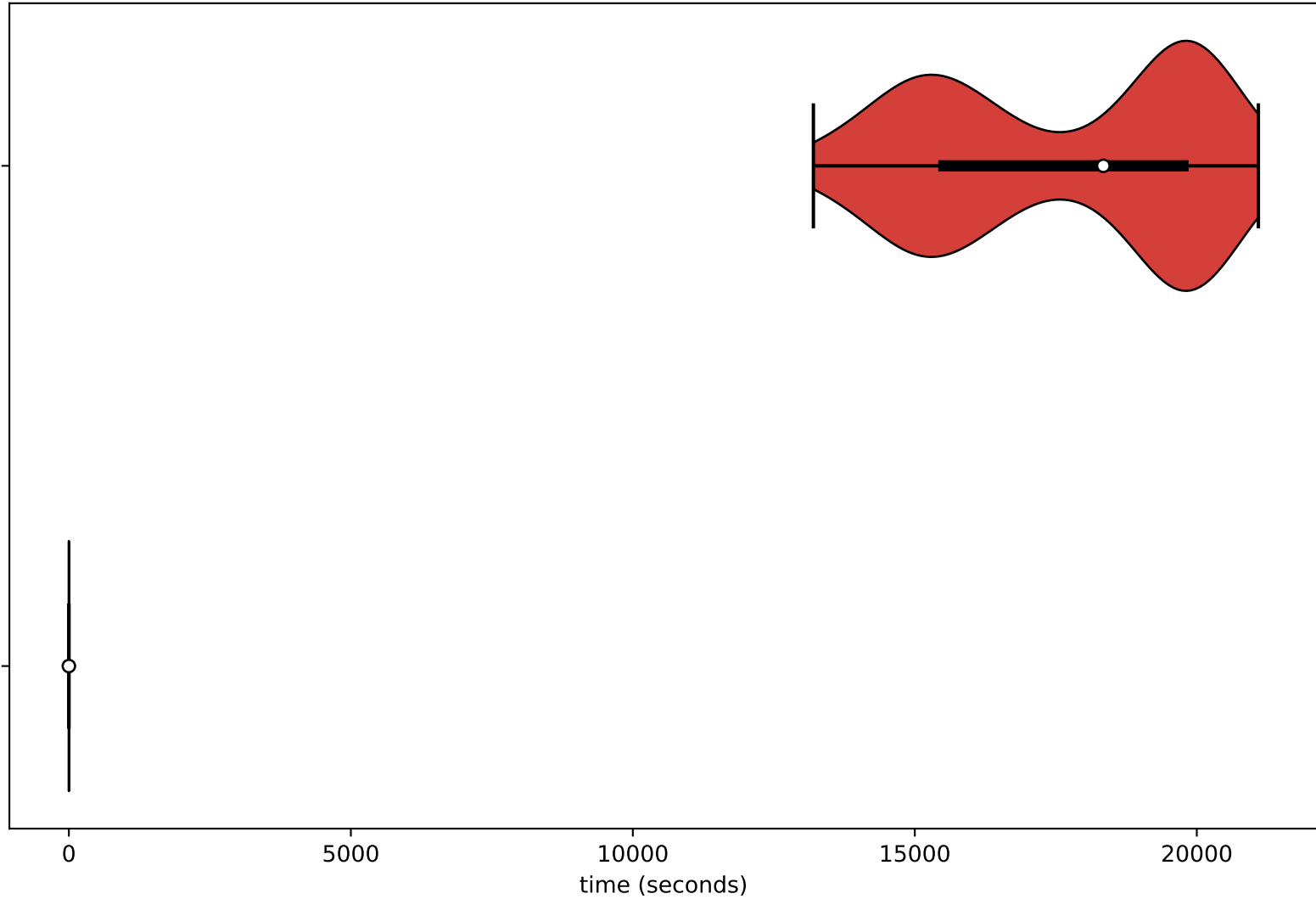


# Run time.

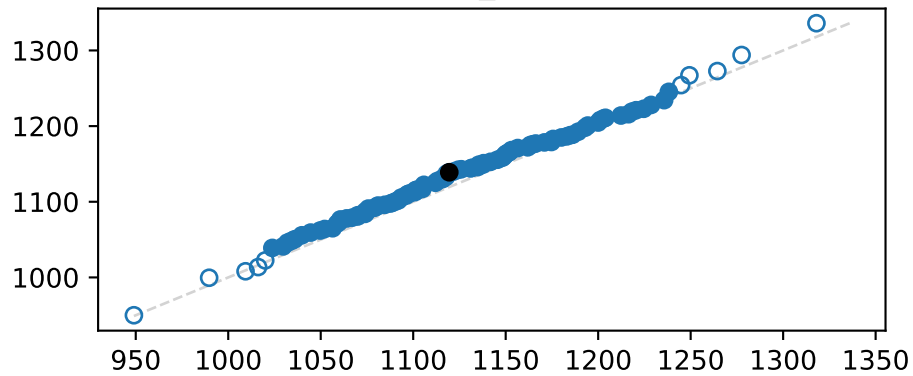
AncientEurasia\_9K19\_slim1

AncientEurasia\_9K19\_msprime1

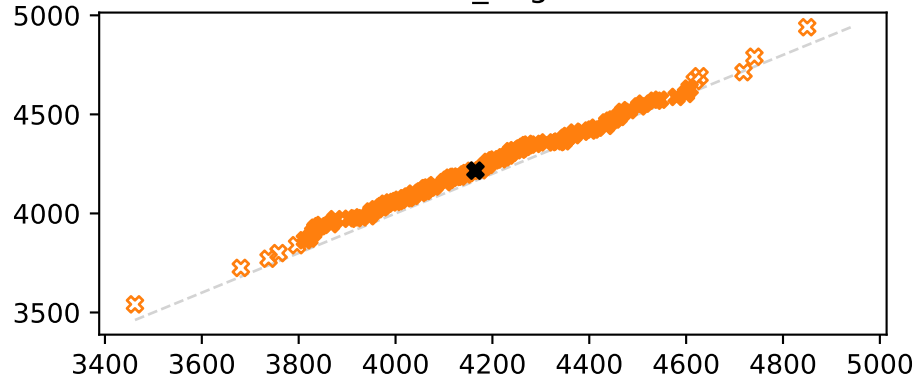


ts\_properties:  
TreeSequence properties.

