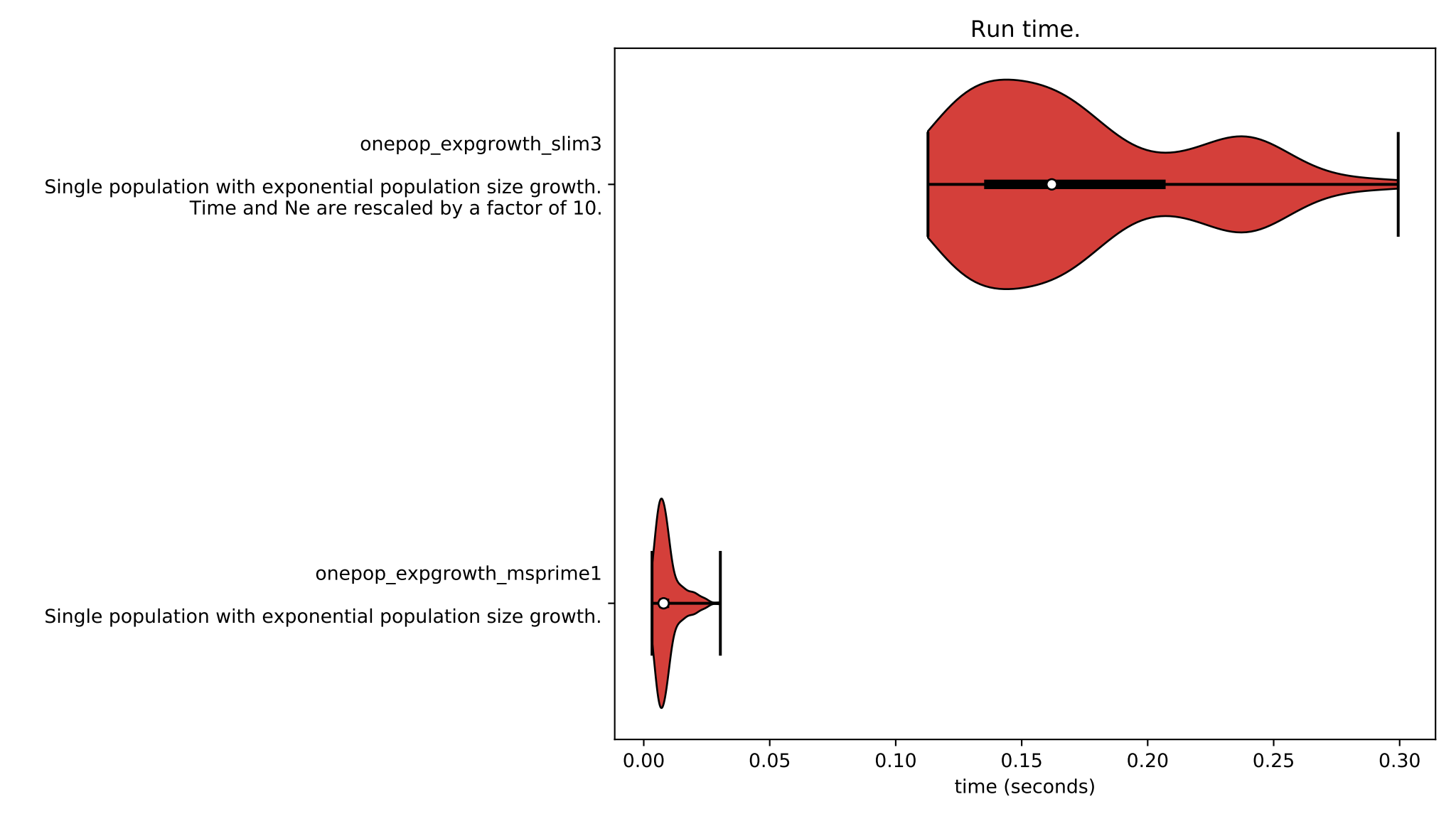
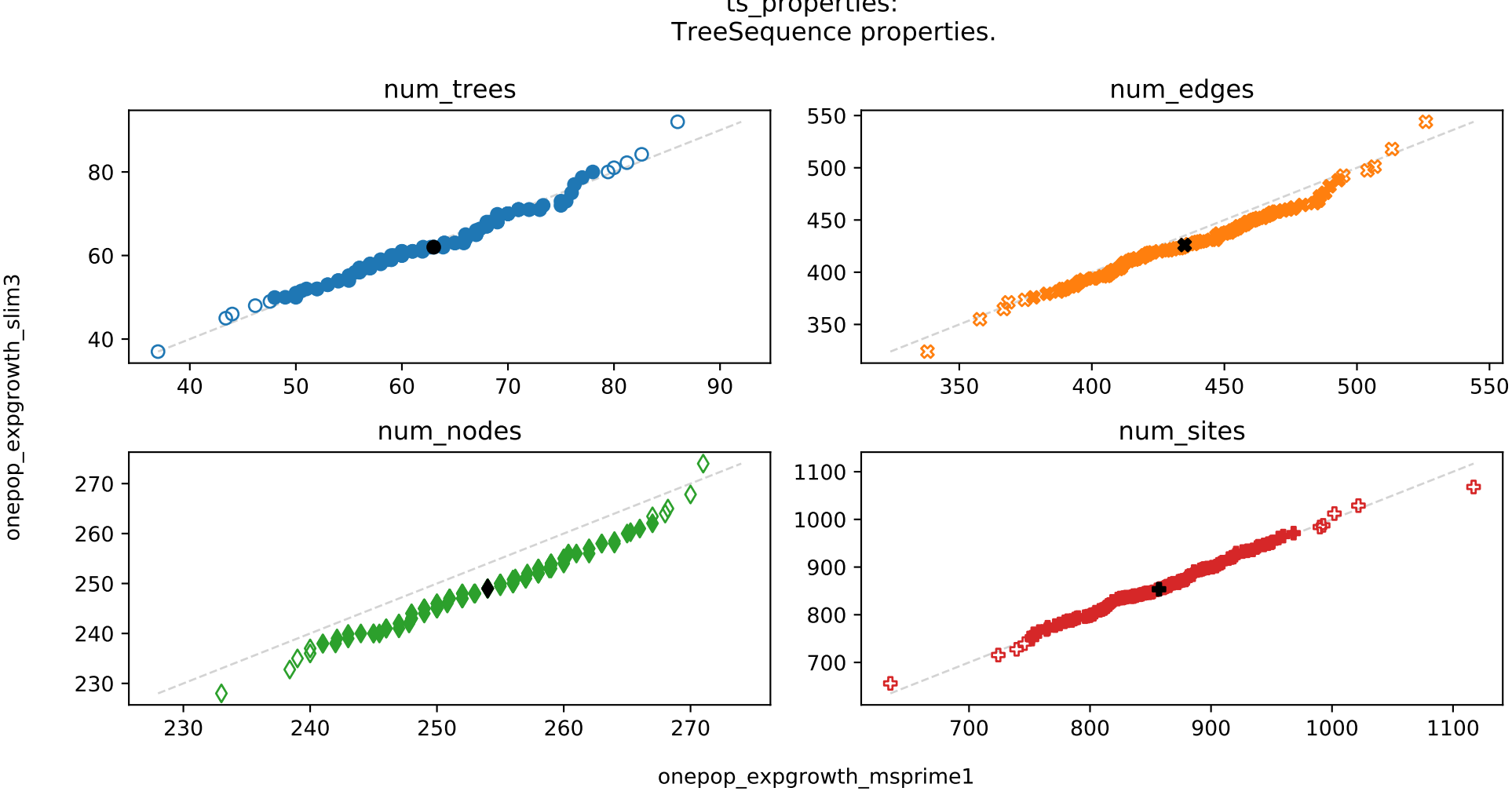
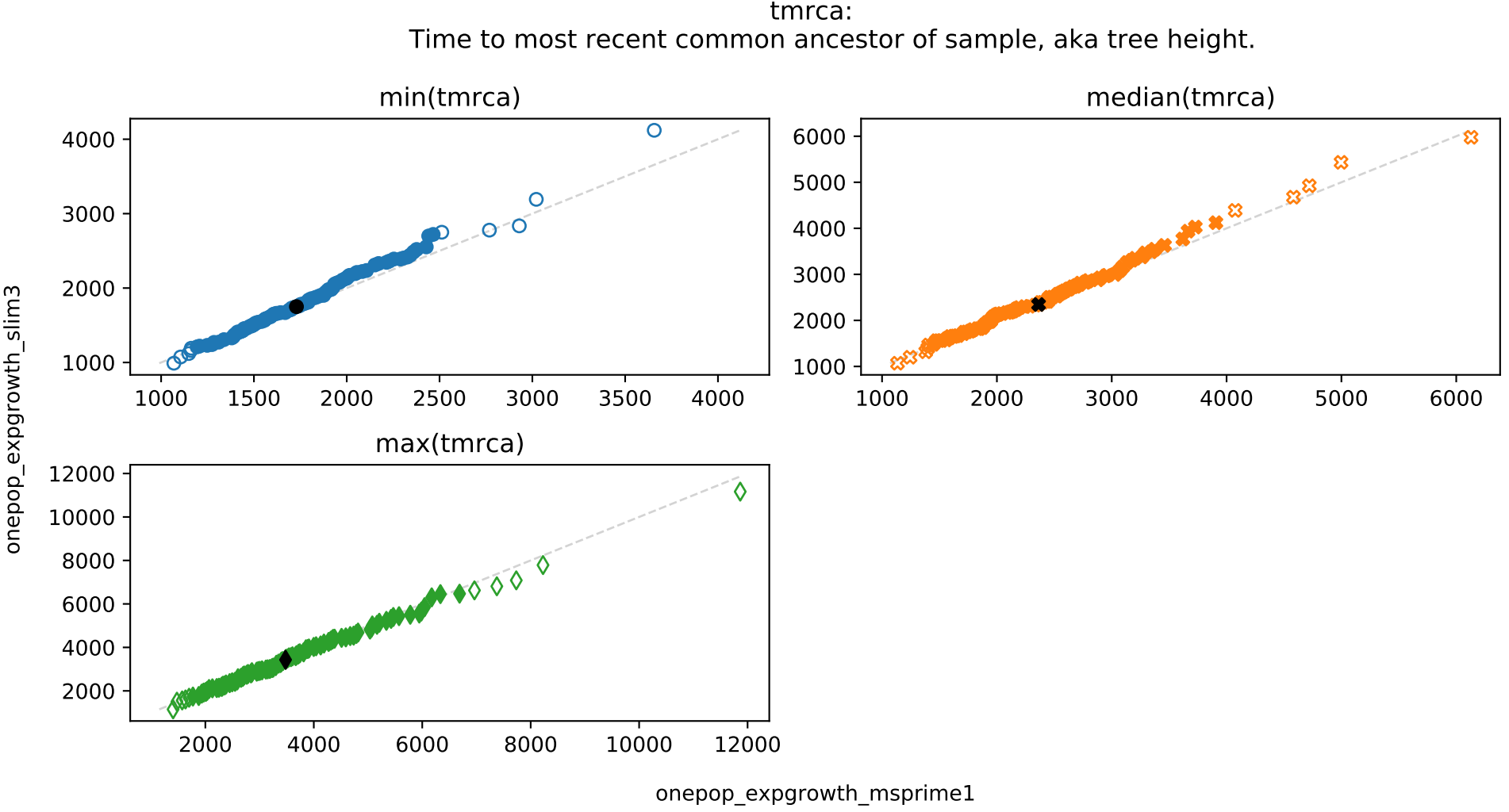
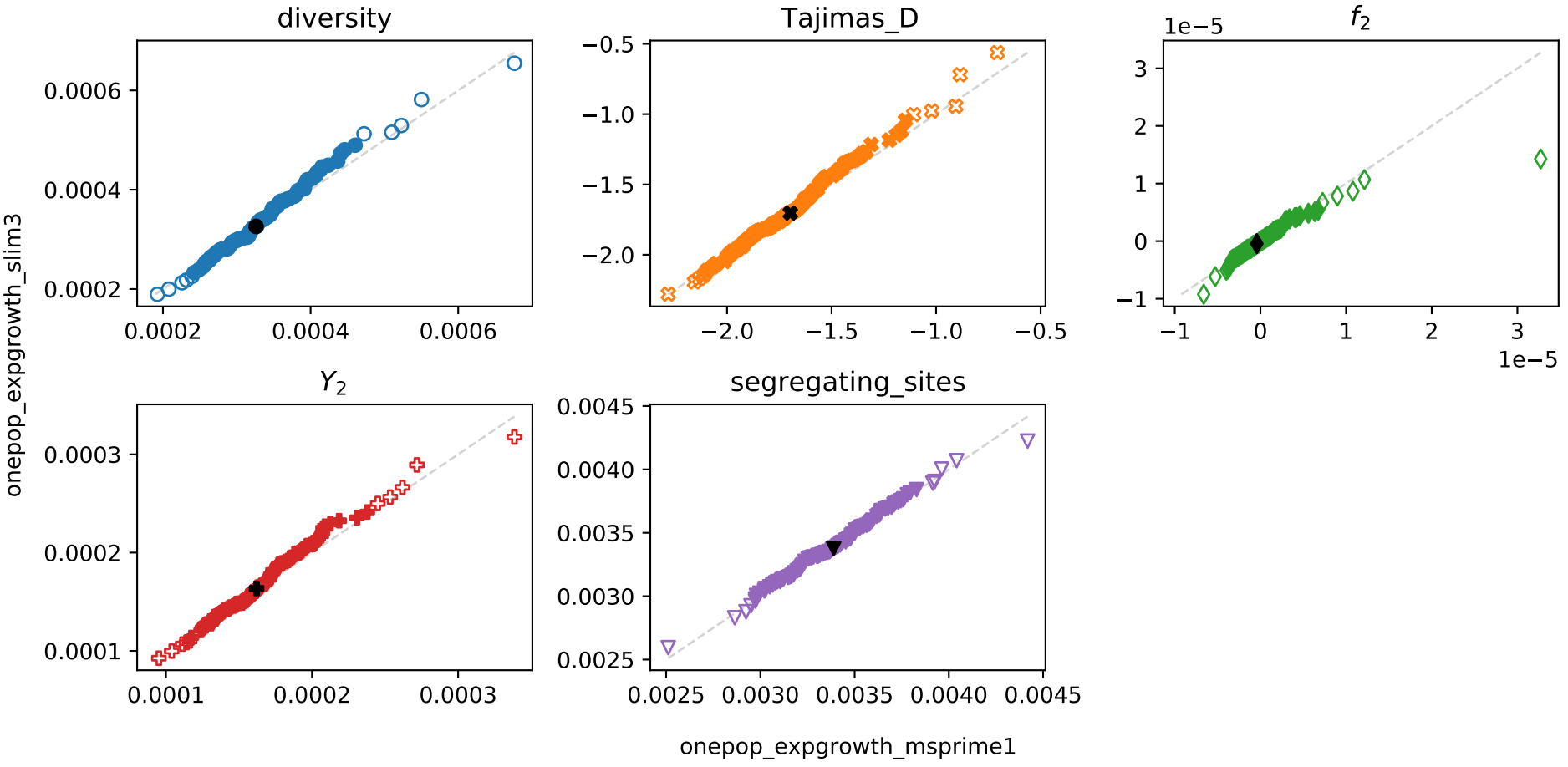
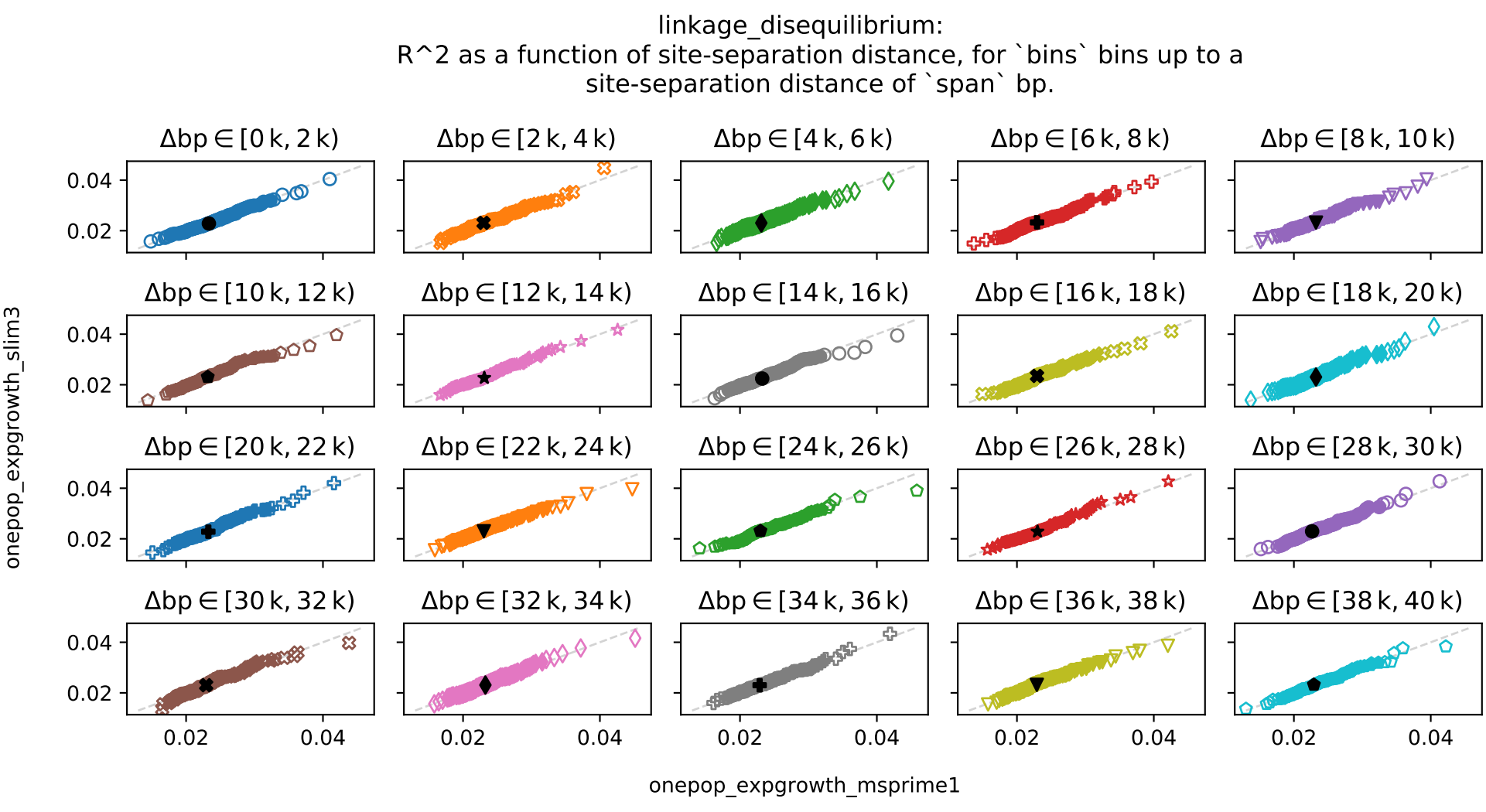

Run time.
onepop_expgrowth_slim3
Single population with exponential population size growth.
