



Tests of selection

- 
1. Tests of diversity / tree shape
 2. Tests of rates

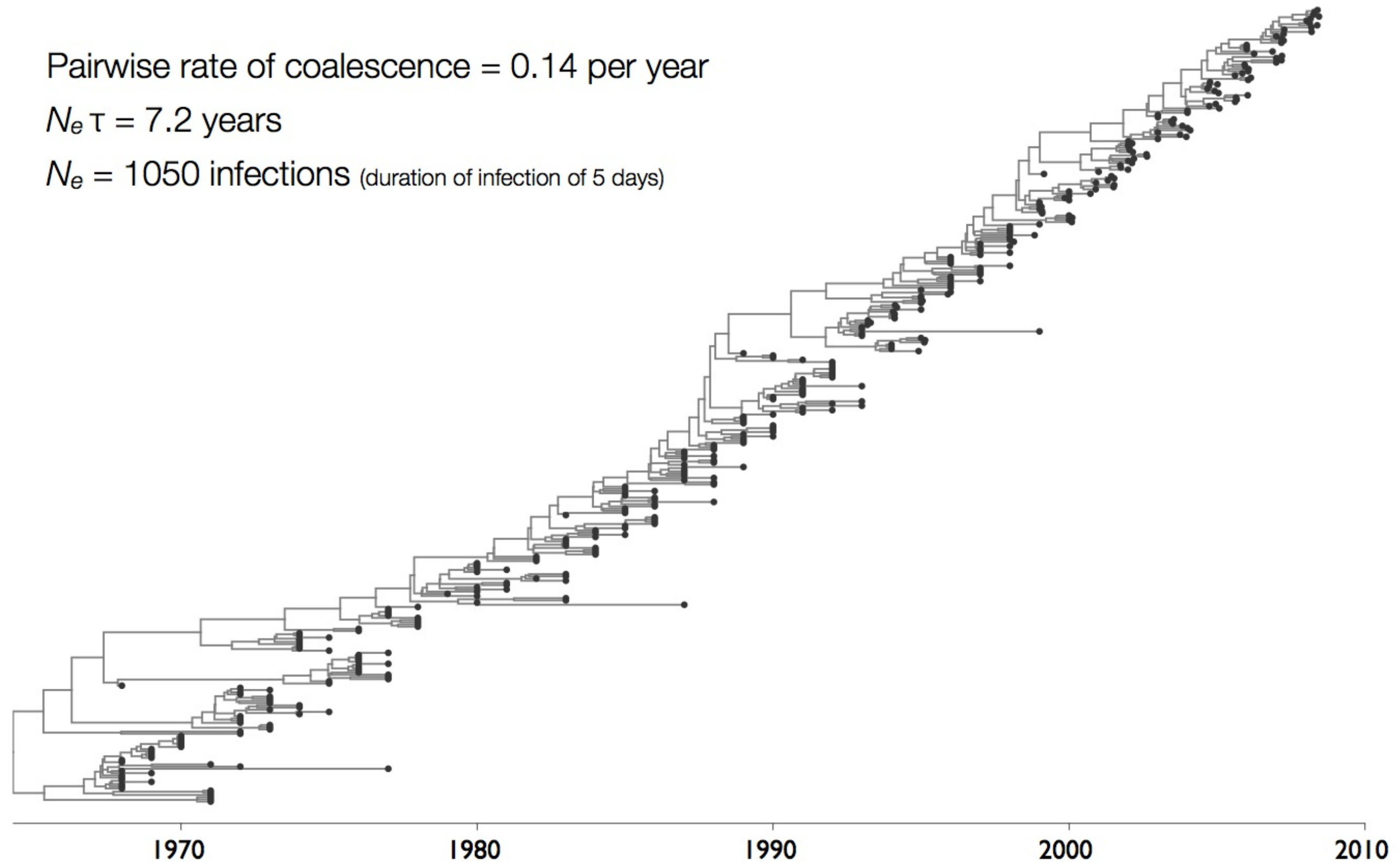
Test: is there less genetic diversity than expected?

