Table 1: Experimental results for the Q^* and NJ method

rates	#sites	$\% e_{fp}(NJ)$	$\% e_{fp}(Q^*)$	$\% e_{T^*}$	$\% e_R$
slow	300	35.14	1.00	54.7	58.6
	1000	14.00	0.71	76.9	82.4
medium	300	11.71	0.57	72.4	88.7
	1000	5.29	0.14	84.7	96.5
fast	300	8.86	0.28	75.1	95.0
	1000	3.57	0.14	86.4	98.7
fast/slow per edge	300	22.14	1.42	59.7	78.3
	1000	12.43	1.14	71.0	90.8
fast/slow per site.	300	22.29	3.43	59.4	95.1
	1000	18.29	4.43	70.9	98.4

Note to Table 1: results (averaged over $25,000$ data sets on 10 species) obtained by the Q^* and the NJ method for reconstructing a phylogeny under various conditions of evolution for sequences of 300 and 1000 sites. The following conditions of evolution were investigated: *slow* rates (≈ 0.02 expected number of mutations per site from root to a leaf), *medium* rates (≈ 0.1 expected mutations), *fast* rates (≈ 0.2 expected mutations), *fast/slow per edges* (fast rate on half of the edges and slow rate on the others), and *fast/slow per site* (fast rate on half of the sites, slow rate on the others). $\% e_{fp}(NJ)$ and $\% e_{fp}(Q^*)$ express (in percent) the number of incorrect edges inferred by the corresponding method divided by the number of internal edges of the correct phylogeny T (*i.e.*, 7). $\% e_{T^*}$ is (in percent) the number of internal edges contained in the tree inferred by the Q^* method divided by the number of internal edges of T. $\% e_R$ is (in percent) the number of internal edges of the model phylogeny where mutations actually occured when generating a data set, divided by the number of internal edges of T.