

Figure S1. Map of the study bioregions (modified from Olson et al. 2001 and Jetz & Fine 2012).

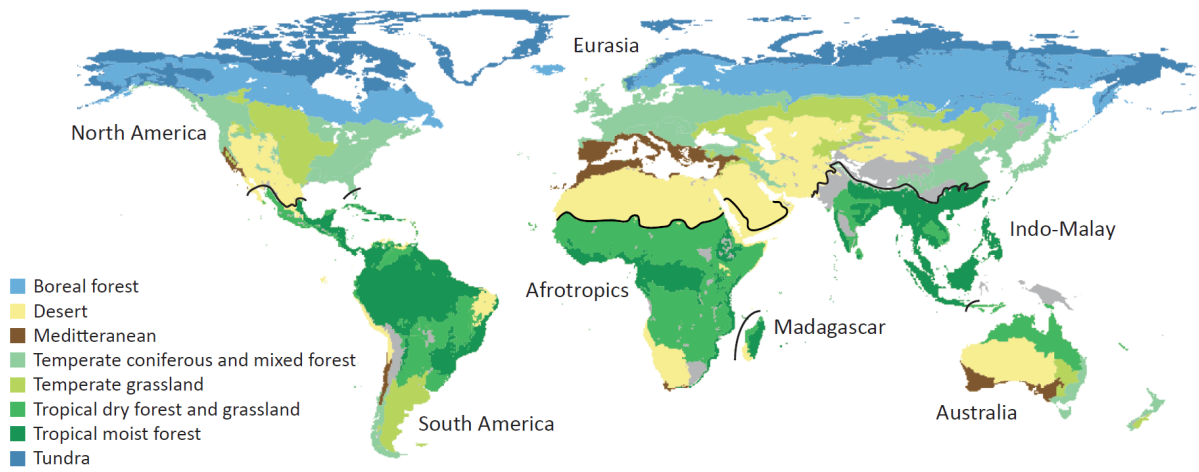


Figure S2. Summary figure of the estimation of direct and indirect variables.

For each bioregion (a) we computed three direct (b, c, d) and three indirect (e, f, g) variables.

Maximum clade age (b) is the age of the oldest clade in which all component species are found in the bioregion. *Speciation rate* (c) is the average speciation rate of the clades belonging to the focal bioregion. *Dispersal rate* (d) is the dispersal rate from any bioregion to the focal bioregion (d_B). *Temperature* (e) is the mean temperature of the focal bioregion, *productivity* (f) is the total productivity of the focal bioregion, and *area through time* (g), our measure of climatic stability, is the integration of the focal bioregion area over the past 55 My (see methods for more details).

