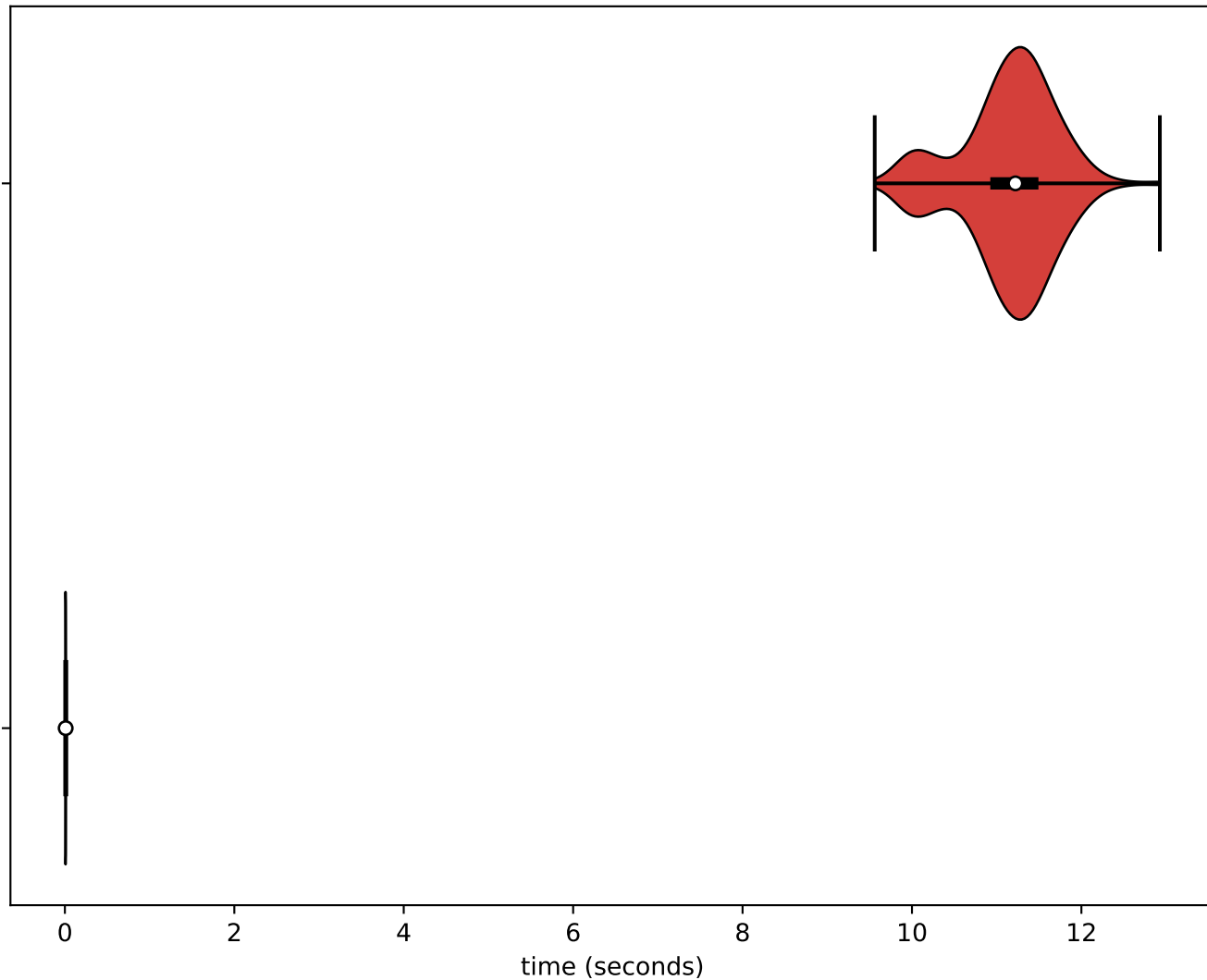


Run time.

