

Measures of sequence diversity

sequence	sites																								
ancestor	·	C	·	·	C	·	·	A	·	·	T	·	·	A	·	·	G	·	·	C	·	·	G	·	
a		C			T			A			G			C			G			C			T		
b		C			T			T			G			C			T			G			T		
c		G			T			A			T			C			G			G			T		
d		G			C			A			T			A			G			C			G		
e		C			T			A			G			C			G			G			T		
f		C			C			A			T			C			G			G			T		

1. What is S (number of segregating sites) for this dataset? What is n (sample size)?
2. Compute the site frequency spectrum (SFS): ξ_i is the number of sites with i copies of the mutant/derived allele and $n - i$ copies of the ancestral allele.
3. Use the SFS to compute the *folded* SFS: η_i is the number of sites with i copies of the minor allele.
4. Find a formula for computing the average pairwise heterozygosity π from the folded SFS. Use your formula to compute π for this dataset.