

Ecography

ECOG-04544

de Camargo, U., Roslin, T. and Ovaskainen, O. 2019.
Spatio-temporal scaling of biodiversity in acoustic
tropical bird communities. – Ecography doi: 10.1111/
ecog.04544

Supplementary material

Appendix 1. Additional information on automated species identification by ASI.

We used ASI (Ovaskainen et al. 2018) to automatically identify the presence of the target species to the minute scale, across all 11,000 hours of audio. To construct and fit the models, we adhered to the steps described by Ovaskainen et al. (2018). In short, we first divided the 11,000 hours of recording in 661,110 audio segments of one minute each. We then let the software find 1,000 letter candidates from 50,000 randomly selected 1-minute segments of field recordings. A letter is a region of the spectrogram containing a vocalization that is informative for species identification (e.g., a song unit or a call). A bird expert (UC) identified the bird species behind the selected letters, and used ASI to fit letter- and species-level models using the 50,000 audio segments as training data. We then applied these models to the entire dataset to predict in which one-minute segments each species vocalizes.

Model validation was done independently for each species by comparing model predictions to manual classifications of 100 audio segments. Fifty segments were selected from each of two groups: segments in which the species is present with probability smaller than 50%, and segments in which the species is present with probability higher than 50%. In the validation phase, ASI selects, shuffles and presents these segments to the user (here the bird expert UC), who classifies them in a blind test.

We used the validation data to calculate precision and false positive rates for each species. Precision was defined as the number of detections by ASI that were true (i.e., classifications that were scored to contain the species by a human listener) divided by the number of segments expected to contain the species. The false positive rate was calculated as the ratio between the number of segments above the threshold which did not contain the species when checked by a human listener (i.e., which had been wrongly categorized as positive by ASI), divided by the number of segments expected to contain the species (i.e., 50 out of the 100 segments).

Our analyses thus involve not all of the ca. 400 species in the study area, but a subset of 60 species. The reason why all species are not included is that some of them are difficult to identify by ASI, e.g. because their vocalizations are not sufficiently distinct from those of other species. This raises the question of whether the included species are a random subset of all species, or a biased subset. Here we address this question related to the commonness versus rarity of the species. The rare species can fall in any of the following three categories:

- 1) The species is so rare that a random search does not find any letter that represents it. In this case, one would either discard the species from the pool of species, or try to use templates to find additional letters (as explained in Ovaskainen et al 2018). If nothing is found even with templates, then letters cannot be defined, and the species is dropped from the study. In our case, we did not apply templates, as we aimed at testing the method's ability to work solely on field data – without the aid of external references from online libraries.
- 2) The species is rare, but some letters are found. Nonetheless, there are not enough audio segments where it occurs, so the fitting and validation of the model is suboptimal (usually some 100 segments are needed to construct good models). In this case, we discarded the species from the pool, as there were no sufficient data to build reliable models to detect it.
- 3) The species is rare, but there are a sufficient number of vocalizations in the dataset for letters to be defined, models to be fit to the data, and validation to be done. Then species classification will perform well. The species was added to the set of study species, and the classification can be expected to found where the species is present in the audio dataset equally well as for common species.

The Figure A1 shows the relationship between the commonness of the species and the precision of the ASI classification (as defined in the main text). The five species with lowest number of recorded occurrences have a lower precision than average, which creates a significant relationship ($p=0.002$) in the linear

regression. These five species are *Campylorhamphus procurvoides*, *Frederickena viridis*, *Monasa atra*, *Ibycter americanus* and *Micrastur ruficollis*. They are not necessarily rare as such, but they may appear rare specifically because the automated identification did not work as well with these species as on average. Beyond these five species, there is no apparent relationships between rarity and ASI performance.

