**Supporting Information** forthe article “*Resolving whole-plant economics from leaf, stem and root traits of 1467 Amazonian tree species*”*.* Vleminckx et al. Oikos.

**Appendix S1.** *Additional details regarding (1) the description of the study area, (2) the functional trait data, (3) the imputation of missing trait values, (4) the post hoc evaluation of trait imputations, (5) the comparison of traits with a phylogenetic comparative method (phylogenetic independent contrasts), (6) the protocol for trait measurements, and (7) further details on the methods used to analyse trait-environment associations.*

# **1. Study area**

Tree species inventories were carried out in ten lowland and lower mountain sites covered by mature tropical moist forests across French Guiana (Fig. 1), at the eastern edge of the Guiana shield. These forests thrive on an old (ca. 1.8 billion-year) Precambrian tableland, with soils that are heavily weathered and highly depleted in soil nutrients. The topography is extremely eroded and generally flat, with elevation rarely exceeding 200 m, except in two mountain ranges with few peaks above 800 m. Mean annual rainfall (calculated over the 2010-2018 period) across inventory sites ranges between 2150 and 3700 mm and is distributed seasonally throughout the year (Gourlet-Fleury et al. 2004, [www.worldclim.org](http://www.worldclim.org); Table 1), with a dry season occurring between August and November (during which monthly rainfall never exceeds 100 mm) and being more pronounced toward the interior of the continent. Mean annual temperature (2010-2018) oscillates around 25°C with low seasonal variation, and around 22°C in a relatively higher site (> 500 m a.s.l.) located at Mont Itoupé in the center of French Guiana. Each of the ten inventory sites comprised two to 12 0.1-ha plots, separated by at least 500 m, and located on contrasted habitats: (i) terra firme, (ii) white-sand and (iii) seasonally flooded forests. Most sites are part of the National Amazonian Park of French Guiana (PAG, [www.pag.fr](http://www.pag.fr)) or the Network of Natural Reserve of French Guiana ([www.guyane-parcregional.fr](http://www.guyane-parcregional.fr)).

# **2. Functional trait data before imputation**

We assembled a dataset characterising 19 functional traits (see Table 2) for 8345 tree individuals belonging to 1625 species distributed in 371 genera, 78 families and 26 orders in the Rosidae, Asteridae and early eudicots (Appendix S3). This dataset represented nearly ten years of collected tissue samples and trait measurements carried out in French Guiana, Peru and Brazil through three research projects (*Nebediv*, *Bridge* and *Amalin*; see the acknowledgment section for details). 5735 of these individuals (68.7%) were inventoried in our 71 French Guiana plots and belonged to 779 out of the 1467 species (53.4%) inventoried in these plots. The other traits measurements were made on samples collected on 1746 and 858 individuals (20.9% and 10.3% of the 8345 individuals) collected outside of our plots, in the Brazilian Amazon near Manaus and in the Peruvian Amazon, respectively (representing, respectively 248 and 541 species, among which 119 and 60 were also observed in our French Guiana plots). We built a matrix of mean values for these 19 traits and 1625 species, hereafter the “*NBA*” matrix (following the initials of the project “*Nebediv*”, “*Bridge*” and “*Amalin*” that collected this database) to facilitate the reading, which was used to address our first question, *i.e*. “*are all economics traits aligned along a single dimension or do they vary along decoupled axes?*”, after imputing missing values in this matrix as well as for the 688 species in our French Guiana plots that were not sampled for trait measurement (1467-779; see next section). We hypothesised that phylogenetic trait conservatism compensates for different geographic locations of the taxa (within a same biome) in determining species trait values (Ackerly 2003; Crisp *et al*. 2012). We further verified this assumption by testing the Pearson correlation between French Guiana and non-French Guiana (Brazil, Peru) for each trait taken individually, for all the species that had observed trait values in both geographic groups, using a *t*-test of the Pearson’s product moment (function *cor.test* in the R *stats* package). Correlations were generally positive, with significant values obtained for 12 out of 18 traits when considering species with at least one trait measurement in each geographic group (Fig. S1). The sapwood wood-specific gravity could not be compared between French Guiana and outside because there were no species in common with measurements for these traits. Non-significant associations, could have partly been due to a lack of statistical power but also to a substantial proportion of the species compared (> 60%) that had only one to three measurements for these traits (potentially not representative of the intra-specific variability) in French Guiana and/or outside. The absence of significant signal for leaf Ca, K and N content may also suggest that these traits are more influenced by the local amounts of soil nutrients than by phylogenetic constraints but we lacked sufficient data to further verify this hypothesis.