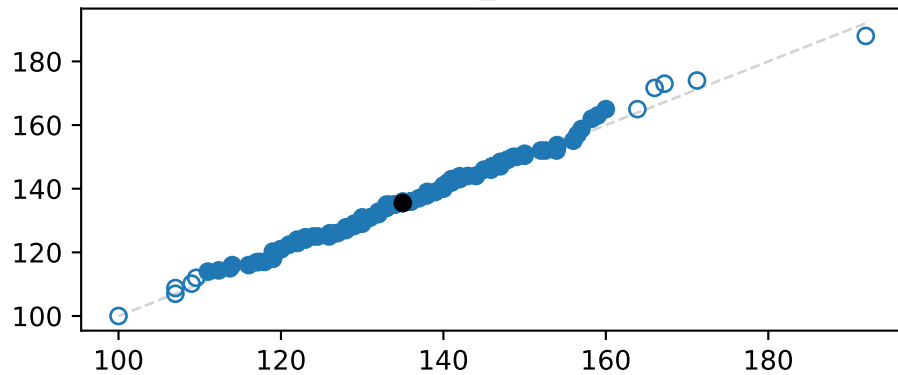
onepop_bottleneck_slim2
Single population with bottleneck and recovery.
Burn-in is disabled.

onepop_bottleneck_msprime1
Single population with bottleneck and recovery.

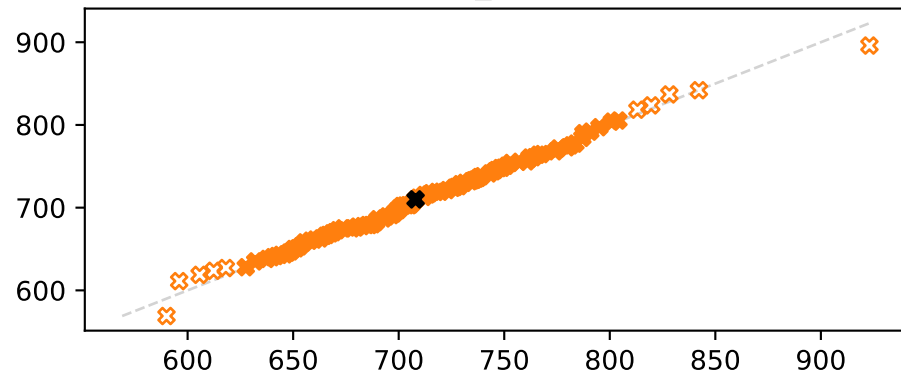


ts_properties:
TreeSequence properties.

