



Supplementary Information for

Dissecting macro-ecological and macro-evolutionary patterns of forest biodiversity across the Hawaiian archipelago

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A. Extended Materials and Methods.

Woodiness Classification

Using the full list of 2,442 species on the Hawaiian Islands provided by the Flora of the Hawaiian Islands (<https://naturalhistory2.si.edu/botany/hawaiianflora>), we classified all species as either woody, herbaceous, or variable following Zanne et al. (2014).

We classified a species as woody if it: (i) was classified as either a ‘tree’, ‘shrub’, or ‘liana’ by either USDA Plants (<http://plants.usda.gov>), Flora of the Hawaiian Islands (<https://naturalhistory2.si.edu/botany/hawaiianflora>), or Hawaiian Ecosystems at Risk (HEAR) (<http://hear.org/plants/>); (ii) was classified as ‘subshrub’ and ‘shrub’ by the previously mentioned data sources; (iii) was classified as ‘vine’ and ‘shrub’, or further confirmation that it is woody by the previously mentioned data sources; or (iv) was classified as having a woody growth form by another reliable data source, such as articles in peer-reviewed journals or governmental reports.

We classified a species as herbaceous if it: (i) was classified as either ‘herb’, ‘forb/herb’ by USDA Plants, Flora of the Hawaiian Islands, or HEAR; (ii) was classified as ‘graminoid’ by the previously mentioned data sources; (iii) was classified as ‘subshrub’ and ‘herb’ by the previously mentioned data sources; was classified as ‘vine’ and ‘herb’ or further confirmation that it is herbaceous by the previously mentioned data sources; or (iv) was classified as having a herbaceous growth form by another reliable data source, such as articles in peer-reviewed journals or governmental reports.

We classified a species as variable if: (i) only a part of the plant was woody (e.g. base of the stem); (ii) it was classified as ‘suffrutescent’ or ‘suffruticose’ by the previously mentioned data sources; or (iii) if there was disagreement across data sources.

In cases where only genus-level information was available and it was unanimous for the entire genus (e.g., the genus contains shrubs), we used classified species using this information. Lastly, if a species was classified as a ‘sub-shrub’ by one of the previously mentioned data sources, we consulted additional data sources and searched for articles in peer-reviewed journals or governmental reports or images.

We provide the full species, including woodiness classification, native status, and data source via GitHub (https://github.com/dylancraven/Hawaii_diversity).

References

Zanne AE, et al. (2014) Three keys to the radiation of angiosperms into freezing environments. *Nature* 506(7486):89.

