

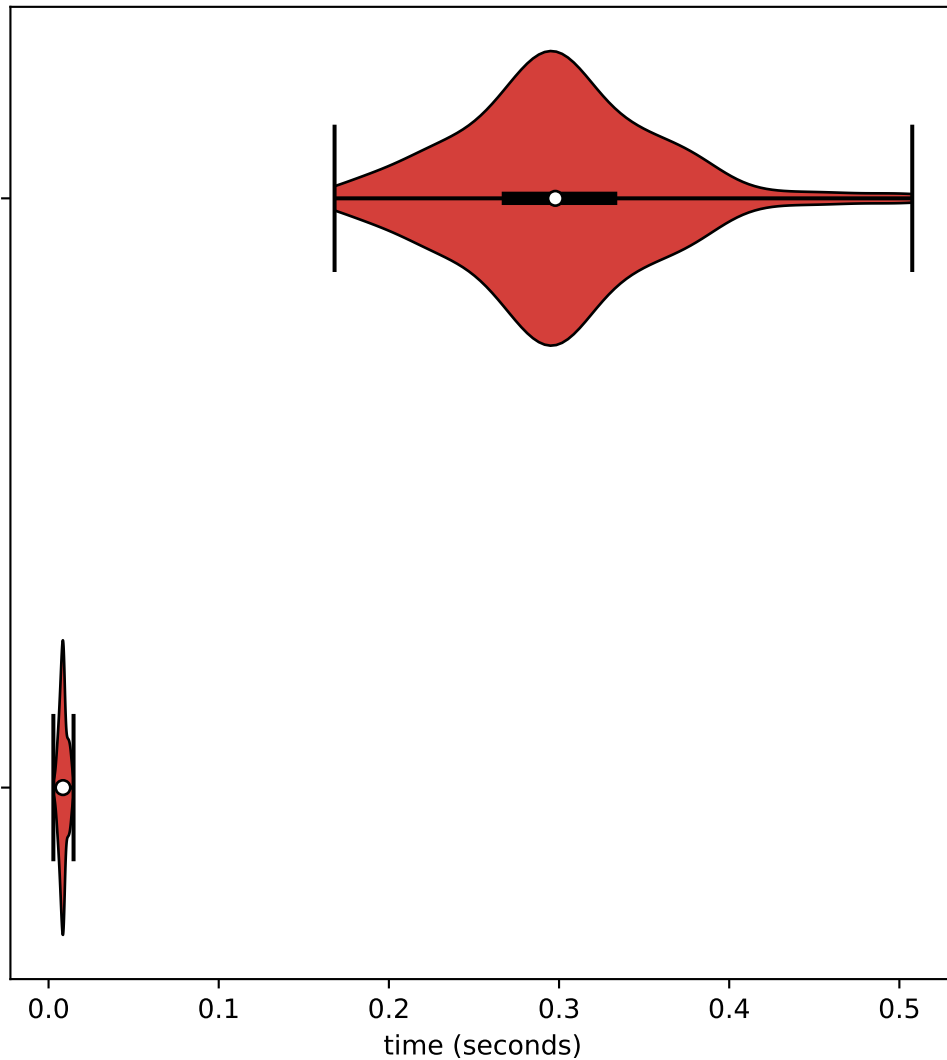
Run time.

onepop_constantN_slim2

Single population with constant population size.
Burn-in is disabled and since there are no demographic_events, SLiM exits immediately. Tree sequences are constructed via recapitation.

