BIOINFORMATIC GENOTYPE-ENRIVONMENT REPEATABILITY **PIPELINE ASSOCIATIONS - GEA TESTING** Fetch climate data for all sampling Orthology assignment Data cleaning & among all ref genomes locations and calculate clim_change trimming worldclim v2.1, 2.5 minutes OrthoFinder2 fastp WGS/Capture data - calculate per-Alignment to reference Filter orthogroups (OG) site allele frequencies max paralogs = 10 genomes **VCFtools** min species = 20 bwa-mem Association between allele Merge OG and per-Data metrics & duplication species, per-gene GEA identification frequencies & climate variation ep-values Picard Tools Kendall's Tau Correlations Test each OG-climate Convert per-SNP pvalues to uniform ep-value vector for Indel realignment empirical pvalues (ep-values) repeatability, length = 20-25 **GATK** qvalue::empPvals() PicMin FDR correct PicMin p-values Genotype Likelihoods Combine per-SNP GEA to per-gene across tested OG (N - 8470) BCFtools - mpileup Weighted-Z Association (WZA) p.adjust() Poolseq WGS/Capture Correct for varying SNP count Quantify interactions among Genotypes Genotypes repeatable OG among genes **BCFtools - Call** Varscan Spline of WZA mean & sd ~ SNP N STRING-db Quality filtering Parametric per-gene p-values Quantify OG pleiotropy GATK & VCFtools converted to uniform ep-values Specificity - Expression Atlas Coexpression - ATTED-II qvalue::empPvals() Combine ep-values for genes with Quantify OG duplications >1 dataset per species OrthoFinder2 Fisher's combined p-value