

Community: Journal table of contents highlights

****published between 1st and last day of **APRIL** (in print *and* early access). **Finish it by May 12th**.**

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](#)**
 - [Intraspecific Variation in Learning: Worker Wasps Are Less Able to Learn and Remember Individual Conspecific Faces than Queen Wasps](#) *Polistes* wasp workers and foundress queens had faces experimentally altered by adding distinctive yellow marks - foundresses showed higher individual recognition.
- **[Bioinformatics](#)**
 - [ASElux: an ultra-fast and accurate allelic reads counter](#)
 - [RecoverY: k-mer-based read classification for Y-chromosome-specific sequencing and assembly](#)
 - [RepLong: de novo repeat identification using long read sequencing data](#) Repeat identification using PacBio reads
 - PREPRINT: [BlockFeST : Bayesian calculation of region-specific FST to detect local adaptation](#) Part of popgenome
 - PREPRINT: [In-silico read normalization using set multi-cover optimization](#)
- **[Cell](#)**
- **[Current Biology](#)**
 - [Unravelling the Molecular Determinants of Bee Sensitivity to Neonicotinoid Insecticides](#) Manjon et al DOI: <https://doi.org/10.1016/j.cub.2018.02.045>. Bumblebee study to check if main components of neonicotinoids affect them the same way as bees, focusing on 450 genes (and enzymes).
 - [How Honeybees Defy Gravity with Royal Jelly to Raise Queens](#) Buttstedt...Moritz DOI: <https://doi.org/10.1016/j.cub.2018.02.022> Sticky royal jelly keeps queen larvae in cell, despite facing downward.
 - [Functional Maps of Mechanosensory Features in the Drosophila Brain](#) Patella & Wilson DOI: <https://doi.org/10.1016/j.cub.2018.02.074> tonotopy (from Greek tono=frequency and topos = place) is the spatial arrangement of where sounds of different frequency are processed in the brain.
 - [Molecular Evolution at a Meiosis Gene Mediates Species Differences in the Rate and Patterning of Recombination](#) Brand et al DOI: <https://doi.org/10.1016/j.cub.2018.02.056>
 - [The Geomagnetic Field Is a Compass Cue in Cataglyphis Ant Navigation](#) Researchers found that the gaze directions during the orientating look-back-to-the-nest behavior change in a predictable way to alterations of the horizontal component of the magnetic field.
- **[eLife](#)**
 - [Reduced expression of C/EBPβ-LIP extends health- and lifespan in mice.](#) DOI: 10.7554/eLife.34985.