Influenza phylogeny and effective number of infections

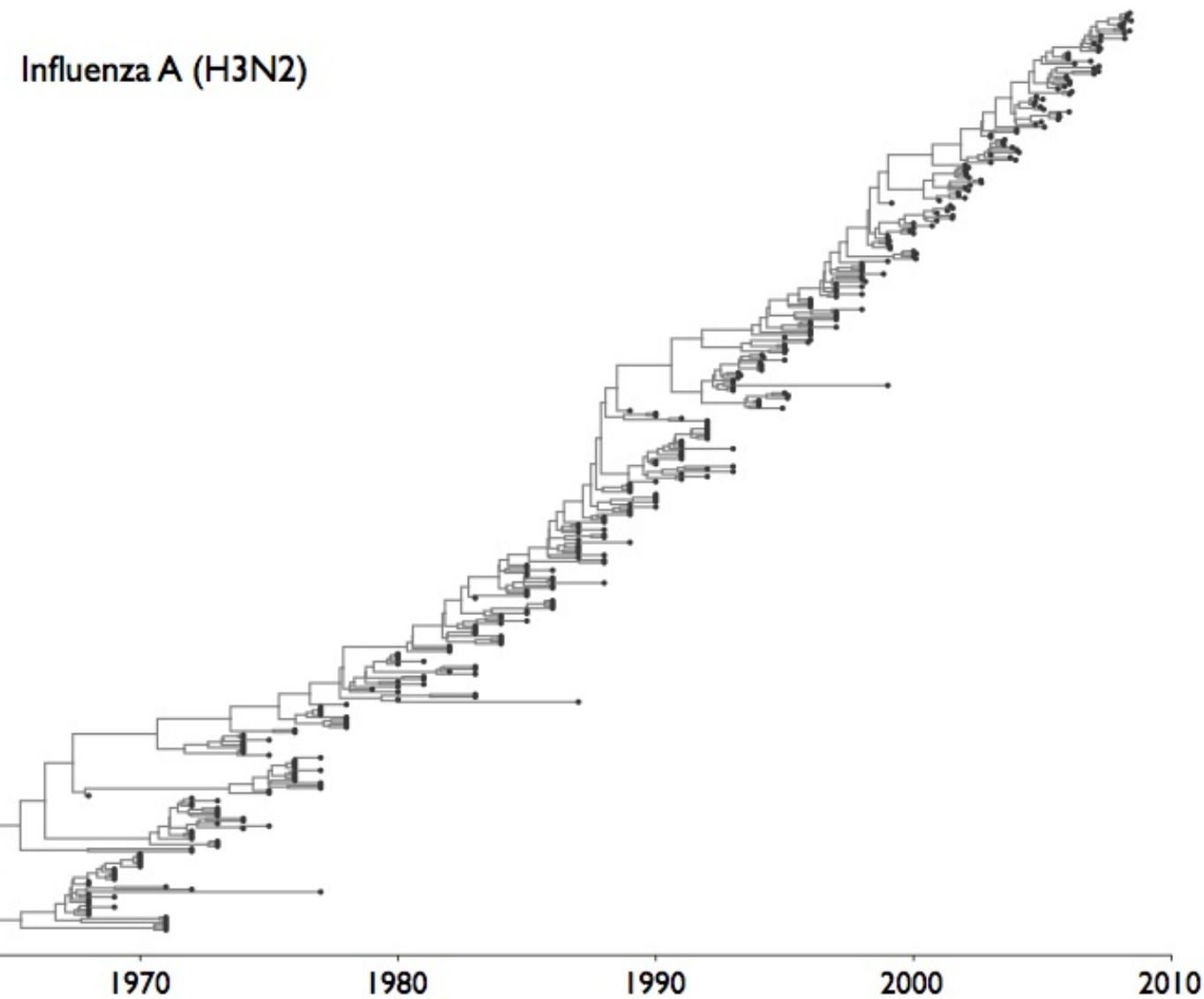
Pairwise rate of coalescence = 0.14 per year

