Wurmlab website

Community: Journal table of contents highlights

published between 1st and last day of **MAY**** (in print *and* early access). **Finish it by June 7th**. Please add everything as nested bullet-points.

CTRL-K for links

CTRL-SHIFT-V paste w/o format

Look at the table of content duties here (github)

• Am Nat

• Bioinformatics

- <u>bcSeq: An R Package for Fast Sequence Mapping in High-throughput shRNA and CRISPR Screens</u>: CRISPR-Cas9 and shRNA high-throughput sequencing screens have abundant applications for basic and translational research. Methods and tools for the analysis of these screens must properly account for sequencing error, resolve ambiguous mappings among similar sequences in the barcode library in a statistically principled manner, and be computationally efficient. Herein we present bcSeq, an open source R package that implements a fast and parallelized algorithm for mapping high-throughput sequencing reads to a barcode library while tolerating sequencing error.
- Combining probabilistic alignments with read pair information improves accuracy of split-alignments: They propose a split-alignment technique that combats the issue of ambiguous alignments by combining information from probabilistic alignment with positional information from paired-end reads. They demonstrate that their method finds accurate split-alignments, and that this translates into improved performance of variant-calling tools that rely on split-alignments.

• Cell

• Current Biology

- The Geomagnetic Field Is a Compass Cue in Cataglyphis Ant Navigation Fleischmann ... Rössler. DOI DOI: https://doi.org/10.1016/j.cub.2018.03.043. This cool study shows that ants not only use visual landmarks and celestial cues, but also geomagnetic compass. Cataglyphis pirouettes when checking where the entrance of the nest is. By disturbing the local geomagnetic field, the authors confused the ants which could not find home anymore.
- Phylogenomics, Diversification Dynamics, and Comparative Transcriptomics across the Spider Tree of Life Fernandez et al DOI https://doi.org/10.1016/j.cub.2018.03.064.
 Impressive phylogenomic study (~160 species). Spiders are old (dating 400mya) and have evolved multiple time the orb web technique.
- <u>Burst Firing in Bee Gustatory Neurons Prevents Adaptation</u> Miriyala et al DOI: https://doi.org/10.1016/j.cub.2018.03.070.

• <u>eLife</u>

- Epigenetic drift of H3K27me3 in aging links glycolysis to healthy longevity in *Drosophila* The researchers show that aging leads to loss of fidelity in epigenetic marking and drift of a highly conserved histone and consequential reduction in the expression of glycolytic genes in *Drosophila*
- Ecological multiplex interactions determine the role of species for parasite spread amplification

The authors present a theoretical 'ecomultiplex' model, where multiple transmission paths among a diverse community of interacting hosts are represented as a spatially explicit multiplex network.

С

Evolution

• GBE

- Comparative Genomics Reveals Thousands of Novel Chemosensory Genes and Massive
 Changes in Chemoreceptor Repertories across Chelicerates
- Regulation of Large Number of Weak Targets—New Insights from Twin-microRNAs
- The Codon Usage of Lowly Expressed Genes Is Subject to Natural Selection

Genome Biol

- o Diversification and independent domestication of Asian and European pears.
- Hundreds of novel composite genes and chimeric genes with bacterial origins contributed to haloarchaeal evolution.
- A major locus controls local adaptation and adaptive life history variation in a perennial plant. "The discovery of a single locus explaining a substantial fraction of the variation in a key life-history trait is remarkable, given that such traits are generally considered to be highly polygenic. These findings provide a dramatic illustration of how loci of large-effect for adaptive traits can arise and be maintained over large geographical scales in natural populations."

Genome Res

• Insectes Sociaux

- The gut microbiome is associated with behavioural task in honey bees Jones et al. https://doi.org/10.1007/s00040-018-0624-9 Using Shannon Diversity Index, taking into consideration abundance and evenness of species present in the community.
- <u>Limited size-related variation in behavioral performance among workers of the exceptionally polymorphic ant Pheidole rhea</u> Gordon, M. Moreau, V. Fourcassie, Traniello.
 https://doi.org/10.1007/s00040-018-0629-4 The main correlation was that supersoldiers are more able to pick up fainter trace of pheromone
- The membrane phospholipid composition of honeybee (Apis mellifera) workers reflects their nutrition, fertility, and vitellogenin stores Wegener et al https://doi.org/10.1007/s00040-018-0623-x They wanted to test if eating more pollen than normal was linked to worker longevity, but it proved more difficult to separate the worker cohorts based on their criteria.