We further examined the phylogenetic signal among the observed values of each trait, using the Pagel’s λ statistic (Pagel 1999); λ = 0 when a trait evolves independently from the phylogeny, while λ = 1 when it evolves accordingly to a Brownian motion (BM) model given the phylogeny. Lambda values that best fit the observed values of each trait, with respect to the observed phylogeny, were estimated using the median of a posterior distribution generated with a Markov Chain Monte Carlo (MCMC) algorithm with 104 iterations, with the precision of these values given by the 2.5 and 97.5% quantiles of the credibility interval from the posterior distribution. We performed a likelihood ratio test (Revell 2012) that compares the likelihood of a BM model given the observed lambda with the likelihood of a BM model with no phylogenetic dependence. All tests indicated that the observed λ value was significantly higher (*P* ≤ 0.001) than a BM model assuming a λ = 0 (phylogenetic independence), suggesting the presence of a phylogenetic influence for each trait (Table S1).



**Fig. S1**. Mean trait values of species in French Guiana plotted against the values of the same species outside of French Guiana (Brazil and Peru), showing the *r*-Pearson correlation between the two populations of values and the significance of the *t*-test of the correlation. Significant values are shown in red (\**P* ≤ 0.05; \*\**P* ≤ 0.01; \*\*\**P* ≤ 0.001), non-significant (ns) ones in green. Tests were limited by the number of species compared, which ranged between N = 6 (Coarse Root wood-specific gravity) to N = 21. Associations could not be plotted for the sapwood wood-specific gravity, as no species with available data for this trait were found in both French Guiana and outside. WSG = Wood-Specific Gravity; SRL = Specific Root Length; SRTA = Specific Root Tip Abundance.

**Table S1**. Median of the posterior distribution of Pagel’s λ values for each traits (column 2), with the credibility interval (CI) characterised by the 2.5th (Lower CI) and 97.5th (Upper CI) quantiles from the posterior distribution of λ values (104 MCMC iterations, burn-in phase = 500 iterations). Values were computed before (Pagel’s λ1) and after (Pagel’s λ2) imputations. The last column shows the difference between the two λ values (λ2-λ1).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Pagel’s λ1** | **Lower CI** | **Upper CI** | **Pagel’s λ2** | **Lower CI** | **Upper CI** | **Diff** |
| ***Chlorophyll content*** | 0.400 | 0.207 | 0.588 | 0.542 | 0.365 | 0.698 | -0.142 |
| ***Thickness*** | 0.473 | 0.262 | 0.655 | 0.539 | 0.339 | 0.702 | -0.066 |
| ***Toughness*** | 0.640 | 0.470 | 0.771 | 0.641 | 0.487 | 0.763 | -0.001 |
| ***Leaf area*** | 0.311 | 0.140 | 0.521 | 0.24 | 0.091 | 0.463 | 0.071 |
| ***SLA*** | 0.671 | 0.504 | 0.789 | 0.711 | 0.571 | 0.809 | -0.04 |
| ***C*** | 0.800 | 0.704 | 0.869 | 0.684 | 0.54 | 0.79 | 0.116 |
| ***N*** | 0.714 | 0.584 | 0.812 | 0.664 | 0.526 | 0.773 | 0.05 |
| ***δ13C*** | 0.136 | 0.026 | 0.459 | 0.57 | 0.346 | 0.722 | -0.434 |
| ***Ca*** | 0.383 | 0.194 | 0.594 | 0.299 | 0.128 | 0.524 | 0.084 |
| ***P*** | 0.678 | 0.530 | 0.790 | 0.688 | 0.545 | 0.794 | -0.01 |
| ***K*** | 0.676 | 0.513 | 0.796 | 0.649 | 0.473 | 0.778 | 0.027 |
| ***Trunk bark thickness*** | 0.423 | 0.246 | 0.601 | 0.42 | 0.234 | 0.597 | 0.003 |
| ***Sapwood WSG*** | 0.932 | 0.888 | 0.958 | 0.879 | 0.823 | 0.917 | 0.053 |
| ***WSG*** | 0.780 | 0.666 | 0.860 | 0.602 | 0.447 | 0.73 | 0.178 |
| ***Diameter*** | 0.669 | 0.409 | 0.841 | 0.577 | 0.405 | 0.723 | 0.092 |
| ***SRL*** | 0.443 | 0.194 | 0.718 | 0.56 | 0.402 | 0.696 | -0.117 |
| ***Fine root tissue density*** | 0.622 | 0.394 | 0.803 | 0.64 | 0.486 | 0.761 | -0.018 |
| ***SRTA*** | 0.582 | 0.321 | 0.795 | 0.662 | 0.514 | 0.775 | -0.08 |
| ***Branchiness*** | 0.329 | 0.134 | 0.642 | 0.606 | 0.422 | 0.75 | -0.277 |

