

## **Errata**

for

Selective Constraints on Amino Acids  
Estimated by a Mechanistic Codon Substitution Model  
with Multiple Nucleotide Changes

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1. Table 9 should be replaced by the new one attached.

The values of  $\Delta\ell$  and  $\Delta\text{AIC}$  are incorrect, although conclusions drawn from this table do not change at all. Their corrected values are marked by red color.

**Table 9. Log-likelihoods of a phylogenetic tree [6]** of the concatenated sequences of 12 protein-coding sequences encoded on the same strand of mitochondrial DNA from 20 vertebrate species with 2 races from human.

Codon Substitution Model <sup>a</sup>	#p <sup>b</sup>	$\ell+$	AIC-	$\hat{\sigma}$	$\hat{m}_{[tc][ag]}$	$\hat{m}_{tc ag}/\hat{m}_{[tc][ag]}$
		<b>116898.6</b>	<b>233917.3</b>			
LG-1-F <sup>c</sup>	60	-1293.8	2587.6			
KHGaa-1-F <sup>cd</sup>	60	-1293.0	2586.1			
WAG-1-F <sup>c</sup>	60	-1108.1	2216.1			
JTT-1-F <sup>c</sup>	60	-836.4	1672.8			
mtREV-1-F <sup>c</sup>	60	0.0	0.0			
No-Constraints-1-F <sup>e</sup>	60	-1731.0	3462.1	(2.46)	(0.040)	(3.24)
WAG-ML91+-1-F <sup>e</sup>	60	1021.4	-2042.7	(2.18)	(0.524)	(3.43)
JTT-ML91+-1-F <sup>e</sup>	60	1237.7	-2475.5	(3.48)	(0.564)	(2.01)
LG-ML91+-1-F <sup>e</sup>	60	1382.2	-2764.4	(3.37)	(0.321)	(3.82)
EI-1-F <sup>e</sup>	60	1395.8	-2791.6	(0.339)	(0.737)	(3.06)
KHG-ML200-1-F <sup>e</sup>	60	1676.9	-3353.9	(2.89)	(0.228)	(1.64)
No-Constraints-11-F	70	772.2	-1524.4	0.906	0.273	3.37
EI-12-F	71	1966.6	-3911.2	0.326	0.549	3.60
WAG-ML91+-12-F	71	2268.3	-4514.5	1.84	0.471	4.16
JTT-ML91+-12-F	71	2275.1	-4528.1	3.57	0.506	2.91
KHG-ML200-12-F	71	2355.7	-4689.4	0.469	0.226	2.50
LG-ML91+-12-F	71	2510.0	-4997.9	1.26	0.357	4.32
No-Constraints-11-F-dG4	71	2495.4	-4968.9	0.000	0.182	3.62
EI-12-F-dG4	72	3742.4	-7460.7	0.000	0.392	3.95
JTT-ML91+-12-F-dG4	72	4156.9	-8289.8	0.064	0.385	3.11
KHG-ML200-12-F-dG4	72	4190.0	-8356.0	0.000	0.147	2.60
WAG-ML91+-12-F-dG4	72	4196.4	-8368.7	0.042	0.342	4.61
LG-ML91+-12-F-dG4	72	4412.6	-8801.1	0.029	0.253	4.83

<sup>a</sup> In all models named with a suffix "F", codon frequencies are taken to be equal to those in coding sequences. A suffix "dG4" means the discrete approximation of the  $\Gamma$  distribution with 4 categories [44] for rate variation. The parameter  $w_0$  in Eq. 11 is optimized in all models.

<sup>b</sup> The number of parameters; the value for the mtREV-1-F is not quite correct, because mtREV was estimated from the almost same set of protein sequences [6].

<sup>c</sup> The exchangeabilities of nonsynonymous and synonymous codon pairs are equal to  $\exp w_0$  multiplied by those of the corresponding amino acid pairs and all equal to the mean amino acid exchangeability in the empirical amino acid substitution matrix specified, respectively.

<sup>d</sup> KHGaa means the amino acid substitution matrix derived from KHG.

<sup>e</sup> All parameters except  $w_0$  and codon frequencies are fixed to those ML estimates of each model fitted to mtREV.