

a) genotype matrix

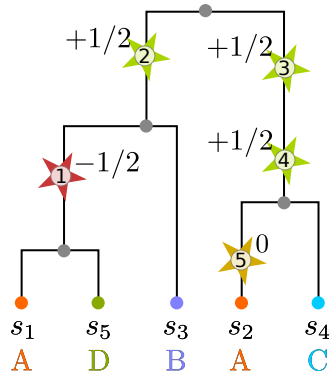
population **A** **A** **B** **C** **D**
 sample s_1 s_2 s_3 s_4 s_5

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

p_A	p_B	p_C	p_D
1/2	0	0	1
1/2	1	0	1
1/2	0	1	0
1/2	0	1	0
1/2	0	0	0

sample
population

b) site $f_4 : 1.0/L$



c) branch $f_4 : 1.5/L$