Time and Ne are rescaled by a factor of 10.
onepop_expgrowth_msprime1
Single population with exponential population size growth.
0.00
0.05
0.10
0.15
0.20
0.25
0.30
time (seconds)

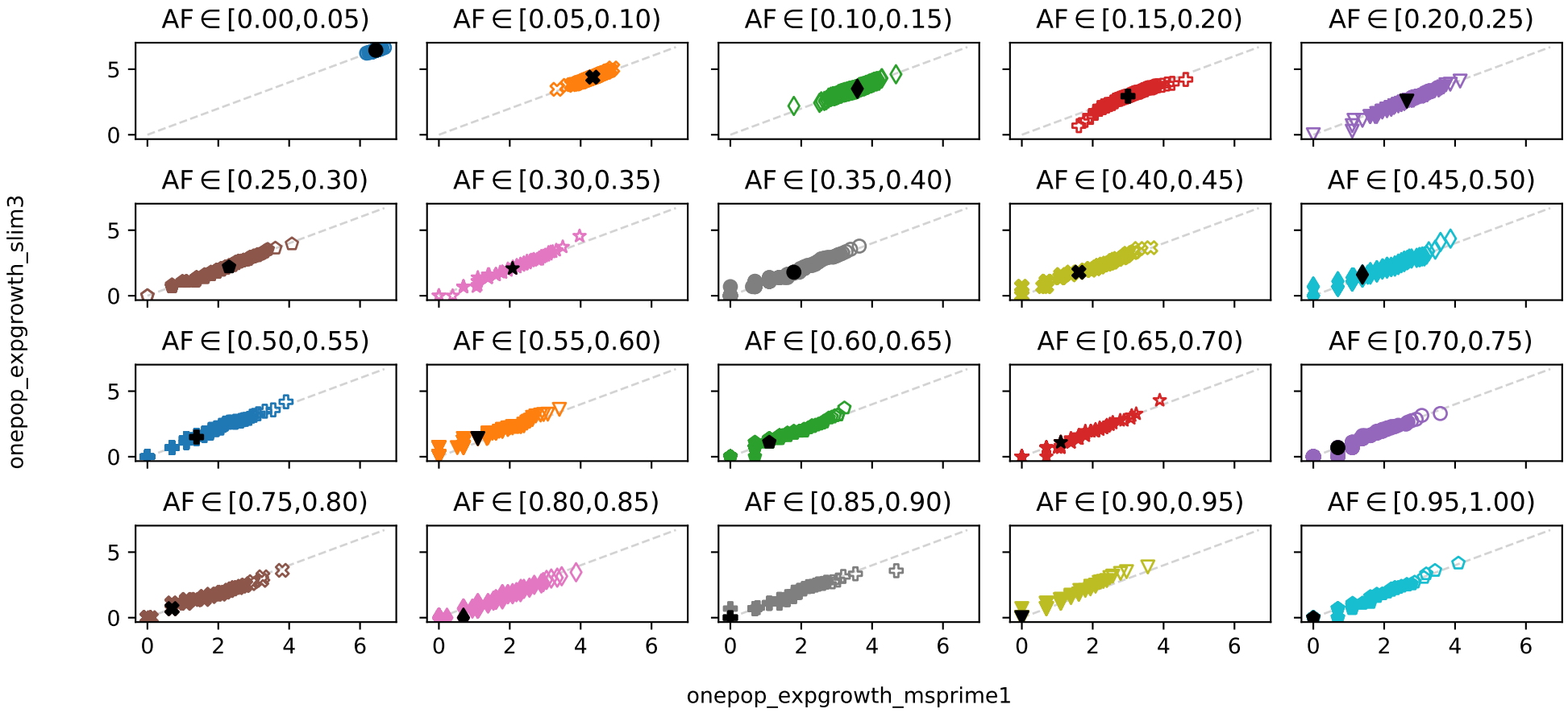

ts_properties:
TreeSequence properties.
num_trees
num_edges
num_nodes
num_sites
onepop_expgrowth_slim3