$N_e \tau = 7.2$ years

$N_e = 1050$ infections (duration of infection of 5 days)



Coalescent rates in flu and measles



$$N_e \tau = 7.2 \text{ years}$$

$$N_e = 1050 \text{ infections (duration of infection of 5 days)}$$

$$N = 7 \times 10^6 \text{ cases per gen (prevalence)}$$

Off by a factor of 6,700



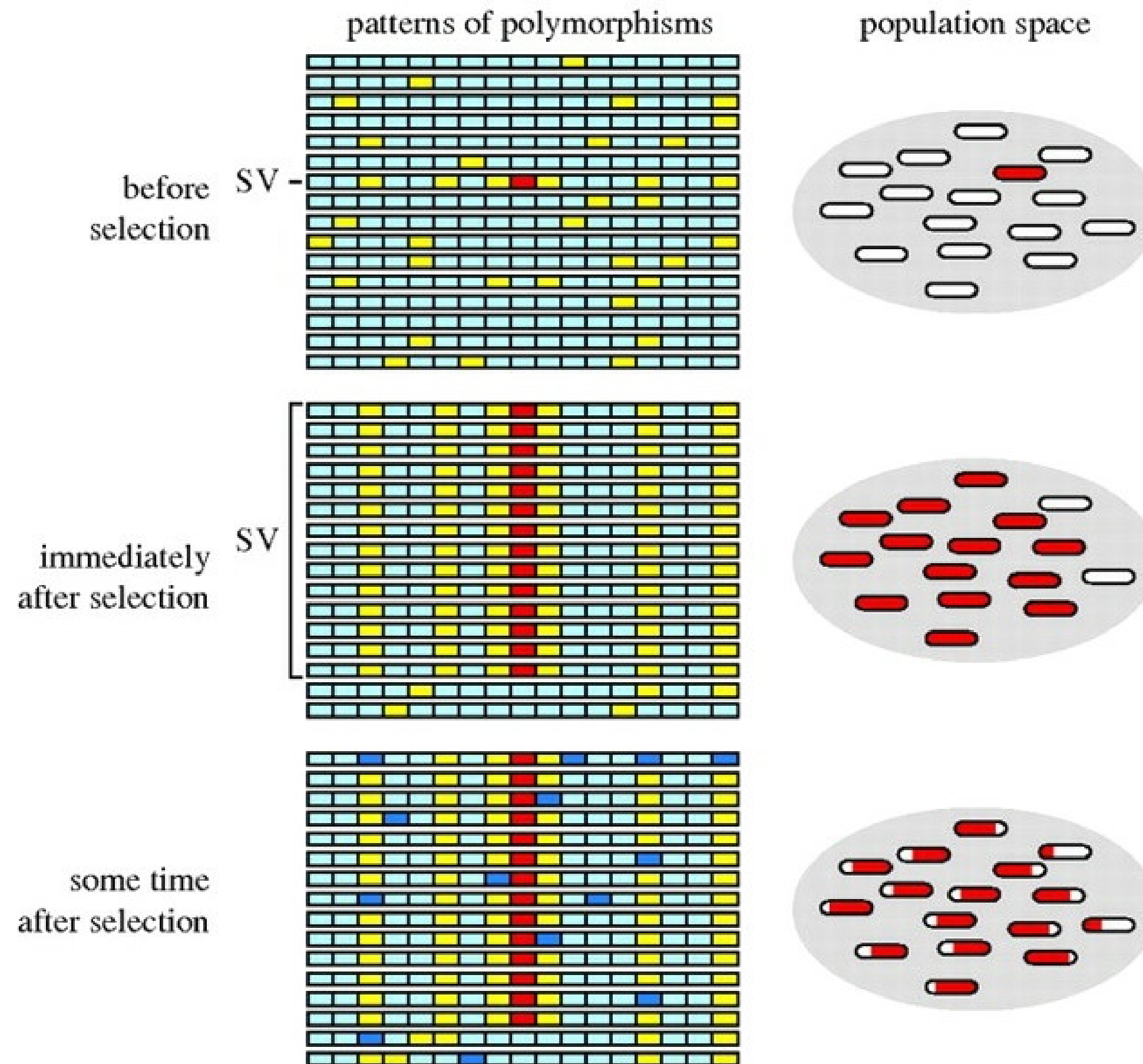
$$N_e \tau = 124.6 \text{ years}$$

$$N_e = 8270 \text{ infections (duration of infection of 11 days)}$$

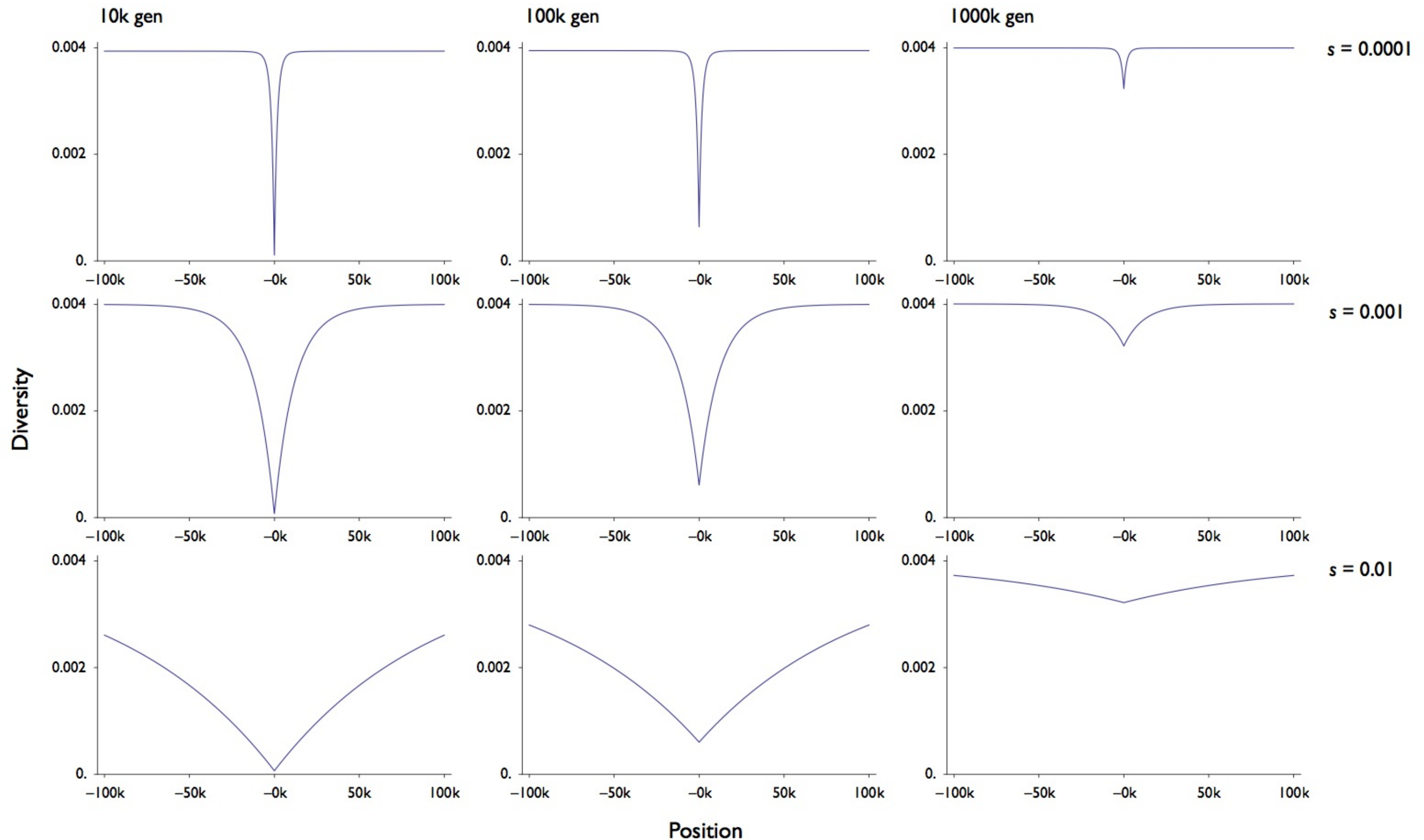
$$N = 9 \times 10^5 \text{ cases per gen (prevalence)}$$

