

SLAC Analysis Results

Nucleotide Model(010010) Fit Results

Log likelihood = -1787.09078680109

Nucleotide substitution rate matrix

	A	C	G	T
A	*	0.162401	1	0.162401
C	-	*	0.162401	1
G	-	-	*	0.162401
T	-	-	-	*

Codon Model Fit Results

Log Likelihood = -1705.12560615312

Tree length (expected substitutions per site) = 0.341605

Global dN/dS = 0.167436

FOUND 1 POSITIVELY SELECTED SITES (0.3 significance level)

Codon	dN-dS	Normalized dN-dS	p-value
151	2.00565	2.36703	0.287108

REL Analysis Results

Codon Model(010010) Fit Results

Log likelihood = -1678.99, AIC = 3453.97

Nucleotide substitution rate matrix

	A	C	G	T
A	*	0.206492	1	0.175733
C	-	*	0.0804541	0.694633
G	-	-	*	0.204151
T	-	-	-	*

Total Tree Length in E[subst/site]:0.388528

Fitted distributions.

Synonymous (dS)		Non-synonymous (dN)		Non-syn and syn difference (dN-dS)	
Rate	Weight	Rate	Weight	Rate	Weight
0.00000000	0.0004947	0.00296214	0.6655950	-1.09329965	0.6071497
0.00000000	0.0873145	0.40204362	0.3187059	-0.69421817	0.2907206
1.09626179	0.9121909	3.35760707	0.0156078	0.00296214	0.0584453
		10.26474971	0.0000913	0.40204362	0.0279853
				2.26134528	0.0142373
				3.35760707	0.0013705
Mean = 1		Mean = 0.183447		9.16848792	0.0000833
Variance = 0.0962618		Variance = 0.203445		10.26474971	0.0000080
				Mean = -0.816553	
				Variance = 0.299707	

FOUND 2 POSITIVELY SELECTED SITES (50 significance level)

Codon	E[dS]	E[dN]	Normalized E[dN-dS]	Posterior{dN>dS}	Bayes Factor{dN>dS}
9	1.08312	3.36074	5.86219	0.980094	432.862
151	1.01061	3.2524	5.76997	0.96414	236.372