Introduction to Computational Biology; An Evolutionary Approach: Testing Evolutionary Hypotheses

Bernhard Haubold & Thomas Wiehe

Data for HKA Test

	5' Flanking			*Adh* locus		
	Length	Sites	Var. sites	Length	Sites	Var. sites
Within species ($n = 81$)	4000	414	9	900	79	8
Between species	4052	4052	210	900	324	18

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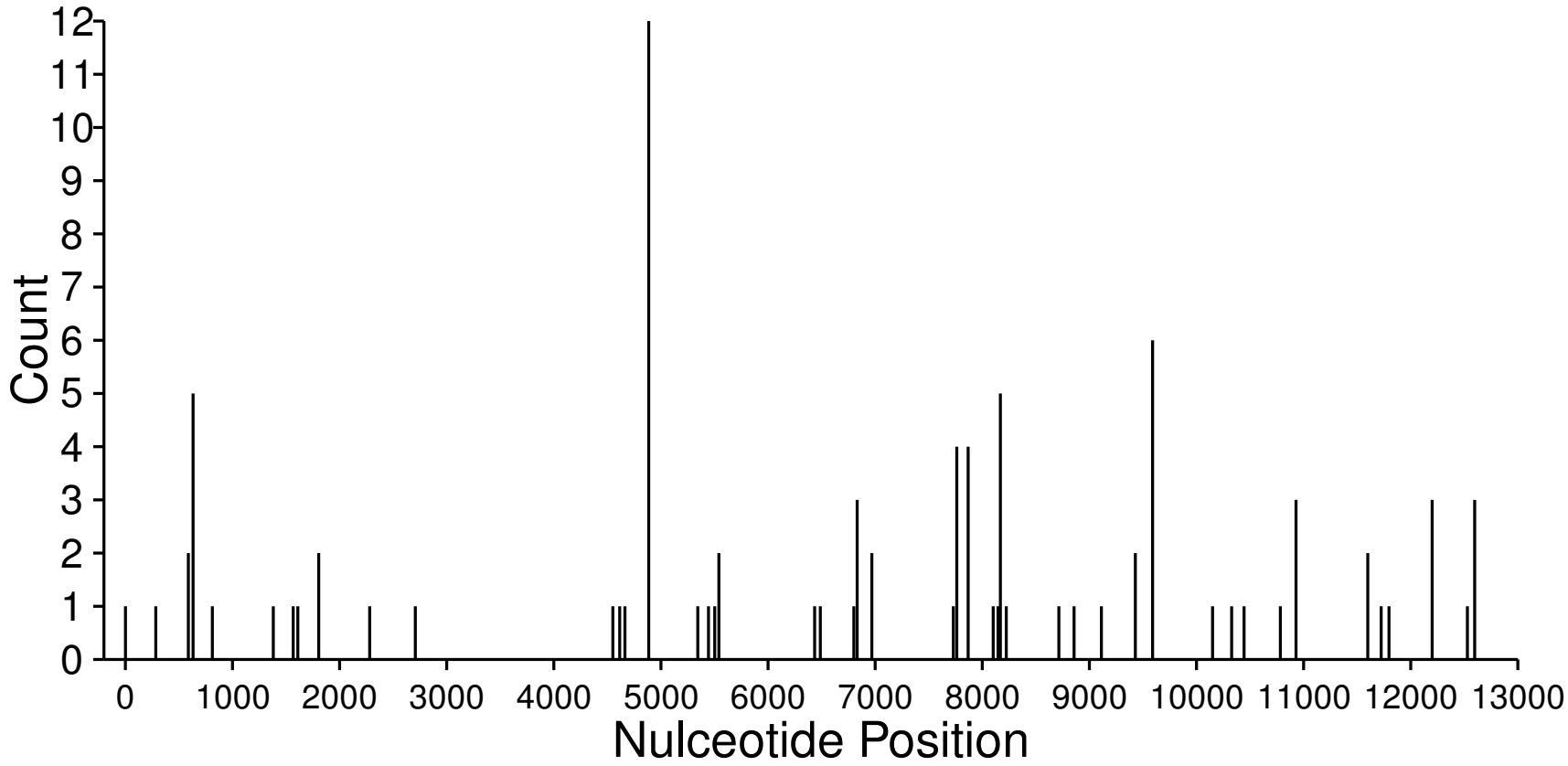
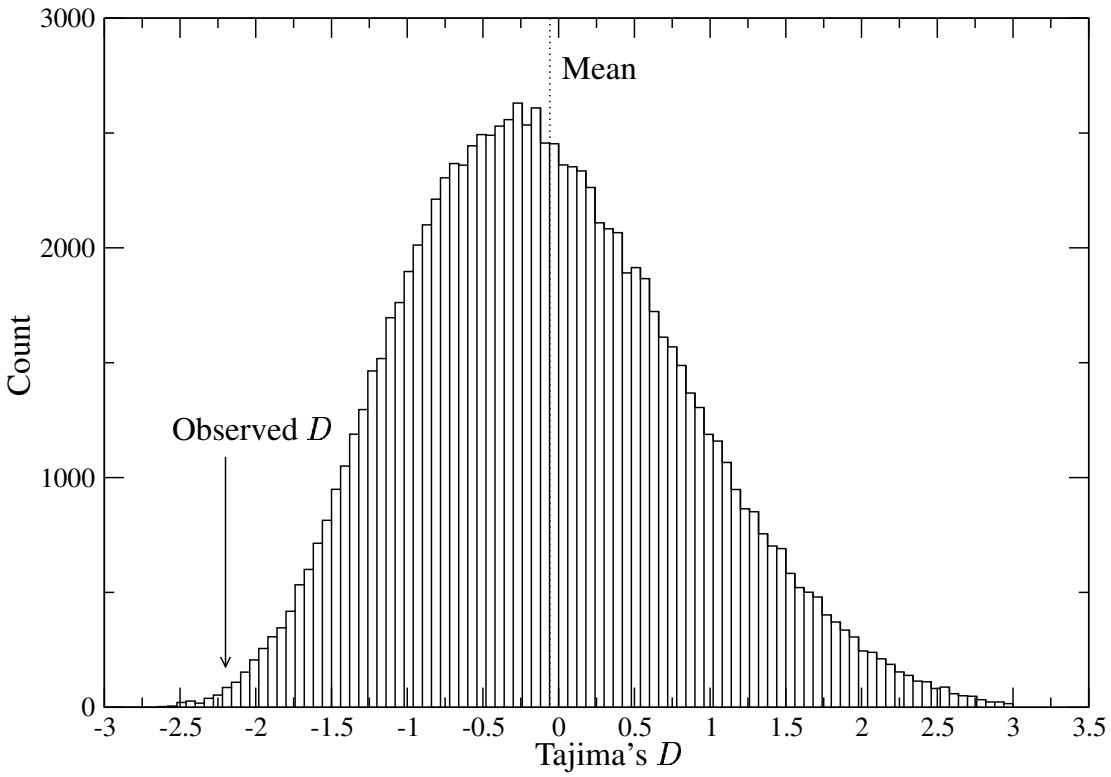
FOXP2 Haplotypes