Off by a factor of 110

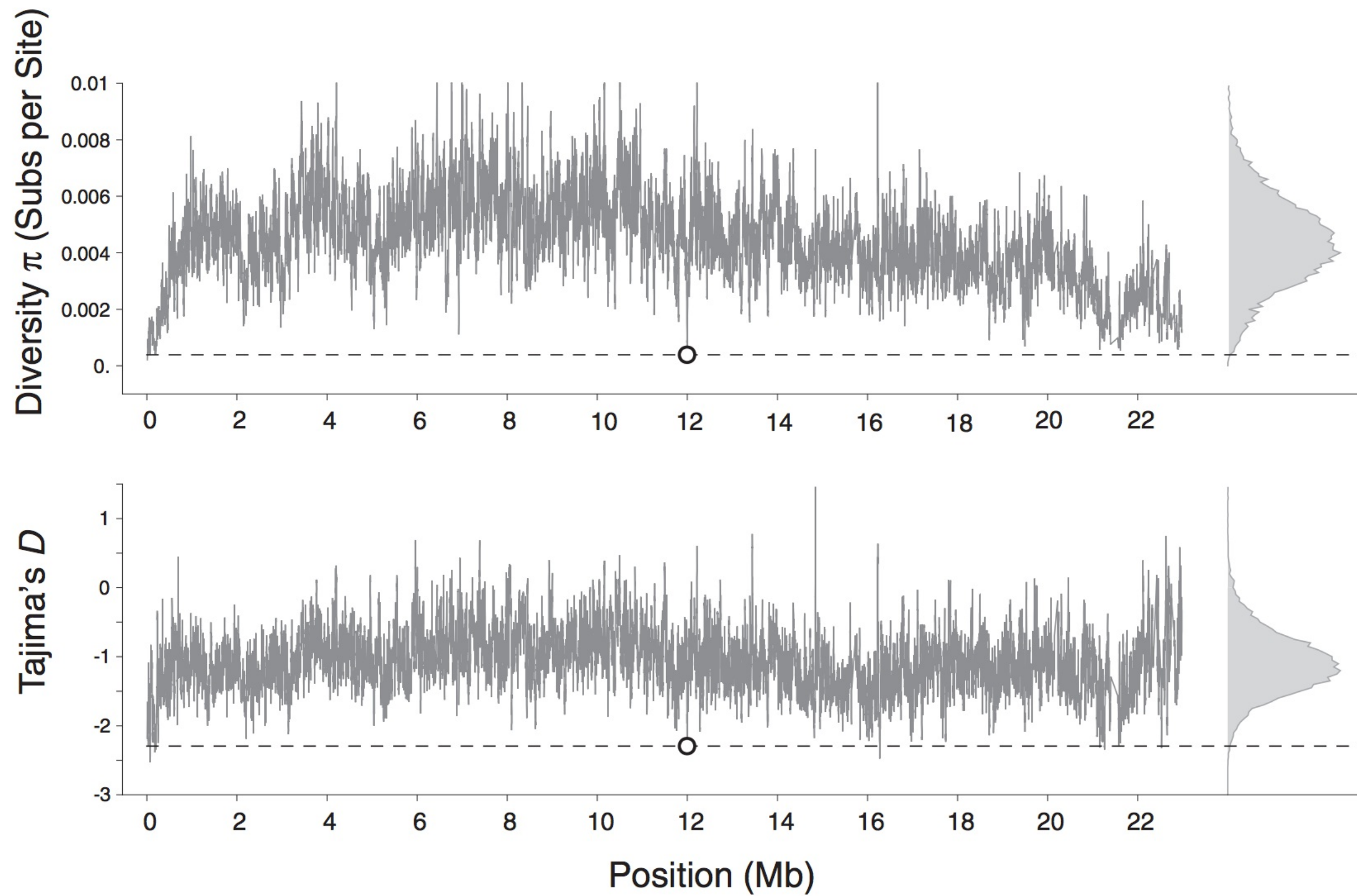
Selective sweeps purge nearby diversity



Depth and breadth indicates