

[Wurmlab](#)

Community: Journal table of contents highlights

****published between 1st and last day of **JANUARY****** (in print ***and*** early access). ****Finish it by February 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](#)
- [Bioinformatics](#)
- [Cell](#)
 - [Characterizing the Major Structural Variant Alleles of the Human Genome](#). The authors identify and annotate nearly 100,000 structural variants in the human genome. DOI: 10.1016/j.cell.2018.12.019
 - [Intrinsic Dynamics of a Human Gene Reveal the Basis of Expression Heterogeneity](#). The authors study in depth (live-cell RNA imaging + Hi-C) the regulatory network and expression variability of a known gene. They characterise gene expression variability and link it to upstream regulation. DOI: 10.1016/j.cell.2018.11.026
- [Current Biology](#)
 - [The genomic footprints of the fall and recovery of the crested ibis \(*Nipponia nippon*\)](#)
- [eLife](#)
- [Evolution](#)
 - [Meiotic drive shapes rates of karyotype evolution in mammals](#). The authors analyse karyotypes from over 1000 mammals and find that taxa with homogeneously shaped chromosomes tend to have more stable chromosome numbers. They hypothesize that meiotic drive may be responsible for this pattern. DOI: 10.1111/evo.13682
 - [Adaptation, chance, and history in experimental evolution reversals to unicellularity](#)
 - [Migration promotes mutator alleles in subdivided populations](#). The authors show through *in silico* and *in vitro* experiments with yeast that mutator alleles (variants that increase mutation rate) are more likely to get fixed in highly structured metapopulations with high migration rates. DOI:10.1111/evo.13681
- [GBE](#)
- [Genome Biol](#)
 - [The site-specific amino acid preferences of homologous proteins depend on sequence divergence](#)
 - [Where is genomics going next?](#)
 - [Accurate prediction of cell type-specific transcription factor binding](#)
- [Genome Res](#)
 - [A quantitative framework for characterizing the evolutionary history of mammalian gene expression](#)
 - [Minerva: an alignment- and reference-free approach to deconvolve Linked-Reads for metagenomics](#)
 - [Nucleosome remodeling at origins of global genome–nucleotide excision repair occurs at the boundaries of higher-order chromatin structure](#)
- [Insectes Sociaux](#)
 - [Intraspecific variation in colony founding behavior and social organization in the honey ant *Myrmecocystus mendax*](#). The authors found that mature colonies from a population of honeypot ants (*Myrmecocystus mendax*) in central Arizona were polygynous, while colonies

sampled in southeastern Arizona were monogynous. In the laboratory, foundresses from the central population showed cooperative behavior, while foundresses from the southeastern population did not.

- [Rhopalomastix is only the second ant genus known to live with armoured scale insects \(Diaspididae\)](#)

- [Journal of Evolutionary Biology](#)

- [An evaluation of the methods to estimate effective population size from measures of linkage disequilibrium](#)
- [Genome size variation and species diversity in salamanders](#)

- [MBE](#)

- [A single SNP turns a social honey bee \(*Apis mellifera*\) worker into a selfish parasite](#)
- [On the Regulatory Evolution of New Genes Throughout Their Life History](#)
- [Detection of Shared Balancing Selection in the Absence of Trans-Species Polymorphism](#)

- [Mol Ecol](#)

- [The specificity of *Burkholderia* symbionts in the social amoeba farming symbiosis: prevalence, species, genetic and phenotypic diversity](#)

- [Myrmecological News](#)

- [Nature](#)

- [Introns are mediators of cell response to starvation](#)

- [Nature Comms](#)

- [Sex peptide receptor-regulated polyandry modulates the balance of pre- and post-copulatory sexual selection in *Drosophila*](#)
- [The evolution of sex determination associated with a chromosomal inversion](#)

- [Nature Genetics](#)

- [Fast and accurate genomic analyses using genome graphs](#)
- [An evolutionary framework for measuring epigenomic information and estimating cell-type-specific fitness consequences](#)
- [A map of constrained coding regions in the human genome](#)

- [Nature Methods](#)

- [Plos Biol](#)