- [Selective eradication of cancer displaying hyperactive Akt by exploiting the metabolic consequences of Akt activation.](#) DOI: 10.7554/eLife.32213.
- [A polymorphism in the tumor suppressor p53 affects aging and longevity in mouse models.](#) DOI: 10.7554/eLife.34701.[
- [An incoherent feedforward loop facilitates adaptive tuning of gene expression](#)
- **Evolution**
 - [Antagonistic pleiotropy in species with separate sexes, and the maintenance of genetic variation in life-history traits and fitness.](#) The authors model the role of antagonistic pleiotropy (alleles of a gene increasing a specific component of fitness at a cost to others) in maintaining polymorphism (and balancing selection). They find that this is plausible under very specific scenarios of sexual antagonism. DOI: doi.org/10.1111/evo.13493
 - [Genome-wide regulatory deterioration impedes adaptive responses to stress in inbred populations of *Drosophila melanogaster*.](#) The authors study the effects of inbreeding depression in gene expression under environmental stress in *D.melanogaster*. They find that inbred individuals have a lower expression response to stress. DOI: 10.1111/evo.13497
- **GBE**
 - [Are Nonsense Alleles of *Drosophila melanogaster* Genes under Any Selection?](#) To investigate the impact of nonsense alleles on the function of affected genes, we performed a direct measurement of the strength of negative selection acting within these alleles in a natural population of *D. melanogaster*. Within those exons that carry nonsense mutations, negative selection, assayed by the ratio of missense over synonymous nucleotide diversity levels, appears to be absent, consistent with total loss of function. In other exons of nonsense alleles, negative selection was deeply relaxed but likely not completely absent, and the per site number of missense alleles declined significantly with the distance from the premature stop codon.
 - [The Most Developmentally Truncated Fishes Show Extensive Hox Gene Loss and Miniaturized Genomes](#)
 - [Signatures of DNA Methylation across Insects Suggest Reduced DNA Methylation Levels in Holometabola](#)
- **Genome Biol**
- **Genome Res**
 - [Whole-genome sequencing of Atacama skeleton shows novel mutations linked with dysplasia](#) This made the news last month
 - [Conserved microRNA targeting reveals preexisting gene dosage sensitivities that shaped amniote sex chromosome evolution](#)
 - [Repeat associated mechanisms of genome evolution and function revealed by the *Mus caroli* and *Mus pahari* genomes](#)
- **Insectes Sociaux**
 - [Different reproductive strategies and their possible relation to inbreeding risk in the bumble bee *Bombus terrestris*:](#) The objective of this study was to determine the probability of inbred mating as a consequence of the simultaneous presence of fertile gynes and males in colonies. We determined the risk of inbreeding through the calculation of a novel index (inbreeding risk index, IRI), proposed here for the first time, and we investigated the relationship between the reproductive strategies of the colonies and their IRI values from an ecological point of view. The inbreeding risk index (IRI) of a colony was a good predictor of the possibility of incestuous mating among gynes and males of a same colony, and it also proved to be a good descriptor of the colony specific reproductive strategy.
 - [Preadaptation for asexual queen succession: queen tytoparthenogenesis produces neotenic queens in the termite *Reticulitermes okinawanus*:](#) In this study, we assessed the evolution of AQS (asexual queen succession) by investigating tytoparthenogenesis in the non-AQS termite *R. okinawanus*. First, we established new colonies by female–female

and female-male reproductive pairs in the laboratory, and compared the number of hatched individuals between them. The ploidy and genotypes of parthenogens produced by female-female pairs were then examined. Finally, caste fate of the parthenogenetically-produced daughters was compared to that of the sexually-produced daughters.

- [Plant pathogenic fungi decrease in soil inhabited by seed-dispersing ants](#): We investigated published *Aphaenogaster* soil fungi data and conducted our own metataxonomic analysis of ant-occupied and unoccupied soils to identify phytopathogenic fungi and investigate whether ant colony presence corresponds with reduced plant fungal pathogens in the soil. We found reduced phytopathogenic fungi presence and richness in soils containing ant colonies as compared to nearby control soils indicating that the presence of ant colonies was concomitant with a reduction in plant pathogens.
- [Journal of Evolutionary Biology](#)
 - [Low levels of hybridization in two species of African driver ants](#)
 - [Conserved roles of Osiris genes in insect development, polymorphism and protection](#)
 - [Laboratory maintenance does not alter ecological and physiological patterns among species: a Drosophila case study](#)
- [MBE](#)
 - [Complex Relationships between Chromatin Accessibility, Sequence Divergence, and Gene Expression in Arabidopsis thaliana](#) “[...] regulatory sites with high levels of sequence variation and differential chromatin accessibility were the most likely to be associated with differential gene expression. Finally, and most surprising, we found that the vast majority of differentially accessible sites show no underlying sequence variation.”
 - [Sex-Chromosome Recombination in Common Frogs Brings Water to the Fountain-of-Youth](#) “: naturally occurring XX males show the same restriction of recombination as XY males (average map length ~2 cM), while XY females recombine as much as XX females (average map length ~150 cM).”
 - [Variable Rates of Simple Satellite Gains across the Drosophila Phylogeny](#)
 - **Advance Articles**
 - [Consequences of Asexuality in Natural Populations: Insights from Stick Insects](#)
 - [Neutral Theory and Phenotypic Evolution](#)
 - [Biology needs evolutionary software tools: Let's build them right](#)
 - [Neutral Theory in Cancer Cell Population Genetics](#)
- [Mol Ecol](#)
- [Myrmecological News](#)
- [Nature](#)
 - [Genome evolution across 1,011 Saccharomyces cerevisiae isolates](#). doi:10.1038/s41586-018-0030-5.
 - [Global warming transforms coral reef assemblages](#)
 - [High male sexual investment as a driver of extinction in fossil ostracods](#)
- [Nature Comms](#)
 - [Population size changes and selection drive patterns of parallel evolution in a host-virus system](#): Here, we examine the degree of parallel evolution shaped through eco-evolutionary dynamics in an algal host population coevolving with a virus. We find high degrees of parallelism at the level of population size changes (ecology) and at the phenotypic level between replicated populations. At the genomic level, we find evidence for parallelism, as the same large genomic region was duplicated in all replicated populations, but also substantial novel sequence divergence between replicates. These patterns of genome evolution can be explained by considering population size changes as an important driver of rapid evolution.