age and strength of sweep

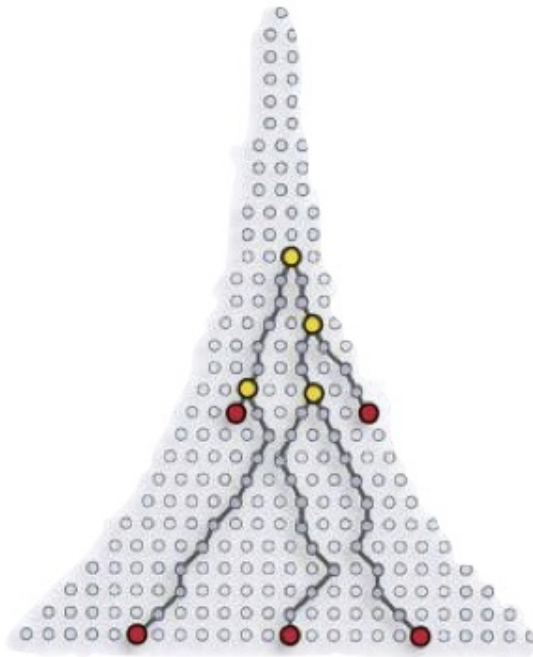


Selective sweeps purge diversity in *Drosophila*

