

Figure 5 Estimates of linear relationships between mean annual temperature (°C) and net ecosystem exchange ($\text{g C m}^{-2} \text{ season}^{-1}$) of CO_2 during the growing season (GS; blue), and winter (red) with 95% confidence intervals, and the annual estimate (black) of the temperature relationship produced by summing predicted values of seasonal trends and their variances. Positive values denote a C source.

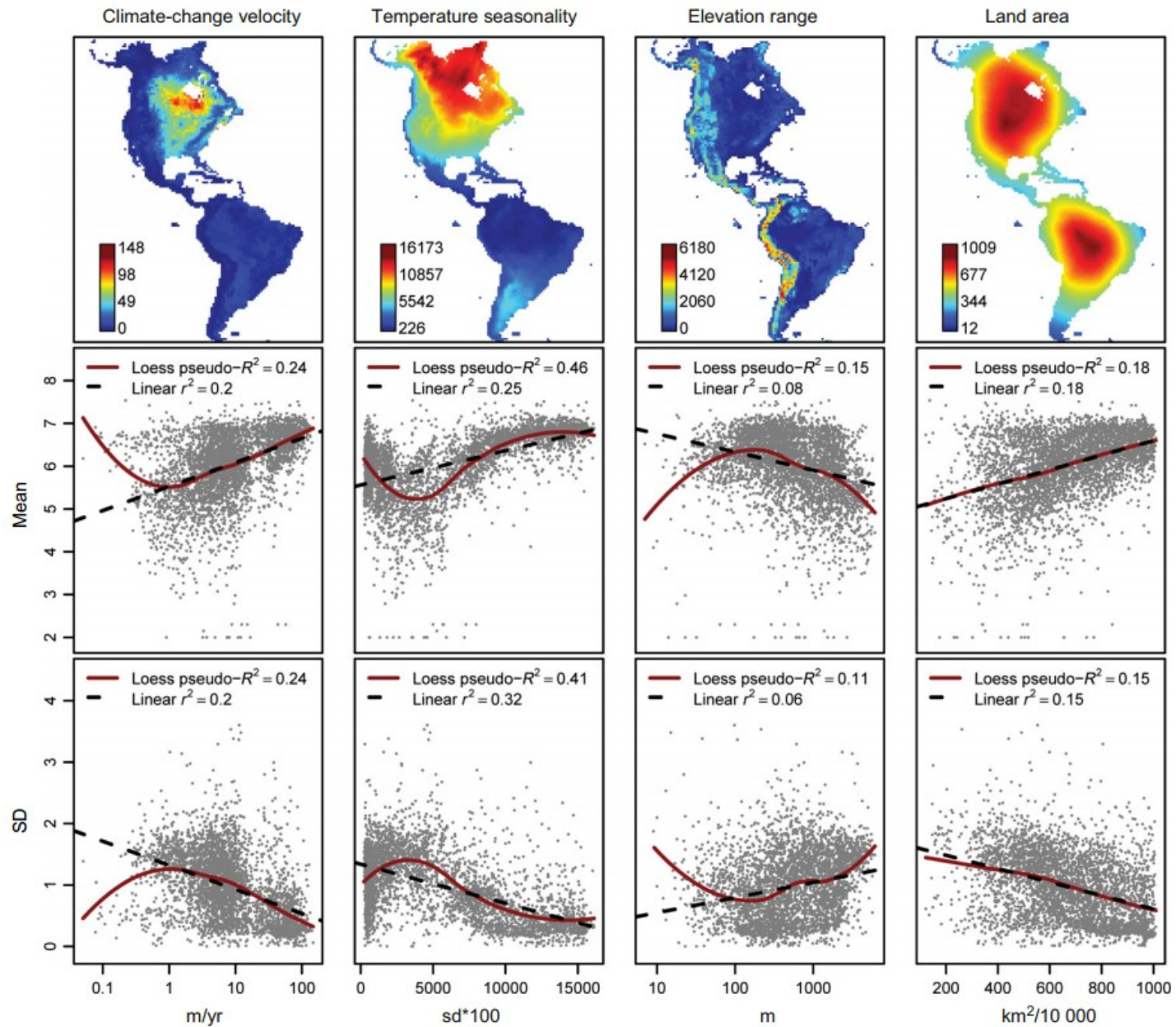
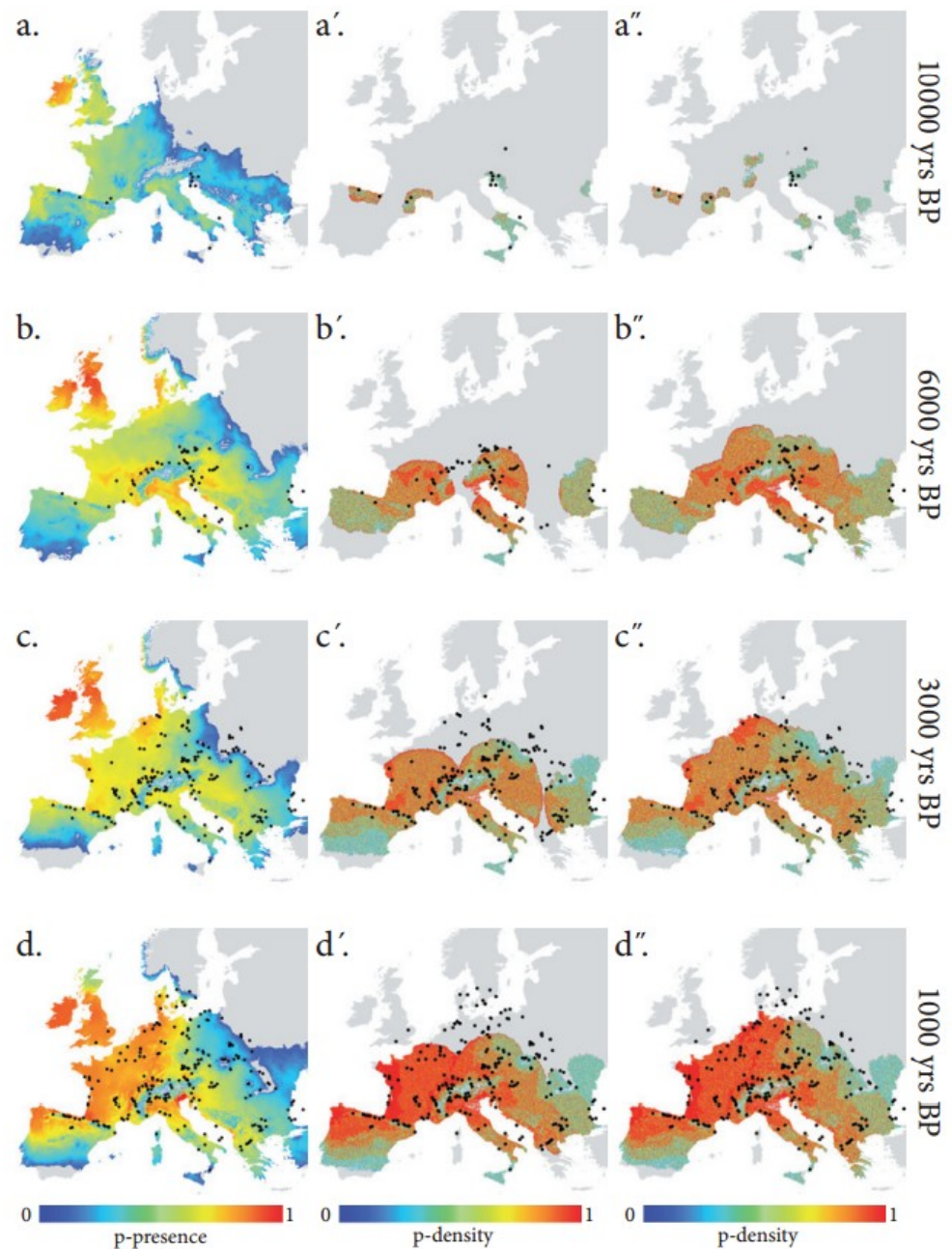


Figure 2 *Fagus sylvatica* distribution maps at 10 (a, a', a''), 6 (b, b', b''), 3 (c, c', c'') and 1 (d, d', d'') kyr BP. Potentially suitable habitats (a–d) derived from probabilities of presence (p-presence) simulated by PHENOFIT. Colonized habitats, starting from the first (a'–d') and the second (a''–d'') refugia scenario, derived from probabilities of density (p-density, number of cohorts in each grid cell) simulated by PHENOFIT and the Gibbs-based model. Grey areas correspond to a simulated absence of beech. Black points correspond to palaeoarchives of beech [pollen > 2% and macrofossils, (Magri et al., 2006)] at the same dates (indicated on the right side of the figure).