# **3. Trait imputations**

The imputations were performed using the matrix of 8345 individuals (belonging to 1625 species) x 19 traits (i.e., the *NBA* matrix). 779 out of the 1467 species of our French Guiana inventories were represented in this matrix. We therefore added 688 lines (1467-779) of empty trait values, corresponding to the species that were not represented in the *NBA* matrix, therefore producing a matrix of 9033 individuals and 2313 species on which we performed the BHPMF imputations. The percentage of missing values in this trait matrix ranged between 34.96% for the leaf area up to 87.9% for the coarse root wood-specific gravity (see Table S2 below for details). Although the latter percentage was high, fine root traits were measured on species covering a wide phylogenetic range (31 families and 9 orders in the Asteridae, Rosidae and Magnoliidae), while previous studies have strongly suggested that phylogenetic trait conservatism represents a major determinant of root functional traits (Valverde-Barrantes *et al*. 2017). To fill the missing trait values, we used the *Bayesian Hierarchical Matrix Factorization* method (BHMF, Fazayeli *et al*. 2014), an imputation procedure based on both (i) covariations among traits and (ii) trait information at higher taxonomic levels (species, genus, family, order, class), in a hierarchical way. The BHPMF method has been proved efficient in assessing missing trait values even with a percentage of missing values higher than 90%, providing that there is a good phylogenetic coverage and/or a sufficient number of traits measured among species (Schrodt et al. 2015). Prior to the imputations, outliers in the distribution of each trait were eliminated following Zuur *et al*. (2010) as the BHMF method is sensitive to extreme values, and traits were normalised (Box-Cox transformation) and standardised (z-score transformation). We also detrended each trait with the height of individuals to remove any ontogenetic variation effect (a factor that is rarely taken into account in ecological studies), by regressing each trait on height and using the residuals of each regression as our trait values. Imputations were then calculated using the *GapFilling* function in the R *BHPMF* package (Fazayeli *et al*. 2014), using observed information available at the genus, family, order, subclass and class level to estimate missing trait values. We used 1000000 iterations in the Markov chain Monte Carlo (MCMC) algorithm, with 10000 iterations in the burning phase to optimise the stability of the posterior parameter estimations of imputed values in the MCMC process. We extracted the resulting imputed values for 6423 lines of the output matrix corresponding to the 1467 species of our French Guiana plots, and verified the precisions of these values using the standard deviation of the imputation distribution for each value. Values with a standard deviation > 3 (≈1.5% of the imputed data) were not taken into account and replaced by “NA”. We then calculated a matrix of mean trait values at the species level, in order to address our research questions. The next section aims at evaluating the reliability of our imputations in terms of their consistence with observed trait data.