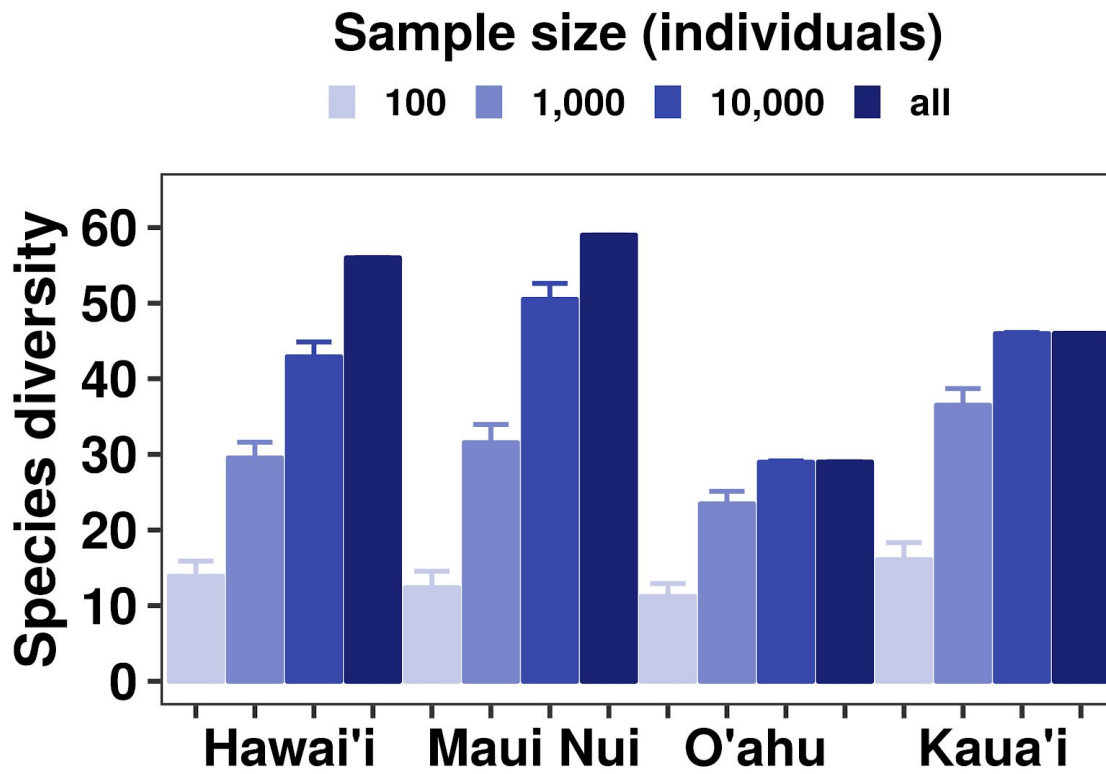


Fig. S1. Species diversity patterns of native woody plants across Hawaiian Islands at the island scale. Species diversity is estimated at the island level for native woody plants by pooling data by island and then using sample-based rarefaction for 100, 1,000, and 10,000 individuals, and all individuals. Islands are ordered by age from youngest to oldest (left to right).

