

Community: Journal table of contents highlights

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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](#)**
 - [Evolution as a Coexistence Mechanism: Does Genetic Architecture Matter?](#)
 - [Multilevel Selection in the Filamentous Ascomycete *Neurospora tetrasperma*](#)
- **[Bioinformatics](#)**
 - [PERF: an exhaustive algorithm for ultra-fast and efficient identification of microsatellites from large DNA sequences](#)
 - [Visualization portal for genetic variation \(VizGVar\): a tool for interactive visualization of SNPs and somatic mutations in exons, genes and protein domains](#)
- **[Cell](#)**
 - [The Biology of CRISPR-Cas: Backward and Forward](#) review
 - [Analysis of Human Sequence Data Reveals Two Pulses of Archaic Denisovan Admixture](#)
- **[Current Biology](#)**
 - [How Honeybees Defy Gravity with Royal Jelly to Raise Queens](#): The female sex in honeybees (*Apis* spp.) comprises a reproductive queen and a sterile worker caste. Nurse bees feed all larvae progressively with a caste-specific food jelly until the prepupal stage. Only those larvae that are exclusively fed a large amount of royal jelly (RJ) develop into queens. RJ is a composite secretion of two specialized head glands: the mandibular glands, which produce mainly fatty acids, and the hypopharyngeal glands, which contribute proteins, primarily belonging to the major royal jelly protein (MRJP) family. Past research on RJ has focused on its nutritional function and overlooked its central role with regard to the orientation of the larva in the royal brood cell.
- **[eLife](#)**
 - [Individual crop loads provide local control for collective food intake in ant colonies](#)
- **[Evolution](#)**
 - [Sex differences in life span: Females homozygous for the X chromosome do not suffer the shorter life span predicted by the unguarded X hypothesis](#). doi:10.1111/evo.13434.
 - [The “unguarded-X” and the genetic architecture of lifespan: Inbreeding results in a potentially maladaptive sex-specific reduction of female lifespan in *Drosophila melanogaster*](#). doi:10.1111/evo.13426.
- **[GBE](#)**
 - [Divergent Evolutionary Trajectories of Two Young, Homomorphic, and Closely Related Sex Chromosome Systems](#) Derived sex chromosomes of one species, *X. laevis*, have a small region of suppressed recombination that surrounds the sex determining locus, and have remained this way for millions of years. In the other species, *X. borealis*, a younger sex chromosome system exists on a different pair of chromosomes, but the region of suppressed recombination surrounding an unidentified sex determining gene is vast, spanning almost half of the sex chromosomes. Differences between these sex chromosome systems are also apparent in the extent of nucleotide divergence between the sex chromosomes carried by females. Our analyses also indicate that in autosomes of both of these species,

recombination during oogenesis occurs more frequently and in different genomic locations than during spermatogenesis

