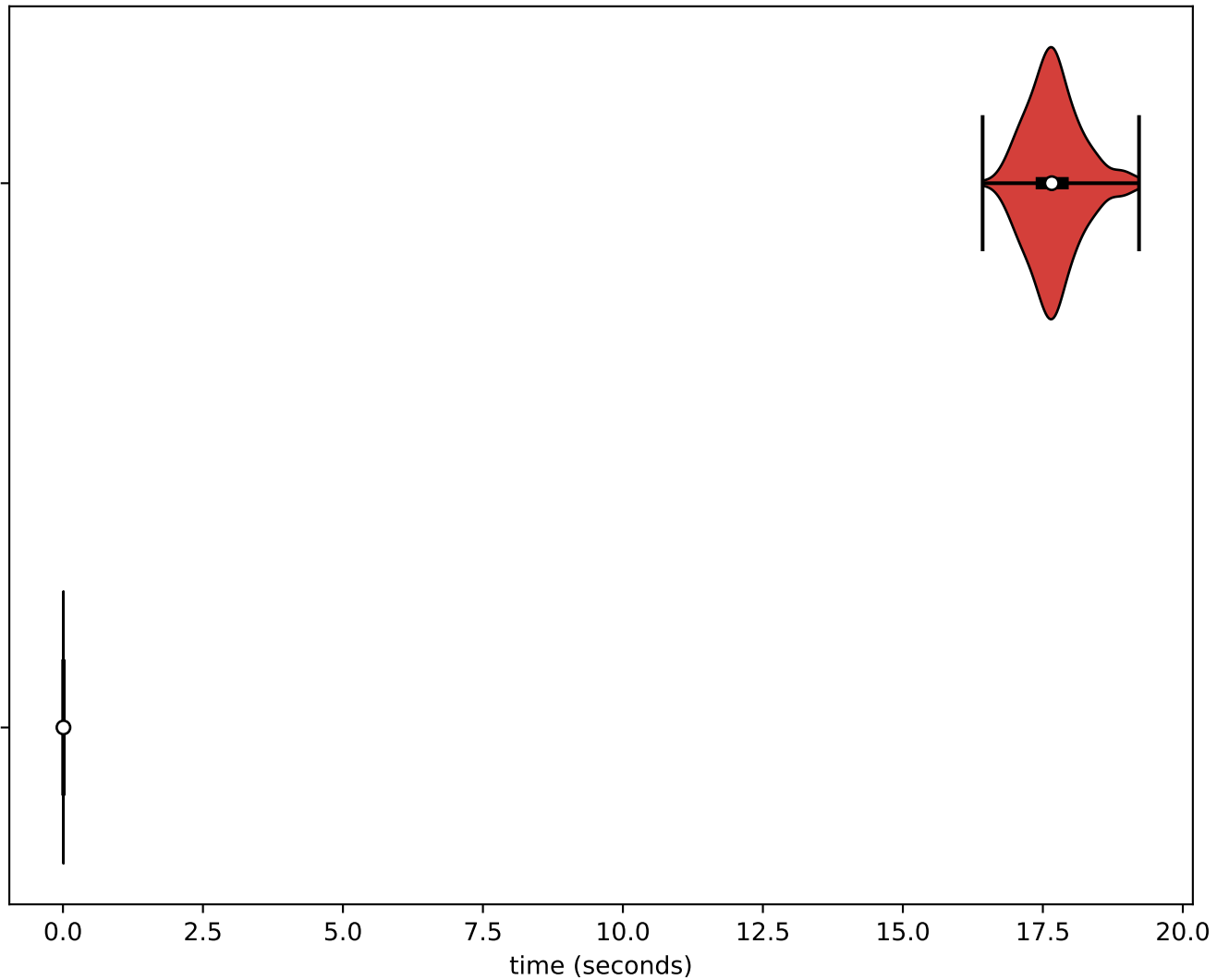


# Run time.

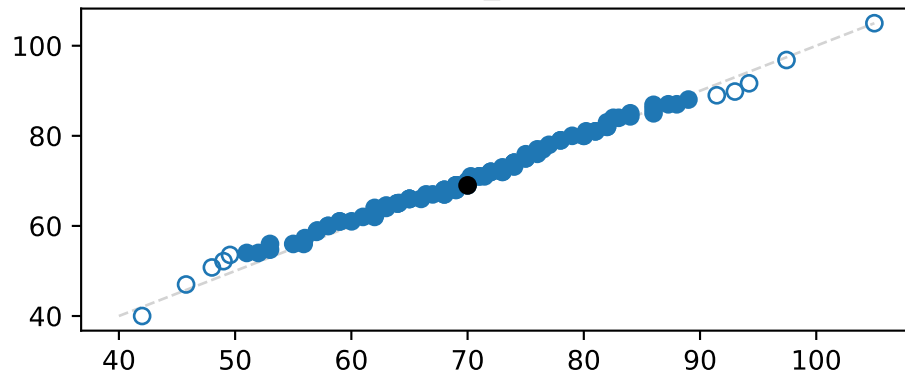
onpop\_constantN\_slim1  
Single population with constant population size.

onpop\_constantN\_msprime1  
Single population with constant population size.

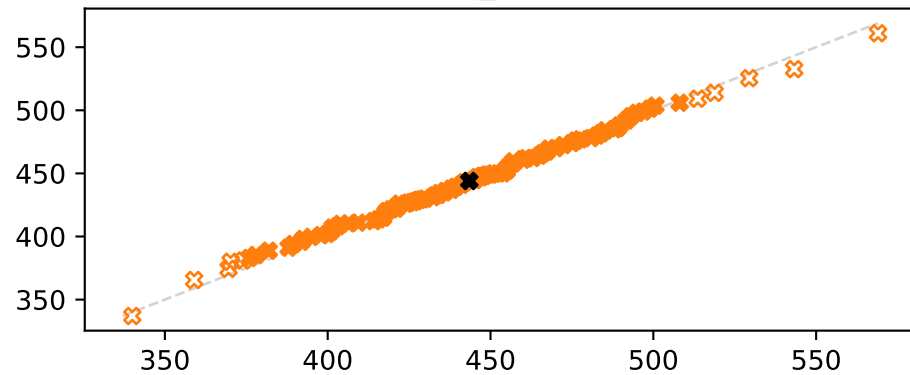


ts\_properties:  
TreeSequence properties.

