

Online Appendix 1

Species Selection Regime and Phylogenetic Tree Shape

G. Anthony Verboom, Florian C. Boucher, David D. Ackerly, Lara M. Wootton and William A. Freyman

Table 1. Best-fit linear models describing the responses of R_{crit} as a function of β , μ (0 and 0.2) and the variable used to identify R_{crit} (i.e. I_c , γ or $r_{rate-trait}$)

The latter is a three-level factor, with γ specified as the reference variable. The best-fit model was determined using stepwise model simplification under the Akaike Information Criterion. Significance of coefficients is indicated as follows: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. The model has adjusted $r^2 = 0.906$ ($p < 0.001$).

Term	Coefficient
Intercept	0.121***
β	2.497***
Variable (I_c)	0.048*
Variable ($r_{rate-trait}$)	0.069**
$\beta : \mu$	8.295***

Figure captions

Fig. 1. Schematic illustrating how the three tree shape metrics relate to variation in tree shape. (a) Colless' (1982) I_c quantifies tree-wide clade imbalance, with a perfectly balanced tree being described by $I_c = 0$ and imbalanced trees having $I_c > 0$. (b) The gamma (γ) statistic (Pybus and Harvey 2000) quantifies the distribution of branching events between the root and the tips, with $\gamma < 0$ describing trees with branching events concentrated near the root, and $\gamma > 0$ describing trees with branching events concentrated close to the present. (c) The diversification rate-trait correlation ($r_{rate-trait}$) describes the extent to which tip-specific values of a putative diversification trait (indicated by filled circles) are correlated with the tip specific diversification rate, the latter quantified as the number of nodes separating the tips from the crown node. Where $r_{rate-trait} = 0$ reflects the lack of any correlation, $r_{rate-trait} < 0$ indicates a negative correlation (as in the left panel) and $r_{rate-trait} > 0$ indicates a positive correlation.

Fig. 2. Variation in the mean size (species number, N ; log-scale), mean Yule-normalized Colless' index (I_c), mean gamma statistic (γ) and mean diversification rate-trait correlation ($r_{rate-trait}$) of trees generated in QuaSSE under a constant model with $\mu = 0$ (i.e. Yule model). β was set arbitrarily to 0.01. The results are plotted against net diversification rate (NDR). Each point is a summary of trees generated by 100 replicate runs, excluding any runs going extinct or yielding a single species.

Fig. 3. Variation in the mean size (species number, N ; log-scale), mean Yule-normalized Colless' index (I_c), mean gamma statistic (γ) and mean diversification rate-trait correlation ($r_{rate-trait}$) of trees generated under static Gaussian-speciation with $\mu = 0$ (black-filled circles) and $\mu = 0.2$ (open circles). Results are presented for $\beta = [0.005, 5]$, and plotted against maximum net diversification rate ($NDR_{max} = \lambda_{max} - \mu$ or $\lambda - \mu_{min}$). Each point is a summary of

trees generated by 100 replicate runs, excluding any runs going extinct or yielding a single species. Solid and dashed lines indicate significant bivariate relationships based on the $\mu = 0$ and $\mu = 0.2$ data, respectively.