# **4. Post Hoc evaluation of our imputations**

The overall trait differences among species were well preserved after imputation, as we found a highly significant relationship (*P* ≤ 0.001; *t*-test of Pearson’s product moment correlation) between the observed and imputed mean species trait dissimilarity (normalised and z-score transformed) calculated using all of the 19 traits (see Fig. S2 below). We also tested the Pearson correlation between the normalised and z-score transformed predicted versus observed values for each trait, for pairs of trait values that did not contain a missing value in the observed trait matrix (Schrodt *et al*. 2015). These correlations were calculated for the matrix of imputed traits at the individual level and the matrix of mean trait values at the species level (for the 1467 species of our French Guiana inventories), and are presented in Table S2. They show that, across all traits, observed values were strongly and significantly correlated with imputed values, for both matrices (*r*-Pearson > 0.66; *P* ≤ 0.001).



**Fig. S2**. Dissimilarity of imputed vs. observed species mean trait values (calculated using all of the 19 traits combined) for the 1625 species of the *Nebediv-Bridge-Amalin* matrix (NBA; yellow) and the 1467 species of the French Guiana floristic matrix (blue). The shaded regions (strongly overlapping for the two linear models) represent two different 95% Bayesian credibility intervals for the predicted imputed trait dissimilarity values. The narrow interval represents the distribution of estimated imputed trait dissimilarity, while the wide interval correspond to the region in which the linear model expects to find 95% of actual imputed trait dissimilarities at each value of observed dissimilarity. Asterisks indicate the *P*-value of the Pearson’s product moment *t*-test for the two plotted relationships (\*\*\**P*≤0.001).

**Table S2.** Percentage of missing trait values (for each of the 21 traits) among individuals before imputation in the matrix combining the observed trait values of the *Nebediv-Bridge-Amalin* (NBA; 8345 individuals belonging to 1625 species) database with the 688 species from the French Guiana floristic inventories that do not have trait data (column 1, shaded in grey). The last two columns correspond to the Pearson correlations between the observed and imputed values (only for the pairs of trait values that did not contain a missing value in the observed trait matrix) for each trait, in the matrix of imputed values at the individual level (Cor-IND) and the matrix of mean trait values per species (Cor-SPE). All correlations were highly significant [*P* ≤ 0.001] using a *t*-test of Pearson’s product moment correlation. The three last lines represent the highest, mean (± standard deviation) and lowest column values.

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |
|  | **%Missing values** | **Cor-IND** | **Cor-SPE** |
| ***Chlorophyll content*** | 34.96 | 0.987 | 0.991 |
| ***Thickness*** | 34.96 | 0.991 | 0.985 |
| ***Toughness*** | 35.24 | 0.995 | 0.992 |
| ***Leaf area*** | 35.54 | 0.987 | 0.974 |
| ***SLA*** | 35.7 | 0.995 | 0.997 |
| ***C*** | 53.24 | 0.954 | 0.920 |
| ***N*** | 53.42 | 0.973 | 0.960 |
| ***δ13C*** | 53.25 | 0.908 | 0.889 |
| ***Ca*** | 75.7 | 0.889 | 0.661 |
| ***P*** | 75.7 | 0.913 | 0.849 |
| ***K*** | 75.7 | 0.859 | 0.812 |
| ***Trunk bark thickness*** | 43.33 | 0.962 | 0.943 |
| ***Sapwood WSG*** | 67.42 | 0.967 | 0.963 |
| ***WSG*** | 87.9 | 0.850 | 0.738 |
| ***Diameter*** | 74.17 | 0.909 | 0.823 |
| ***SRL*** | 74.17 | 0.922 | 0.780 |
| ***Fine root tissue density*** | 74.17 | 0.934 | 0.749 |
| ***SRTA*** | 74.18 | 0.903 | 0.793 |
| ***Branchiness*** | 74.17 | 0.932 | 0.834 |
| ***Highest*** | 87.900 | 0.995 | 0.997 |
| ***Mean (±SD)*** | 59.627 (±0.18) | 0.932 (±0.06) | 0.876 (±0.10) |
| ***Lowest*** | 34.960 | 0.850 | 0.661 |