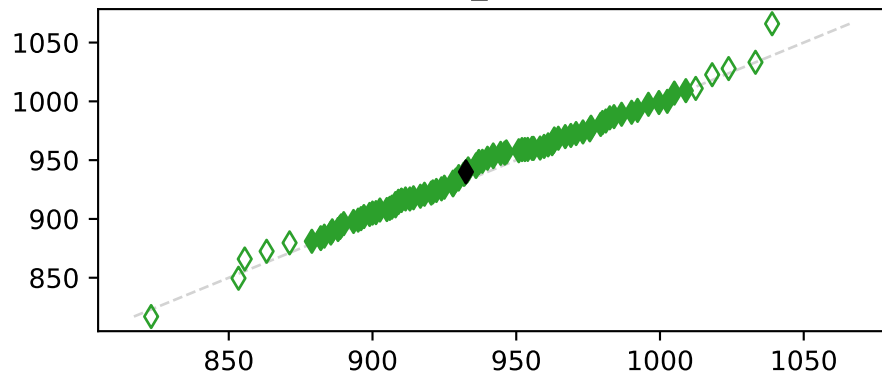
num\_trees



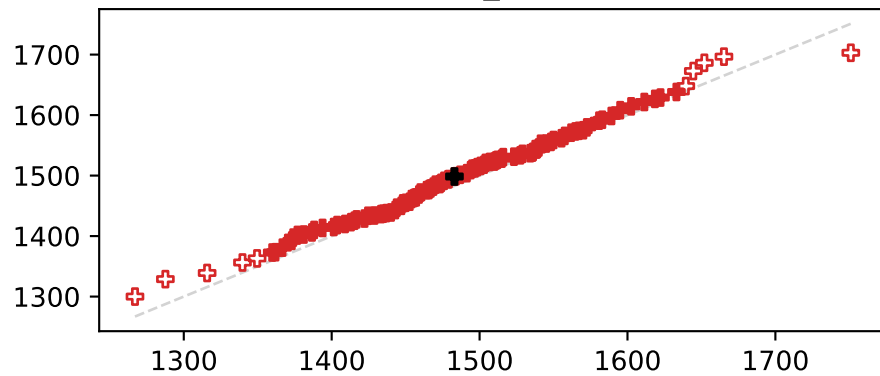
num\_edges



num\_nodes



num\_sites

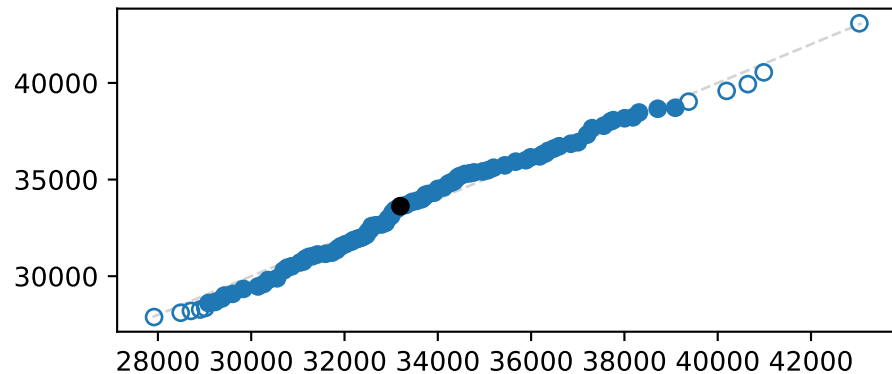


AncientEurasia\_9K19\_msprime1

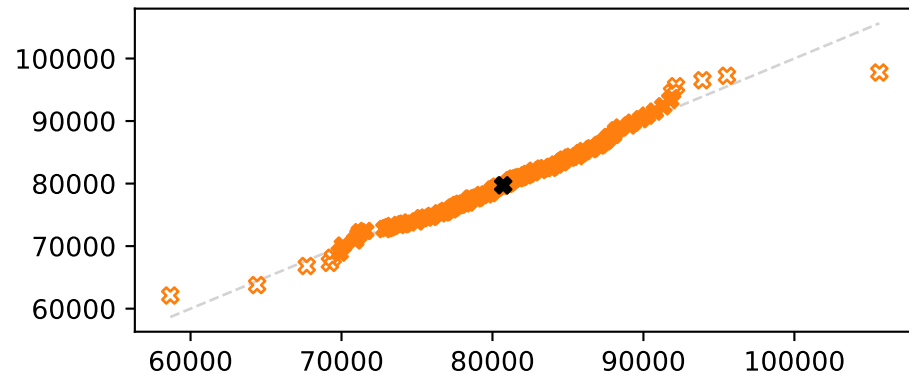
tmrca:

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

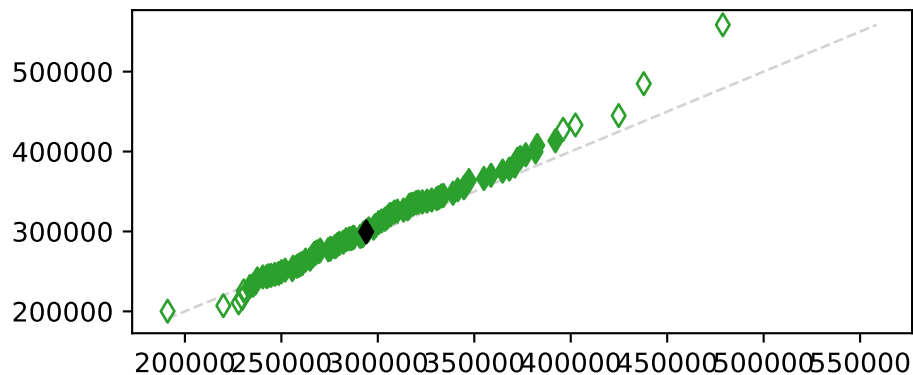
min(tmrca)



median(tmrca)