- [Signatures of Long-Term Balancing Selection in Human Genomes](#) describe the *Non-central Deviation (NCD)*, a simple yet powerful statistic to detect long-term balancing selection (LTBS) that quantifies how close frequencies are to expectations under LTBS, and provides the basis for a neutrality test. *NCD* can be applied to a single locus or genomic data, and can be implemented considering only polymorphisms (*NCD1*) or also considering fixed differences with respect to an outgroup (*NCD2*) species
- **The DNA Methylation Landscape of Stickleback Reveals Patterns of Sex Chromosome Evolution and Effects of Environmental Salinity** compared genome-wide DNA methylation patterns between threespine stickleback males and females and between stickleback reared at different environmental salinities. Apparent hypermethylation of the younger evolutionary stratum of the stickleback X chromosome in females relative to males suggests a potential role of DNA methylation in the evolution of heteromorphic sex chromosomes. We also demonstrate that rearing salinity has genome-wide effects on DNA methylation levels
- [Patterns of Population Variation in Two Paleopolyploid Eudicot Lineages Suggest That Dosage-Based Selection on Homeologs Is Long-Lived](#) analyzed the At-α genome duplication that is the most recent polyploidy in the model plant *Arabidopsis thaliana* and a more recent hexaploidy shared by *Brassica* and its relatives. By comparing the strength and direction of the natural selection acting at the population and at the species level, we find evidence for continued intensified purifying selection acting on retained duplicates from both polyploidies even down to the present. The constraint observed in preferentially retained genes is not a result of the polyploidy event: the orthologs of such genes experience even stronger constraint in nonpolyploid outgroup genomes. In both the *Arabidopsis* and *Brassica* lineages, we further find evidence for segregating mildly deleterious variants, confirming that the population-level data uncover patterns not visible with between-species comparisons. Using
- [Intragenomic Conflict and Immune Tolerance: Do Selfish X-Linked Alleles Drive Skewed X Chromosome Inactivation?](#) Very cool idea. “proteins expressed from the primarily inactivated X-chromosome are incompletely tolerated, leading to an autoimmune response. This has potentially important implications for pregnancy, given that each targeted X-linked allele has a 50% chance of being inherited by a given fetus. If fetal expression of these targeted alleles triggers the maternal immune response, SXCI could lead to a higher rate of spontaneous abortion”
- **Influence of Effective Population Size on Genes under Varying Levels of Selection Pressure** For genes under high selective constraints, the ω estimated for the subspecies with small N_e (*M. m. musculus*) was three times higher than that observed for that with large N_e (*M. m. castaneus*). However, this difference was only 18% for genes under relaxed selective constraints. Also, for highly expressed genes, the ω of *M. m. musculus* was 2.1 times higher than that of *M.m. castaneus* and this difference was only 27% for genes with low expression levels. These results suggest that the effect of effective population size is more pronounced in genes under high purifying selection.
- **Genome Biol**
 - [SUPPA2: fast, accurate, and uncertainty-aware differential splicing analysis across multiple conditions](#)
 - [FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods](#) Combines BreakDancer [8], BreakSeq2 [9], cnMOPS [10], CNVnator [11], DELLY [12], GenomeSTRiP [13, 14]¹, Hydra [15], and LUMPY. But I don't know if it will run without a “truth set of SV calls from one or more samples”

- [Predicting double-strand DNA breaks using epigenome marks or DNA at kilobase resolution](#)
- [Quartz-Seq2: a high-throughput single-cell RNA-sequencing method that effectively uses limited sequence reads](#)
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- **[Genome Res](#)**
 - [SvABA: genome-wide detection of structural variants and indels by local assembly](#): SvABA is an efficient and accurate method for detecting SVs from short-read sequencing data using genome-wide local assembly with low memory and computing requirements. It was evaluated SvABA's performance on the NA12878 human genome and in simulated and real cancer genomes. SvABA demonstrates superior sensitivity and specificity across a large spectrum of SVs and substantially improves detection performance for variants in the 20–300 bp range, compared with existing methods.
 - [Whole-genome sequencing of Atacama skeleton shows novel mutations linked with dysplasia](#): Over a decade ago, the Atacama humanoid skeleton (Ata) was discovered in the Atacama region of Chile. The Ata specimen carried a strange phenotype—6-in stature, fewer than expected ribs, elongated cranium, and accelerated bone age. To determine the possible genetic drivers of the observed morphology, DNA from the specimen was subjected to whole-genome sequencing using the Illumina HiSeq platform with an average 11.5× coverage of 101-bp, paired-end reads. The detailed whole-genome analysis showed that Ata is a female of human origin, likely of Chilean descent, and its genome harbors mutations in genes (COL1A1, COL2A1, KMT2D, FLNB, ATR, TRIP11, PCNT) previously linked with diseases of small stature, rib anomalies, cranial malformations, premature joint fusion, and osteochondrodysplasia (also known as skeletal dysplasia).
 - [Enhancer RNA profiling predicts transcription factor activity](#) enhancer RNAs (eRNA) seem to be produced when enhancers become activated by association with a transcription factor - they can be used as an assay of enhancer function, but they are transient and thus very hard to sequence.
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- **[Insectes Sociaux](#)**
 - [Using T- and Y-mazes in myrmecology and elsewhere: a practical guide](#) Czaczkes V nice overview of risks and recommendations
 - [Preadaptation for asexual queen succession: queen tycho parthenogenesis produces neotenic queens in the termite Reticulitermes okinawanus](#) Matsuura lab
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- **[Journal of Evolutionary Biology](#)**
 - [Sex- antagonistic genes, XY recombination and feminized Y chromosomes](#)
 - [Linking genotype to phenotype in a changing ocean: inferring the genomic architecture of a blue mussel stress response with genome- wide association](#)
 - [Male–male aggression is unlikely to stabilize a poison frog polymorphism](#)
- **[MBE](#)**
 - [Multiple Factors Confounding Phylogenetic Detection of Selection on Codon Usage](#). The authors show how sensitive the CUYN test (used to detect codon use selection) is to natural levels of CpG mutation rates. They develop a new method to control for this bias. DOI: 10.1093/molbev/msy047
 - [The Birth and Death of Olfactory Receptor Gene Families in Mammalian Niche Adaptation](#). The authors reconstruct the species-specific evolutionary history of olfactory receptors across the mammalian phylogeny. They analysed >70,000 olfactory receptor genes. DOI: 10.1093/molbev/msy028
 - [BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics](#)
- **[Mol Ecol](#)**