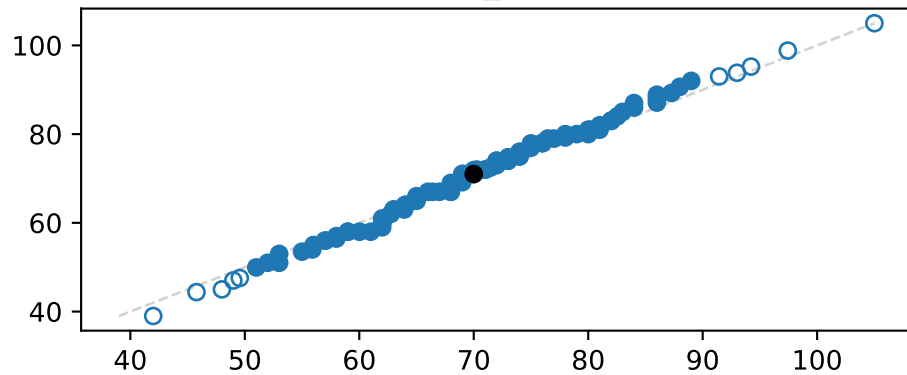
onepop_constantN_msprime1

Single population with constant population size.

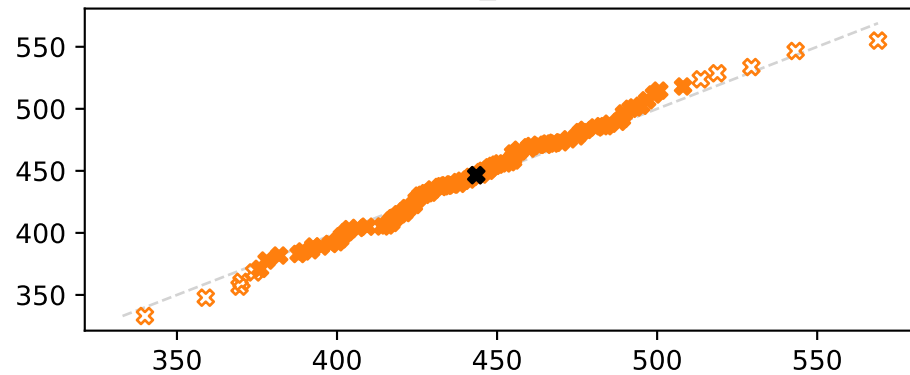


ts_properties:
TreeSequence properties.