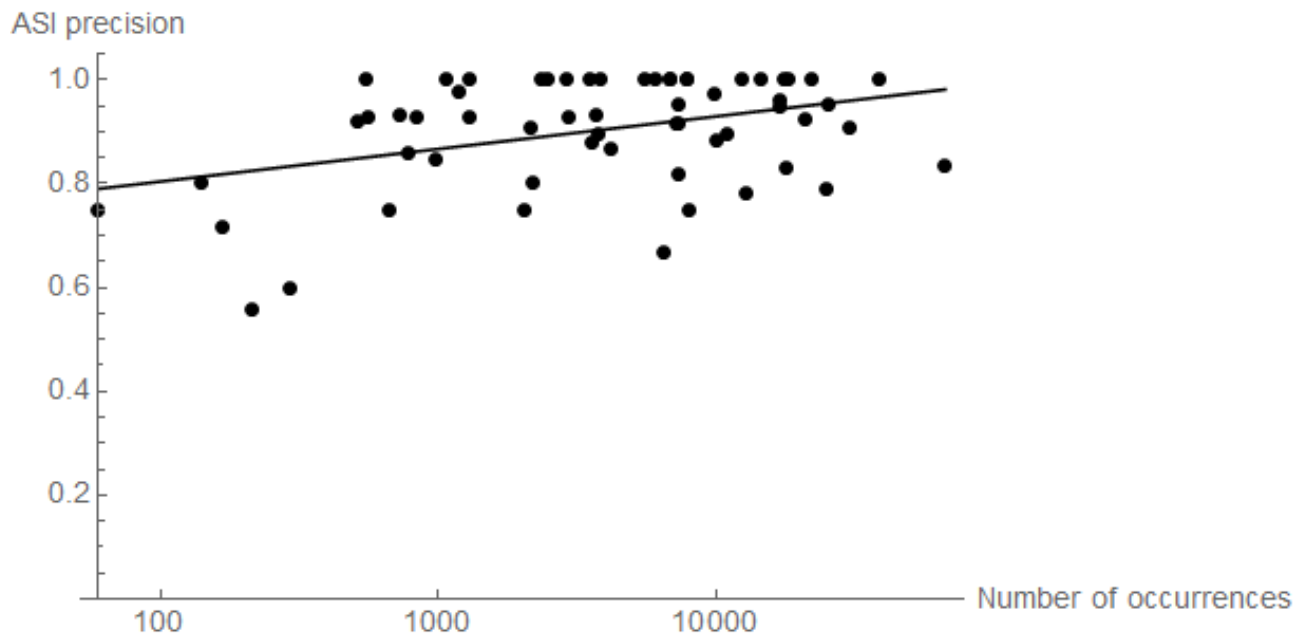


Fig. A1. The relationship between ASI precision and species rarity. In the figure, each dot is one species, and the line shows a linear relationships ($p=0.002$).

Appendix 2. Further details and primary data on the classification of functional diversity.

As a basis for our analysis of functional diversity, we used the classification of Wilman et al. (2014) to score each of the 60 bird species encountered in this study for 22 numerical traits describing their functional foraging attributes. Of these traits, eight showed no variation among the set of species encountered (see Table A2 and A3)

Table A1. A key to the traits used, as adopted from Wilman et al. (2014).

Data on unshaded variables are given in Table A2A, data on shaded variables are given in Table A2B. Eight traits exhibited no variation among the species encountered: for DietVend, DietVfish and DietScav, ForStratwatbelowsurf, ForStratwataroundsurf, ForStrataerial, PelagicSpecialist, and Nocturnal, all species scored a zero. These variables are identified by an asterisk and excluded from Tables 2A and TablesA2B.

Variable	Description	Type	Variable codes
Scientific_name	Species scientific name	Character	NA
Family	Family name	Character	NA
DietInv	Percent use of: Invertebrates-general, aquatic invertebrates, shrimp, krill, squid, crustaceans, molluscs, cephalopod, polychaetes, gastropods, orthoptera, terrestrial Invertebrates, ground insects, insect larvae, worms, orthopterans, flying insects	Integer	estimated % use ($\Sigma 100\%$)
DietVend*	Percent use of: Mammals, Birds	Integer	estimated % use ($\Sigma 100\%$)
DietVect	Percent use of: Reptiles, snakes, amphibians, salamanders	Integer	estimated % use ($\Sigma 100\%$)
DietVfish*	Percent use of: Fish	Integer	estimated % use ($\Sigma 100\%$)
DietVunk	Percent use of: Vertebrates-general or unknown	Integer	estimated % use ($\Sigma 100\%$)
DietScav*	Percent use of: Scavenge, garbage, offal, carcasses, trawlers, carrion	Integer	estimated % use ($\Sigma 100\%$)
DietFruit	Percent use of: Fruit, drupes	Integer	estimated % use ($\Sigma 100\%$)
DietNect	Percent use of: Nectar, pollen, plant exudates, gums	Integer	estimated % use ($\Sigma 100\%$)
DietSeed	Percent use of: Seed, maize, nuts, spores, wheat, grains	Integer	estimated % use ($\Sigma 100\%$)
DietPlantO	Percent use of: Other plant material, Grass, ground vegetation, seedlings, weeds, lichen, moss, small plants, reeds, cultivated crops, forbs, vegetables, fungi, roots, tubers, legumes, bulbs, leaves, above ground vegetation, twigs, bark, shrubs, herbs, shoots, aquatic vegetation, aquatic plants	Integer	estimated % use ($\Sigma 100\%$)
ForStratwatbelowsurf*	Prevalence of: Foraging below the water surfaces	Integer	estimated % use ($\Sigma 100\%$)
ForStratwataroundsurf*	Prevalence of: Foraging on or just (<5 inches) below water surface	Integer	estimated % use ($\Sigma 100\%$)
ForStratground	Prevalence of: Foraging on ground	Integer	estimated % use ($\Sigma 100\%$)
ForStratunderstory	Prevalence of: Foraging below 2m in understory in forest, forest edges, bushes or shrubs	Integer	estimated % use ($\Sigma 100\%$)
ForStratmidhigh	Prevalence of: Foraging in mid to high levels in trees or high bushes (2m upward), but below canopy	Integer	estimated % use ($\Sigma 100\%$)