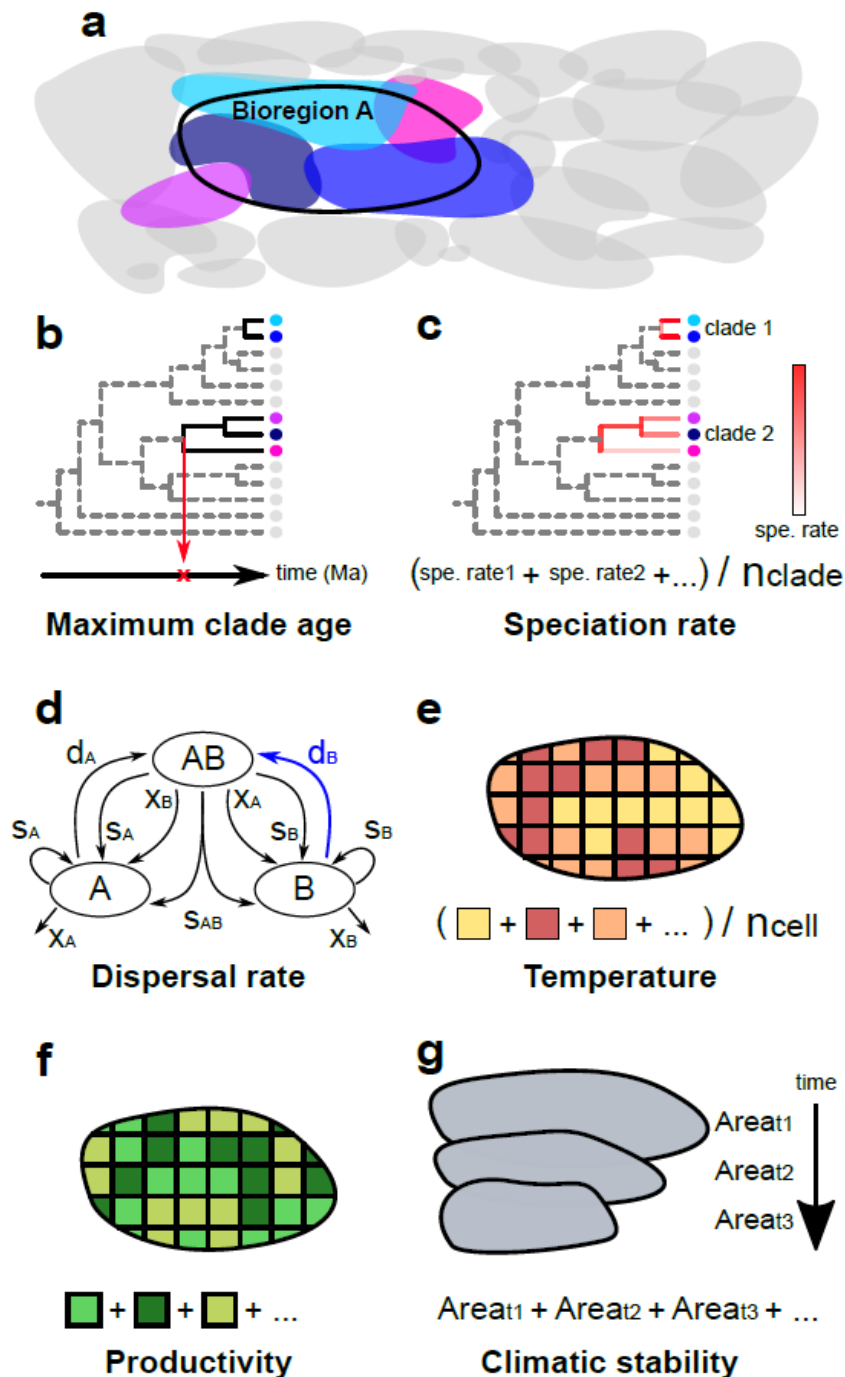


Figure S3. Structural equation models depicting the associations of direct and indirect variables with species richness (full model, model 1). *Maximum clade age, speciation rate, and dispersal rate* are the direct variables and *area through time, productivity, and temperature* the indirect variables, for tetrapods, amphibians, birds, mammals, and squamates. Bold path arrows represent significant (at $P < 0.05$) associations. Numbers adjacent to arrows represent β -standardised regression coefficients. R^2 value associated with each exogenous variable are in italics. For amphibians we also indicated β -standardised regression coefficients and R^2 values after the removal of the outlier clade of Mediterranean Alytidae (12 species) if the result changed (value in second position). Max.: maximum.