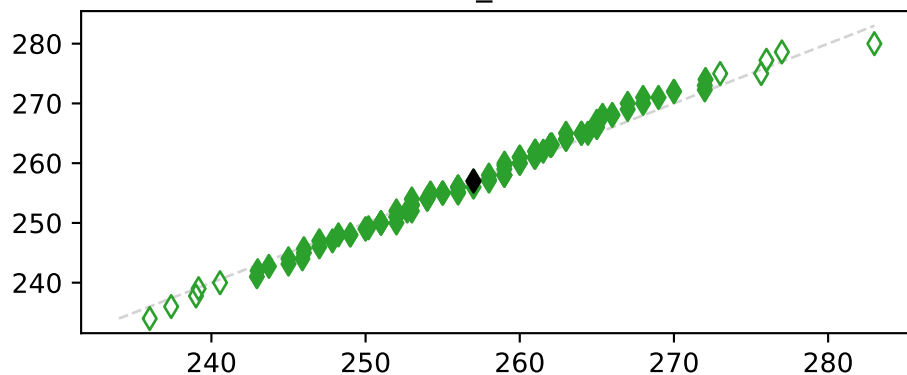
num_trees



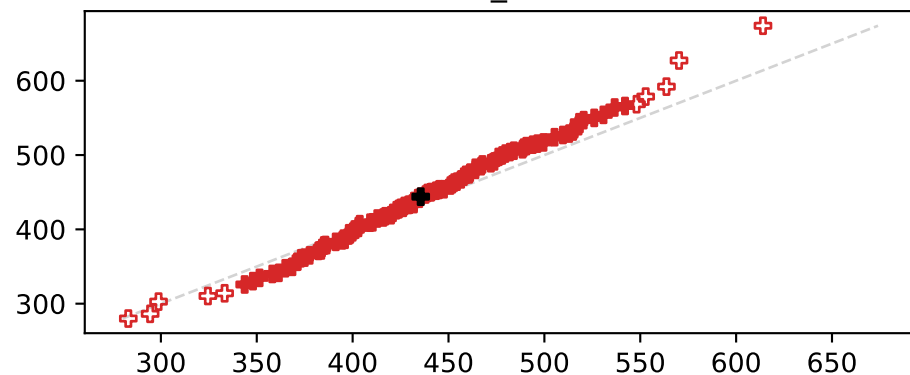
num_edges



num_nodes



num_sites

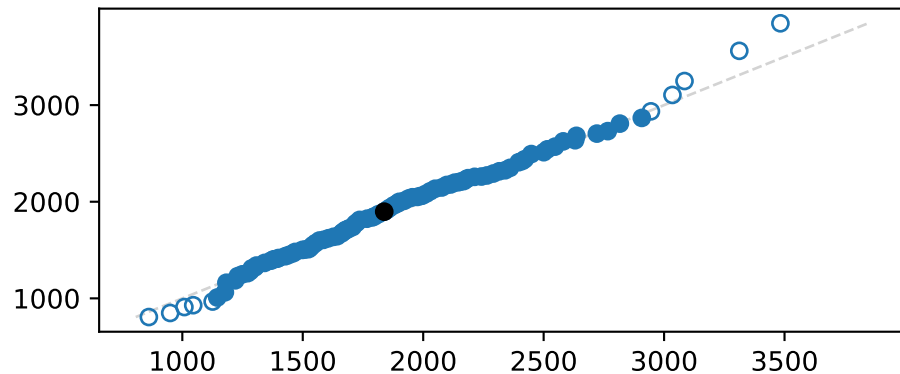


onepop_constantN_msprime1

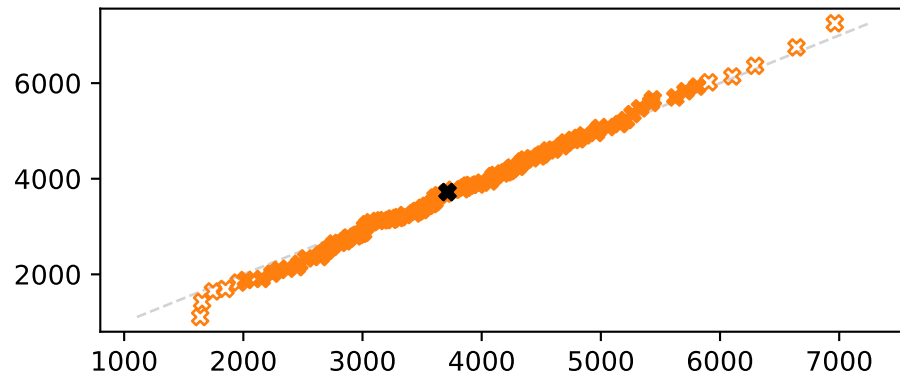
tmrca:

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

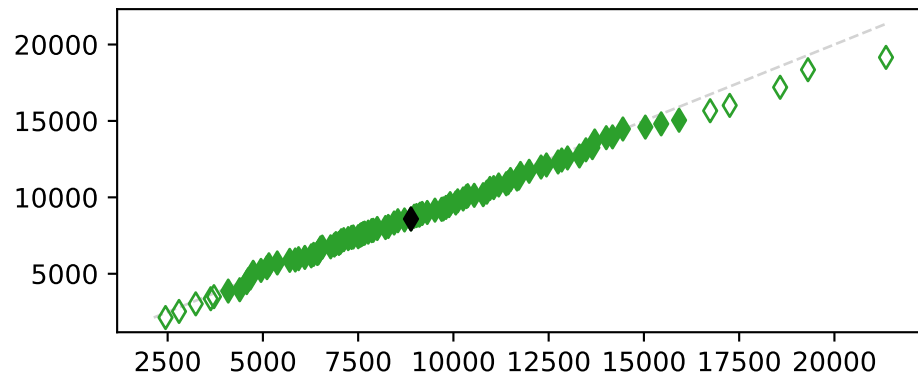
min(tmrca)



median(tmrca)