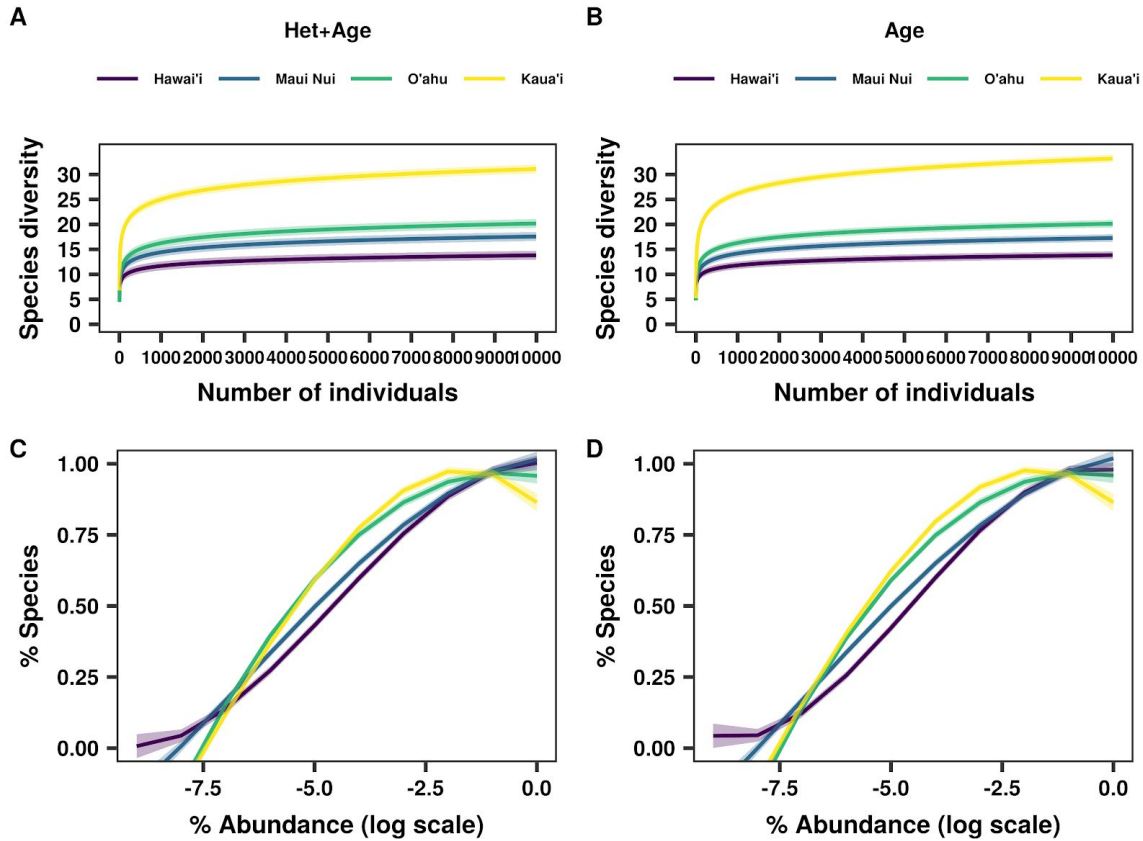


Fig. S2. Rarefaction curves and relative abundance distributions of native forest communities across the Hawaiian archipelago, estimated for two sampling scenarios that influence biodiversity. In the first scenario ('Het+Age' ; **A** & **C**) sampling effort was controlled for and in the second scenario, both sampling effort and habitat heterogeneity were controlled for ('Age' ; **B** & **D**). Individual-based rarefaction curves (**A** and **B**) were estimated with interpolation and extrapolation up to 10,000 individuals. Relative abundance distributions (**C** & **D**) are presented as re-scaled empirical cumulative distribution functions. Individual-based rarefaction curves and relative abundance distributions were estimated for the 'Het+Age' and 'Age' scenarios by randomly selecting ten plots per island one hundred times to control for sampled area. For the 'Age' scenario, habitat heterogeneity was controlled for by randomly selecting ten plots per island with a restricted range in *elevation* (Table S5). Colored bands are 95% confidence intervals and solid lines are fitted using linear mixed-effects models.

