

Supplementary Information for: A random effects branch-site model for detecting episodic diversifying selection.

Sergei L Kosakovsky Pond^{1,*}, *Ben Murrell*^{2,3}, *Mathieu Fourment*⁴, *Simon DW Frost*⁵, *Wayne Delport*⁴ and *Konrad Scheffler*².

¹Department of Medicine, University of California San Diego, San Diego, California; ²Computer Science Division, Department of Mathematical Sciences, University of Stellenbosch, Stellenbosch, South Africa; ³Biomedical Informatics Research Division, eHealth Research and Innovation Platform, Medical Research Council, Tygerberg, South Africa; ⁴Department of Pathology, University of California San Diego, San Diego, California; ⁵Department of Veterinary Medicine, University of Cambridge, Cambridge, United Kingdom.

Key words: episodic selection, random effects model, evolutionary model, branch-site model

E-mail: spond@ucsd.edu

Mol. Biol. Evol. 24(1):1–3, 2008

doi:10.1093/molbev/msl161

Advance Access publication October 25, 2008

© The Author 2008. Published by Oxford University Press on behalf of the Society for Molecular Biology and Evolution. All rights reserved. For permissions, please e-mail: journals.permissions@oxfordjournals.org

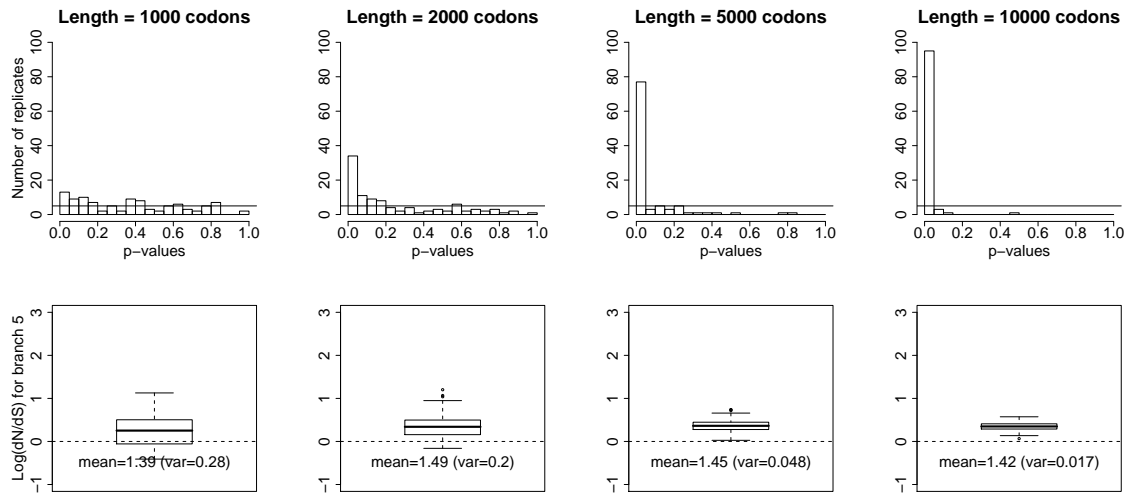


FIG. S1.—P-values of the test for selection along branch 5 for RS1 based on 100 replicates, and estimates of ω along branch 5 under the alternative (M_A) model. The horizontal line on p-value plots shows the expected distribution of p-values if the null model were true. ω estimates for the rBS model are plotted on the log scale to include outliers, but means and variances for the actual values are given (dashed line corresponds to the correct value $\omega = 1$).

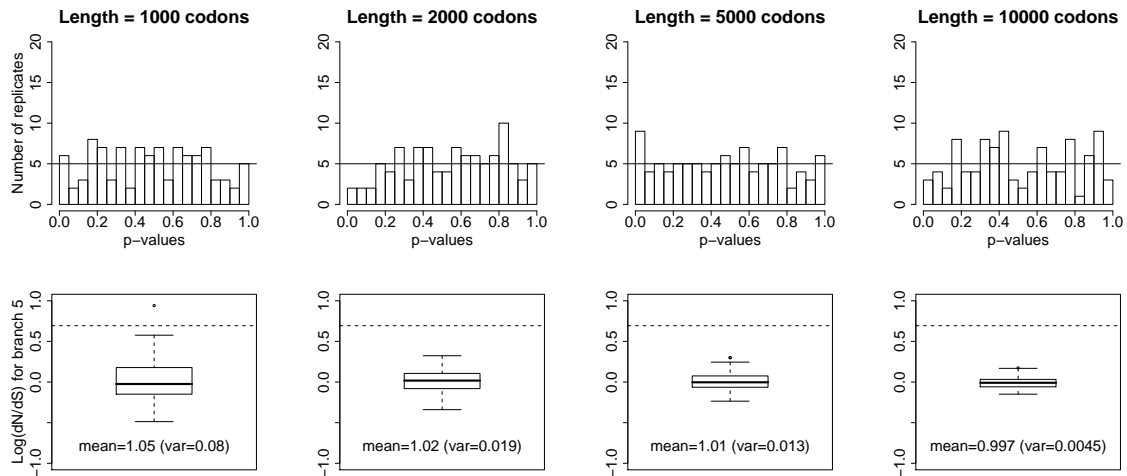


FIG. S2.—P-values of the test for selection along branch 5 for RS2 based on 100 replicates, and estimates of ω along branch 5 under the alternative (M_A) model. The horizontal line on p-value plots shows the expected distribution of p-values if the null model were true. ω estimates for the rBS model are plotted on the log scale to include outliers, but means and variances for the actual values are given (dashed line corresponds to the correct value $\omega = 2$).

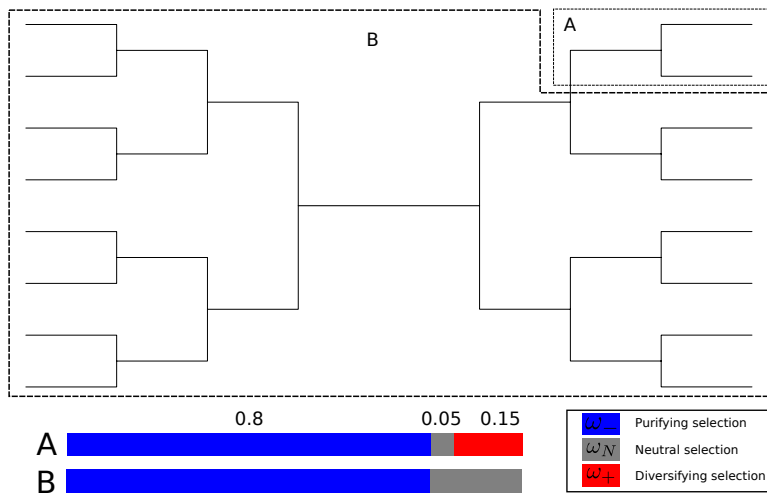


FIG. S3.—The 16-taxon tree used for simulations, each branch is 0.1 substitutions long, except for the middle branch which is 0.2 substitutions long). Branches in box (A) had an evolutionary configuration depicted in the colored bar (A) and the rest of the branches had configuration (B).