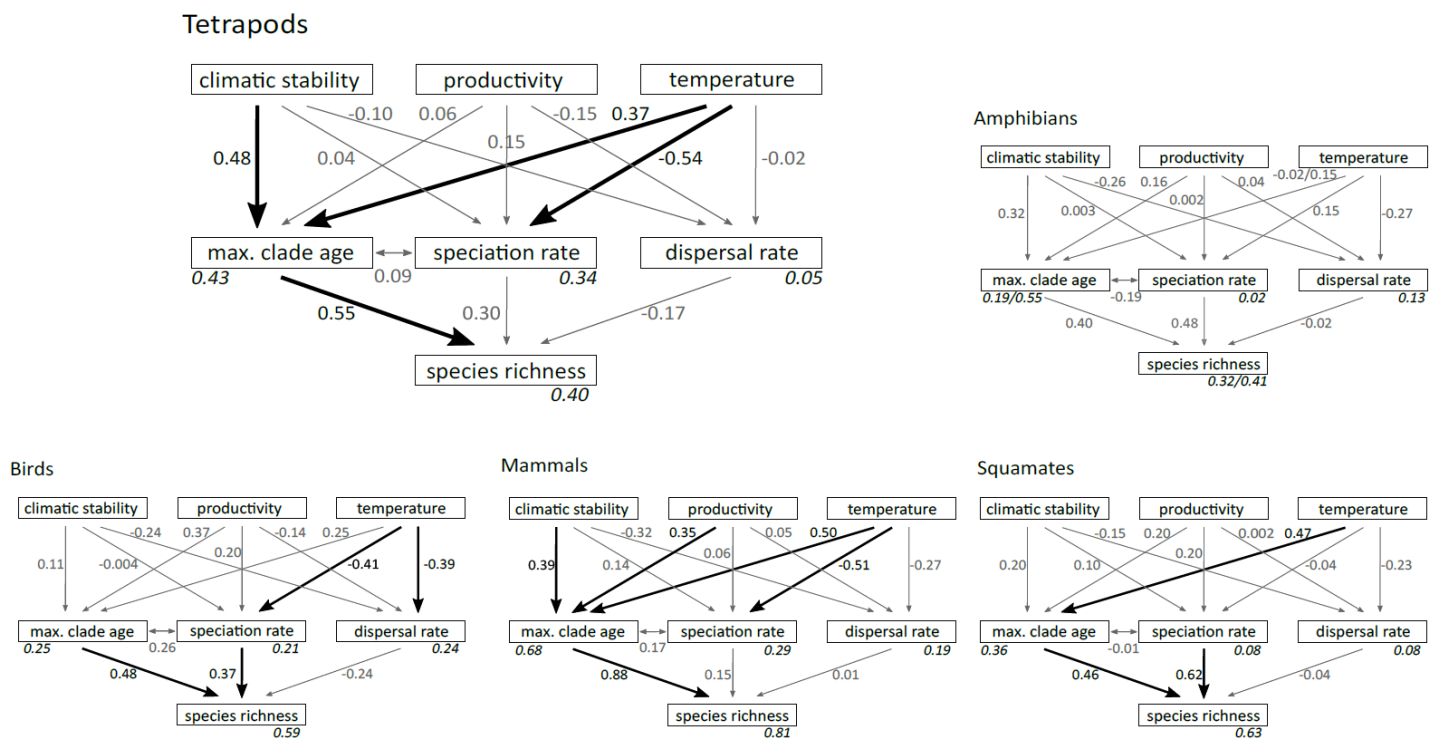


Figure S4. Structural equation models depicting the associations of direct (*maximum clade age*, *diversification rate*, and *dispersal*) and indirect (*area through time*, *productivity*, and *temperature*) variables with species richness (model 1) for tetrapods, amphibians, birds, mammals, and squamates. Bold path arrows represent significant (at $P < 0.05$) associations. Numbers adjacent to arrows represent β -standardised regression coefficients. R^2 value associated with each exogenous variable are in italics. For amphibians we also indicated β -standardised regression coefficients and R^2 values after the removal of the outlier clade of Mediterranean Alytidae (12 species) if the result changed (value in second position). Div.: diversification, max.: maximum.