ForStratcanopy	Prevalence of: Foraging in or just above (from) tree canopy	Integer	estimated % use ($\Sigma 100\%$)
ForStrataerial*	Prevalence of: Foraging well above vegetation or any structures	Integer	estimated % use ($\Sigma 100\%$)
PelagicSpecialist*	Foraging predominantly pelagic. Source for all: Handbook of the Birds of the World	Binary	0: no; 1: yes
ForStratSource	Source of estimates for foraging stratum	Character	Link to Ref_ID in Table 3
ForStratSpecLevel	Indicates whether foraging stratum estimates are based on species-level data	Binary	0: no; 1: yes
Nocturnal*	Main foraging activity at night. Source for all: Handbook of the Birds of the World	Binary	0: no; 1: yes
BodyMassValue	Body mass (g). For Source Dunning08: Geometric mean of average values provided for both sexes (Dunning08). For Source GenAvg: genus average as provided by other source	Floating Point	NA

Table A2A. Species classified for traits related to diet (see the unshaded part of Table A1 for a key to these trait).

Scientific_name	Family	DietInv	DietVect	DietVunk	DietFruit	DietNect	DietSeed	DietPlantO
<i>Attila spadiceus</i>	Tyrannidae	50	30	0	10	0	10	0
<i>Automolus infuscatus</i>	Furnariidae	90	10	0	0	0	0	0
<i>Automolus ochrolaemus</i>	Furnariidae	80	20	0	0	0	0	0
<i>Cacicus haemorrhous</i>	Icteridae	60	0	0	20	20	0	0
<i>Campylorhamphus procurvoides</i>	Furnariidae	100	0	0	0	0	0	0
<i>Cercomacra cinerascens</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Corythopsis torquatus</i>	Tyrannidae	90	20	0	0	0	0	0
<i>Dendrocolaptes certhia</i>	Furnariidae	80	0	0	0	0	0	0
<i>Fam Psittacidae</i>	Psittacidae	0	0	0	0	0	0	0
<i>Formicarius analis</i>	Formicariidae	80	0	10	10	0	0	0
<i>Formicarius colma</i>	Formicariidae	100	0	0	0	0	0	0
<i>Frederickena viridis</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Galbula albirostris</i>	Galbulidae	100	0	0	0	0	0	0
<i>Glyphorhynchus spirurus</i>	Furnariidae	100	0	0	0	0	0	0
<i>Grallaria varia</i>	Grallariidae	100	0	0	0	0	0	0
<i>Hemitriccus zosterops</i>	Tyrannidae	100	0	0	0	0	0	0
<i>Herpsilochmus dorsimaculatus</i>	Thamnophilidae	100	10	0	0	0	0	0
<i>Hylexetastes perrotii</i>	Furnariidae	90	0	10	0	0	0	0
<i>Hylophilus muscicapinus</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Willisornis poecilinotus</i>	Thamnophilidae	90	0	0	0	0	0	0
<i>Hypocnemis cantator</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Ibycter americanus</i>	Falconidae	100	0	0	0	0	0	0