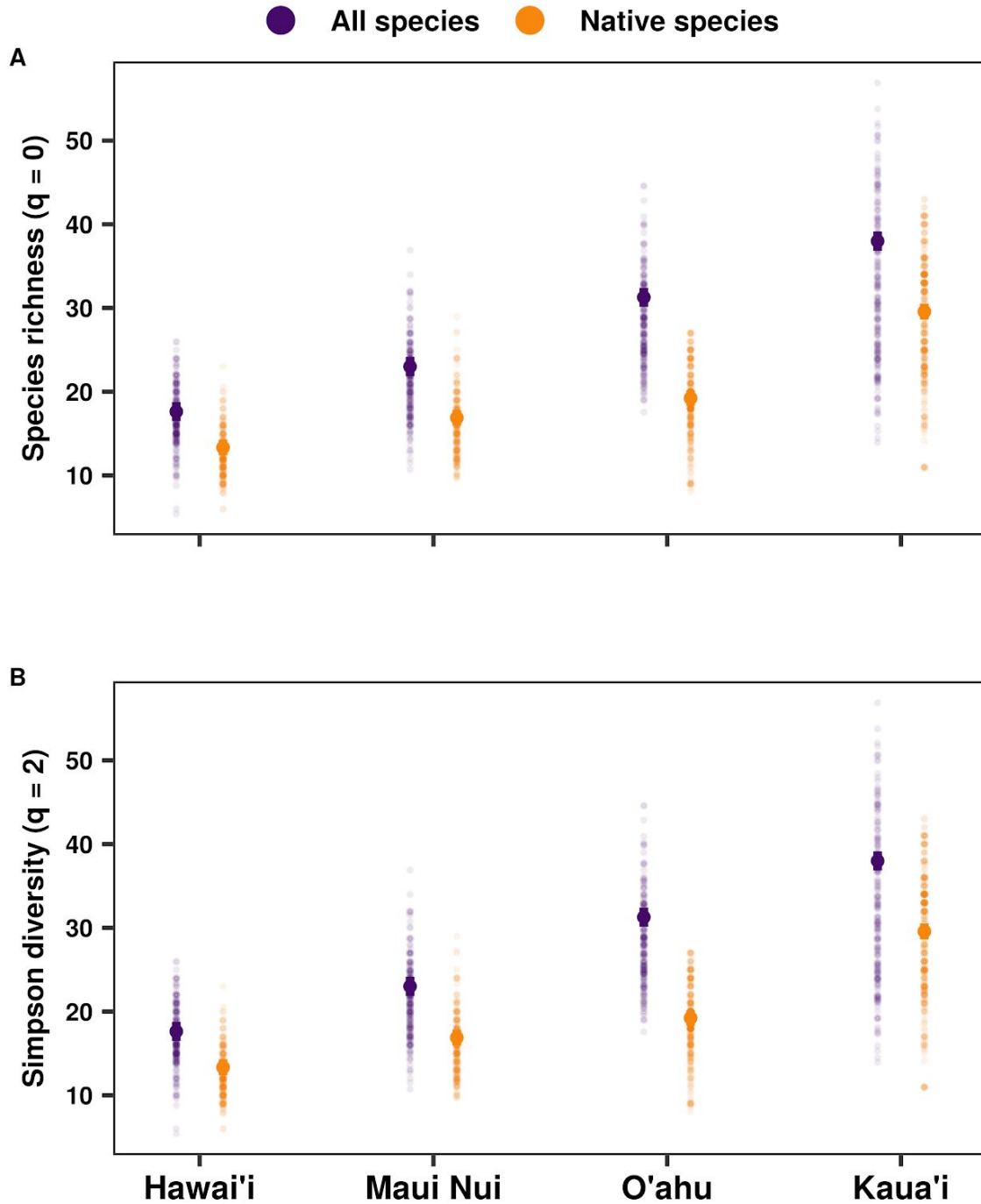


Fig. S3. Species diversity patterns of forest communities across the Hawaiian archipelago for all species (native and alien) and only native species. Species diversity was estimated as species richness (A; Hill number 0) and Simpson diversity (B; Hill number 2) using sample-based interpolation for 10,000 individuals; both diversity indices are expressed in terms of effective species numbers. Species diversity was estimated using a sampling scenario ('Het +Age') that only controlled for sampling effort by selecting a fixed number of plots (ten) per island. Means and 95% confidence intervals are estimated with one-way ANOVAs (see Table S8).