# **5. Comparing traits with a phylogenetic comparative method (phylogenetic independent contrasts).**

We verified the influence of species evolutionary history on the correlations among traits. To do so, we tested whether the whole correlation structure obtained when using original traits (observed values only, or imputed) was consistent with the correlation structure obtained with phylogenetic independent contrasts (PIC, Felsenstein 1985), using a Procrustes correlation test between ordinations, following a similar approach as in Schrodt et al. (2015) to evaluate the consistency between imputed and observed traits. These tests showed highly significant concordance between trait scores from a principal coordinate analysis (PCoAs) obtained using original traits and PIC data (Table S3 below). PCoA was performed to model, with eigenvectors, the inertia of the matrix of observed and imputed correlations among traits, following recommendations in Dray & Josse. (2015). These results suggest that species evolutionary history had a moderate effect on the correlation patterns among traits, which was consistent with patterns described by Fortunel et al. (2012) with Amazonian tree communities. Appendix S13 (presented in an excel file due to limited space here) shows in more details the correlations observed for each pair of traits using original (observed and imputed) trait values and PIC data, separately.

Finally, we also show that the PCA obtained using original or using phylogenetic contrasts (PIC), calculated with the imputed traits of the NBA matrix, showed highly consistent patterns of trait correlation with the PCAs obtained using the 1467 species of our French Guiana inventories presented in Fig. 2 (Fig. S3, Table S3). We thus chose to keep presenting in the main text the PCA obtained for the French Guiana species only, in order to follow a logical framework with our second question that addresses the associations between traits and environmental variables in the 71 French Guiana plots.



**Fig. S3.** Projection of traits on axes 1-2 (above) and 3-4 (below) of a PCA performed on the matrix of 19 traits for the 1625 species from the *Nebediv-Amalin-Bridge* dataset, with trait data corresponding to either measured and imputed traits (PCA, left) or phylogenetic contrasts (PCAPIC, right). Leaf, stem, coarse root and fine root traits are emphasised with different colours indicated in the bottom tables. The latter tables show the relative contribution of each organ (in%) to the inertia expressed by each axis, calculated for each organ as the sum of the squared trait loadings divided by the total sum of squared loadings among all traits. For each axis, the one to three organ(s) contributing for a total of at least 78.1% are emphasised in bold. Chlo = leaf chlorophyll content; Thick = leaf thickness; Tough = leaf toughness; Ca/K/P/N = leaf Ca/K/P/N content; Area = leaf area; WSG = wood-specific gravity of the trunk (orange) and the coarse roots (blue); TBT = trunk bark thickness; Branch = fine root branchiness; Diam = fine root diameter.

**Table S3**. Procrustes correlation quantifying the degree of rotated configuration matching among principal coordinate analyses (axes 1 to 4) obtained using original traits (observed and imputed; in lines) and phylogenetic independent contrasts (columns), for the matrix of 1467 species in French Guiana (FG) and the NBA matrix. All values were highly significant (*P* ≤ 0.001; Procrustes correlation test performed using the function protest in R vegan package).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Phylogenetic independent contrasts** | | | |
| ***Observed traits*** | **FG matrix** |  | **NBA matrix** |  |
|  | **Imputed traits** | **Observed traits** | **Imputed traits** | **Observed traits** |
| ***FG matrix*** |  |  |  |  |
| ***Imputed traits*** | 0.895 | 0.660 | 0.960 | 0.692 |
| ***Observed traits*** | 0.781 | 0.835 | 0.777 | 0.875 |
| ***NBA matrix*** |  |  |  |  |
| ***Imputed traits*** | 0.943 | 0.682 | 0.891 | 0.701 |
| ***Observed traits*** | 0.756 | 0.856 | 0.750 | 0.884 |

# **6. Protocol for trait measurements**

The protocol follows the same procedure as described in Fortunel *et al*. (2012). The number of individuals sampled per species ranged from min. = 1 to max. = 183 for *Eschweilera coriacea* (Lecythidaceae), one of the most abundant species in our floristic inventories, with an average of 5 samples per species. We could not examine whether conspecific individuals showed trait variation along environmental gradients since we did not have accurate estimates of intraspecific trait variation