<i>Lepidothrix serena</i>	Pipridae	40	0	0	60	0	0	0
<i>Lophotriccus vitiensis</i>	Tyrannidae	100	0	0	0	0	0	0
<i>Micrastur gilvicollis</i>	Falconidae	40	0	0	0	0	0	0
<i>Micrastur mirandollei</i>	Falconidae	0	0	0	0	0	0	0
<i>Micrastur ruficollis</i>	Falconidae	0	0	0	0	0	0	0
<i>Microbates collaris</i>	Poliophtilidae	100	0	0	0	0	0	0
<i>Microcerculus bambla</i>	Troglodytidae	80	0	0	0	0	0	0
<i>Momotus momota</i>	Momotidae	50	0	0	30	0	0	0
<i>Monasa atra</i>	Bucconidae	80	0	0	0	0	0	0
<i>Myrmeciza ferruginea</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Myrmothera campanisona</i>	Grallariidae	100	0	0	0	0	0	0
<i>Myrmotherula brachyura</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Myrmotherula menetriesii</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Ortalis motmot</i>	Cracidae	0	0	0	100	0	0	0
<i>Pachyramphus marginatus</i>	Tityridae	50	0	0	50	0	0	0
<i>Patagioenas plumbea</i>	Columbidae	0	0	0	50	0	50	0
<i>Percnostola rufifrons</i>	Thamnophilidae	80	0	0	10	0	0	0
<i>Perissocephalus tricolor</i>	Cotingidae	20	0	0	80	0	0	0
<i>Phaethornis superciliosus</i>	Phaethornidae	10	0	0	0	90	0	0
<i>Pipra erythrocephala</i>	Pipridae	20	0	0	80	0	0	0
<i>Pithys albifrons</i>	Thamnophilidae	90	0	0	0	0	0	0
<i>Platyrrinchus coronatus</i>	Tyrannidae	100	0	0	0	0	0	0
<i>Psarocolius viridis</i>	Icteridae	60	0	0	40	0	0	0
<i>Ramphastos tucanus</i>	Ramphastidae	10	0	0	50	10	0	10
<i>Ramphastos vitellinus</i>	Ramphastidae	20	0	0	60	0	0	0
<i>Ramphotrigon ruficauda</i>	Tyrannidae	80	0	0	20	0	0	0
<i>Rhytipterna simplex</i>	Tyrannidae	80	0	0	20	0	0	0
<i>Schiffornis turdina</i>	Tityridae	50	0	0	50	0	0	0
<i>Sittasomus griseicapillus</i>	Furnariidae	90	0	0	0	0	0	10
<i>Thamnomanes ardesiacus</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Thamnomanes caesius</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Thamnophilus murinus</i>	Thamnophilidae	100	0	0	0	0	0	0
<i>Tolmomyias assimilis</i>	Tyrannidae	90	0	0	10	0	0	0
<i>Trogon melanurus</i>	Trogonidae	30	0	0	70	0	0	0

<i>Trogon rufus</i>	Trogonidae	60	0	0	40	0	0	0
<i>Trogon violaceus</i>	Trogonidae	20	0	0	80	0	0	0
<i>Vireolanius leucotis</i>	Vireonidae	100	0	0	0	0	0	0
<i>Xiphorhynchus pardalotus</i>	Furnariidae	100	0	0	0	0	0	0

Table A2B. Species classified for traits related to habitat use (forest strata) and body mass (see the shaded part of Table A1 for a key to these trait).

Scientific_name	ForStratground	ForStratunderstory	ForStratmidhigh	ForStratcanopy	ForStratSource	ForStratSpecLevel	BodyMassValue
<i>Attila spadiceus</i>	10	10	40	40	9	1	3.67
<i>Automolus infuscatus</i>	0	80	20	0	8	1	3.49
<i>Automolus ochrolaemus</i>	10	70	20	0	8	1	3.69
<i>Cacicus haemorrhous</i>	0	20	60	20	35	1	4.43
<i>Campylorhamphus procurvoides</i>	0	40	60	0	8	1	3.51
<i>Cercomacra cinerascens</i>	0	0	100	0	8	1	2.66
<i>Corythopsis torquatus</i>	80	20	0	0	9	1	2.66
<i>Dendrocolaptes certhia</i>	0	10	90	0	8	1	4.23
Fam Psittacidae	0	0	0	0	0	0	6.21
<i>Formicarius analis</i>	100	0	0	0	8	1	4.13
<i>Formicarius colma</i>	80	20	0	0	8	1	3.85
<i>Frederickena viridis</i>	40	60	0	0	8	1	4.33
<i>Galbula albirostris</i>	0	50	50	0	7	1	3.10
<i>Glyphorhynchus spirurus</i>	0	0	40	60	8	1	2.68
<i>Grallaria varia</i>	100	0	0	0	8	1	4.78
<i>Hemitriccus zosterops</i>	0	40	60	0	9	1	2.17
<i>Herpsilochmus dorsimaculatus</i>	0	0	100	0	8	1	2.29
<i>Hylexetastes perrotii</i>	0	50	50	0	8	1	4.64
<i>Hylophilus muscicapinus</i>	0	0	50	50	33	1	2.46
<i>Willisornis poecilinotus</i>	60	40	0	0	8	1	2.91
<i>Hypocnemis cantator</i>	30	40	30	0	8	1	2.51
<i>Ibycter americanus</i>	10	20	50	20	2	1	6.44
<i>Lepidothrix serena</i>	0	70	30	0	9	1	2.43
<i>Lophotriccus vitiosus</i>	0	0	50	50	9	1	1.90
<i>Micrastur gilvicollis</i>	10	50	40	0	2	1	5.34
<i>Micrastur mirandollei</i>	0	50	50	0	2	1	6.31

