

13	Marine - Le Gal	In 1771, a major tsunami hit the Yaeyama islands (Japan). Among them, Ishigaki Island was severely impacted with 30m run-ups on the south east coast. Like many other islands in the Pacific, Ishigaki Island is characterized by an irregular coastline with reefs. While, the propagation and inundation of tsunamis as well as current and reef interactions have been numerously analyzed, the interactions between tsunami and reef have been little studied. Moreover, most of the previous works focused on one-dimensional idealized reefs, and few real reef tsunami events have been presented. In the present study, a two-dimensional numerical approach is suggested to measure the influence of the reef for the inundation of the 1771 tsunami along the south-east coast of Ishigaki. First a reference model, simulating the historical event, was developed with a Nonlinear Shallow Water model. Second, modifed models were build from the reference model by altering the reef topography. Three situations were tested : the absence of reef, the absence of channels in the reef and changes in the reef depth. In order to measure the influence of these different modifications, a new ratio, quantifying their impact along the coastline, was defined. Overall, in our simulations, the reef protected the coast reducing the maximum wave heights by an average of 12.5%. However, at local scales, the channels increased the maximum wave height by up to 40% on the nearby coasts. Finally, changes in the reef depths showed a global positive correlation with the maximum wave height at the coast. This study brought new elements to better understand the protective function of the reef. These conclusions can help to better forecast the inundation behind this given reef, resulting in more appropriate management of the coast.	Marine Science	-
14	Sam Ross	Understanding the drivers of ecological stability is a central goal of ecology given current global environmental change. Field experiments tackling these questions by manipulating temperature have largely not matched climate change projections, clouding our inference of global change impacts on ecosystems. Here, we examine the temporal and spatial stability of algal function (biomass) and composition in response to artificially induced heatwaves through a novel aquatic mesocosm experiment in Horonai stream, Hokkaido, Japan. We expose naturally assembled communities of algae and macroinvertebrates to combinations of predator removal (extinction) and aquatic heatwaves at two levels (current [+2.8C] versus projected future heatwave [+6.1C]) using statistically downscaled values to produce locally realistic temperature increases. We found that algal dynamics were resistant to both heatwave conditions, and that the effect of predators on algae and macroinvertebrates remained constant across heatwave conditions. However, when considering time-varying interaction strengths between algal groups and the contribution of predators to algal dynamics, our heatwaves decoupled the spatial and temporal dimensions of functional and compositional stability. Our results highlight the complexity of climate change impacts on aquatic systems and the need to consider community dynamics over simple measures of biomass or composition when assessing global change impacts on ecological communities.	Environmental & Ecological Sciences	X
15	William Ashworth	Multi-omics analysis of CNOT4 CNOT4, a ubiquitin E3 ligase with RNA binding activity, regulates several proteins through the ubiquitin-proteasome degradation pathway. It plays an important role in embryonic development and knockout mouse embryos are not viable after around e9.5. However, the cause of this embryonic lethality has yet to be identified. Here, the role of CNOT4 in regulation of mRNA and protein expression was studied through a multi-omics approach. RNA-seq and qPCR were used to measure changes in mRNA levels and stability. Binding partners and ubiquitination targets were identified through co-immunoprecipitation experiments followed by mass-spec. Whole proteome mass-spec was used to identify proteins degraded by CNOT4. Consistent with yeast NOT4, co-IP with ribosome components was observed suggesting a conserved role in co-translational quality control. CNOT4 also co-immunoprecipitated with several histone components suggesting an additional role in DNA folding or modification. CNOT4 coimmunoprecipitated with members of the CCR4-NOT complex. In addition, CNOT4-dependent ubiquitination of CCR4-NOT member CNOT1 was observed but was not associated with proteasomal degradation. Several other novel ubiquitination targets were identified. Pathway analysis showed groups of proteins involved in cell-cell adhesion and cell cycle/differentiation. RNAseq of CNOT4 knockout cells identified changes in a small number of genes primarily involved in development and cellular differentiation. Computational analysis showed these changes did not occur due to changes in stability. These identified changes in mRNA and protein expression may contribute to the embryonic lethality seen in CNOT4 knockout embryos.	Molecular, Cellular, and Developmental Biology	-