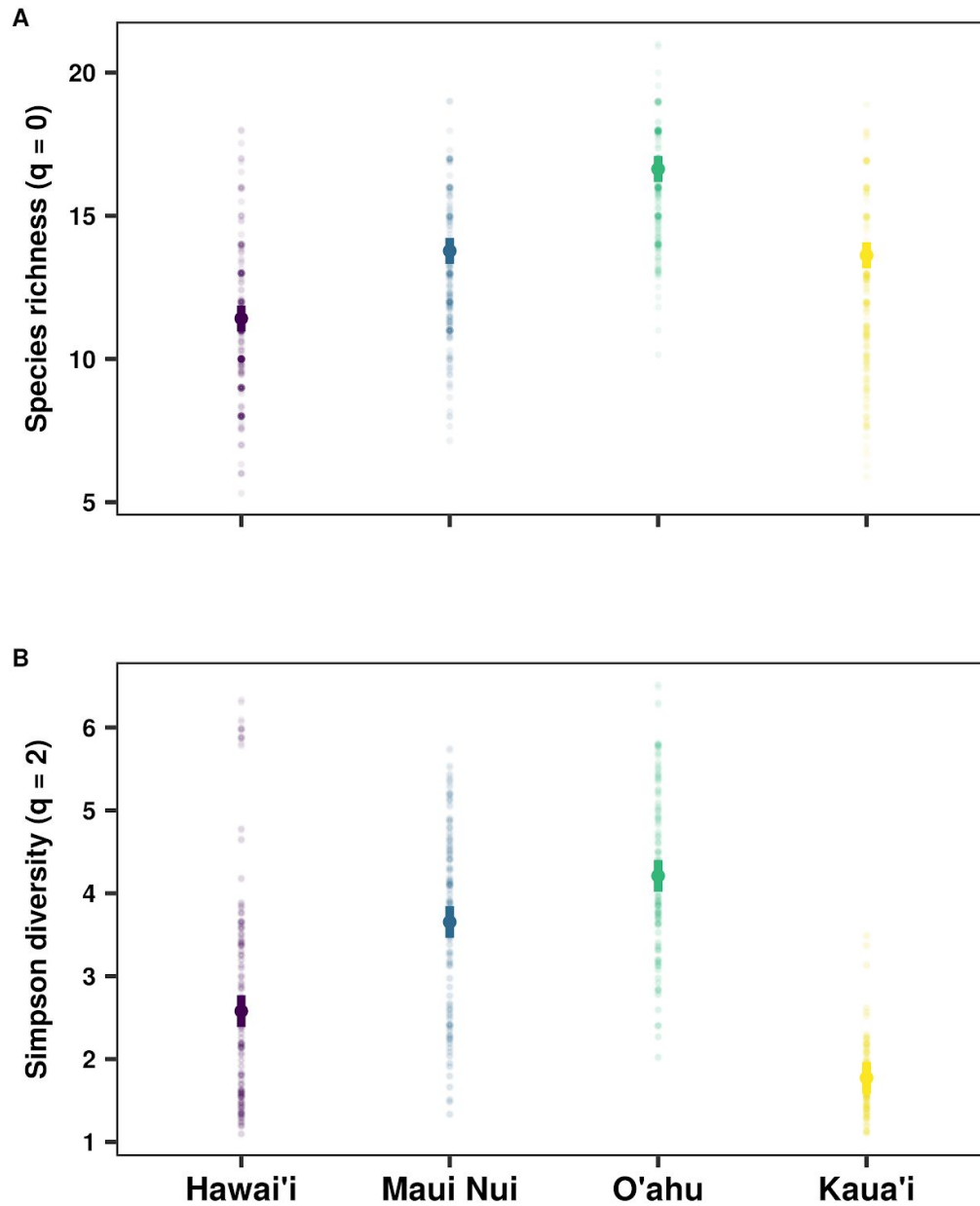


Fig. S4. Species diversity patterns of forest communities across the Hawaiian archipelago for only alien species. Species diversity was estimated as species richness (A; Hill number 0) and Simpson diversity (B; Hill number 2) using sample-based interpolation for 10,000 individuals; both diversity indices are expressed in terms of effective species numbers. Species diversity was estimated using a sampling scenario ('Age') that controlled for sampling effort and habitat heterogeneity by selecting a fixed number of plots per island (ten) with a restricted range in aridity. Means and 95% confidence intervals are estimated with one-way ANOVAs (species richness: $R^2 = 39.3\%$, F-statistic = 85.5, $P < 0.001$; Simpson diversity: $R^2 = 48.7\%$, F-statistic = 125.2, $P < 0.001$).

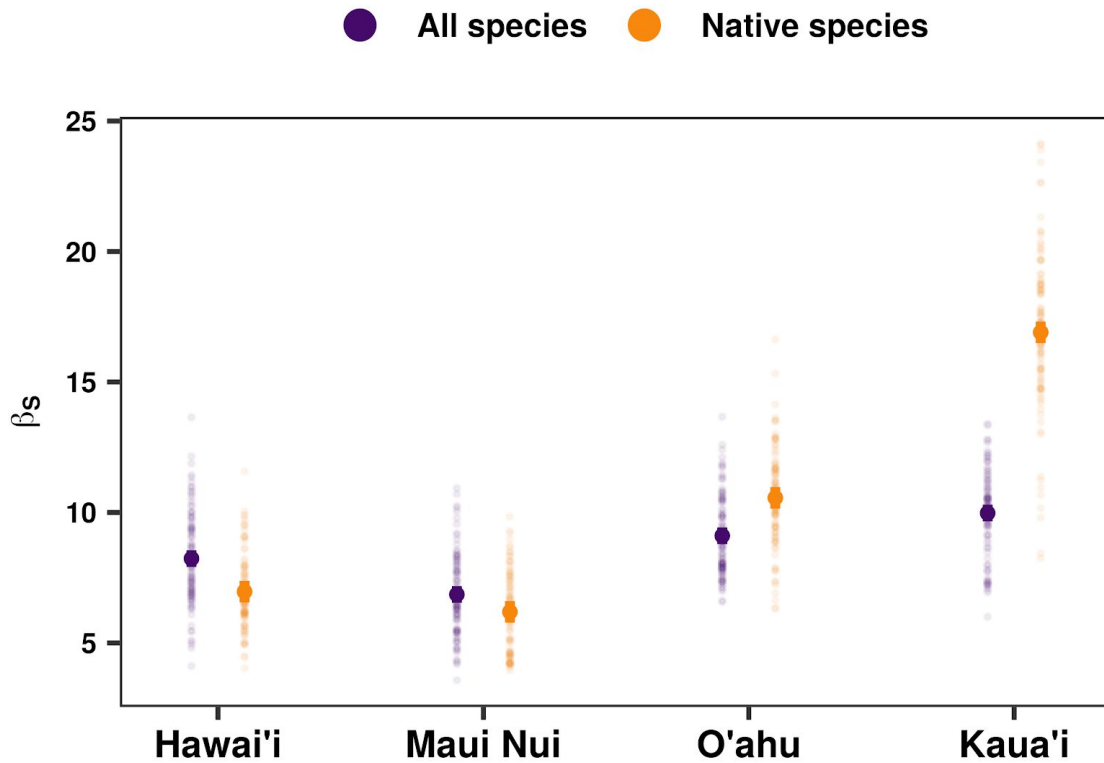


Fig. S5. Beta diversity patterns of forest communities across the Hawaiian archipelago estimated for all species (native and alien) and only native species. Beta diversity (for each plot) was calculated multiplicatively using species richness, which highlights contributions of rare species. Beta diversity was estimated using a sampling scenario ('Het +Age') that only controlled for sampling effort by selecting a fixed number of plots (ten) per island one hundred times, and then calculated mean beta diversity for each island per sample. Means and 95% confidence intervals are estimated with one-way ANOVAs (All species: $R^2 = 33.5\%$, F-statistic = 66.6, $P < 0.001$; Native species: $R^2 = 80.3\%$, F-statistic = 537.4, $P < 0.001$).