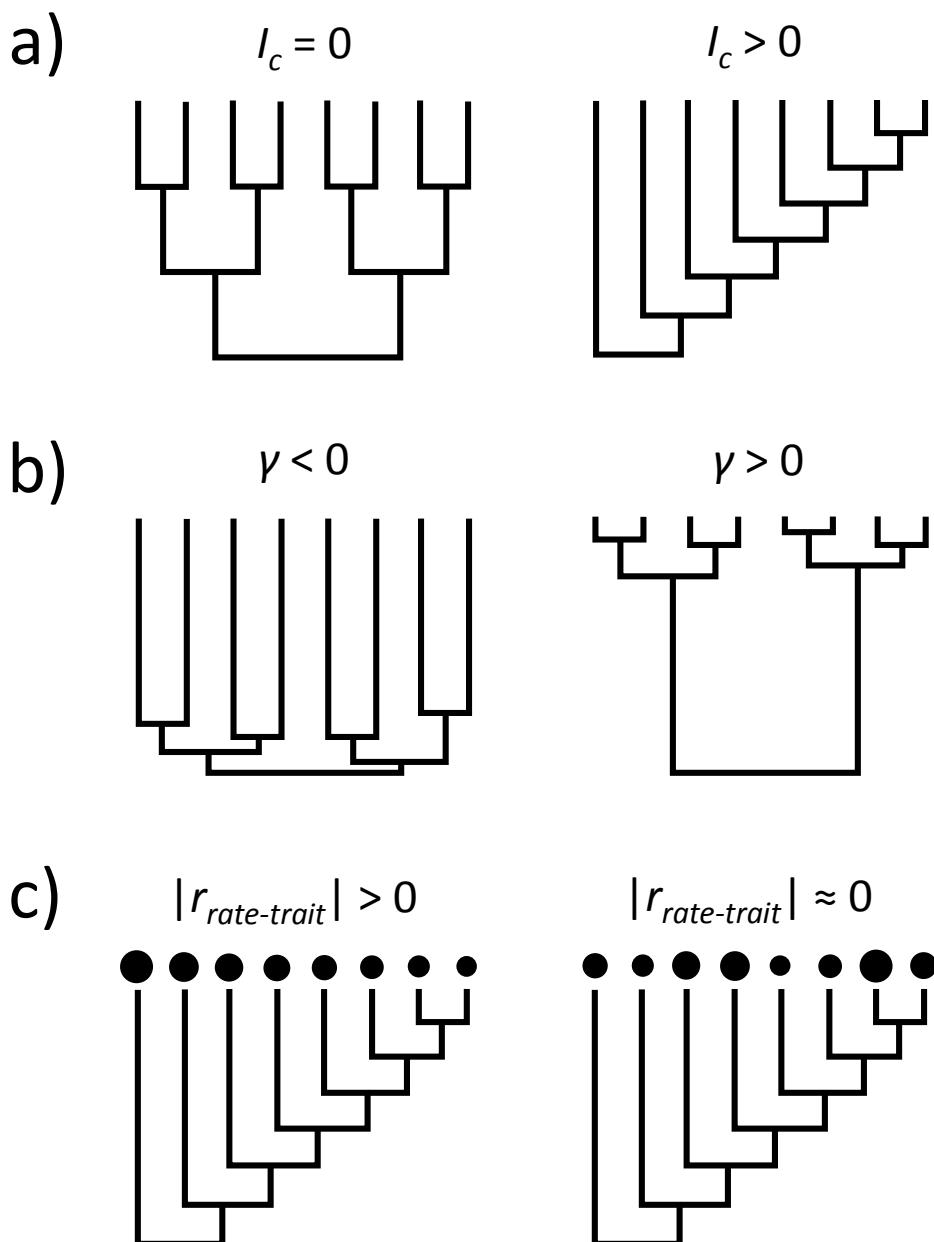
Fig. 4. The relationships of R_{crit} , as identified on the basis of I_c (circles, solid lines), γ (squares, dashed lines) and $r_{rate-trait}$ (triangles, dotted lines), to β for simulations done under $\mu = 0$ (filled symbols) and $\mu = 0.2$ (open symbols). Lines represent the significant bivariate linear relationships of R_{crit} to β for each combination of I_c , γ or $r_{rate-trait}$ and μ .

Fig. 5. Variation in the mean size (species number, N ; log-scale), mean Yule-normalized Colless' index (I_c), mean gamma statistic (γ) and mean diversification rate-trait correlation ($r_{rate-trait}$), plotted against the shift rate of the diversification function (R_{shift}), of trees generated under shifting Gaussian-speciation with $\mu = 0$ (black-filled circles) and $\mu = 0.2$ (open symbols). Results are presented for $\beta = [0.005, 5]$ and only for simulations run under $NDR_{max} (\lambda_{max} - \mu \text{ or } \lambda - \mu_{min}) = 0.6$. Each point is a summary of trees generated by 100 replicate runs, excluding any runs going extinct or yielding a single species.

Fig. 6. Application of breakpoint regression to the relationships of mean Yule-normalized Colless' index (I_c), mean gamma statistic (γ) and mean diversification rate-trait correlation ($r_{rate-trait}$) to the shift rate of the diversification function (R_{shift}), for trees generated under Gaussian-extinction. Results are presented for $\beta = [0.005, 0.1]$ and only for simulations run under $NDR_{max} = 0.6$. Each point is a summary of trees generated by 100 replicate runs, excluding any runs going extinct or yielding a single species. Bold circles indicate the positions of breakpoints identified as significant by the Davies (2002) test.