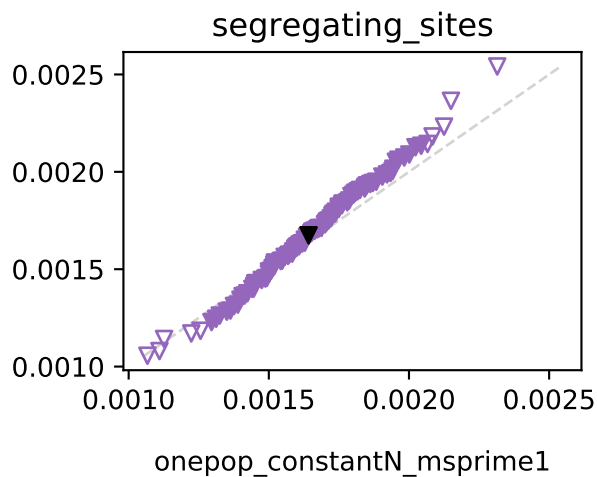
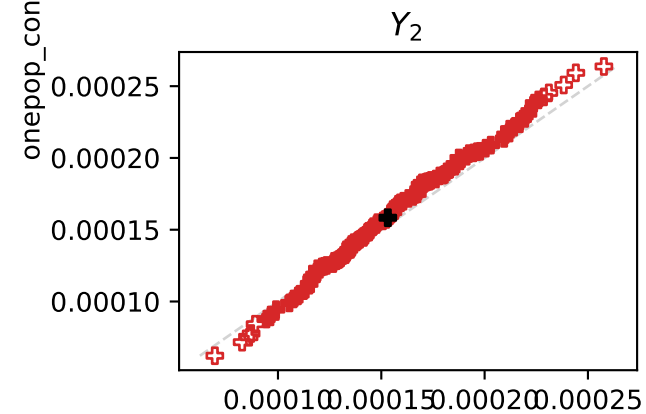
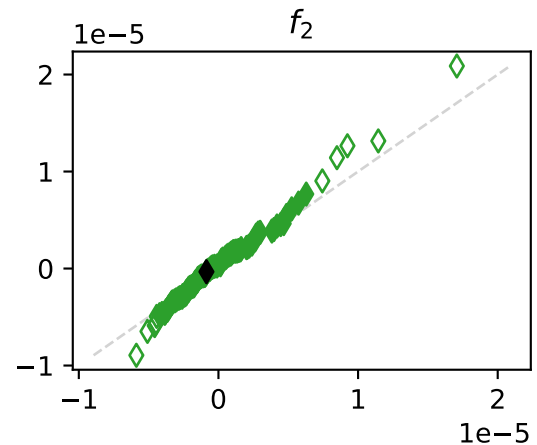
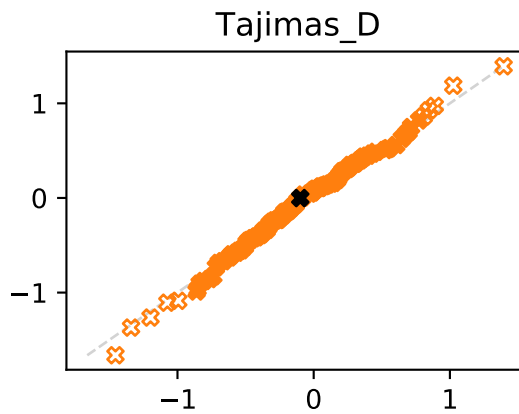
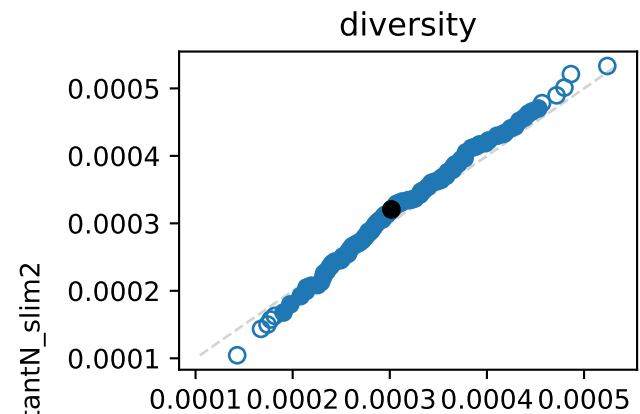


max(tmrca)

