

The 'slog through it together' bioinformatics reading group

Purpose: to create a welcoming space to read and critique current papers in 'omic biology.

Goals: to understand: 1) the analytical pipelines used and why, 2) the validation techniques used and why, 3) their interpretation of results, and 4) how each figure serves the manuscript as a whole.

TOPICS:

Part 1: Genomes shedding light on interesting questions

Week 1- Genome evolution, homeology, ploidy in the African clawed frog

(Session et al 2016, doi:10.1038/nature19840)

Week 2- How to make an oddly shaped fish Pt. 1—the seahorse genome

(Lin et al 2016, doi:10.1038/nature20595)

Week 3- How to make an oddly shaped fish Pt. 2—the flatfish genome

(Shao et al 2017, doi:10.1038/ng.3732)

Week 4- Asgard Archaea, the origins of 'eukaryotic' genes, and early complexity

(Zaremba-Niedzwiedzka et al 2017, doi:10.1038/nature21031)

Week 5- Synteny, amniotes, homology in the painted turtle

(Badenhorst et al 2015, doi:10.1093/gbe/evv119)

Week 6- Phylogenomics and challenging relationships on the tree of life

(Arcila et al 2017, doi: 10.1038/s41559-016-0020)

Part 2: Genome variation, lessons from humans

Week 7- Tissue-specific mutation variability in humans

(Blokzijl et al 2016, doi:10.1038/nature19768)

Week 8- Variation in protein-coding genes, a human case study

(Lek et al 2016, doi:10.1038/nature19057)

Week 9- Back to basics—Tajima and population structure

(Tajima 1983, *Genetics* 105:437–460)

Part 3: Gene flow and adaptation in genomics

Week 10- Pinpointing historical admixture in non-human primates

(de Manuel et al 2016, doi: 10.1126/science.aag2602)

Week 11- Local adaptation, review and directions

(Hoban and Kelley et al 2017, DOI: 10.1086/688018)

The 'slog through it together' bioinformatics reading group

Week 12- Inferring historical demography: PSMC vs MSMC vs SMC++

(Li and Durban 2011, doi:10.1038/nature10231; Schiffels and Durbin 2014, doi:10.1038/ng.3015; Terhorst et al 2017, doi:10.1038/ng.3748)

Part 4: Progress in genomic/transcriptomic methods

Week 13- Statistical dispersion, log fold changes and algorithms for RNAseq analysis

(Love et al 2014, doi: 10.1186/s13059-014-0550-8; Williams et al 2017, doi: 10.1186/s12859-016-1457-z)

Week 14- Hi-C: what can it do and what analytical pipelines exist?

(Lazaris et al 2017, doi: 10.1186/s12864-016-3387-6)

Week 15- Read mapping with highly polymorphic data

(Sedlazeck et al 2014, doi: 10.1093/bioinformatics/btt468) –not so new, but a quick read