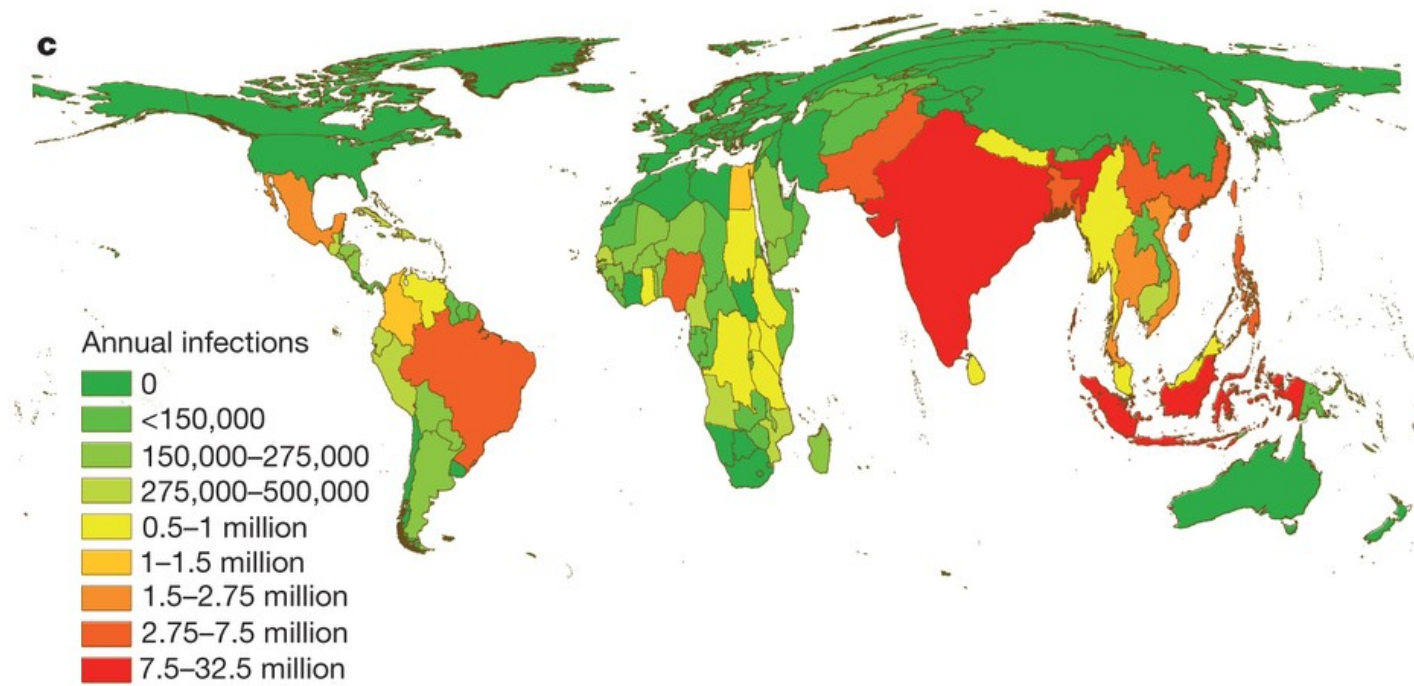
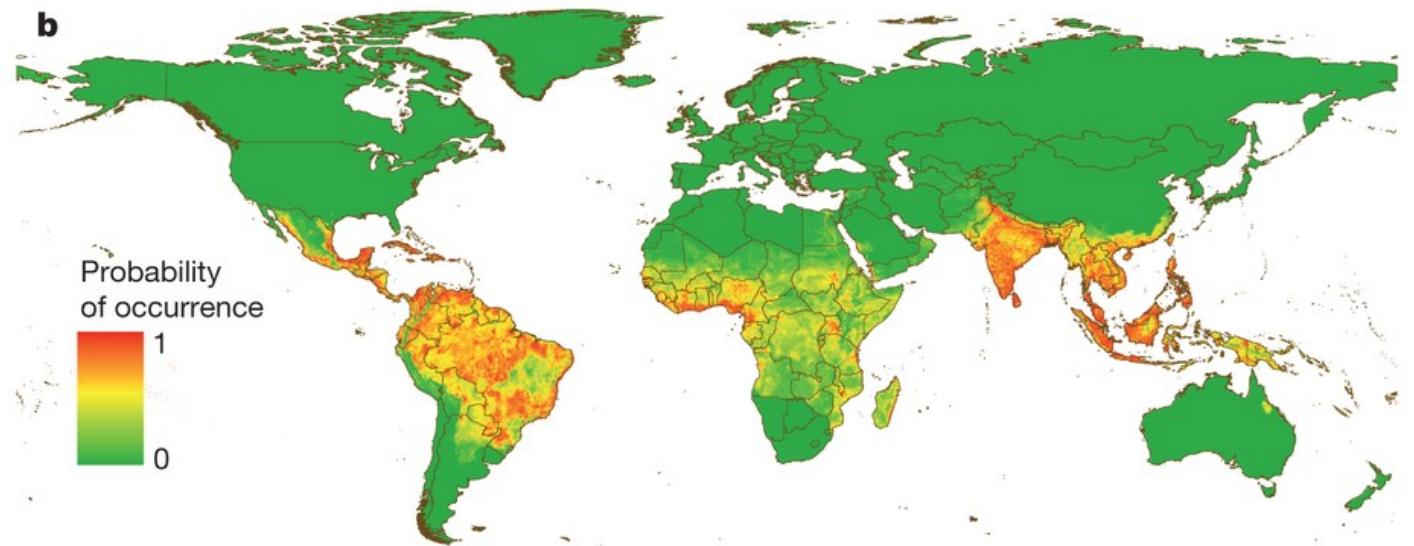


Figure 1 Spatial variation in phylogenetic species variability (PSV) (a) and net relatedness index (NRI) (b).

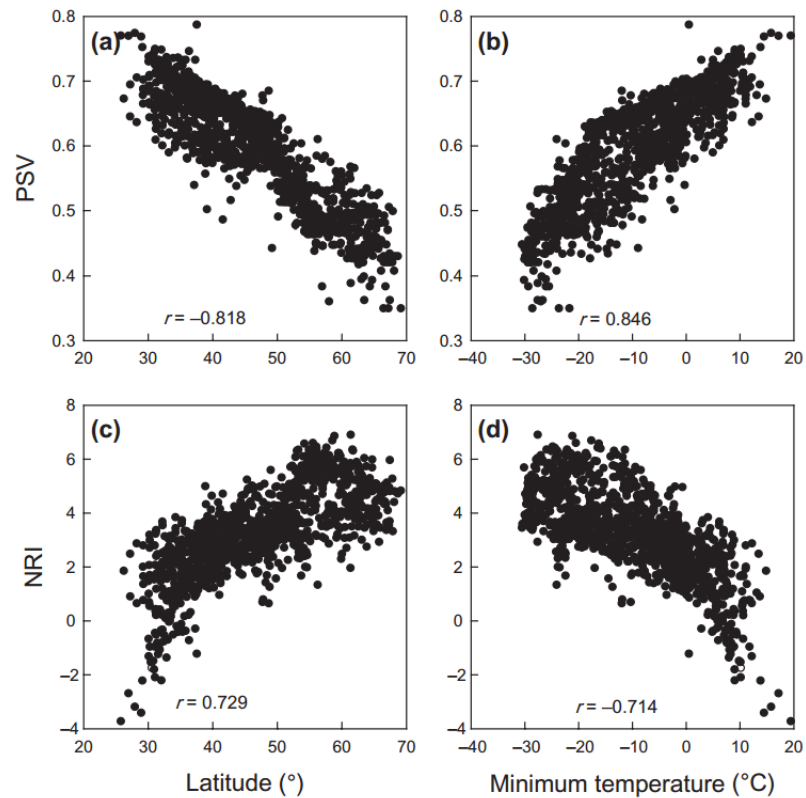
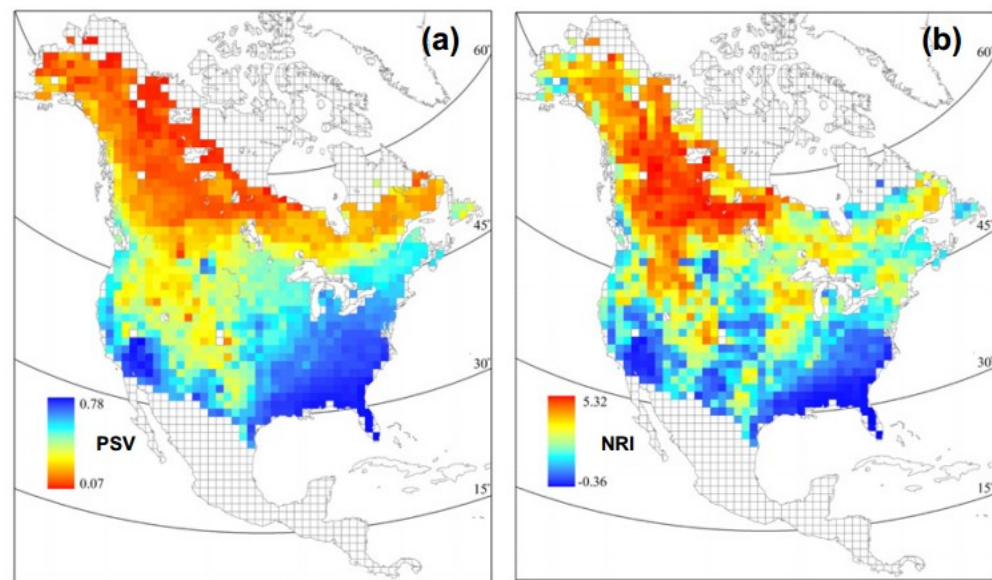
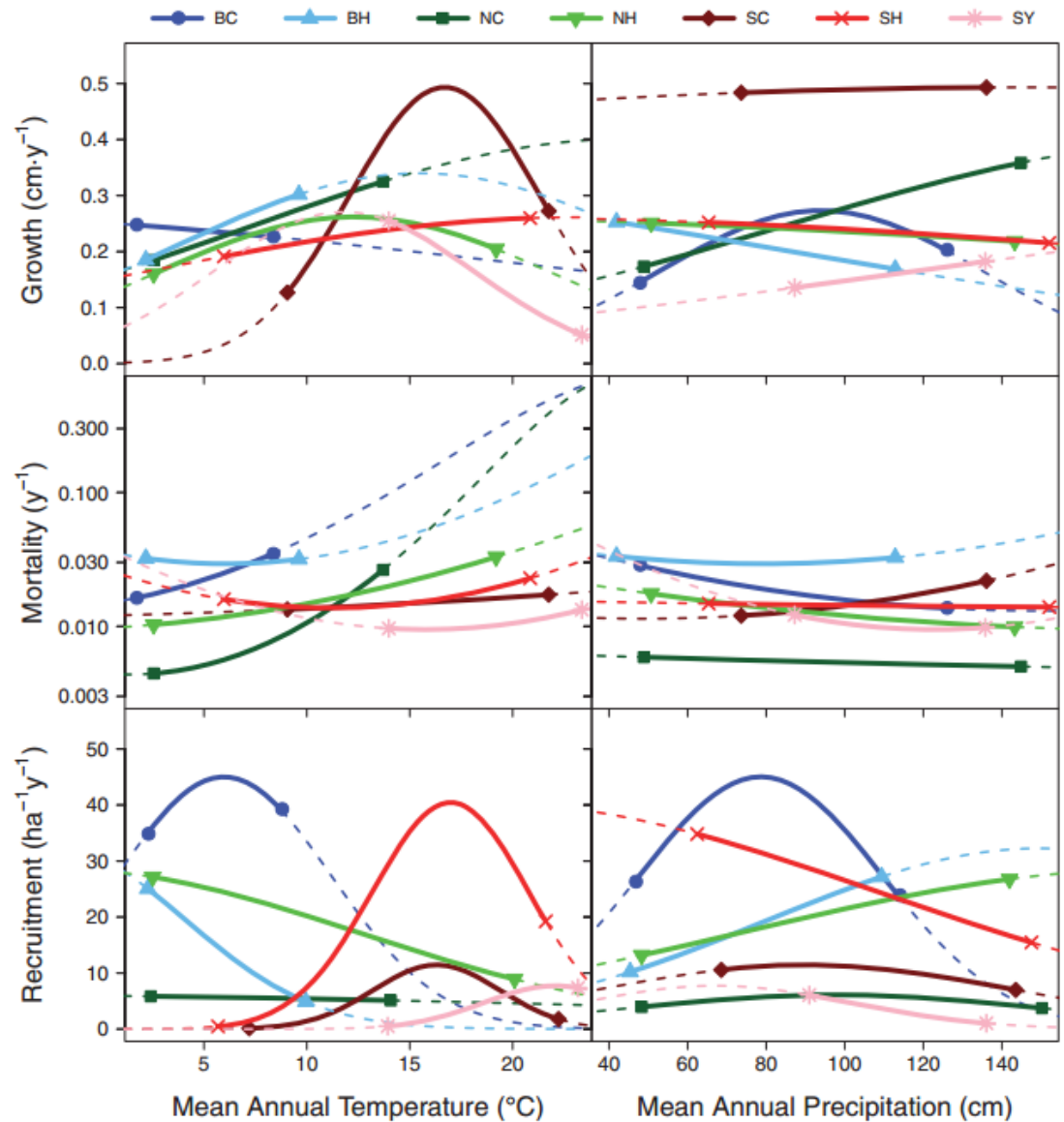