<i>Micrastur ruficollis</i>	40	30	30	0	2	1	5.18
<i>Microbates collaris</i>	80	20	0	0	11	1	2.32
<i>Microcerculus bambla</i>	50	50	0	0	10	1	2.95
<i>Momotus momota</i>	30	30	30	10	6	1	4.74
<i>Monasa atra</i>	33	33	33	0	7	1	4.50
<i>Myrmeciza ferruginea</i>	50	50	0	0	8	1	3.26
<i>Myrmothera campanisona</i>	100	0	0	0	8	1	3.85
<i>Myrmotherula brachyura</i>	0	0	100	0	8	1	1.86
<i>Myrmotherula menetriesii</i>	0	0	100	0	8	1	2.15
<i>Ortalis motmot</i>	33	0	33	33	2	1	6.25
<i>Pachyramphus marginatus</i>	0	0	100	0	9	1	2.91
<i>Patagioenas plumbea</i>	0	0	30	70	4	1	5.19
<i>Percnostola rufifrons</i>	50	50	0	0	8	1	3.17
<i>Perissocephalus tricolor</i>	0	60	40	0	9	1	5.83
<i>Phaethornis superciliosus</i>	0	100	0	0	5	1	1.84
<i>Pipra erythrocephala</i>	0	50	50	0	9	1	2.60
<i>Pithys albifrons</i>	60	40	0	0	8	1	2.97
<i>Platyrinchus coronatus</i>	0	80	20	0	9	1	2.21
<i>Psarocolius viridis</i>	0	0	50	50	35	1	5.66
<i>Ramphastos tucanus</i>	0	0	20	80	7	1	6.49
<i>Ramphastos vitellinus</i>	10	10	50	30	7	1	5.89
<i>Ramphotrigon ruficauda</i>	0	50	50	0	9	1	2.91
<i>Rhytipterna simplex</i>	0	50	50	0	9	1	3.46
<i>Schiffornis turdina</i>	0	100	0	0	9	1	3.46
<i>Sittasomus griseicapillus</i>	0	0	50	50	8	1	2.57
<i>Thamnomanes ardesiacus</i>	0	30	70	0	8	1	2.87
<i>Thamnomanes caesius</i>	0	10	90	0	8	1	2.75
<i>Thamnophilus murinus</i>	0	10	90	0	8	1	2.96
<i>Tolmomyias assimilis</i>	0	10	90	0	9	1	2.83
<i>Trogon melanurus</i>	0	10	30	60	6	1	4.74
<i>Trogon rufus</i>	10	60	30	0	6	1	3.99
<i>Trogon violaceus</i>	0	70	20	10	6	1	3.84
<i>Vireolanius leucotis</i>	0	0	20	80	33	1	3.26
<i>Xiphorhynchus pardalotus</i>	0	80	20	0	8	1	3.54

Appendix 3. Validation of species diversity and functional diversity versus sampling time -relations using alternative species detection criteria.

We note that when applying automatic species identifications, the number of species observed per time unit is naturally affected by the stringency of the criterion used to score a species as “reliably detected” (see the Discussion of the main paper, section *Bioacoustics offer useful descriptors of community structure*). To validate the findings of the main paper, we thus recreated Figures 2 and 3 using the very same methods as applied in the main paper, but scoring a species as present when detected with a probability of >0.5 . With this threshold, the rarest species was detected 59 times among the 656,698 one minute segments included in the analyses and the most common 66142 times. On average, each species was detected 8622 times. For 55% (360,929) of the one-minute segments, not a single species was detected. The fraction (number) of segments for which we detected 1 species was 25% (161,378), whereas the corresponding number for 2 species was 12% (78,208), for 3 species 5% (34,913), and for 4 species 2% (14,158), for 5 species 0.8% (5018), and for 6 species or more, it was 0.3% (2094).

We note that this results in higher diversity per time unit (compare the absolute scale of data points in the y-dimension between Figures 2 and 3 of the main paper and Figures A2 and A3 below), but in qualitatively identical species accumulation (compare slopes among Figures 2 and 3 of the main paper and Figures A2 and A3 below, and among Table 1 of the main paper and Table A3 below).