- [Drosophila melanogaster cloak their eggs with pheromones, which prevents cannibalism](#)
- [Bio-On-Magnetic-Beads \(BOMB\): Open platform for high-throughput nucleic acid extraction and manipulation](#)
- [An opposing function of paralogs in balancing developmental synapse maturation](#)
- [Evidence that nonsignificant results are sometimes preferred: Reverse *P*-hacking or selective reporting?](#)
- [Developing a modern data workflow for regularly updated data](#)

- [Plos Comp Biol](#)

- [Plos Genet](#)

- [Intronic CNVs and gene expression variation in human populations](#). The authors explore the hypothesis that intron length affects gene expression, even in trans. They find extensive evidence for this in a human genomic DNA dataset. DOI: 10.1371/journal.pgen.1007902
- [Allele-specific RNA imaging shows that allelic imbalances can arise in tissues through transcriptional bursting](#)
- [Integrating predicted transcriptome from multiple tissues improves association detection](#)

- [PNAS](#)

- [Conserved transcriptomic profiles underpin monogamy across vertebrates](#)

- [Proc B](#)

- [Leaf-cutter ants engineer large nitrous oxide hot spots in tropical forests](#)
- [Pathogen shifts in a honeybee predator following the arrival of the *Varroa* mite](#)

- [Insecticide resistance genes affect *Culex quinquefasciatus* vector competence for West Nile virus](#)
- [A selective fungal transport organ \(mycangium\) maintains coarse phylogenetic congruence between fungus-farming ambrosia beetles and their symbionts](#)
- [Phenotypic evolution shaped by current enzyme function in the bioluminescent courtship signals of sea fireflies](#)

- [Science](#)

- [Linking a mutation to survival in wild mice](#)
- [A sleep-inducing gene, *nemuri*, links sleep and immune function in *Drosophila*](#)
- [Agriculturally dominated landscapes reduce bee phylogenetic diversity and pollination services](#)
- [Termites mitigate the effects of drought in tropical rainforest](#)

- [TREE](#)

- [Environmentally Mediated Social Dilemmas](#)
- [Evolution in the light of fitness landscape theory](#)

- [Trends in Genetics](#)

- [Translation of small open reading frames: Roles in regulation and evolutionary innovation](#)

- Other papers/tools that you feel someone should have seen:

- Ann Rev of Entomology
 - [The ecology of collective behavior in ants](#)
 - [Molecular evolution of the major arthropod chemoreceptor gene families](#)
 - [Epigenetics in insects: Genome regulation and the generation of phenotypic diversity](#)
 - [Molecular mechanisms of wing polymorphism in insects](#)
 - [Bee viruses: Ecology, pathogenicity, and impacts](#)
- BioRxiv
 - [Transcriptomic basis and evolution of the ant social interactome](#)
 - [Methylation and gene expression differences between reproductive castes of bumblebee workers](#)
 - [Host evolutionary history predicts virus prevalence across bumblebee species](#)
 - [Müllerian mimicry in bumble bees is a transient continuum](#)
 - [Genomic analyses of sibling honey bee ectoparasitic mite species show divergent strategies of adaptation](#)
 - [The spread of resistance to imidacloprid is restricted by thermotolerance in natural populations of *Drosophila melanogaster*](#)
 - [Incipient species or social polymorphism? Diversity in the desert ant *Cataglyphis*](#)
 - [Population genomics perspectives on convergent adaptation](#)
 - [The variability of expression of many genes and most functional pathways is observed to increase with age in brain transcriptome data](#)
 - [Genes lost during the transition from land to water in cetaceans highlight genomic changes involved in aquatic adaptations](#)