Figure 2 Predicted tree diameter growth rate, mortality rate and recruitment rate (ingrowth of stems surpassing 2.54 cm diameter) for seven plant functional types (PFTs) in the eastern USA against mean annual temperature and precipitation. The climate dependency of each rate was modelled as a Gaussian-shaped response to a linear combination of temperature and precipitation. The solid portion of each line indicates the interval between the 1st and 99th percentiles of temperature or precipitation for each PFT; the dashed portion represents extrapolations outside this range. All other covariates were fixed to their mean values in calculating these responses. PFT legend abbreviations are as in Fig. 3.





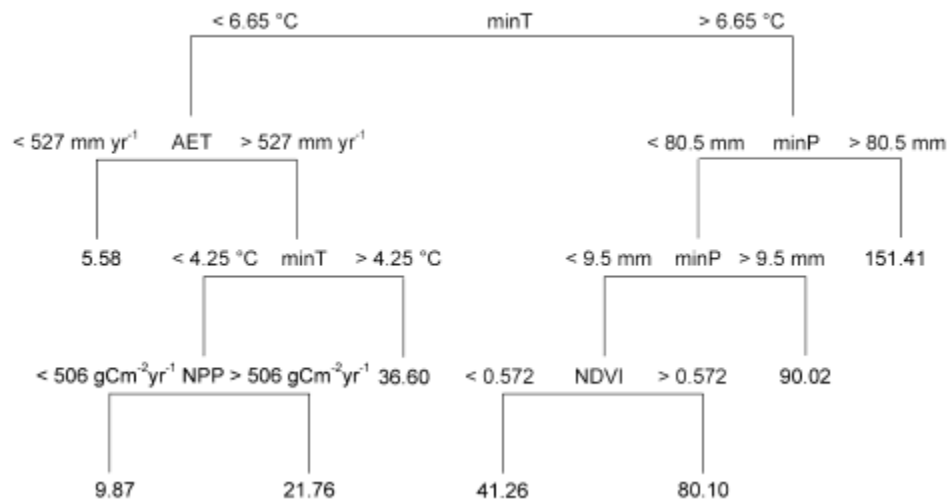


Figure 4 Regression tree for species richness of forest plots based on binary recursive variance partitioning. As explanatory variables we used all single-term variables from Table 1. Names of the splitter variables and their split value are indicated at each node. Geometric means for species richness in each terminal group are given at each terminal branch.