- [Does genomic variation in a foundation species predict arthropod community structure in a riparian forest?](#) Yes! Significant correlations between genomic distance of alder trees and arthropod community structure were found.
- [The search for loci under selection: trends, biases and progress](#) An interesting review of the use, biases and trends of *FST* outlier analysis (OA) and environmental association analyses (EAA) with recommendations for improved design and analysis factors.
- [Myrmecological News](#)
 - [Sociometry of *Solenopsis geminata* \(Hymenoptera: Formicidae\) reveals variation in colony-level phenotypes in fire ants](#) Tribble, W., Shoemaker, D.D. & Gotzek, D. PDF available (Emeline)
- [Nature](#)
 - [Altruism in a volatile world.](#) The authors (Including S.Sumner) link through theoretical models environmental stochasticity and Hamilton's rule. They find that under specific circumstances, altruism can evolve even when seemingly counter productive for inclusive fitness. **COOL ARTICLE.** DOI: 10.1038/nature25965
 - [Dysregulation of expression correlates with rare-allele burden and fitness loss in maize.](#) The authors examine a large database for maize that includes tissue-specific expression data, a range of phenotypes and genomic data. They find that through domestication maize has been accumulating ancestral rare alleles that tend to be detrimental for maize production. DOI: 10.1038/nature25966
 - [The cis-regulatory dynamics of embryonic development at single-cell resolution.](#) *Drosophila* paper, the authors trace single-cell RNA expression through the early stages of development. Not hugely relevant to us but pretty cool. DOI:10.1038/nature25981
- [Nature Comms](#)
 - [Genomic evidence of speciation reversal in ravens](#)
 - [Circular DNA elements of chromosomal origin are common in healthy human somatic tissue](#) 20kb long. Contain genes. May be a mechanism to increase transcription? Transcription from eccDNAs suggests that eccDNAs reside in nuclei and recurrence of certain eccDNAs in several individuals implies DNA circularization hotspots.
 - [Convergent genomic signatures of domestication in sheep and goats](#)
 - [Elongator and codon bias regulate protein levels in mammalian peripheral neurons](#)
 - [Strong selection during the last millennium for African ancestry in the admixed population of Madagascar](#)
 - [Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese](#)
 - [Gene refashioning through innovative shifting of reading frames in mosses](#)
 - [Strong phenotypic plasticity limits potential for evolutionary responses to climate change](#)
 - [A genomics approach reveals insights into the importance of gene losses for mammalian adaptations](#) Very cool approach. gene loss is an evolutionary mechanism for adaptation that may be more widespread than previously anticipated.
 - [Random sequences rapidly evolve into de novo promoters](#) *E. coli* was under selection to reduce accidental promoters inside genes by avoiding promoter-like sequences.
- [Nature Genetics](#)
 - [Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection](#)
 - [Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals](#)
- [Nature Methods](#)
- [Plos Biol](#)