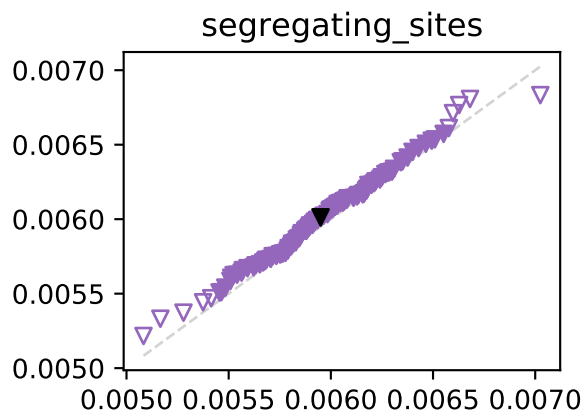
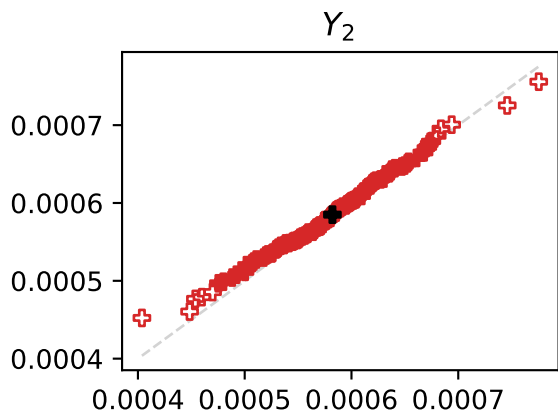
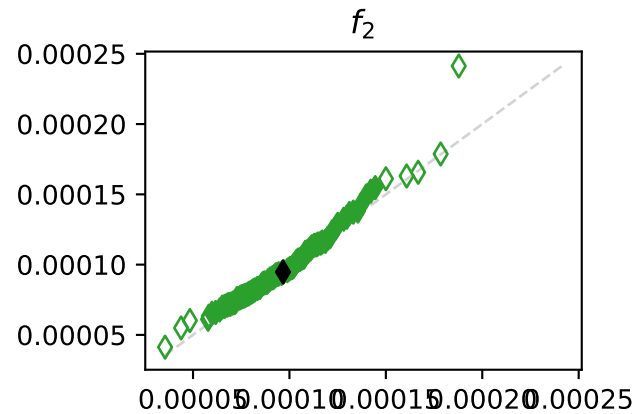
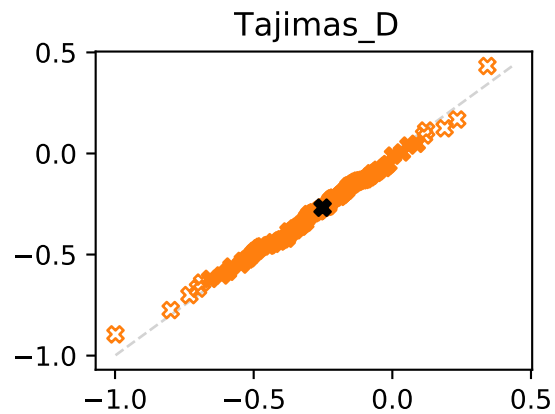
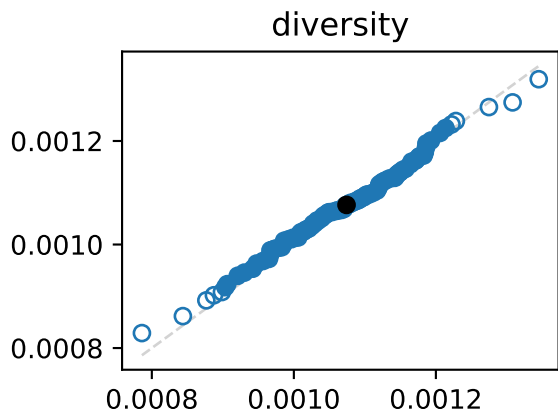


max(tmrca)