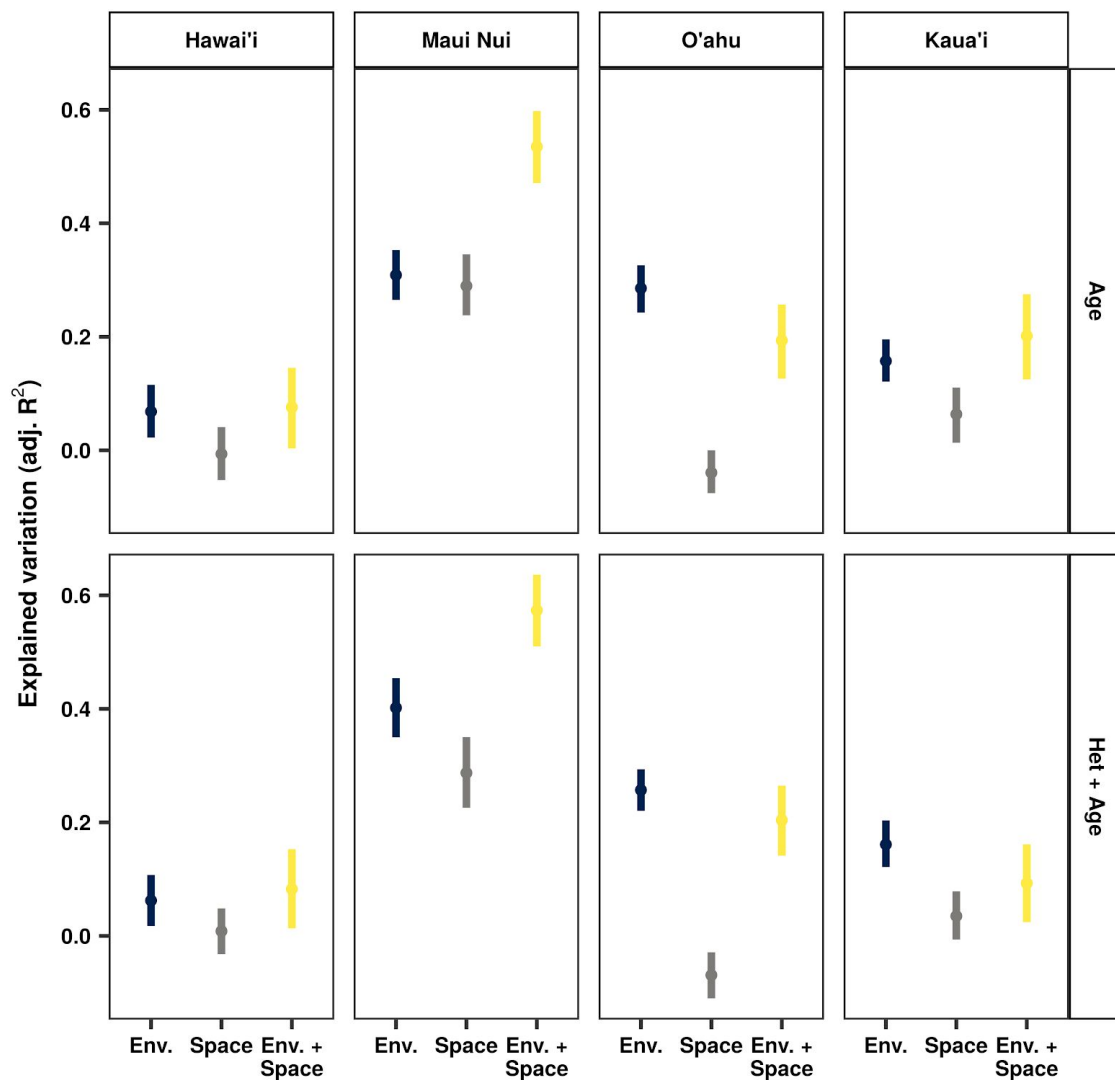


Fig. S6. Partitioning of variation in beta diversity within each island of the Hawaiian archipelago among environmental factors (black), spatial factors (dark grey), and spatially structured environmental factors (yellow). Explained variation is the adjusted unique contribution (adj. R^2) of environmental, spatial, and spatially structured environmental factors calculated by partial regression. The 'Het + Age' scenario controlled for sampling effort by selected a fixed number of plots (ten) per island and the 'Age' scenario controlled for sampling effort and habitat heterogeneity by selecting a fixed number of plots (ten) per island with a restricted range in aridity. Mean and 95% confidence intervals were calculated across one hundred samples for each sampling scenario.