• Journal of Evolutionary Biology

- Successful despite poor flight performance: range expansion is associated with enhanced exploratory behaviour and fast development
 By comparing core populations with edge populations of the European range-shifting butterfly Lycaena tityrus, the authors find adaptation to local climates and an enhanced dispersal ability in edge populations. The edge populations had shorter development times and smaller size, were more sensitive to higher temperatures, had a higher diapause incidence, and showed enhanced exploratory behaviour.
- Mitochondrial complementation: a possible neglected factor behind early eukaryotic sex. The
 authors use modelling approaches to test the hypothesis that fusion in early eukaryotes
 emerged as a way to overcome the negative effects of mutation load in mitochondria.
 DOI:10.1111/jeb.13293

• MBE

- o Review: The State of Software for Evolutionary Biology
- Codon Usage Bias in Animals: Disentangling the Effects of Natural Selection, Effective
 Population Size, and GC-Biased Gene Conversion

 Rates of Mutation and Recombination in Siphoviridae Phage Genome Evolution over Three Decades

Mol Ecol

- Rapid genetic adaptation to a novel environment despite a genome-wide reduction in genetic diversity: Introduced species often colonize regions that have vastly different ecological and environmental conditions than those found in their native range. As such, species introductions can provide a deeper understanding into the process of adaptive evolution. In the 1890s, steelhead trout (Oncorhynchus mykiss) from California were introduced into Lake Michigan (Laurentian Great Lakes, North America) where they established naturally-reproducing populations. In their native range, steelhead hatch in rivers, migrate to the ocean, and return to freshwater to spawn. Steelhead in Lake Michigan continue to swim up rivers to spawn, but now treat the freshwater environment of the Great Lakes as a surrogate ocean. To examine the effects of this introduction, we sequenced the genomes of 264 fish. By comparing steelhead from Lake Michigan to steelhead from their ancestral range, we determined that the introduction led to consistent reductions in genetic diversity across all 29 chromosomes. Despite this reduction in genetic diversity, three chromosomal regions were associated with rapid genetic adaptation to the novel environment.
- Signatures of diversifying selection and convergence acting on passerine Toll-like receptor 4 in an evolutionary context: We show that 55 passerine species vary substantially in the distribution of electrostatic potential on the surface of the receptor, and based on these distinct patterns we identified four species clusters. Seven out of the 34 evolutionarily non-conservative and positively selected residues correspond topologically to sites previously identified as being important for lipopolysaccharide, lipid IVa or MD-2 binding. Five of these positions co-determine the identity of the charge clusters. Groups of species that host related communities of pathogens were predicted to cluster based on their TLR4 LBR charge. Despite some evidence for convergence among taxa there were no clear associations between the TLR4 LBR charge distribution and any of the general ecological characteristics compared (migration, latitudinal distribution, and diet). Closely related species, however, mostly belonged to the same surface charge cluster indicating that phylogenetic constraints are key determinants shaping TLR4 adaptive evolution. Our results suggest that host innate immune evolution is consistent with Fahrenholz's rule on the co-speciation of hosts and their parasites.
- Phylogenetic patterns of ant-fungus associations indicate that farming strategies, not only a superior fungal cultivar, explain the ecological success of leafcutter ants. The authors examine the phylogeny of leaf-cutter ants and their associated funghi. They show that interactions between the two are not as simple as previously thought and that they can be ecosystem-specific. DOI: 10.1111/mec.14588
- Meta-analysis of chromosome-scale crossover rate variation in eukaryotes and its significance to evolutionary genomics. The authors examine genome-wide cross-over sites in 62 eukaryote genomes. They find a general pattern of low cross-over frequency at the center of the chromosomes (independently of centromere position). They also show that smaller chromosomes have higher cross-over rates. VERY COOL ARTICLE. WORTH A READ. DOI:10.1111/mec.14699
- The "two rules of speciation" in species with young sex chromosomes. The author looks at the Haldane Rule and the large X effect rule in the recently diverged sex chromosomes of two different plant species. DOI:10.1111/mec.14721