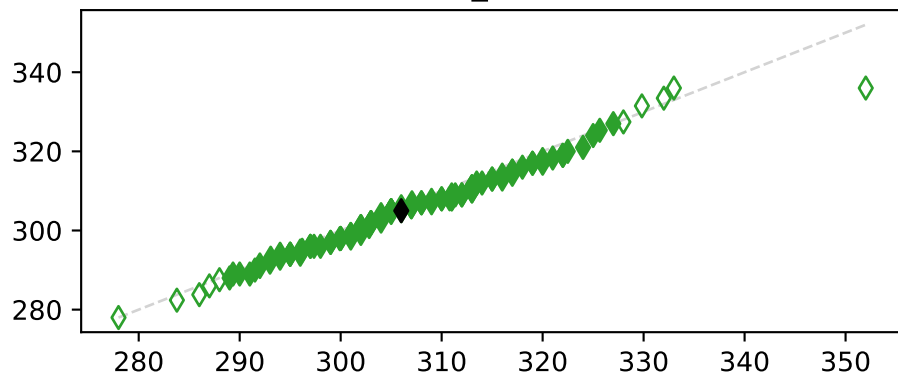
num_trees



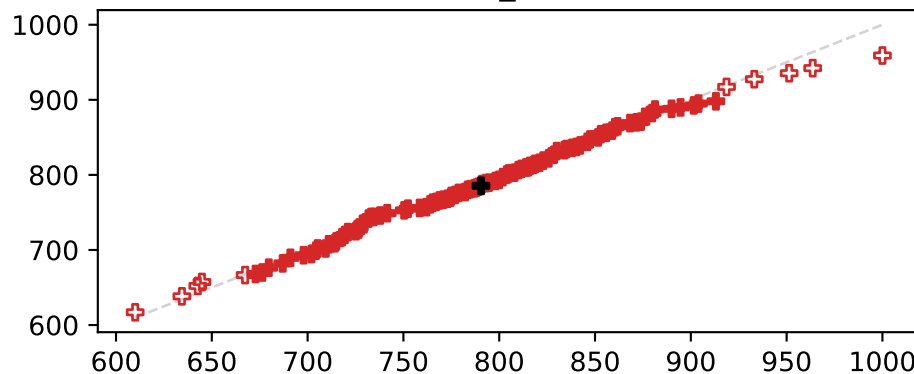
num_edges



num_nodes



num_sites



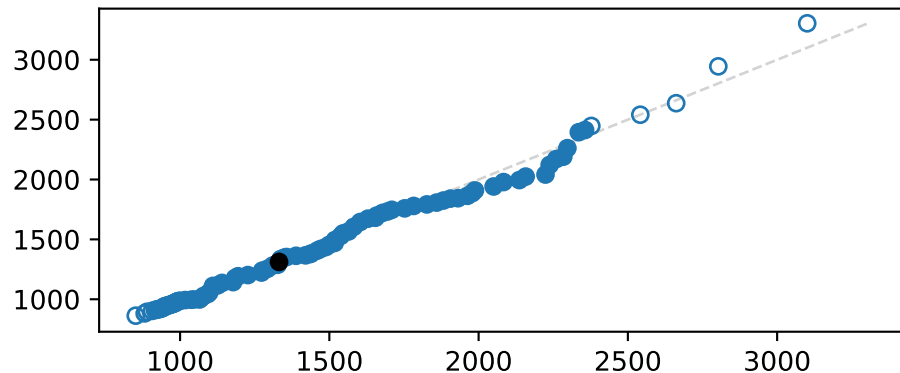
onepop_bottleneck_msprime1

onepop_bottleneck_slim2

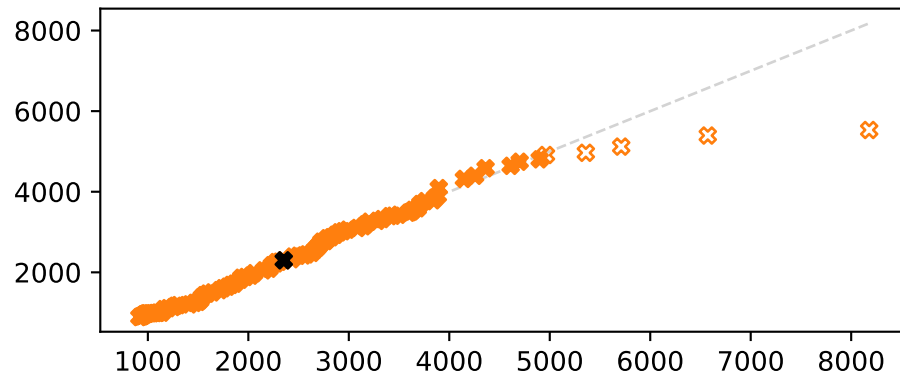
tmrca:

Time to most recent common ancestor of sample, aka tree height.

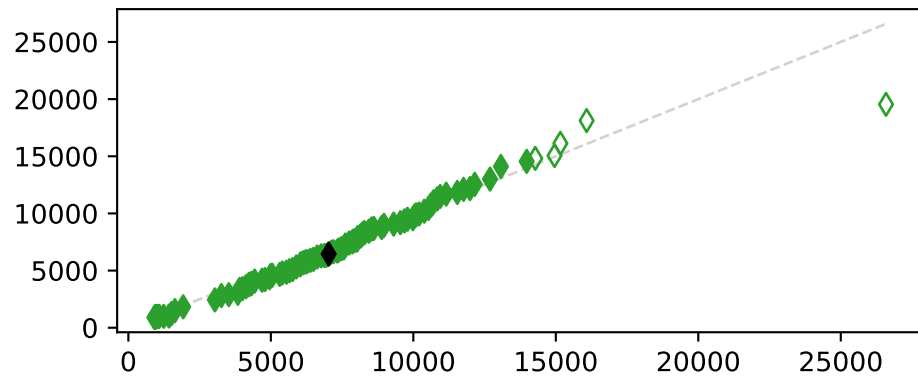
min(tmrca)



median(tmrca)