Table S1. Summary of number of plots (including native and alien species), sampled area, and environmental conditions of forests across the Hawaiian archipelago. Mean annual temperature (MAT) and precipitation (MAP), mean aridity, range in aridity, range in elevation, and soil substrate age were extracted for each plot. Sampled area is the total area of plots per island and individuals is the total number of individuals of native and alien species in plots per island. Aridity is the ratio of mean annual precipitation to mean annual potential evapotranspiration (MAP/PET).

Island	Plots (#)	Sampled area (m²)	MAT (°C)	MAP (mm yr⁻¹)	Aridity	Aridity range	Elevation range (m)	Soil substrate age (y)
Hawai'i	369	275759	17.7	2702	1.2	3.9	2653	16370
Maui Nui	95	83759	16.0	3965	1.9	4.8	2132	758484
O'ahu	31	19927	21.1	1840	0.6	2.0	852	2570400
Kaua'i	22	15388	19.7	1919	0.7	1.8	1124	3910526

Table S2. Summary of sampled area, aridity range, and elevation range for each sampling scenario (based on 100 random samples of 10 plots per island; only including native species) of forests across the Hawaiian archipelago. For ‘Het+Age’ and ‘Age’ sampling scenarios, sampled area (m²), aridity range, and elevation range are mean values calculated from 100 samples of 10 plots per island. ‘Age’ controlled for sampling effort and habitat heterogeneity by selecting a fixed number of plots per island (ten) with a restricted range in aridity. 95% confidence intervals are included in parentheses for sampled area.

Island	Het+Age			Age		
	Sampled area (m ²)	Aridity range	Elevation range	Sampled area (m ²)	Aridity range	Elevation range
Hawai’i	7469 (7371 , 7566)	2.3	1926.7	7416 (7319 , 7512)	1.6	1890.1
Maui Nui	7904 (7860 , 7949)	3.8	1332.7	7922 (7874 , 7970)	3.2	1370.7
O’ahu	7448 (7364 , 7533)	1.3	672.0	7389 (7302 , 7476)	0.8	706.4
Kaua’i	7209 (7070 , 7347)	1.3	1057.2	7302 (7208 , 7396)	0.7	1062.6

Table S3. Fixed effects and model fit information for linear mixed-effects models of species accumulation curves for ‘Het+Age’ and ‘Age’ sampling scenarios (native species only). Satterthwaite’s method was used to calculate denominator degrees-of-freedom and F-statistics. Marginal and conditional R² represent model variation explained by fixed effects and the combination of fixed and random effects, respectively.

Sampling Scenario	Fixed Effects	F statistic	<i>P</i>	Marginal R ²	Conditional R ²
Het + Age	log(individuals)	872781.9	<0.001	0.63	0.98
	Island	4.8	0.003		
	log(individuals) x Island	42002.2	<0.001		
Age	log(individuals)	882704.5	<0.001	0.69	0.97
	Island	4.1	0.007		
	log(individuals) x Island	53843.7	<0.001		

Table S4. Fixed effects and model fit information for linear mixed-effects models of relative abundance distributions for ‘Het+Age’ and ‘Age’ sampling scenarios (native species only). In both models, we included relative abundance (natural-log transformed to meet normality assumptions) and two orthogonal polynomial terms. Satterthwaite’s method was used to calculate denominator degrees-of-freedom and F-statistics. Marginal and conditional R² represent model variation explained by fixed effects and the combination of fixed and random effects, respectively.

Sampling Scenario	Fixed Effects	F statistic	<i>P</i>	Marginal R²	Conditional R²
Het + Age	log(rel. abundance)	33482.0	<0.001	0.89	0.94
	Island	37.9	<0.001		
	log(rel. abundance) <i>x</i> Island	202.2	<0.001		
Age	log(rel. abundance)	33983.7	<0.001	0.90	0.94
	Island	47.0	<0.001		
	log(rel. abundance) <i>x</i> Island	188.4	<0.001		

Table S5. Summary of sampled area, aridity range, and elevation range for each sampling scenario (based on 100 random samples of 10 plots per island; native species only) of forests across the Hawaiian archipelago. For the ‘Age’ scenario, habitat heterogeneity was controlled by selecting plots with a restricted range in elevation. For ‘Het+Age’ and ‘Age’ sampling scenarios, sampled area (m²), aridity range, and elevation range are mean values calculated from 100 samples of 10 plots per island. 95% confidence intervals are included in parentheses for sampled area.