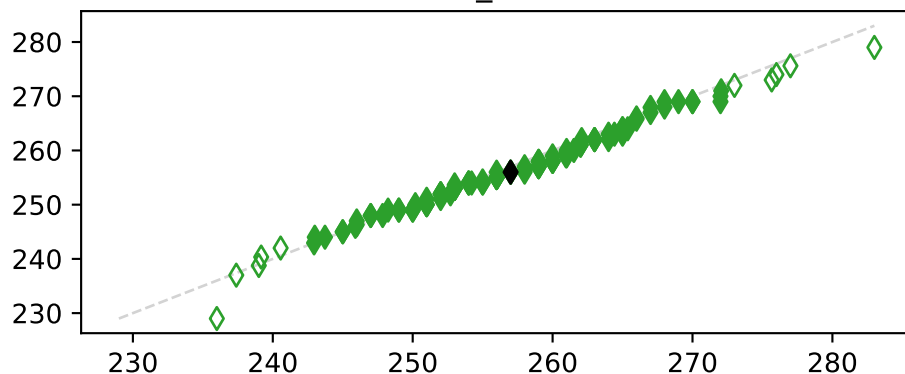
num\_trees



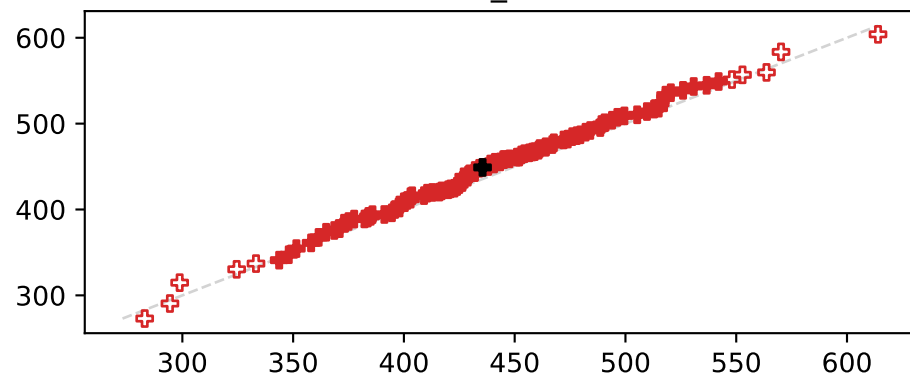
num\_edges



num\_nodes



num\_sites



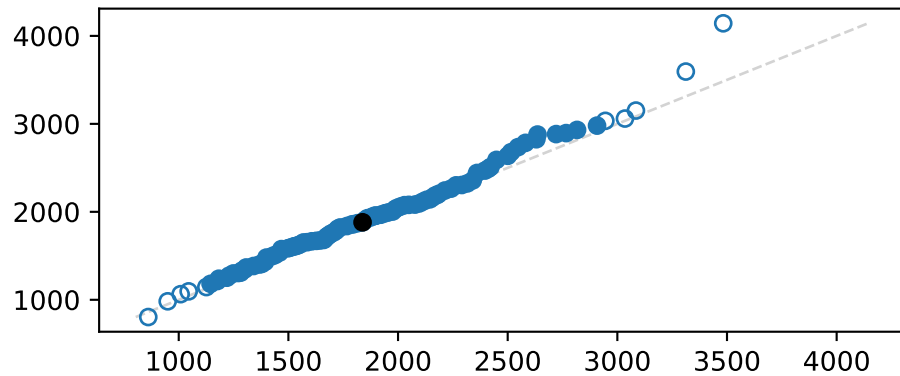
onepop\_constantN\_msprime1

onepop\_constantN\_slim1

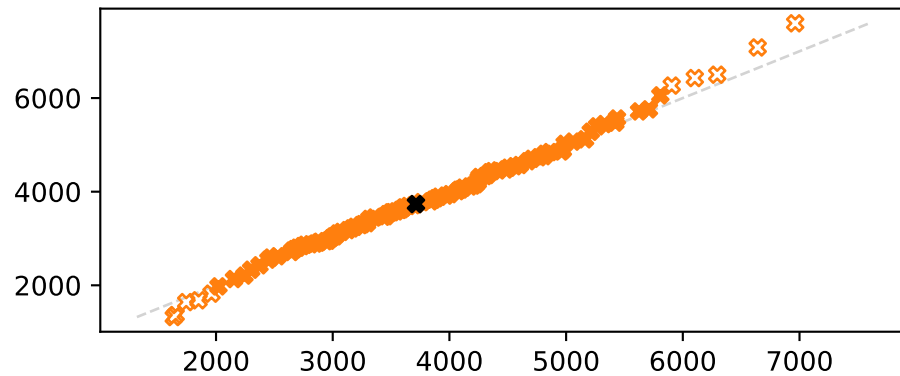
tmrca:

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

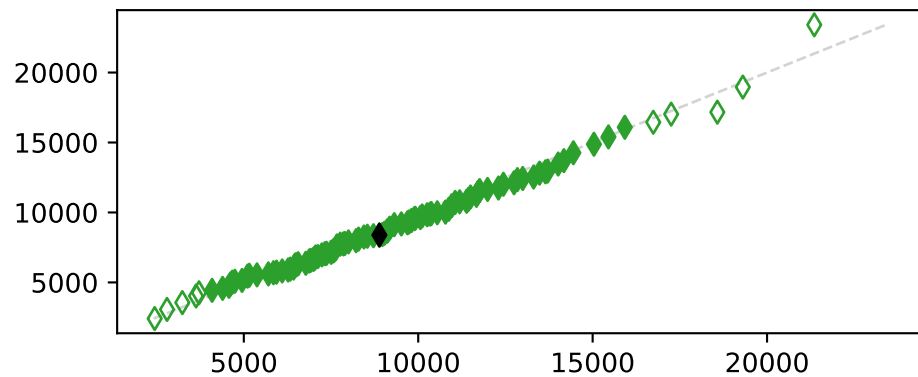
min(tmrca)



median(tmrca)