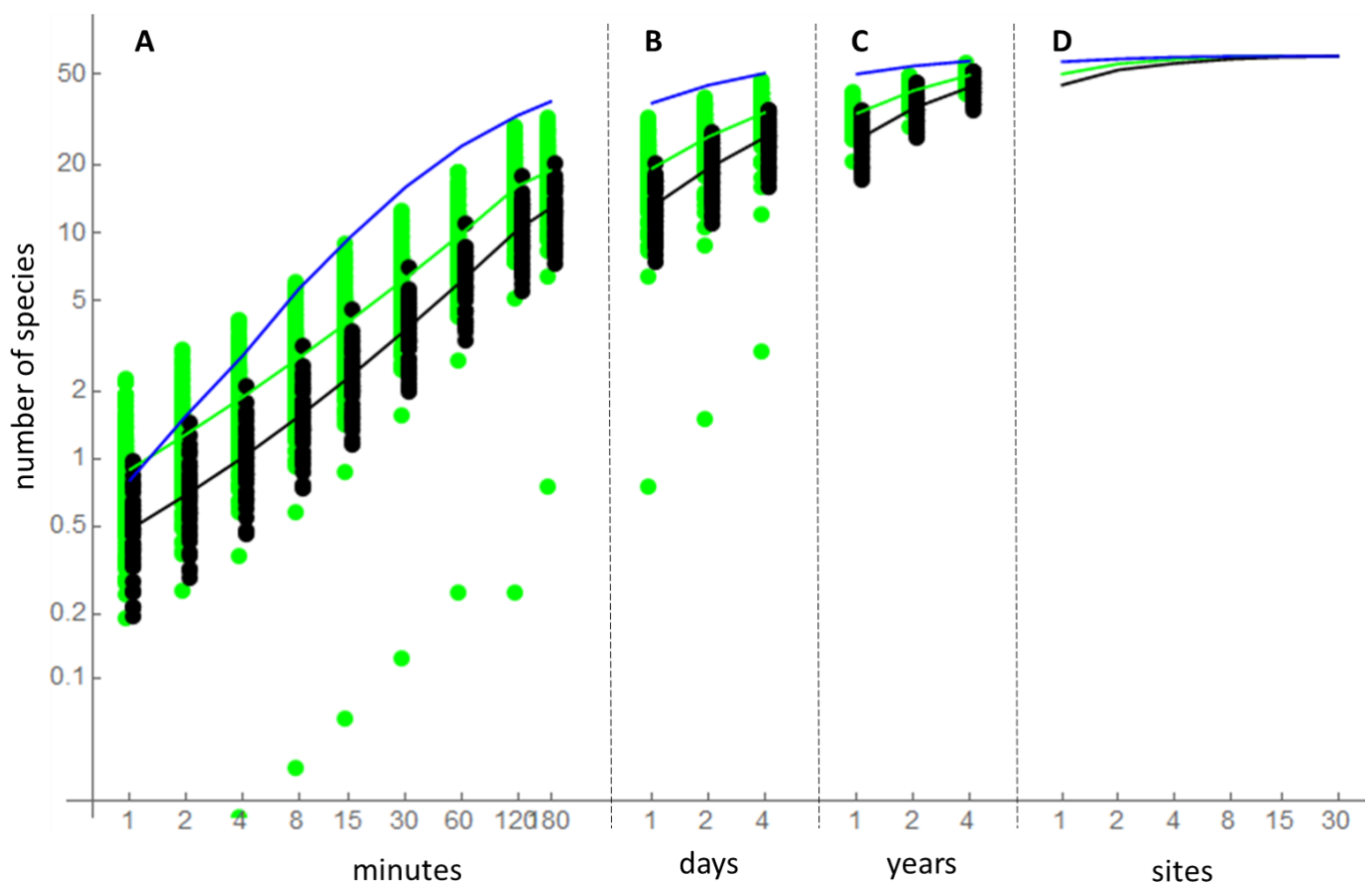


Fig. A2. Local species diversity versus sampling time and number of sites.

Mirroring Fig. 2 of the main paper, we show species accumulation with increasing sampling in time and space, resolving patterns at the level of minutes within a day (panel A), among days within a year (panel B), among years (panel C), and among sites (panel D). Contrasting with Fig. 2, we score a species as present when detected with a probability of >0.5 . In all cases, green dots show primary forest and black dots secondary forest locations, and the

line shows the average over the sampling locations. The data points shown in the figure each correspond to a separate sampling location. Panel A shows the expected species number if we listen to a sample of a given length, e.g. 15 consecutive minutes of the three hour recording. Panel B shows the expected number of species if we listen to the full three hour-recording for a given number of days of the same year. Note that the starting point of panel B is the end point of panel A, as in both cases three hours of one day have been listened to. Panel C shows the expected species number if we listen to four days of three hour -recordings for a given number years. Note that the starting point of panel C is the end point of panel B, as in both cases four days of three hours have been listened to. Panel D continues by asking how new species accumulate when new sites are added. All sites are listened to for four years of four days of three hours. Here, the green and black sites show how new species accumulate when sites from primary or secondary forest are included, whereas the blue lines shows how new species are accumulated if the sites are selected randomly among all sites regardless of habitat.