Island	Het+Age			Age		
	Sampled area (m ²)	Aridity range	Elevation range	Sampled area (m ²)	Aridity range	Elevation range
Hawai'i	7469 (7371 , 7566)	2.3	1926.7	7375 (7274 , 7477)	2.5	1649.3
Maui Nui	7904 (7860 , 7949)	3.8	1332.7	7962 (7921 , 8002)	3.8	1088.6
O'ahu	7448 (7364 , 7533)	1.3	672.0	7519 (7439 , 7599)	1.4	564.9
Kaua'i	7209 (7070 , 7347)	1.3	1057.2	7307 (7224 , 7390)	1.2	1011.2

Table S6. Fixed effects and model fit information for linear mixed-effects models of species accumulation curves for ‘Het+Age’ and ‘Age’ sampling scenarios (native species only). For the ‘Age’ scenario, habitat heterogeneity was controlled by selecting plots with a restricted range in elevation. Satterthwaite’s method was used to calculate denominator degrees-of-freedom and F-statistics. Marginal and conditional R² represent model variation explained by fixed effects and the combination of fixed and random effects, respectively.

Sampling Scenario	Fixed Effects	F statistic	<i>P</i>	Marginal R ²	Conditional R ²
Het + Age	log(individuals)	872781.9	<0.001	0.63	0.98
	Island	4.8	0.003		
	log(individuals) x Island	42002.2	<0.001		
Age	log(individuals)	942004.2	<0.001	0.74	0.98
	Island	1.1	0.37		
	log(individuals) x Island	66948.	<0.001		

Table S7. Fixed effects and model fit information for linear mixed-effects models of relative abundance distributions for ‘Het+Age’ and ‘Age’ sampling scenarios (native species only). For the ‘Age’ scenario, habitat heterogeneity was controlled by selecting plots with a restricted range in elevation. In both models, we included relative abundance (natural-log transformed to meet normality assumptions) and two orthogonal polynomial terms. Satterthwaite’s method was used to calculate denominator degrees-of-freedom and F-statistics. Marginal and conditional R² represent model variation explained by fixed effects and the combination of fixed and random effects, respectively.

Sampling Scenario	Fixed Effects	F statistic	<i>P</i>	Marginal R ²	Conditional R ²
Het + Age	log(rel. abundance)	33482.0	<0.001	0.89	0.94
	Island	37.9	<0.001		
	log(rel. abundance) <i>x</i> Island	202.2	<0.001		
Age	log(rel. abundance)	34120.1	<0.001	0.90	0.94
	Island	57.2	<0.001		
	log(rel. abundance) <i>x</i> Island	207.1	<0.001		

Table S8. Model summary and model fit information for one-way ANOVAs that test for variation in species richness and Simpson diversity across islands for ‘Het+Age’ and ‘Age’ sampling scenarios and different species groups. For the ‘Age’ scenario, habitat heterogeneity was controlled by selecting plots with a restricted range in aridity. R² represents explained model variation.

Sampling Scenario	Species group	Response Variable	F statistic	<i>P</i>	R²
Het + Age	All species	Species richness	238.3	<0.001	64.4%
	Native species		211.4	<0.001	61.6%
Het + Age	All species	Simpson diversity	87.4	<0.001	39.8%
	Native species		40.0	<0.001	23.2%
Age	All species	Species richness	330.6	<0.001	71.5%
	Native species		283.9	<0.001	68.3%
Age	All species	Simpson diversity	64.1	<0.001	32.7%
	Native species		51.4	<0.001	28.0%

Table S9. Summary of sampled area, aridity range, and elevation range for each sampling scenario (based on 100 random samples of 10 plots per island; including native and alien species) of forests across the Hawaiian archipelago. For the ‘Age’ scenario, habitat heterogeneity was controlled by selecting plots with a restricted range in aridity. For ‘Het+Age’ and ‘Age’ sampling scenarios, sampled area (m²), aridity range, and elevation range are mean values calculated from 100 samples of 10 plots per island. 95% confidence intervals are included in parentheses for sampled area.

Island	Het+Age			Age		
	Sampled area (m ²)	Aridity range	Elevation range	Sampled area (m ²)	Aridity range	Elevation range
Hawai'i	7248 (7151 , 7345)	2.4	1895.9	7286 (7186 , 7386)	1.6	1896.9
Maui Nui	7611 (7531 , 7691)	4.0	1530.0	7677 (7600 , 7755)	3.2	1537.6
O'ahu	6887 (6794 , 6981)	1.2	664.6	6667 (6595 , 6738)	0.8	672.0
Kaua'i	7076 (6931 , 7221)	1.2	1057.7	7079 (6989 , 7169)	0.9	1072.2