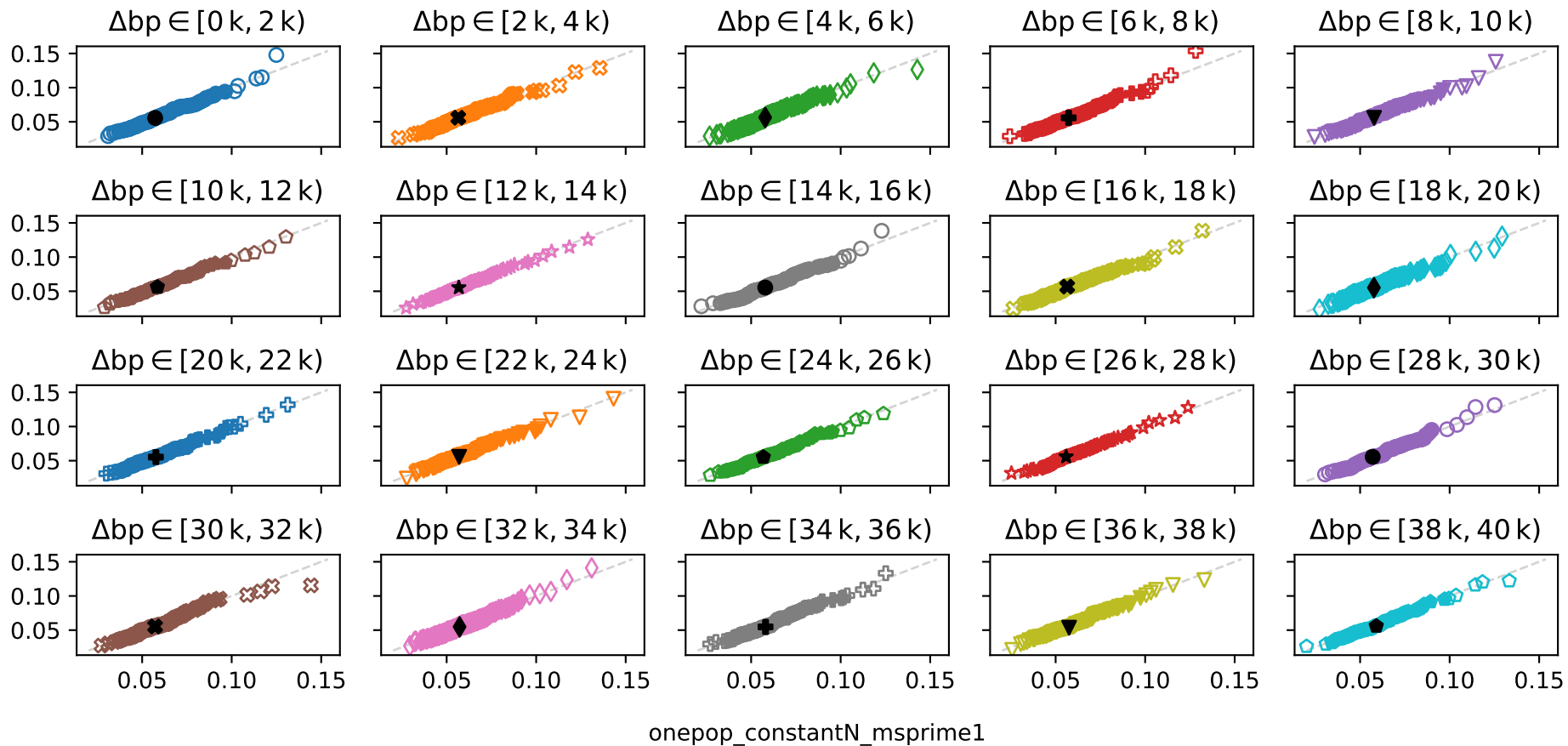


onepop_constantN_msprime1

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



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.

onepop_constantN_slim2