Fig. 7. Ordinations of trees with ≥ 100 species generated under Gaussian-speciation (with $\mu = 0$ and $\mu = 0.2$), skewed-speciation (negatively and positively skewed) and Gaussian extinction, based on linear discriminant analyses applied to I_c , γ and $r_{rate-trait}$ scores. Separate

analyses were done for $R_{shift} < 0.05$, $0.05 < R_{shift} < 0.15$, $0.15 < R_{shift} < 0.25$ and $R_{shift} > 0.25$, each column presenting the result of a different analysis. Within each column, the trees associated with each model are plotted separately (rows 1-5) and together (row 6). Within each plot the x- and y-axes describe the first and second linear discriminant functions.

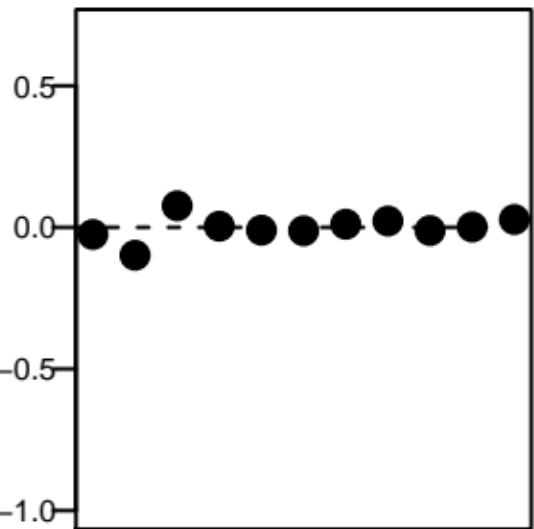
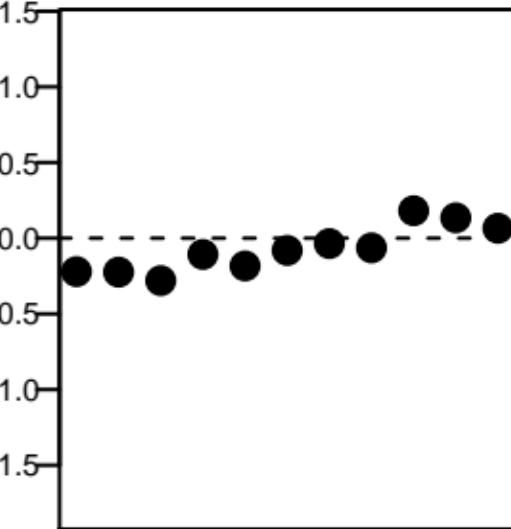
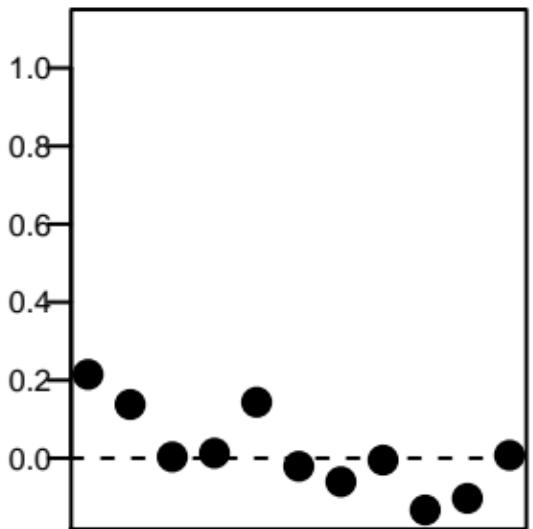
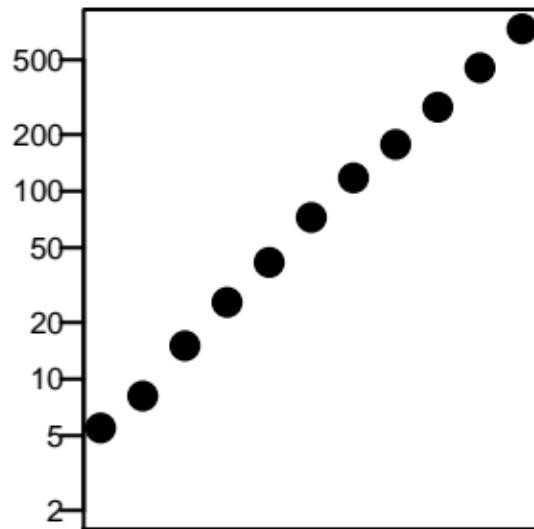