- [Manipulation of insulin signaling phenocopies evolution of a host-associated polyphenism](#): We present evidence that *J. haematoloma* wing polyphenism is adaptive in females, but maladaptive in males of the native host ecotype. This sexual conflict is partially resolved in the derived *Koelreuteria* ecotype, in which the reaction norm offset has evolved to make short-winged individuals more common. The frequency of morphs is determined nutritionally and associated with differences in the expression of genes encoding insulin signaling components. Manipulation of the insulin signaling pathway alters this reaction norm, phenocopying its evolution in natural populations.
- [Crab spiders impact floral-signal evolution indirectly through removal of florivores](#)
- [Spatial fidelity of workers predicts collective response to disturbance in a social insect](#)
- **[Nature Genetics](#)**
 - [Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits](#). The authors carry out a comprehensive comparison of tools used to estimate heritability based on SNP data. DOI: 10.1038/s41588-018-0108-x
 - [Single-cell RNA sequencing identifies celltype-specific cis-eQTLs and co-expression QTLs](#). The authors use single-cell RNA seq and co-expression module analyses to detect trans-regulatory element effects on phenotypes. DOI: 10.1038/s41588-018-0089-9
 - [Signatures of negative selection in the genetic architecture of human complex traits](#). The authors develop a new method to detect signatures of selection based on SNP data. DOI: 10.1038/s41588-018-0101-4
- **[Nature Methods](#)**
 - [Identifying the favored mutation in a positive selective sweep](#) (tool).
- **[Plos Biol](#)**
 - [Full disclosure: Genome assembly is still hard](#): Two recent papers highlight the fascinating comparative genomics of anhydrobiosis, the ability to withstand complete desiccation, in bdelloid rotifers and tardigrades. However, both groups had to openly deal with the significant difficulties of generating and interpreting short-read draft assemblies—especially challenging in microscopic species with high sequence polymorphism. These exemplars demonstrate the need to go beyond single draft-quality reference genomes to high-quality multiple species comparative genomics if we are to fully capture the value of genomics.
- **[Plos Comp Biol](#)**
 - [Divergent genome evolution caused by regional variation in DNA gain and loss between human and mouse](#): Our analysis provides a novel method for capturing the regional variation of lineage-specific DNA gain and loss events in their respective genomic contexts. To further understand this connection we used comparative genomics to identify genome-wide individual DNA gain and loss events in the human and mouse genomes. Focusing on the distribution of DNA gains and losses, relationships to important structural features and potential impact on biological processes, we found that in autosomes, DNA gains and losses both followed separate lineage-specific accumulation patterns. However, in both species chromosome X was particularly enriched for DNA gain, consistent with its high L1 retrotransposon content required for X inactivation. We found that DNA loss was associated with gene-rich open chromatin regions and DNA gain events with gene-poor closed chromatin regions
 - [Bayesian reconstruction of transmission within outbreaks using genomic variants](#): Here we propose a new Bayesian approach to transmission inference, BadTrIP (BAYesian epiDemiological TRansmission Inference from Polymorphisms), that explicitly models evolution of pathogen populations in an outbreak, transmission (including transmission bottlenecks), and sequencing error. BadTrIP enables the inference of host-to-host transmission from pathogen sequencing data and epidemiological data. By assuming that genomic variants are unlinked, our method does not require the computationally intensive and unreliable reconstruction of individual haplotypes. Using simulations we show that

BadTrIP is robust in most scenarios and can accurately infer transmission events by efficiently combining information from genetic and epidemiological sources; thanks to its realistic model of pathogen evolution and the inclusion of epidemiological data, BadTrIP is also more accurate than existing approaches. BadTrIP is distributed as an open source package (<https://bitbucket.org/nicofmay/badtrip>) for the phylogenetic software BEAST2.