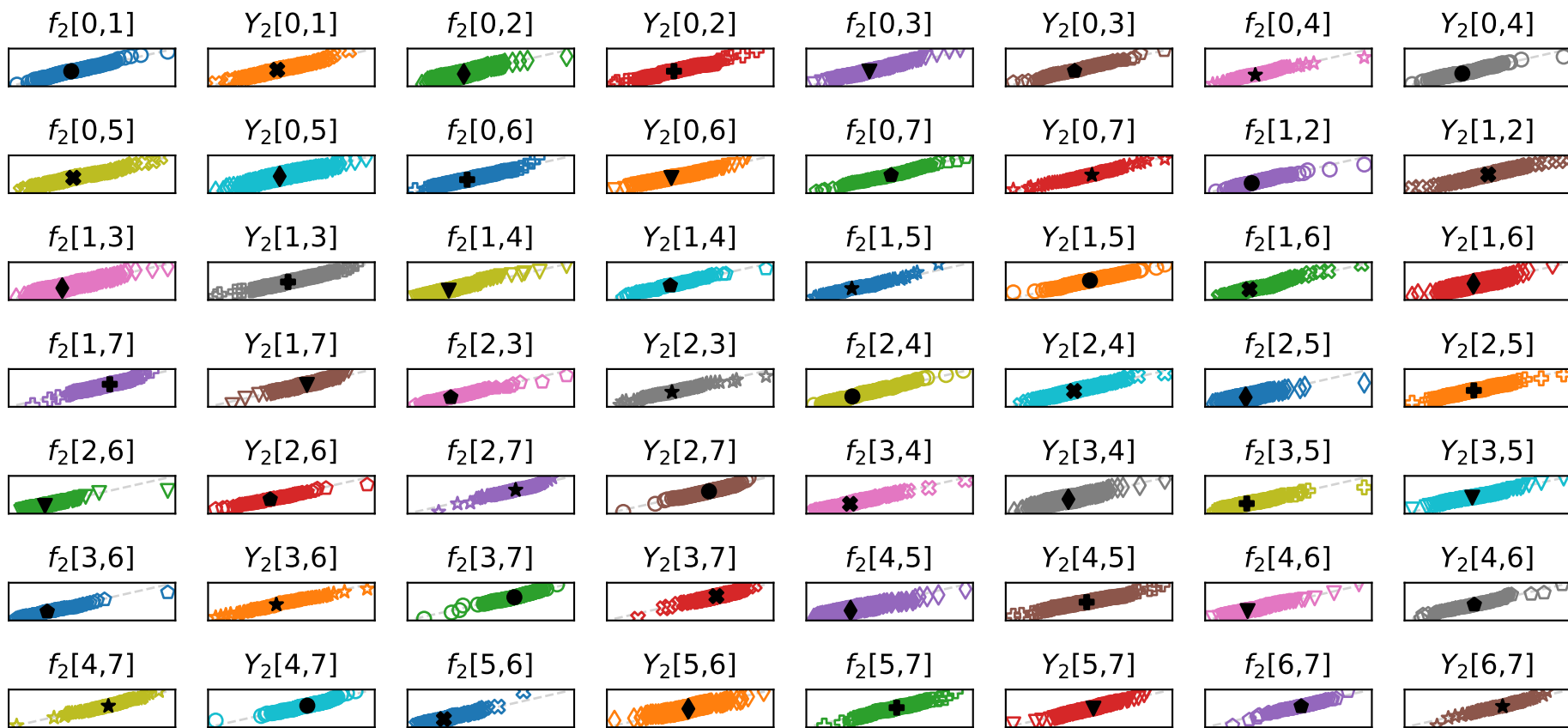
AncientEurasia\_9K19\_msprime1

pooled\_pop\_stats:  
Population statistics, with samples pooled from all populations.



AncientEurasia\_9K19\_msprime1

pairwise\_pop\_stats:  
Pairwise population statistics, calculated for all pairs of populations.



AncientEurasia\_9K19\_msprime1

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