N

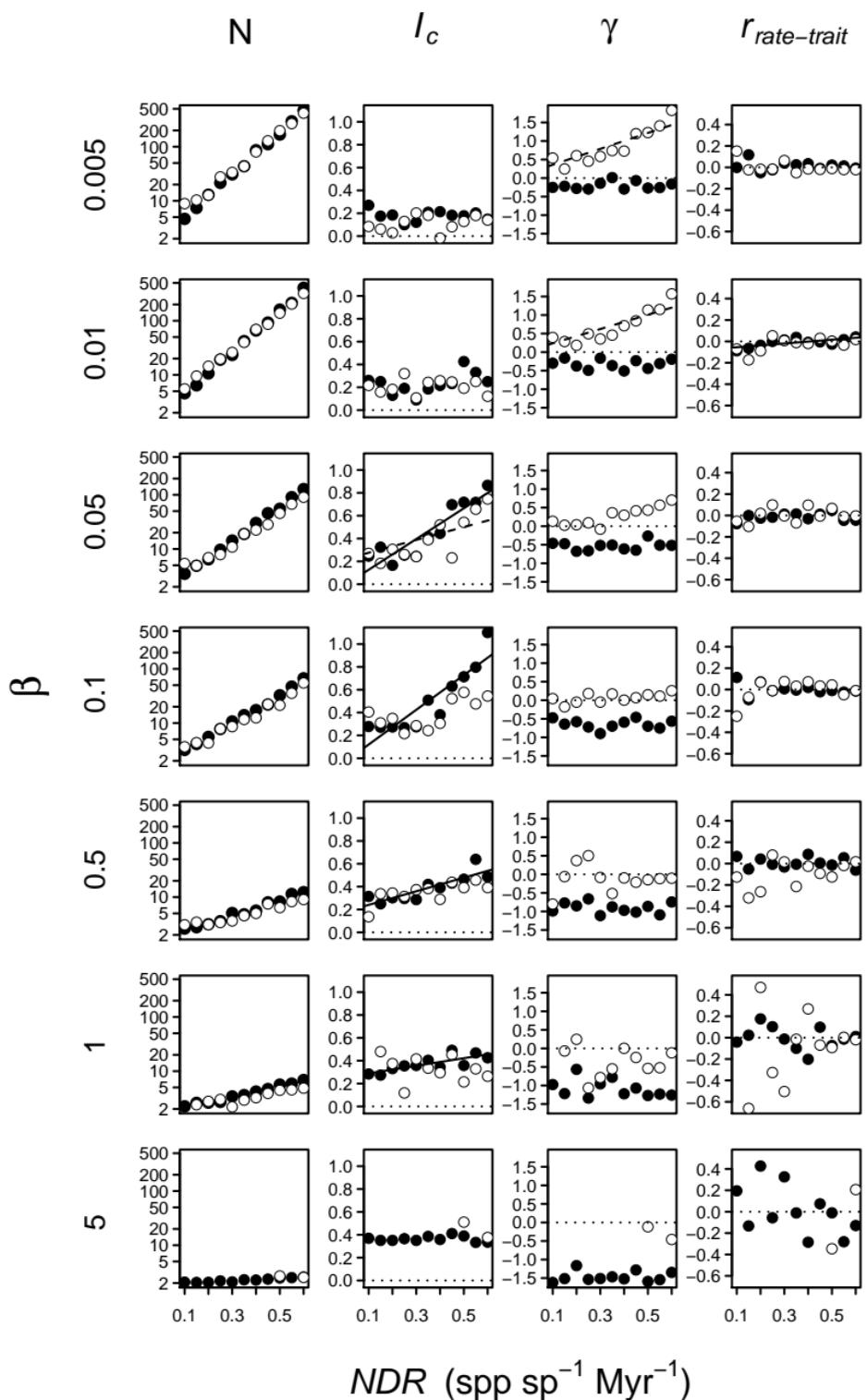
I_c

γ

$r_{rate-trait}$



NDR (spp sp $^{-1}$ Myr $^{-1}$)



R_{crit}

0.6
0.5
0.4
0.3
0.2
0.1

0.02 0.04 0.06 0.08 0.10

 β 