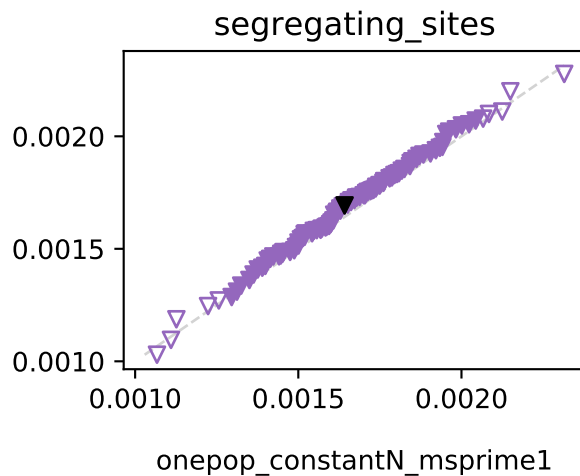
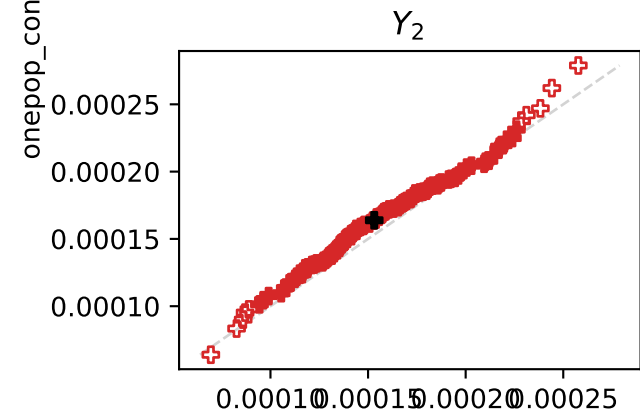
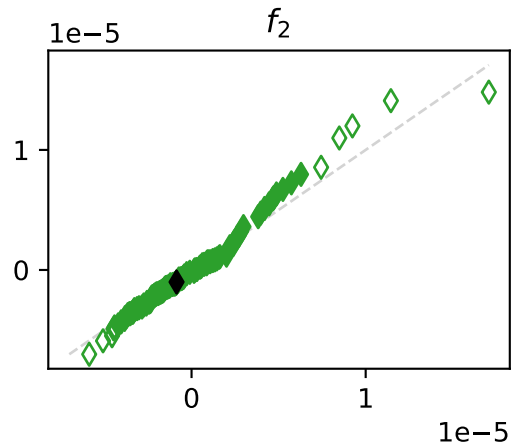
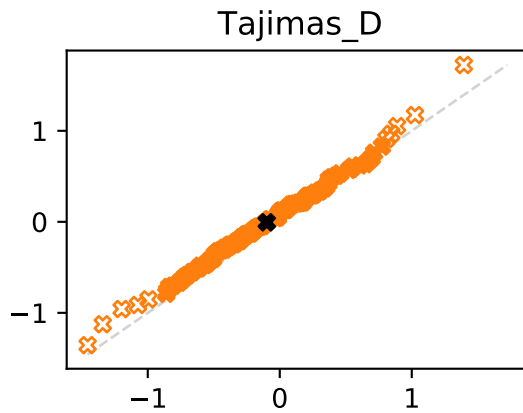
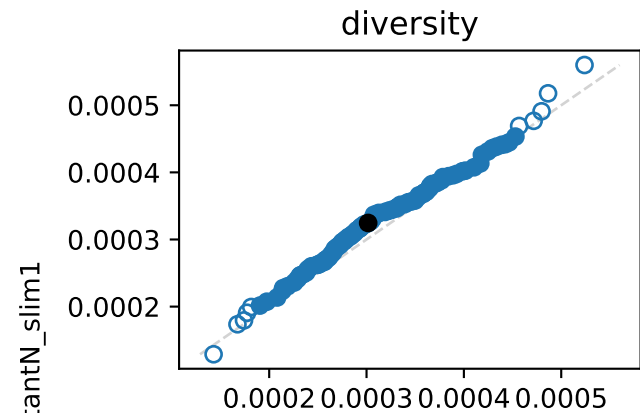


max(tmrca)