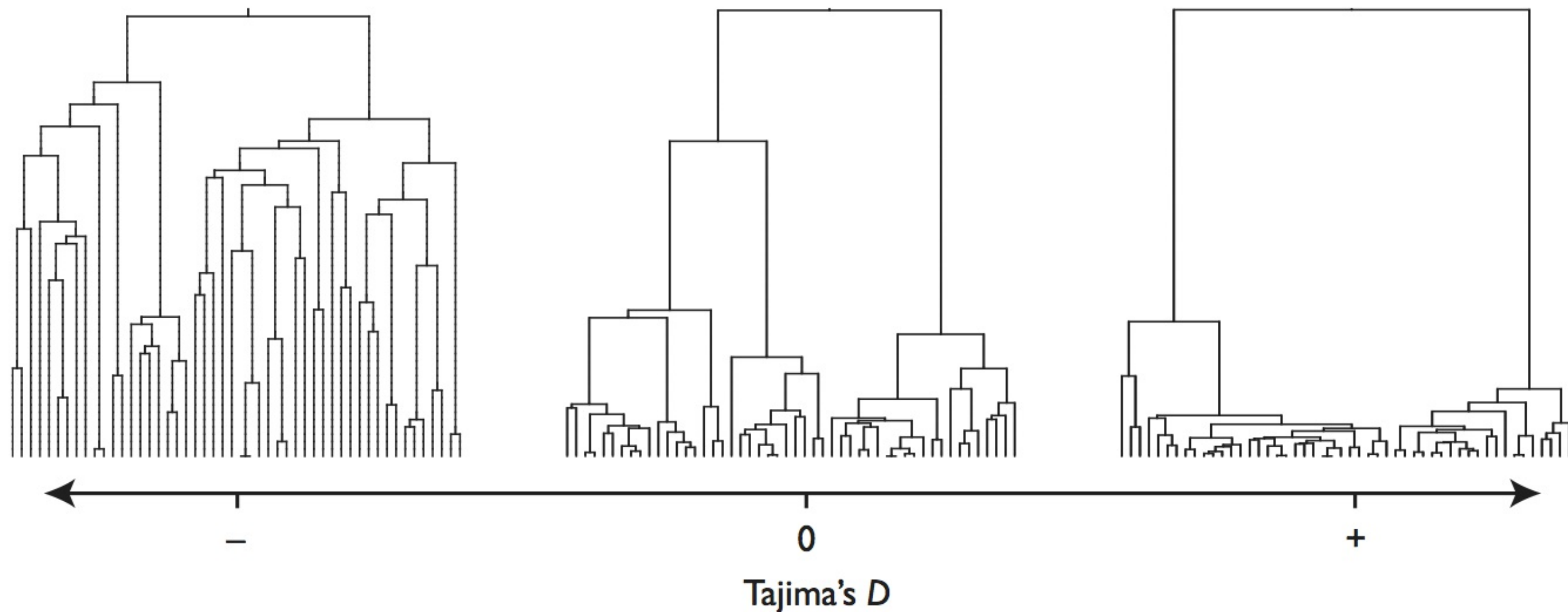
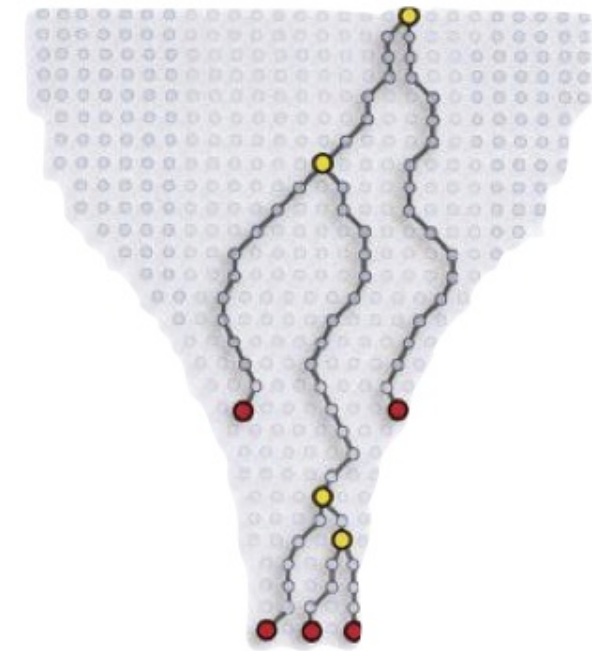


Test: is the tree shape different from the neutral expectation?