16	Jelena Katic	How social interactions affect attention and song perception in juvenile zebra finches during song learning Juvenile male zebra finches learn to sing via vocal communications with adults during development. Song learning is improved by socially interacting with adults, possibly through an increase in attention level. Here I investigated whether social interaction with adult tutors modulates attention level as well as auditory information processing. I recorded neuronal activities from the auditory area that stores tutor song memories, the caudomedial nidopallium (NCM), while inhibiting the activity of the neurons in the attention control area, the nucleus locus coeruleus (LC).	Neuroscience	-
17	Lazzat Aibekova	Ants are one of the most diverse and ecologically successful groups on Earth. They play an important role in many ecosystems and can be found in almost all habitats. They are adapted to many different lifestyles; they can be found underground, leaf litters and on trees. Ant's legs are involved in many different locomotion like climbing, catching prey, jumping and running. Therefore, it is important to understand how ants modified their skeletomuscular configurations for different locomotion and how they adapted to walk on different surfaces. The aim of this project is to study the evolution of functional morphology using the leg of ants as a model system. Objectives: 1. To illuminate the skeletomuscular system involved in ant legs movement; 2. To investigate the proximate basis of convergent evolution of jumping ability by comparing the muscle insertion, attachment, and volume between jumping ants and closely related non-jumping ants; 3. To Identify how morphology co-evolves with posture and function across different stages of ant evolution; 4. To compare the attachment structures between arboreal and terrestrial ants.	Environmental & Ecological Sciences	-
18	Florian Lalande	The first exoplanet has been confirmed in 1995 by"Michel Mayor and Didier Queloz (University of Geneva)."This discovery has been awarded the 2019 Nobel Prize"of Physics. Since this first evidence of worlds outside"the Solar System, astrophysicists have been looking"for exoplanets to compare with our own Earth. Exoplanets characterization allows to look for planetary candidates that could harbour life, giving hints for the quest of extraterrestrial life biomarkers. In this respect, Kepler (March 2009 – October 2018, NASA) brought us more than 2,500 new exoplanets using the transit method. However we still know very little on long period exoplanets. The"exoplanets found by Kepler are biased towards very short"period orbits (see graph below), which does not compare"with our Solar System. Looking for Earth-like planets"requires to develop new methods of detections that"do not require several transits do confirm a planet. Furthermore, NASA launched Kepler's successor in April 2018 : TESS (Transiting Exoplanet Survey Satellite). This space telescope"is expecting to bring more than 20,000 new exoplanets via"the transit method. Again, detecting long period planets will be a challenge given the discontinued observation of stars.	Mathematical and Computational Sciences	X
19	Yuka Suzuki	Ecological systems are very complex due to many entities involved and the interplay of multiple processes, such as dispersal, drift, selection, and speciation. Moreover, connections among species and across geographic space can make them even more complex at a large spatial scale. Network analysis is a powerful tool to describe and analyze biological complex systems. I apply network analysis to understand biodiversity dynamics among local communities connected by dispersal in a metacommunity. Dispersal limitation is one of the fundamental processes shaping diversity patterns and has been suggested that dispersal network structure has a large influence on pattern formation. Using theoretical and computational approaches, I investigate how spatial structure in a metacommunity influence the metacommunity dynamics.	Environmental & Ecological Sciences	X
20	Kevin Dorgans	In vivo calcium imaging of mouse inferior olive neuronsAbstractThe importance of inferior olive (IO) neurons in motor behaviour had been shown bystudies on their output, climbing fibers, and purkinje cell complex spikes activated by climbing fibers. The intrinsic properties of IO neurons had also been intensively investigated in vitro. Considering that IO receiving inputs from a great number of brain and spinal cord areas and its function relying on an intact olivo-cerebellar complex, it is essential to examine IO neurons activity in vivo to validate previous studies and to have a better understanding of olivo-cerebellar complex. We developed in vivo whole-field calcium imaging method for IO network recording to achieve this purpose. For the first time, we show the in vivo calcium imaging of IO neurons in both anesthetised and awake mice.	Neuroscience	-

| 21 | Zifcakova Lucia | The assembly of fungal communities in termite guts is affected by diet and taxonomy.
Termites are one of the most abundant insects in tropical and subtropical regions and play crucial role as ecosystem engineers feeding and degradation different substrates. Although it is known that gut symbionts are necessary for termites in order to effectively use their feeding substrate, such as wood, there is a little knowledge about role of fungal community in termite guts.We tried to fill this gap of knowledge and have sequenced two fungal markers - ITS and LSU, in more than 50 termite species for each marker. We have covered different feeding groups as well as different locations and taxonomical groups. There was a obvious trend in low diversity and abundance of fungal species in the guts of lower termites. On the other hand, highest diversity and richness of fungal species was recorded for soil feeders. Termitomyces fungus was present in all fungal-growers (Macrotermitinae) as expected. Interestingly, fungal community of fungal-grower Macrotermes was unexpectedly rich and abundant in fungal orders Hypocreales and Pleosporales. Lichen-feeders, fungus-growers and lower termites were significantly different in the composition of their fungal microbiota from other groups. Occurrence of some fungal orders was influenced by the location as well. For example, ubiquitous order Eurotiales were significantly more often found in the guts of termites from Africa. Overall, to our knowledge, this is the first comprehensive study on fungal communities in termite guts. | Environmental & Ecological Sciences | X |