**► Leaf traits**: For each species in each plot, we chose the stem nearest to 5 cm DBH, to standardize trait measures for the majority of taxa to understorey light conditions and the small tree stage. Leaves were collected from a lateral branch in the understorey using a pruning pole. We sampled three leaves per individual. Leaf chlorophyll content was estimated using three values from a Minolta SPAD 502DL meter (Spectrum Technologies, Illinois, USA) with calibrations based on Coste *et al*. (2010). Leaf thickness was measured as the mean of three measurements with a micrometer (Mitutoyo Instruments, Singapore), and leaf toughness was measured as the average of three punch tests with a Chatillon penetrometer of 5 mm-diameter punch rod (Ametek, Florida, USA). The leaves were scanned using a portable scanner (Canon LiDE 60, Canon Inc., Tokyo, Japan) and their area was determined by image analyses with WinFolia software (Regent Instruments, Toronto, Canada). The leaves were dried at 60 °C for 72 h and their dry mass was weighed to determine specific leaf area (SLA, leaf area divided by its dry mass). Leaf carbon and nitrogen concentrations were determined using an elemental analyser and mass spectrometer at the Mass Spectrometry Facility at Florida International University (FIU, Miami). Leaf phosphorus and base cation analyses were performed in the Soil and Plant Agricultural Laboratory at the Louisiana State University, using an Inductively Coupled Spectrometer on HNO3-H2O2 digests of 500 mg of plant tissue. Foliar 13C composition (‰) was determined using the conventional Pee Dee Belemnite standard (Farquhar, Ehleringer & Hubick 1989).

**► Stem traits:** The stem fragment was taken in the last growth unit with a diameter of 1–2 cm. We measured bark thickness at a height of 1-4 m with increment hammers (Haglöf Sweden AB, Langsele, Sweden), a method that provides precise measurements for barks thinner than 15 mm (Paine *et al*. 2010). Branch samples collected from lateral branches using a pruning pole in the understorey were saturated with water, then their saturated volume was measured based on the principle of water displacement, using the Sartorius density determination kit (Goettingen, Germany). Samples were then dried at 103 °C for 72 h, then their dry mass was measured. We measured the stem specific gravity (Williamson & Wiemann 2010), as the dry mass divided by the saturated volume.

**► Root traits**: Root traits were divided between coarse woody samples and fine root samples. For root wood tissue samples, outer bark was removed. Woody root samples were saturated with water and their saturated volume was estimated using the Sartorius density determination kit (Goettingen, Germany), which is based on the principle of water displacement. After measuring the saturated volume, samples were dried at 103 °C for 72 h, and their dry mass was determined. Root wood density, was measured as the dry mass divided by the saturated volume. In addition, cross sections of each woody root sample was mounted and stained to calculate parenchyma, fiber and vessel fractions following the same procedures done in stems. Fine roots were obtained from root systems that were traced from the trunk of each individual to the most distal portion of the roots. From each traced roots, we selected a ca. 10 cm-long entire root system comprising at least the first three root orders. Each cluster was tagged, sealed in a plastic bag and stored in ice to transport to the laboratory. Two to four root samples from each root segment were separated and washed before measurements. Each root sample was scanned using a high resolution flatbed scanner (600 DPI resolution, 256-level gray-scale, TIFF format; Epson Scanner Perfection V700 Photo, USA). Morphological measurements were calculated for each root sample using WinRhizo image analysis (2007 Pro version, Regent Instruments, Inc, Quebec, Canada). We analyzed three morphological traits typically associated with tradeoffs between organ cost per potential return in trees [specific root length (SRL), root tissue density (RTD) and average diameter; Comas *et al*. 2002]; and two traits associated with plant root foraging strategies [specific root tip abundance (SRTA, Hertel *et al*. 2003; Meinen *et al*. 2009) and branch intensity (B, Pregitzer *et al*. 2002; Dupuy *et al.* 2010).

