

a) genotype matrix

sample	s_1	s_2	s_3	s_4	s_5
site 1	A	T	T	T	A
site 2	C	A	C	A	C
site 3	T	A	T	A	T
site 4	G	C	G	C	G
site 5	C	T	C	C	C

derived
allele
frequency

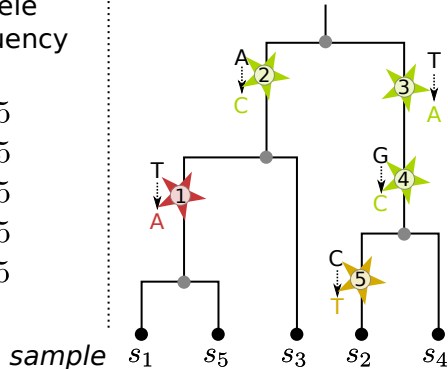
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1/5

b) location of mutations
on the treec) number of samples
below each node