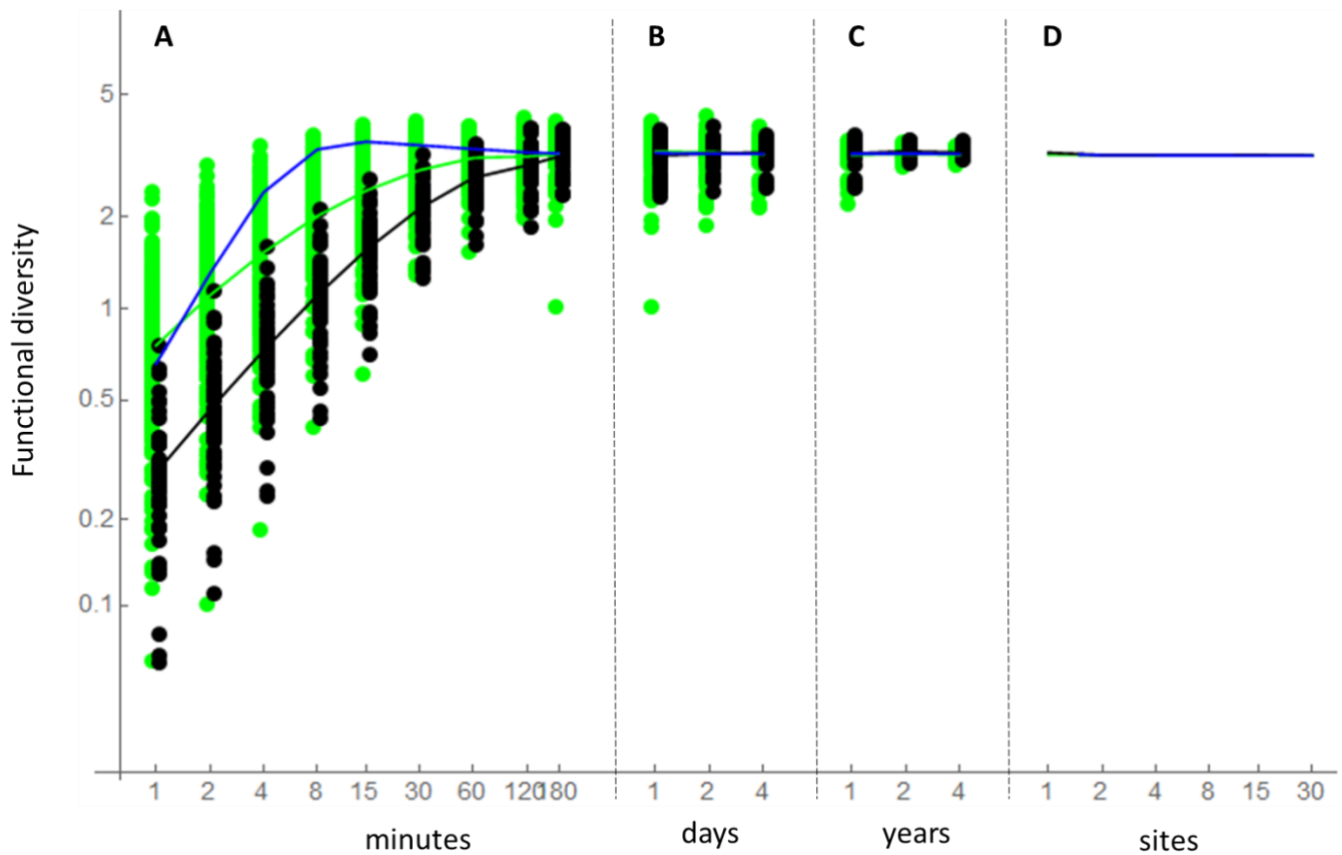


Fig. A3. Local functional diversity versus sampling time.

Mirroring Fig. 3 of the main paper, the figure is otherwise identical to Fig. A2 (hence, see legend of Fig. A2 for explanation), but instead of number of species, the y-axis is functional diversity. Contrasting with Fig. 3, we score a species as present when detected with a probability of >0.5 .

Table A3. Influence of habitat and sampling time on species richness and functional species richness. Mirroring Table 1 of the main paper, the table shows the results of the linear mixed model, where the explanatory variables were the categorical variable of habitat H (primary forest set as baseline, so the coefficient shows the effect of the habitat being secondary forest) and sampling time S. The day-location combination was included in the model as a random effect. Contrasting with Table 1, we score a species as present when detected with a probability of >0.5.