# ***7. Further details on the methods used to analyse trait-environment associations***

Two complementary approaches were used to address question 2 (Is there a convergent filtering among economics traits across environmental gradients, and do traits respond differently to soil fertility and climate gradients?): (i) a comparison of the mean functional traits values of species among habitats and (ii) a more detailed approach identifying trait significantly associated with soil fertility and climatic gradients.

The first approach consisted of testing the differences in mean trait values among species present in the four inventoried habitats (terra firme, seasonally flooded, white-sand and cloud forests), using a one-way ANOVA complemented by a Tukey test of comparison for each pair of habitats. The second approach aimed at examining in more details the pairwise associations between traits and environmental variables, using the Fourth-Corner Analysis (FCA; Legendre et al. 1997). The FCA quantifies these associations by combining three matrices (a plot by environmental variables matrix, a plot by species abundance matrix and a species by traits matrix) into a single matrix quantifying trait-environment associations. Species abundances were Hellinger-transformed (Legendre & Gallagher 2001) to equilibrate the weight of abundant and rare species. To take spatial autocorrelation, as well as phylogenetic autocorrelation into account, the FCA statistic that quantifies the strength of trait-environment association (ter Braak 2017) was tested by comparing its observed values with 4999 null values obtained using a procedure based on Moran Spectral Randomisations (MSR, Wagner & Dray 2015) to following Braga et al. (2018) to account for both spatial and phylogenetic autocorrelation. The MSR method allows considering the multiscale spatial autocorrelation structures in any type of quantitative data. To do so, the method uses information on spatial connectivity among sampling points (*i.e*., the 71 plot in our case), which is obtained from the selection of Moran’s Eigenvector Maps (MEMs, Dray et al. 2006). MEMs are commonly used to model multi-scale spatial structures in any type of numerical variable. The selection of MEMs was optimised following the procedure described in Bauman et al. (2018a,b) to take into account the nested pattern of our sampling design (using a Gabriel’s graph to model connectivity among plots). The connectivity information is then used in a constrained randomisation algorithm in the MSR method to reproduce variables that accurately mimic the observed spatial structures of the randomised variable(s). The procedure is similar when taking phylogenetic autocorrelation into account, expect that phylogenetic eigenvectors are used instead of Moran’s eigenvectors. The ultrametric tree of the phylogeny for the 1467 species was obtained using the package V.PhyloMaker (Jin et al. 2019).

Values of the FCA association statistic were considered significant when they were lower than the 2.5th quantile (if negative) or higher than the 97.5th quantile (if positive) of null values. To avoid inflating the number of tests (14 environmental variables × 19 traits = 266 tests), we used plot scores from the first two axes of the PCA performed on environmental variables (explaining, 42.9 and 19.2% of the overall environmental inertia, respectively) instead of each environmental variable, as these axes were well interpretable and corresponded to a soil fertility gradient (axis 1) and a seasonality gradient (axis 2) (see results). This resulted in a reduced number of tests performed (n = 44).

All analyses described in the methods were performed in R (version 3.6.3) statistical environment (R Development Core Team 2020). The environmental, species abundance and trait data matrices, as well the R code and packages to reproduce all of our analyses and the trait imputations are available in supplementary material (Appendices S3 to S7).

# **Literature cited**

Ackerly, D.D. 2003. Community assembly, niche conservatism, and adaptive evolution in changing environments. International Journal of Plant Sciences 164:165–184.

Bauman, D., Drouet, T., Fortin, M. J., and S. Dray. 2018a. Optimizing the choice of a spatial weighting matrix in eigenvector-based methods. Ecology 99(10):2159–2166.

Bauman, D., Drouet T., Dray, S., and J. Vleminckx. 2018b. Disentangling good from bad practices in the selection of spatial or phylogenetic eigenvectors. Ecography 41:1–12.

Comas, L. H., Bouma, T. J., and D. M. Eissenstat. 2002. Linking root traits to potential growth rate in six temperate tree species. Oecologia 132:34–43.