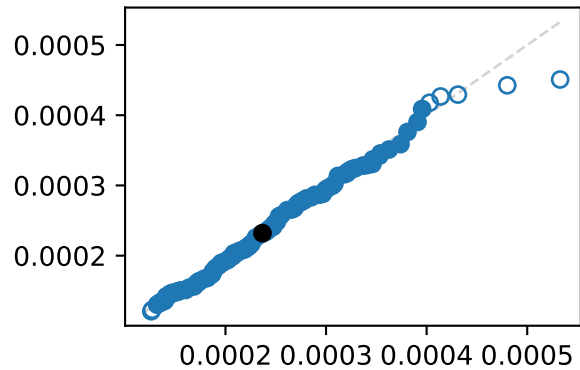
max(tmrca)



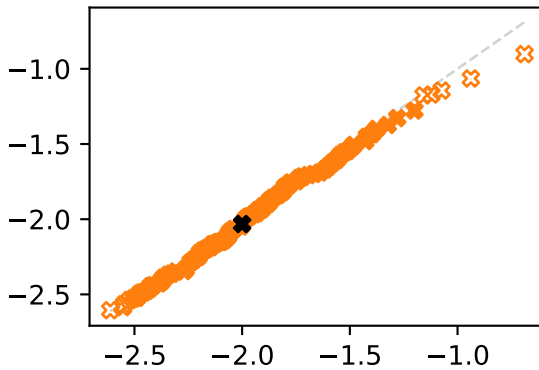
onepop_bottleneck_msprime1

pooled_pop_stats:
Population statistics, with samples pooled from all populations.