- [Integrating Hi-C links with assembly graphs for chromosome-scale assembly](#)
- [Fast and accurate reference-guided scaffolding of draft genomes](#)
- [A comprehensive evaluation of long read error correction methods](#)
- [ELECTOR: Evaluator for long reads correction methods](#)
- [NanoR: An user-friendly R package to analyze and compare nanopore sequencing data](#)
- [Detecting convergent adaptive amino acid evolution](#)
- [Memory-driven computing accelerates genomic data processing](#)
- [GToTree: a user-friendly workflow for phylogenomics](#)
- [BEHST: genomic set enrichment analysis enhanced through integration of chromatin long-range interactions](#)
- [Fast and accurate long-read assembly with wtdbg2](#) Potential bioinformatics breakthrough. A new long-read assembler developed by Heng Li. 100 times faster for human genome assembly compared to Falcon, achieving similar contiguity and accuracy. For assembly of the *D. melanogaster* genome, Canu's CPU time was 16 hours, while wtdbg2's CPU time was 26 minutes.
- BMC Evol Biol
 - [Diversity and evolution of the transposable element repertoire in arthropods with particular reference to insects](#)
 - [Decrease of gene expression diversity during domestication of animals and plants](#)
 - [Supercolonial structure of invasive populations of the tawny crazy ant *Nylanderia fulva* in the US](#)
 - [Improved inference of site-specific positive selection under a generalized parametric codon model when there are multinucleotide mutations and multiple nonsynonymous rates](#)
- BMC Bioinformatics
 - [BPG: Seamless, automated and interactive visualization of scientific data](#)
- BMC Genomics
 - [Genomic changes associated with adaptation to arid environments in cactophilic *Drosophila* species](#)
 - [Stability of methods for differential expression analysis of RNA-seq data](#)
 - [Evaluation of strategies for the assembly of diverse bacterial genomes using MinION long-read sequencing](#)
 - [Sequence and structural properties of circular RNAs in the brain of nurse and forager honeybees \(*Apis mellifera*\)](#)
- Behav Ecol

- [Horizontal partner exchange does not preclude stable mutualism in fungus-growing ants](#)
- Ecol Entomol
 - [Assessing the density of honey bee colonies at ecosystem scales](#)
- Curr Zool
 - [Role of conspecifics and personal experience on behavioural avoidance of contaminated flowers by bumblebees](#)
- G3: Genes, Genomes, Genetics
 - [Draft genome assembly and population genetics of an agricultural pollinator, the solitary alkali bee \(Halictidae: *Nomia melanderi*\)](#)
- Genetics
- Genome Biol Evol
 - [Evolutionary potential of *cis*-regulatory mutations to cause rapid changes in transcription factor binding](#)
- Sci Data
 - [De novo transcriptome assembly and its annotation for the black ant *Formica fusca* at the larval stage](#)
- Life Sci Alliance
 - [A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs](#)
- Methods Ecol Evol
 - [Challenges and solutions for analysing dual RNA-seq data for non-model host-pathogen systems](#)
- Mol Ecol Res
 - [Minor allele frequency thresholds strongly affect population structure inference with genomic datasets](#)
- Nat Biotech
 - [Errors in long-read assemblies can critically affect protein prediction](#) The authors evaluated how indel errors affect gene predictions in three long-read human genome assemblies. The three assemblies were generated using different technologies (PacBio and ONT), and presumably all had accuracy (99.7-99.8%). Here the authors show, however, that the three assemblies differ considerably in the amount of indels disrupting protein-coding gene models. The most errors occurred in a PacBio-only assembly (Pendleton, M. et al. 2015. Nat. Methods 12), with nearly 9,000 protein-coding gene models disrupted by indels. In contrast, a different PacBio-only assembly (Koren, S. et al. 2017. Genome Res. 27) included about 400 protein coding genes with indel errors. The high quality of the Koren et al. assembly is likely the result of various factors: longer and more accurate reads (P6-C4 chemistry), high coverage (142X), two rounds of Quiver polishing, and the use of haploid cells.

- Nat Ecol Evol
 - [A systems approach reveals urban pollinator hotspots and conservation opportunities](#)
 - [Direct estimation of mutations in great apes reconciles phylogenetic dating](#)
- Nat Protocols
 - [Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap](#)
- Oecologia
 - [Habitats shape taxonomic and functional composition of Neotropical ant assemblages](#)
- Syst Biol
 - [Convergent evolution of the army ant syndrome and congruence in big-data phylogenetics](#)
- Heredity
- Aging
- Mol Cell Biol
- J Gerontol
- Curr Opin Insect Sci
 - [Plant chemical mediation of ant behavior](#)
 - [Detoxifying enzyme complements and host use phenotypes in 160 insect species](#)
 - [Mining insect genomes for functionally affiliated genes](#)
 - [Comparative genomics and transcriptomics of host–pathogen interactions in insects: evolutionary insights and future directions](#)
 - [Sex loss in insects: causes of asexuality and consequences for genomes](#)