- **[Plos Genet](#)**

- **[PNAS](#)**

- [Cooption of an appendage-patterning gene cassette in the head segmentation of arachnids](#)
RNAi-mediated knockdown of the spider *Sp6-9* ortholog resulted in diminution or loss of *Dll* expression and truncation of appendages, as well as loss of the two body segments specified by the early *Dll* function
- [Identification of a queen and king recognition pheromone in the subterranean termite *Reticulitermes flavipes*](#)
Identification of a royal-specific hydrocarbon—heneicosane—and several previously unreported and highly royal enriched long-chain alkanes. When applied to glass dummies, heneicosane elicited worker behavioral responses identical to those elicited by live termite queens.

- **[Proc B](#)**

- [Frequency dependence shapes the adaptive landscape of imperfect Batesian mimicry](#)
Experimental evidence examining *Adelpha* butterflies shows that imperfect Batesian mimicry is frequency-dependent on the relative abundance of models and mimics in natural populations.
- [Genome-wide single nucleotide polymorphism scan suggests adaptation to urbanization in an important pollinator, the red-tailed bumblebee \(*Bombus lapidarius* L.\)](#)
Using 110 314 single nucleotide polymorphisms generated by restriction-site-associated DNA sequencing, researchers investigated the genome-wide effects of urbanization on putative neutral and adaptive genomic diversity in a bumblebee.
- [Rapid comeback of males: evolution of male-killer suppression in a green lacewing population](#)
“We demonstrated here that lacewing hosts rapidly evolved suppressors against selfish reproductive manipulation by a *Spiroplasma* endosymbiont.”
- [Systematic conservation planning for intraspecific genetic diversity](#)
By examining freshwater fish species at the Garonne-Dordogne river basin in France researchers found that with the exception of private allelic richness, classical genetic diversity indices (allelic richness, genetic uniqueness) were poor predictors for identifying priority conservation areas.
- [Restoration and repair of Earth's damaged ecosystems](#)
“Active restoration did not result in faster or more complete recovery than simply ending the disturbances ecosystems face”

- **[Science](#)**

- [CRISPR-Cas12a target binding unleashes indiscriminate single-stranded DNase activity](#)
- [Ancient genomes revisit the ancestry of domestic and Przewalski's horses](#)
- [Quantitative analysis of population-scale family trees with millions of relatives](#)
- [Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding](#)

- **[TREE](#)**

- [Microplastics: No Small Problem for Filter-Feeding Megafauna](#)
Another horrible effects of all-pervasive microplastics
- [Towards the Integration of Niche and Network Theories](#)

- **[Trends in Genetics](#)**

- [Supervised Machine Learning for Population Genetics: A New Paradigm](#)

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

- BioRxiv
 - [RefSeq database growth influences the accuracy of k-mer-based species identification](#)
- Biological Journal

- [A dolichoderine ant that constructs traps to ambush prey collectively: convergent evolution with a myrmicine genus](#)
- Ecology & Evolution
 - [A land classification protocol for pollinator ecology research: An urbanization case study](#)
 - [Brain gene expression analyses in virgin and mated queens of fire ants reveal mating-independent and socially regulated changes](#)
- Genetics
- Heredity
- Aging
- Mol Cell Biol
- J Gerontol
- Methods in Ecology and Evolution
- Current Opinion in Insect Science
- Zookeys
 - [Colobopsis explodens sp. n., model species for studies on “exploding ants” \(Hymenoptera, Formicidae\), with biological notes and first illustrations of males of the Colobopsis cylindrica group](#)