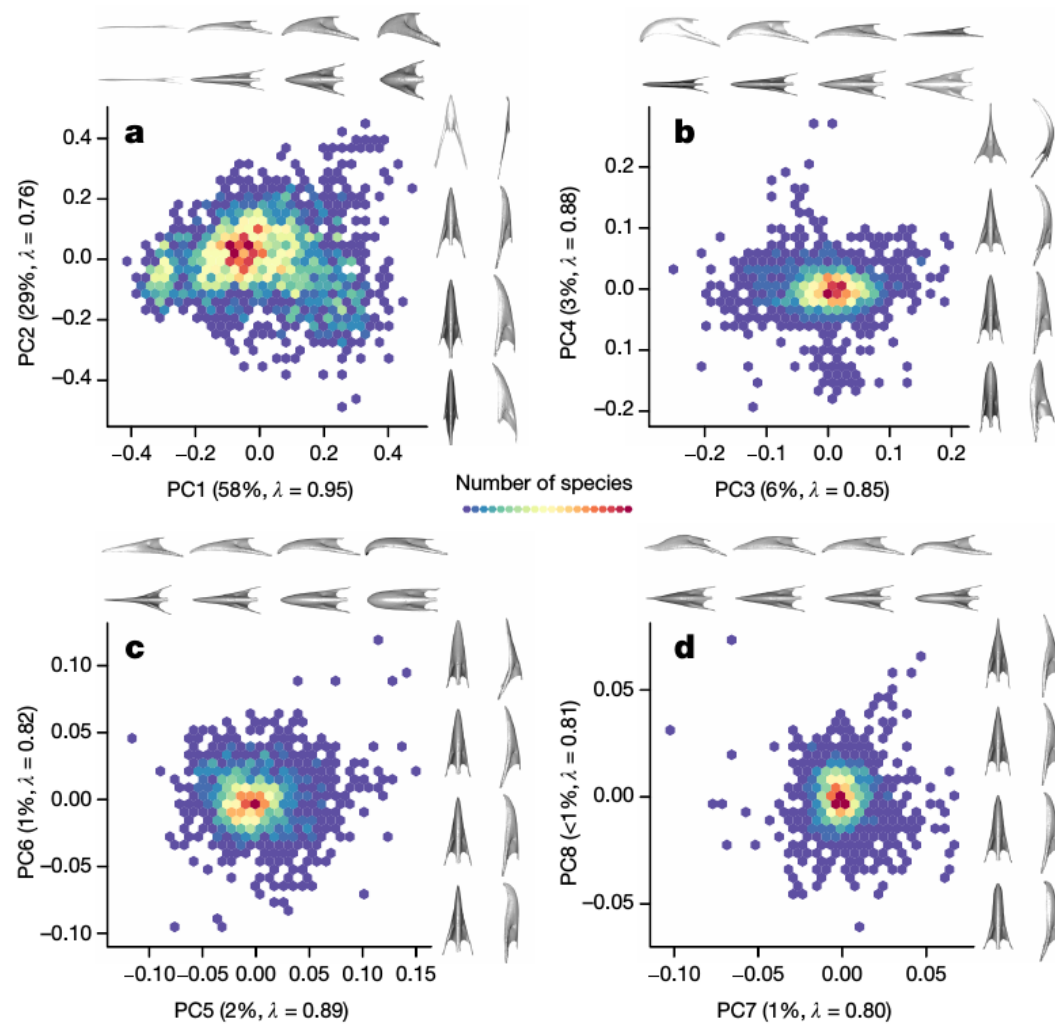


Figure 1 | Bird bill morphospace density plots. PC axes 1–8 are shown as pairwise scatter plots, along with warps representing the change in bill shape ($n = 2,028$ species) along each axis in dorsal and lateral views. Each axis is labelled with the proportion of variance explained and estimates of phylogenetic signal (Pagel's λ). The colour scale refers to the number of species in 20 bins with minimum and maximum richness of 1–23 (a), 1–72 (b), 1–64 (c) and 1–98 (d) species, respectively.