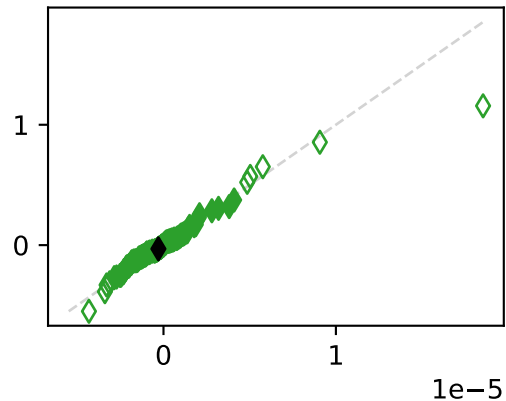
diversity



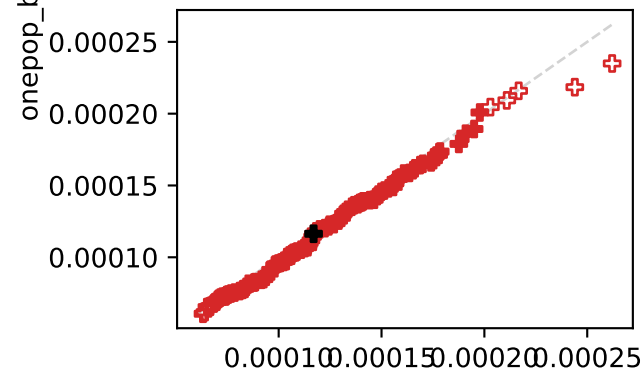
Tajimas_D



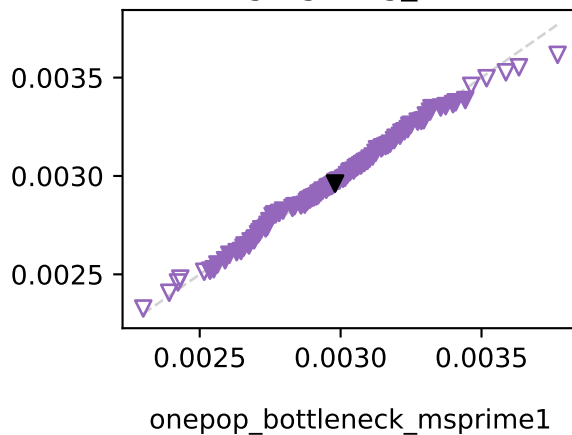
f_2



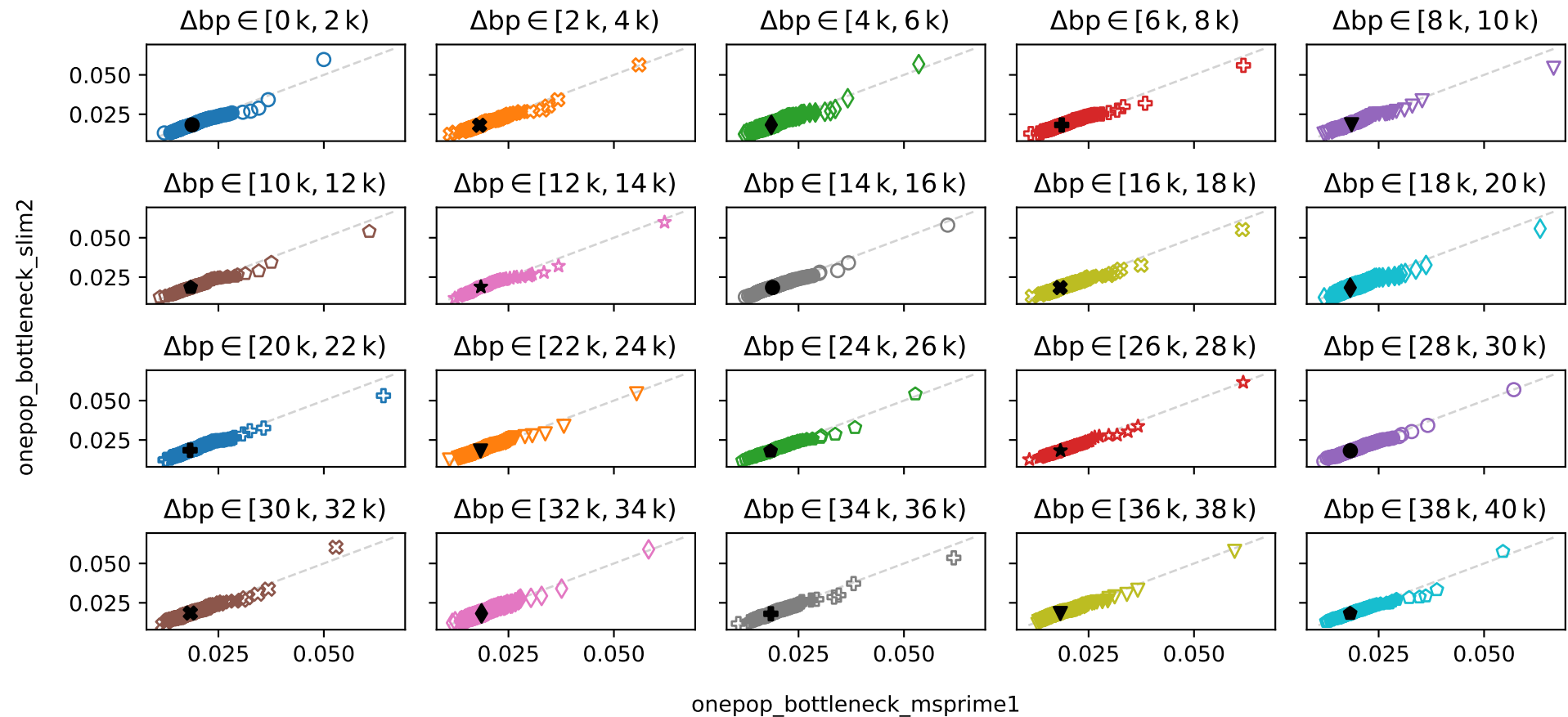
Y_2



segregating_sites



linkage disequilibrium:
 R^2 as a function of site-separation distance, for `bins` bins up to a
site-separation distance of `span` bp.



allele_frequency_spectrum:
Allele frequency spectrum for `bins` allele frequency bins.
Values are log(1+counts) for each bin.