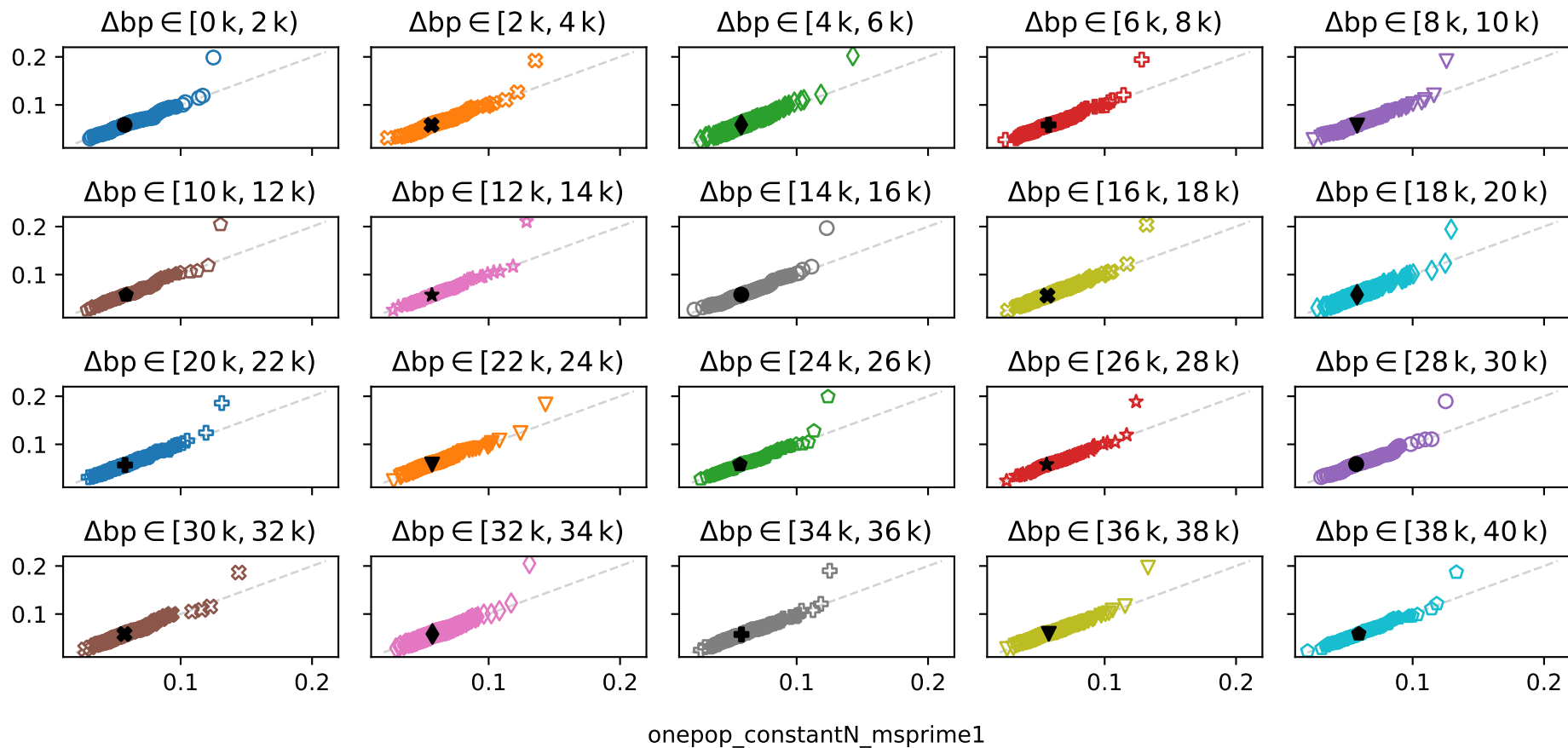
onepop\_constantN\_msprime1

pooled\_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.

onepop\_constantN\_slim1



allele\_frequency\_spectrum:  
Allele frequency spectrum for `bins` allele frequency bins.  
Values are  $\log(1+\text{counts})$  for each bin.

onepop\_constantN\_slim1