#	Count	Haplotype
1	21	AAATAGAAACACCAGAGAGAGACGTCCGATACGTGCTATAATGATCG
2	2	.....A.....T.....
3	2	..G.....
4	2	...G.....A.....T..TA..A.....G...C.A
5	1	.....A.....
6	1	.....A.....
7	1	.....A.....C..A.....A....
8	1	.....A.....T.
9	1	C..G.AGT...TTGA....TA.....CA..CC..A.GT...G...
10	1	.....G.....
11	1	.....G.....A.....G.....T.....
12	1	.....G.....A.....T.....
13	1	...G.....A.....T..TA..A.T.....G...C.A
14	1	....G.....G.....
15	1	...G.....G...A.AGC.....TA..A....TT.....C.....
16	1	.T.....
17	1	.....T....A...C.....TT.C...C.....

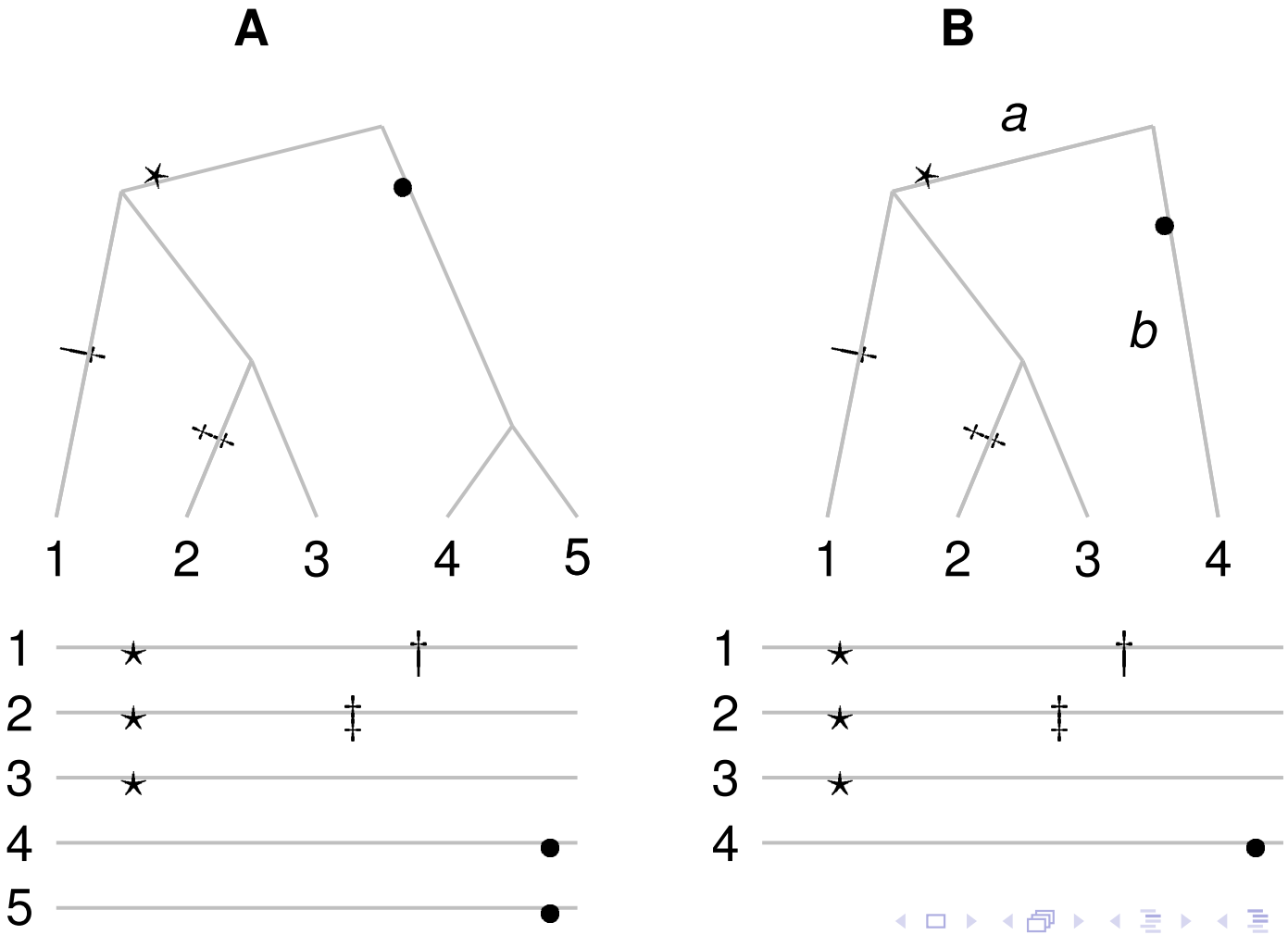
Position & Count of Rare Allele



Distribution of Tajima's *D*



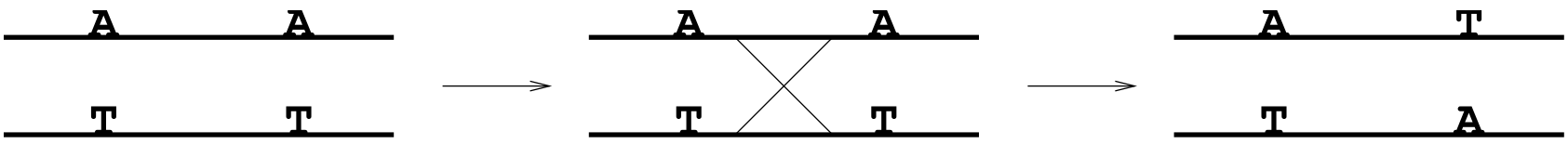
Coalescent and Singletons



Polymorphism Data for *D. melanogaster Adh*

	Fixed differences	Polymorphisms
Non-synonymous	7	2
Synonymous	17	42

Reciprocal Recombination



Index of Association

	L_1	L_2	L_3
H_1	1	1	1
H_2	1	2	1
H_3	2	2	1
H_4	2	2	2

	H_1	H_2	H_3	H_4
H_1	-			
H_2	1	-		
H_3	2	1	-	
H_4	3	2	1	-

$\longrightarrow V_{\mathrm{D}} = 0.67$

$\{h_1 = 0.67, h_2 = 0.5, h_3 = 0.5\} \rightarrow V_{\mathrm{e}} = 0.72$

$I_{\mathrm{A}}^{\mathrm{S}} = -0.04$