Myrmecological News

<u>Diversity and distribution of Solenopsis (Hymenoptera: Formicidae) thief ants belowground:</u>
 In this study, we sampled the subterranean ant community of central Florida, a region with conspicuously high subterranean thief ant abundance. We used a stratified-random

sampling protocol and collected soil environmental variables at each sampling plot to model subterranean ant diversity in relation to abiotic conditions in the soil environment. Furthermore, we utilized non-parametric ordination methods and permutation-based analyses of variance to visualize and quantify associations of species based on habitats and soil strata. This study finds that thief ants dominate belowground and respond predictably to soil habitat conditions. Biotic effects among ant species may be important given their purported lestobiotic behaviors.

Reconstructing the relatedness of cooperatively breeding queens in the Panamanian leaf-cutting ant Acromyrmex echinatior (Hymenoptera: Formicidae): permanent inquiline social parasites in ants has been conjectured to be facilitated by secondary polygyny, that is, the re-adoption of new queens into existing mature colonies. However, these scenarios hinge on two vital conditions that have not been quantitatively documented: 1. That host sister species are secondarily polygynous and primarily recruit close kin, and 2. That such adoptions are prone to occasional mistakes that would select for the condition-dependent expression of exploitative traits and reproductive isolation by disruptive selection. Here, we use a long-term data set on the leaf-cutting ant Acromyrmex echinatior (ForEl, 1899), known to have a closely related inquiline social parasite A. insinuator schultz, BEKKEvoID & Boomsma, 1998, to address the first of these conditions. We estimate the frequency of secondary polygyny and the degree to which cooperatively breeding gueens are related. We find that the overall frequency of polygynous colonies is ca. 8% and that polygynous colonies typically have two queens. Most queen pairs are first-degree relatives, consistent with colonies adopting one or two daughters either before or just after becoming orphaned.

Nature

Nature Comms

- Macroecology and macroevolution of the latitudinal diversity gradient in ants Economo...
 Guénard. Doi https://doi.org/10.1038/s41467-018-04218-4 Impressive dataset
 "encompassing nearly all described ant species". Species outside tropics are younger.
 Similar rates of diversification throughout the phylogeny.
- Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics Barbeira et al doi https://doi.org/10.1038/s41467-018-03621-1 Mathematical model to improve the biological implications (such as human disease) from expression data.
- Hygroscopic compounds in spider aggregate glue remove interfacial water to maintain adhesion in humid conditions
 Singla et al doi: https://doi.org/10.1038/s41467-018-04263-z
 Hygroscopy is the phenomenon of attracting and holding water molecules from the surrounding environment, which is usually at normal or room temperature.

• Nature Genetics

- The fecal metabolome as a functional readout of the gut microbiome Zierer et al. doi:10.1038/s41588-018-0135-7. In this comprehensive description of the human fecal metabolome, 1,116 metabolites from 786 individuals from a population-based twin study were examined. The fecal metabolome was found to be only modestly influenced by host genetics.
- Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits Evan et al doi:10.1038/s41588-018-0108-x. Review. Authors

suggest to employ methods that group SNPs "according to minor allele frequency and linkage disequilibrium" (less sensitive than other methods)

Nature Methods

o Computational correction of index switching in multiplexed sequencing libraries.

Plos Biol

 Death and population dynamics affect mutation rate estimates and evolvability under stress in bacteria Frenoy & Bonhoeffer. https://doi.org/10.1371/journal.pbio.2005056. Population model includes for the first time death rate to understand consequences on mutation rates of high-evolving bacteria under stress (think antibiotic effects).