onepop_expgrowth_msprime1


tmrca:
Time to most recent common ancestor of sample, aka tree height.
min(tmrca)
median(tmrca)
max(tmrca)
onepop_expgrowth_slim3
onepop_expgrowth_msprime1
1000
1500
2000
2500
3000
3500
4000
5000
6000
8000
10000
12000

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.
Δbp ∈ [0 k, 2 k)
Δbp ∈ [2 k, 4 k)
Δbp ∈ [4 k, 6 k)
Δbp ∈ [6 k, 8 k)
Δbp ∈ [8 k, 10 k)
Δbp ∈ [10 k, 12 k)
Δbp ∈ [12 k, 14 k)
Δbp ∈ [14 k, 16 k)
Δbp ∈ [16 k, 18 k)
Δbp ∈ [18 k, 20 k)
Δbp ∈ [20 k, 22 k)
Δbp ∈ [22 k, 24 k)
Δbp ∈ [24 k, 26 k)
Δbp ∈ [26 k, 28 k)
Δbp ∈ [28 k, 30 k)
Δbp ∈ [30 k, 32 k)
Δbp ∈ [32 k, 34 k)
Δbp ∈ [34 k, 36 k)
Δbp ∈ [36 k, 38 k)
Δbp ∈ [38 k, 40 k)
0.02
0.04
onepop_expgrowth_slim3
onepop_expgrowth_msprime1


allele_frequency_spectrum:
Allele frequency spectrum for `bins` allele frequency bins.
Values are log(1+counts) for each bin.
AF ∈ [0.00,0.05)
AF ∈ [0.05,0.10)
AF ∈ [0.10,0.15)
AF ∈ [0.15,0.20)
AF ∈ [0.20,0.25)
AF ∈ [0.25,0.30)
AF ∈ [0.30,0.35)
AF ∈ [0.35,0.40)
AF ∈ [0.40,0.45)
AF ∈ [0.45,0.50)
AF ∈ [0.50,0.55)
AF ∈ [0.55,0.60)
AF ∈ [0.60,0.65)
AF ∈ [0.65,0.70)
AF ∈ [0.70,0.75)
AF ∈ [0.75,0.80)
AF ∈ [0.80,0.85)
AF ∈ [0.85,0.90)
AF ∈ [0.90,0.95)
AF ∈ [0.95,1.00)
0
5
0
2
4
6
onepop_expgrowth_slim3
onepop_expgrowth_msprime1