Tajima's D statistic summarizes deviation from neutrality



Compares singleton mutations
to shared diversity



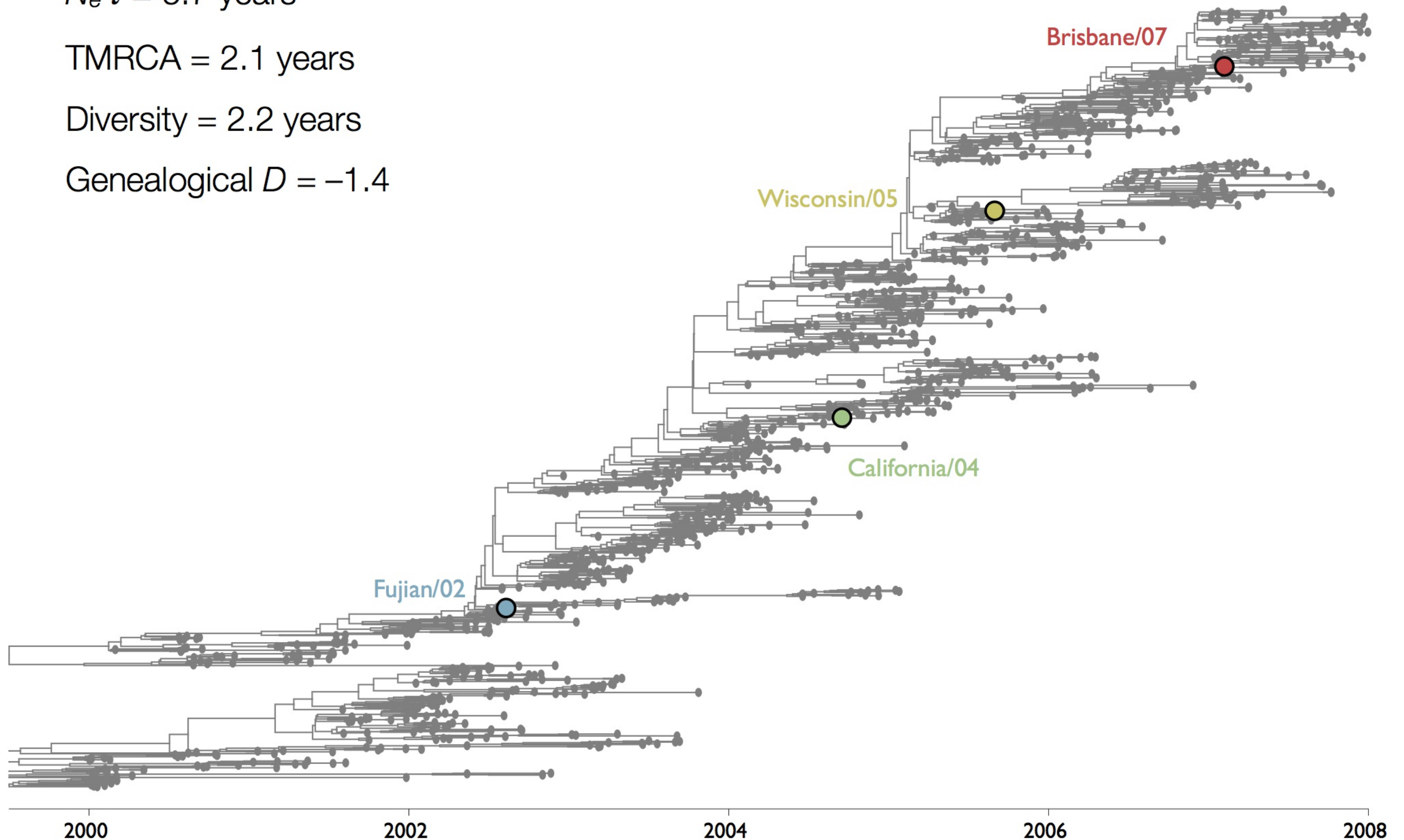
Influenza has negative Tajima's D

$N_e \tau = 6.7$ years

TMRCA = 2.1 years

Diversity = 2.2 years

Genealogical $D = -1.4$



Test: is there an
overabundance of fixed non-
synonymous mutations?

"Trunk" branches show an excess of non-synonymous change at epitope sites in influenza

Protein sites	d _N /d _S ratio; tree partition		
	All branches	Trunk branches	Other branches
H3N2 HA	0.27 ± 0.02	0.35 ± 0.08	0.26 ± 0.02
H3N2 HA1	0.37 ± 0.04	0.57 ± 0.15	0.34 ± 0.04
H3N2 HA2	0.13 ± 0.02	0.10 ± 0.05	0.14 ± 0.03
H3N2 epitopes	0.63 ± 0.09	1.85 ± 0.82	0.53 ± 0.08
H3N2 non-epitopes	0.15 ± 0.02	0.09 ± 0.04	0.16 ± 0.02

Wolf et al. 2006