Coste, S., Baraloto, C., Leroy, C., Marcon, E., Renaud, A., Richardson, A. D., Roggy, J. C., Schimann, H., Uddling, J., and B Herault. 2010. Assessing foliar chlorophyll contents with the SPAD-502 chlorophyll meter: a calibration test with thirteen tree species of tropical rainforest in French Guiana. Annals of Forest Science, 67:5.

Crisp, M. D., and L. G. Cook. 2012. Phylogenetic niche conservatism: what are the underlying evolutionary and ecological causes? New Phytologist 196:681–694.

Dray, S., Legendre, P., and P. R. Peres-Neto. 2006. Spatial modelling: a comprehensive framework for principal coordinate analysis of neighbour matrices (PCNM). Ecological Modelling 196:483–493.

Dray, S., and Josse, J. 2015. Principal component analysis with missing values: a comparative survey of methods. Plant Ecology 216:657–667.

Dupuy, L., Vignes, M., Mckenzie, B. M., and P. J. White. 2010 The dynamics of root meristem distribution in the soil. Plant, Cell & Environment 33:358–369.

Farquhar, G.D., Ehleringer, J.R. & Hubick, K.T. (1989) Carbon isotope discrimination and photosynthesis. Annual Review in Plant Physiology, 40, 503–537.

Fazayeli, F., Banerjee, A., Kattge, J., Schrodt, F., and P. Reich. 2014. Uncertainty quantified matrix completion using Bayesian hierarchical matrix factorization. Proceedings of the 13th International Conference on Machine Learning and Applications.

Felsenstein, J. 1985. Phylogenies and the Comparative Method. The American Naturalist. 125 (1): 1–15.

Fortunel, C., Fine, P. V. A., and C. Baraloto. 2012. Leaf, stem and root tissue strategies across 758 Neotropical tree species. Functional Ecology 26:1153–1161.

Hertel, D., Leuschner, C., and D. Hölschner. 2003. Size and structure of fine root systems in old-growth and secondary tropical montane forests (Costa Rica). Biotropica 35:143–153.

Jin, Y., and Qian H. 2019 V.PhyloMaker: an R package that can generate very large phylogenies for vascular plants. Ecography 42(8):1353-1359.

Meinen, C., Hertel, D., and C. Leuschner. 2009. Biomass and morphology of fine root in temperate broad-leaved forest differing in tree species diversity: is there evidence of below-ground overyielding? Oecologia 161:99–111.

Paine, C. E. T., Stahl, C., Courtois, E. A., Patiño, S., Sarmiento, C., and C. Baraloto. 2010. Functional explanations for variation in bark thickness in tropical rain forest trees. Functional Ecology 24:1202–1210.

Pregitzer, K. S., DeForest, J. L., Burton, A. J., Allen, M. F., Ruess, R. W., and R. L. Hendrick. 2002. Fine root architecture of nine North American trees. Ecological Monographs 72:293–309.

Revell, L. J. 2012. phytools: An R package for phylogenetic comparative biology (and other things). Methods in Ecology and Evolution 3:217–223.

Schrodt, F., et al. 2015. BHPMF - a hierarchical Bayesian approach to gap-filling and trait prediction for macroecology and functional biogeography. Global Ecology and Biogeography 24:1510–1521.

ter Braak, C. J. F. 2017. Fourth-corner correlation is a score test statistic in a log-linear trait–environment model that is useful in permutation testing. Environmental and Ecological Statistics 24: 219–242.

Valverde-Barrantes, O. J., Freschet, G. T., Roumet, C., and C. B. Blackwood. 2017. A worldview of root traits: the influence of ancestry, growth form, climate and mycorrhizal association on the functional trait variation of fine-root tissues in seed plants. New Phytologist 215:1562–1573.

Williamson, G. B., and M. C. Wiemann. 2010. Measuring wood specific gravity… correctly. American Journal of Botany 97:519–524.

Zuur, A., Ieno, E. N, and C. S. Elphick. 2010. A protocol for data exploration to avoid common statistical problems. Methods in Ecology and Evolution 1:3–14.