Analysis	Scale	Variable	Coefficient	P-value
Species richness	minutes	H	-0.21	0.003
		S	0.59	<0.001
		H*S	0.06	<0.001
	days	H	-0.12	0.08
		S	0.41	<0.001
		H*S	0.10	<0.001
	years	H	-0.12	<0.001
		S	0.28	<0.001
		H*S	0.11	<0.001
Functional diversity	minutes	H	-0.34	<0.001
		S	0.29	<0.001
		H*S	0.19	<0.001
	days	H	0.02	0.66
		S	-0.01	0.04
		H*S	0.03	0.003
	years	H	0.004	0.39
		S	0.002	0.77
		H*S	0.007	0.50

Appendix 4. Validation of temporal and spatial distance decay curves using alternative species detection criteria

To validate the findings of the main paper, we recreated Figure 4 using the same methods as applied in the main paper, but scoring a species as present when detected with a probability of >0.5 . We note that the results are qualitatively similar regardless of the data selection criteria (compare Figure 4 of the main paper and Figure A4 below, and Table 2 of the main paper and Table A4 below), except that in these results community similarity is higher within primary than within secondary forests. Community similarity (correlation in species content) decreased with distance in both time (Fig. 4A, Fig. A4A) and space (Fig. 4B, Fig. A4B), but the decay in space was much steeper than in time. These patterns were mildly affected by habitat (Table 2 and Table A4): community similarity was higher in primary than secondary forests.

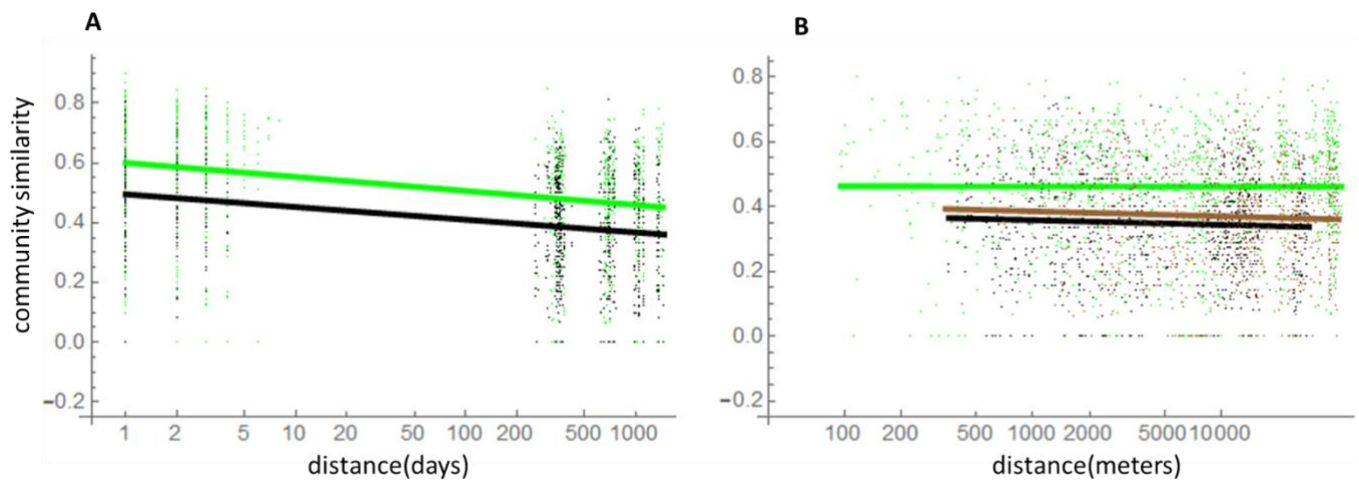


Fig. A4. Temporal and spatial distance decay curves.

To validate the results of the main paper, we recreated Fig. 4, but using 0.5 rather than 0.9 as the probability threshold for considering a species to be detected. Mirroring Fig. 4, we plot similarity of community composition as a function of time between the samples taken in the same location (panel A), and the spatial distance between two locations here sampled in the same year during the same week (panel B). Temporal and spatial distance decay curves are shown separately for primary forests (green) and for secondary forests (black). For spatial distance decay curves, we also show the case where one site is in primary and the other one in secondary forest (brown).

Table A4. Temporal and spatial distance decay curves.

The table shows the intercepts and slopes of the distance decay curves depicted in Fig. A3, and thus mirrors the results shown in Table 2 of the main paper, but for a different data selection: here, species was considered detected if the probability of detection was at least 0.5, whereas in the main manuscript the probability of 0.9 was applied. The values in brackets show the proportion of 1000 replicate analyses in which the intercept was greater in the primary forest than in the habitat of comparison, and in which the slope was smaller (and hence distance decay steeper) in the primary forest than in the habitat of comparison.

Analysis	Habitat	Intercept	Slope
Temporal	Primary	0.47	-0.06
	Secondary	0.39 (1.00)	-0.05 (0.83)
Spatial	Primary	0.51	-0.01
	Secondary	0.43 (0.96)	-0.02 (0.23)
	Mixed	0.41 (0.97)	-0.01 (0.59)

References

- Ovaskainen, O., et al. 2018. Animal Sound Identifier (ASI): software for automated identification of vocal animals. - *Ecol. Lett.* 21: 1244-1254.
- Wilman, H., et al. 2014. EltonTraits 1.0: Species-level foraging attributes of the world's birds and mammals. - *Ecology* 95: 2027-2027.