

Exercise 3 help file: The box below contains part of the results output by codeml for a ML analysis. This box indicates the log likelihood score required to carry out the likelihood ratio tests of exercise 3.

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TREE # 1: (1, 2, (5, ((3, 4), (((6, (8, 9)), (7, 10))), (11, 12)))); MP score: -1
check convergence..
lnL(ntime: 21 np: 23): -6018.633010 ← 10.000
  13..1  13..2  13..14  14..5  14..15  15..17  17..18  18..19
19..6  19..20  20..8  20..9  18..21  22..11  22..12
  0.165986 0.145030 0.060255 0.252090 0.030239 0.125411 0.692353 0.249467
0.205980 0.294515 0.131299 0.213038 0.174959 0.290395 0.356760 2.401783
0.136656

Note: Branch length is defined as number of mutations per codon (not per nucleotide
site).

tree length = 4.50360

(1: 0.165986, 2: 0.145030, (5: 0.252090, ((3: 0.133936, 4: 0.101768): 0.230094, (((6: 0.205980, (8:
0.131299, 9: 0.213038): 0.294515): 0.249467, (7: 0.155890, 10: 0.172753): 0.174959): 0.692353, (11:
0.290395, 12: 0.356760): 0.321380): 0.125411): 0.030239): 0.060255);

(X02152Hom: 0.165986, U07178Sus: 0.145030, (M22585rab: 0.252090, ((NM017025Rat: 0.133936, U13687Mus:
0.101768): 0.230094, (((AF070995C: 0.205980, (X04752Mus: 0.131299, U07177Rat: 0.213038): 0.294515):
0.249467, (U95378Sus: 0.155890, U13680Hom: 0.172753): 0.174959): 0.692353, (X53828OG1: 0.290395,
U28410OG2: 0.356760): 0.321380): 0.125411): 0.030239): 0.060255);
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This is the log likelihood score (lnL) computed for a dataset of 12 sequences.

The likelihood was computed for a user-supplied tree topology. That topology is shown in newick format in the line starting with "TREE # 1:"

Note: The next page contains a different part of the results for the same analysis. That output will help you identify the branch specific estimates of ω under H1, H2 and H3.

Exercise 3 help file: The box below contains output that can be found at the very bottom of the result file. These results are for a model having the same ω in all branches of the tree. Your "branch models" (specified as H1, H2 & H3) will have different ω 's for different branches, and the column marked "dN/dS" will have different values in your files (depending on the model).

		dN & dS for each branch								
		branch	t	N	S	dN/dS	dN	dS	N*dN	S*dS
Branches labeled A1 in figure (pro-orthologous <i>Ldh-A</i> sequences)	→	13..1	0.166	729.3	269.7	0.1367	0.0205	0.1497	14.9	40.4
		13..2	0.145	729.3	269.7	0.1367	0.0179	0.1308	13.0	35.3
		13..14	0.060	729.3	269.7	0.1367	0.0074	0.0543	5.4	14.7
		14..5	0.252	729.3	269.7	0.1367	0.0311	0.2273	22.7	61.3
		14..15	0.030	729.3	269.7	0.1367	0.0037	0.0273	2.7	7.4
		15..16	0.230	729.3	269.7	0.1367	0.0283	0.2075	20.7	55.9
Branches labeled C0 in figure (the proximal post-duplication branch for <i>Ldh-C</i>)		16..3	0.134	729.3	269.7	0.1367	0.0165	0.1208	12.0	32.6
		16..4	0.102	729.3	269.7	0.1367	0.0125	0.0918	9.1	24.7
	→	17..18	0.692	729.3	269.7	0.1367	0.0853	0.6242	62.2	168.3
Branches labeled C1 in figure (the distal post-duplication branches for <i>Ldh-C</i>)		18..19	0.249	729.3	269.7	0.1367	0.0307	0.2249	22.4	60.7
		19..6	0.206	729.3	269.7	0.1367	0.0254	0.1857	18.5	50.1
	→	19..20	0.295	729.3	269.7	0.1367	0.0363	0.2655	26.5	71.6
		20..8	0.131	729.3	269.7	0.1367	0.0162	0.1184	11.8	31.9
		20..9	0.213	729.3	269.7	0.1367	0.0262	0.1921	19.1	51.8
		18..21	0.175	729.3	269.7	0.1367	0.0216	0.1577	15.7	42.5
Branches labeled A0 in figure (post-duplication event <i>Ldh-A</i> sequences)		21..7	0.156	729.3	269.7	0.1367	0.0192	0.1406	14.0	37.9
		21..10	0.173	729.3	269.7	0.1367	0.0213	0.1558	15.5	42.0
	→	17..22	0.321	729.3	269.7	0.1367	0.0396	0.2898	28.9	78.1
	22..11	0.290	729.3	269.7	0.1367	0.0358	0.2618	26.1	70.6	
	22..12	0.357	729.3	269.7	0.1367	0.0440	0.3217	32.1	86.7	
tree length for dN:				0.55489						
tree length for dS:				4.06047						
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		.								