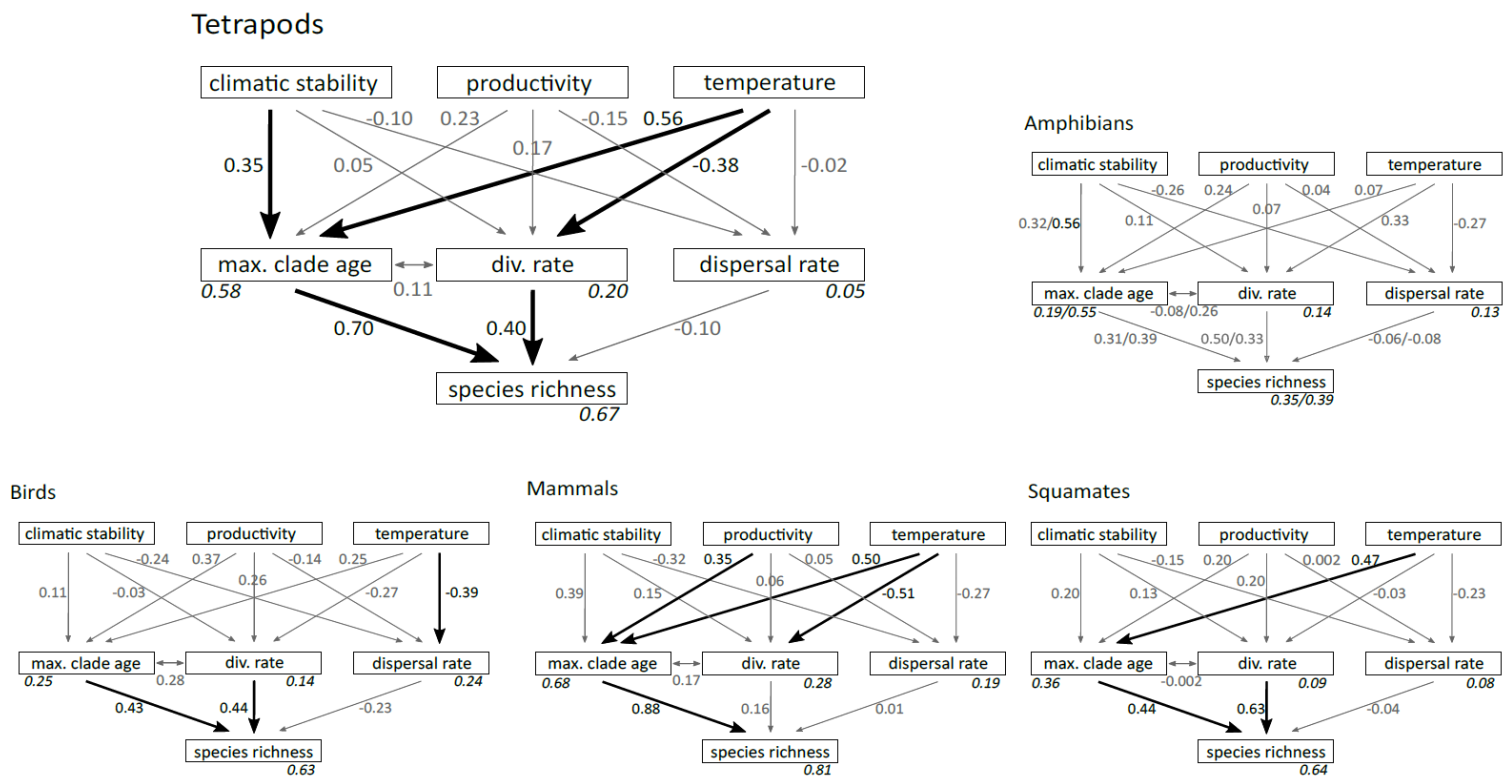


Figure S5. Path models depicting the associations of direct (*maximum clade age* and *diversification rate*) and indirect (*area through time*, *productivity*, and *temperature*) variables with species richness (model 2) for tetrapods, amphibians, birds, mammals, and squamates. Bold path arrows represent significant (at $P < 0.05$) associations. Numbers adjacent to arrows represent β -standardised regression coefficients. R^2 value associated with each exogenous variable are in italics. For amphibians we also indicated β -standardised regression coefficients and R^2 values after the removal of the outlier clade of Mediterranean Alytidae (12 species) if the result changed (value in second position). Div.: diversification, max.: maximum.