- [Population genetics and GWAS: A primer](#) Background info from George Grigson (Georgia Tech) which helps explain why thousands of variants of small effect contribute to complex traits.
- [Taxonomy based on science is necessary for global conservation](#) Response to [Garnet & Christidis 2017](#) which claims that taxonomy hampers conservation. The authors maintain that taxonomy underpins all biological research (not just conservation). They also propose a new framework for legislation that does not rely on the false premise that species are “fixed entities” as biodiversity & conservation assessments tend to imply.
- [Meta-research: Why research on research matters](#) A short overview of meta-research by John Ionnidis from Stanford, exploring its significance as an interdisciplinary research form.
- **[Plos Comp Biol](#)**
 - [Stoichiometric balance of protein copy numbers is measurable and functionally significant in a protein-protein interaction network for yeast endocytosis](#)
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- **[Plos Genet](#)**
- **[PNAS](#)**
 - [Rapid regulatory evolution of a nonrecombining autosome linked to divergent behavioral phenotypes](#) supergene and allele-specific expression
 - [Ants avoid superinfections by performing risk-adjusted sanitary care](#)
 - [Sign of selection on mutation rate modifiers depends on population size](#)
 - [Reintroductions of birds and mammals involve evolutionarily distinct species at the regional scale](#) This paper is more about the “psychology” of conservationists than conservation itself. The authors show that conservationists have mostly selected phylogenetically distinct species despite this not being a major aim of conservation (at least until recently)
 - [Regional pest suppression associated with widespread Bt maize adoption benefits vegetable growers](#) But evolution of resistance...
 - [Reconstructing a metazoan genetic pathway with transcriptome-wide epistasis measurements](#)
- **[Proc B](#)**
 - [Male spiders control offspring sex ratio through greater production of female-determining sperm](#): There is evidence that species with the chromosomal sex determination system can adjust sex ratio strategically. The results show the production of more female- than male-determining sperm cells as the likely mechanism underlying female-biased sex ratio in two social *Stegodyphus* spider species. This supports the hypothesis of sex ratio adjustment through a bias in gamete production in the heterogametic sex. The paper also show that five common genera of bacterial endosymbionts known to affect sex ratio are largely absent, ruling out that endosymbiont bacteria influence sex ratio bias in social spiders.
 - [Migratory behaviour predicts greater parasite diversity in ungulates](#): Long-distance animal movements can increase exposure to diverse parasites, but can also reduce infection risk through escape from contaminated habitats or culling of infected individuals. Using a comparative approach, the researchers analyse the parasite communities of 93 migratory, nomadic and resident ungulate species. They find that migrants have higher parasite species richness than residents or nomads, even after considering other factors known to influence parasite diversity, such as body size and host geographical range area.
 - [The ecology of insect–yeast relationships and its relevance to human industry](#): The researchers propose a ‘dispersal–encounter hypothesis’ whereby yeasts are dispersed by insects between ephemeral, spatially disparate sugar resources, and insects, in turn, obtain the benefits of an honest signal from yeasts for the sugar resources. They review the relationship between yeasts and insects through three main examples: social wasps, social bees and beetles, with some additional examples from fruit flies.
 - [Social enforcement depending on the stage of colony growth in an ant](#)

- **Science**
 - [A research behemoth is born in Britain](#)
 - [Diurnal transcriptome atlas of a primate across major neural and peripheral tissues](#)
 - [Proteoforms as the next proteomics currency](#)
 - [Evolution of alluvial mudrock forced by early land plants](#)
- **TREE**
 - **[Quantifying Temporal Genomic Erosion in Endangered Species](#)** Comparative analyses of genomic data from several endangered species suggest little concordance between genome-wide diversity and current population sizes. *They argue that comparing current to museum samples one should calculate “delta estimators” of “genomic erosion” that represent temporal changes in, for example, heterozygosity (Δh), inbreeding (ΔF), genetic load (ΔL), and genomic deletions (Δd).*
 - **[Finding Evolutionary Processes Hidden in Cryptic Species](#)**
 - We propose a conceptual framework that recognizes cryptic species based on their low levels of phenotypic (morphological) disparity relative to their degree of genetic differentiation and divergence times as compared with non-cryptic species.
 - **[Breaking Barriers: Causes, Consequences, and Experimental Utility of Human-Mediated Hybridization](#)** Different scenarios - can help understand introgression. Can we find evidence of adaptive human-mediated introgression?
 - [Rabbits and the Specious Origins of Domestication](#)
- **Trends in Genetics**
 - **[Supervised Machine Learning for Population Genetics: A New Paradigm](#)**: ML methods are powerful approaches that have revolutionized many fields, but their use in population genetics inference is only beginning. These methods are able to take advantage of high dimensional input – an important asset for population genetics inference – and are often more robust than other statistical approaches. The early applications of ML to population genetics demonstrate that they outperform traditional approaches. In this review it's introduce ML to a biology audience, discuss examples of their application to evolutionary and population genetics, and lay out future directions that we view as promising.

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

- BioRxiv
- Genetics
- Heredity
- Aging
- Mol Cell Biol
- J Gerontol
- Methods in Ecology and Evolution
- Current Opinion in Insect Science