Plos Comp Biol

Plos Genet

- Adaptive genome duplication affects patterns of molecular evolution in Saccharomyces cerevisiae: Laboratory evolution experiments initiated with haploid Saccharomyces cerevisiae cultures repeatedly experience whole-genome duplication (WGD). We report recurrent genome duplication in 46 haploid yeast populations evolved for 4,000 generations. We find that WGD confers a fitness advantage, and this immediate fitness gain is accompanied by a shift in genomic and phenotypic evolution. The presence of ploidy-enriched targets of selection and structural variants reveals that autodiploids utilize adaptive paths inaccessible to haploids. We find that autodiploids accumulate recessive deleterious mutations, indicating an increased susceptibility for nonadaptive evolution.
- Machine learning identifies signatures of host adaptation in the bacterial pathogen Salmonella enterica: . Here, we measure the burden of atypical mutations in protein coding genes across independently evolved Salmonella enterica lineages, and use these as input to train a random forest classifier to identify strains associated with extraintestinal disease. Our random forest classifier learned to perfectly discriminate long-established gastrointestinal and invasive serovars of Salmonella. Additionally, it was able to discriminate recently emerged Salmonella Enteritidis and Typhimurium lineages associated with invasive disease in immunocompromised populations in sub-Saharan Africa, and within-host adaptation to invasive infection. We dissect the architecture of the model to identify the genes that were most informative of phenotype, revealing a common theme of degradation of metabolic pathways in extraintestinal lineages.

PNAS

Proc B

- Multiple large inversions and breakpoint rewiring of gene expression in the evolution of the fire ant social supergene
- o Sex-specific effects of inbreeding on reproductive senescence
- Sexual selection predicts species richness across the animal kingdom
- Mitochondrial genetic effects on reproductive success: signatures of positive intrasexual, but negative intersexual pleiotropy

• Science

• TREE

<u>Bridgehead Effects and Role of Adaptive Evolution in Invasive Populations</u>: This review is presented as it follows: Biological invasions are a major threat to biodiversity, agriculture, and human health. Invasive populations can be the source of additional new introductions, leading to a self-accelerating process whereby invasion begets invasion. This phenomenon, coined bridgehead effect, has been proposed to stem from the evolution of higher invasiveness in a primary introduced population. There is, however, no conclusive evidence that the success of bridgehead populations stems from the evolution of increased

invasiveness. Instead, we argue that a high frequency of secondary introductions can be explained by increased abundance in the bridgehead region or the topology of human transport networks. We outline the type of evidence and experiments that are needed to demonstrate adaptive evolution and higher invasion success of introduced populations.

- Social Information Links Individual Behavior to Population and Community Dynamics: This review is presented as it follows: When individual animals make decisions, they routinely use information produced intentionally or unintentionally by other individuals. Despite its prevalence and established fitness consequences, the effects of such social information on ecological dynamics remain poorly understood. Here, we synthesize results from ecology, evolutionary biology, and animal behavior to show how the use of social information can profoundly influence the dynamics of populations and communities. We combine recent theoretical and empirical results and introduce simple population models to illustrate how social information use can drive positive density-dependent growth of populations and communities (Allee effects).
- o Eco-Evolutionary Genomics of Chromosomal Inversions
- Trends in Genetics
 - Through Sex. Nature Is Telling Us Something Important
 A review of "The Magnificent Four Mechanisms for the Evolutionary Advantage of
 - Amphimixis" and the possible gradual loss of amphimixis.
 - Why Do Sex Chromosomes Stop Recombining? The authors review the existing evidence supporting different hypotheses by which sex chromosomes evolve suppressed recombination. DOI:10.1016/j.tig.2018.04.001

[1]. Other papers/tools that you feel someone should have seen:

- o BioRxiv:
 - De novo assembly of a young Drosophila Y chromosome using Single-Molecule
 sequencing and Chromatin Conformation capture
- Genetics
- Heredity
- Aging
- o Mol Cell Biol
- J Gerontol
- Nature Ecology and Evolution
 - Division of labour and the evolution of extreme specialization
- Methods in Ecology and Evolution
- o Current Opinion in Insect Science
- Molecular Phylogenetics & Phylogenetic
 - Early Cretaceous greenhouse pumped higher taxa diversification in spiders
- o PeerJ
 - A brief introduction to mixed effects modelling and multi-model inference in ecology