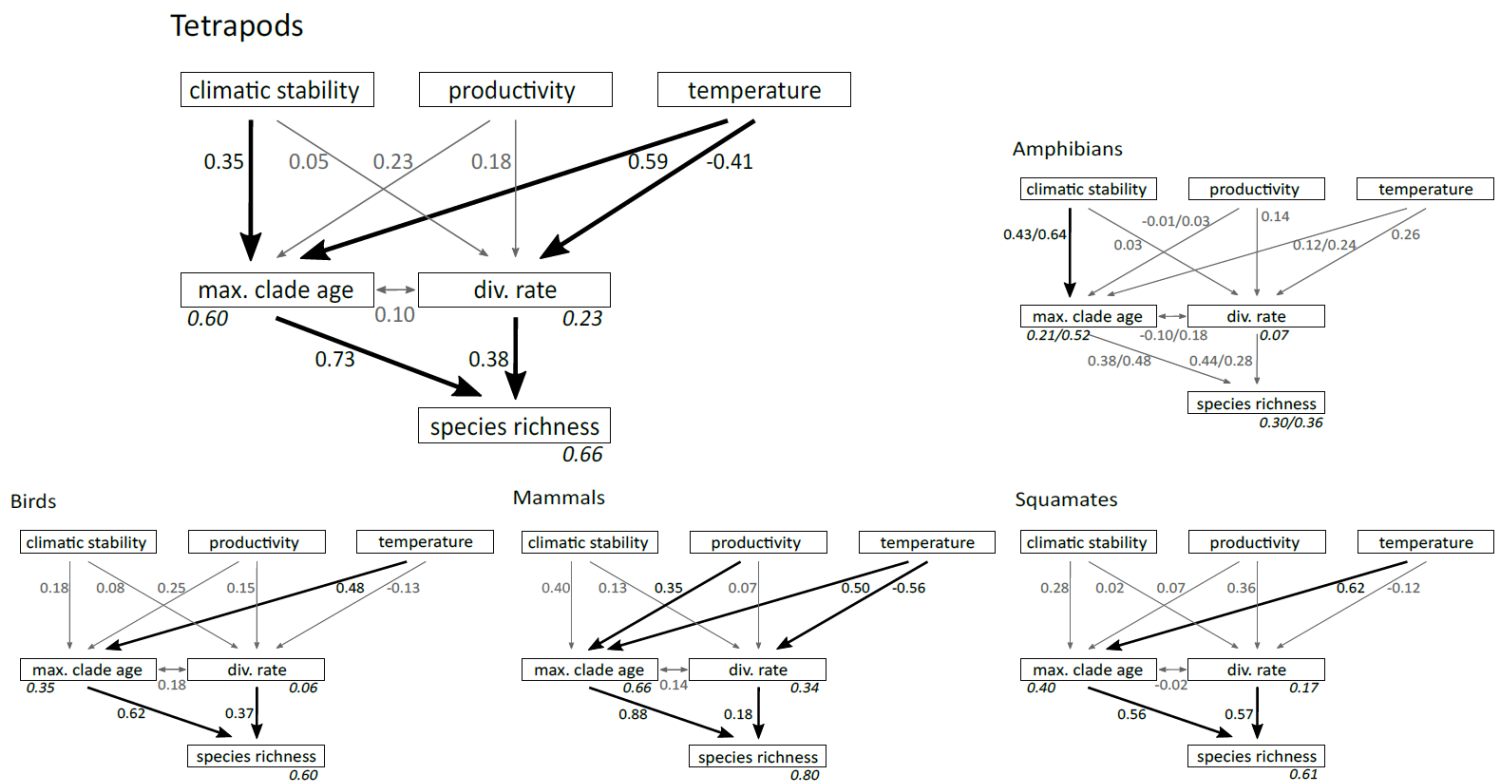


Figure S6. Distribution of the correlation coefficients between *maximum clade age* and *richness*. The correlation was calculated 1000 times over 100 regions for which X clades were sampled from a variable birth-death simulated timetree (see methods). The black line represents the 0.95 upper limit of the distribution and the red lines the estimated correlation coefficients of amphibians (a; without the outlier clade), birds (c), mammals (e), squamates (b), and tetrapods (d).

