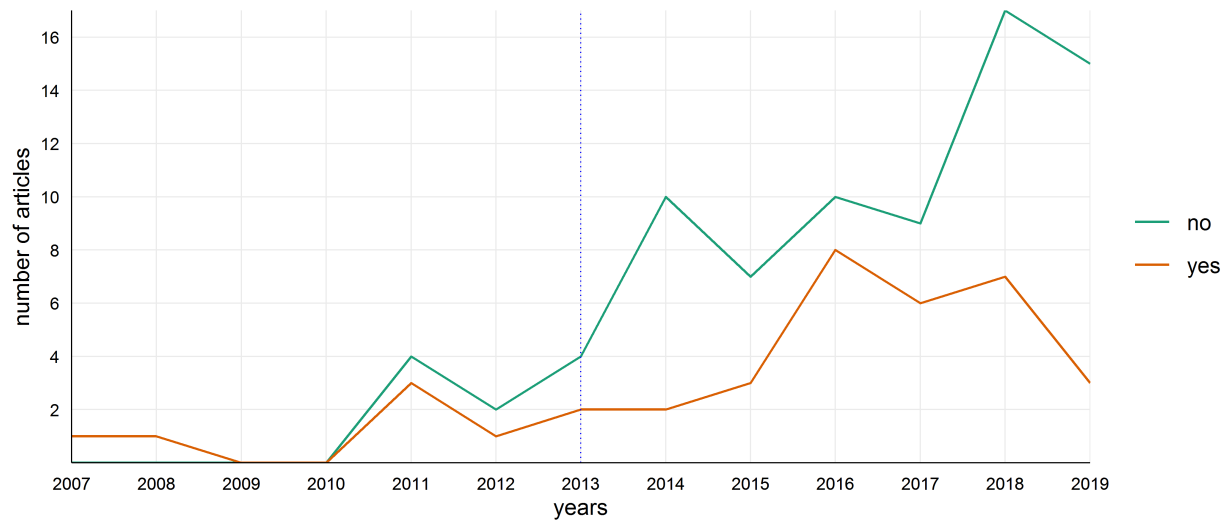


Acoustic diversity indices as biodiversity indicators: a meta-analysis

Supplementary material

A neat presentation of the supplementary material can be found in <https://irene-alcocer.github.io/Acoustic-Indices/>

Data descriptions



Supplementary Figure 1: Temporal evolution (2007 – 2019) of the validation data from the total of 142 articles. Articles which correlate the acoustic indices with real biological data are represented with an orange line and studies which do not correlate with a green line

Supplementary Table 1: Dataset used in the study. Due to the size of this table it is only available at <https://irene-alcocer.github.io/Acoustic-Indices/>

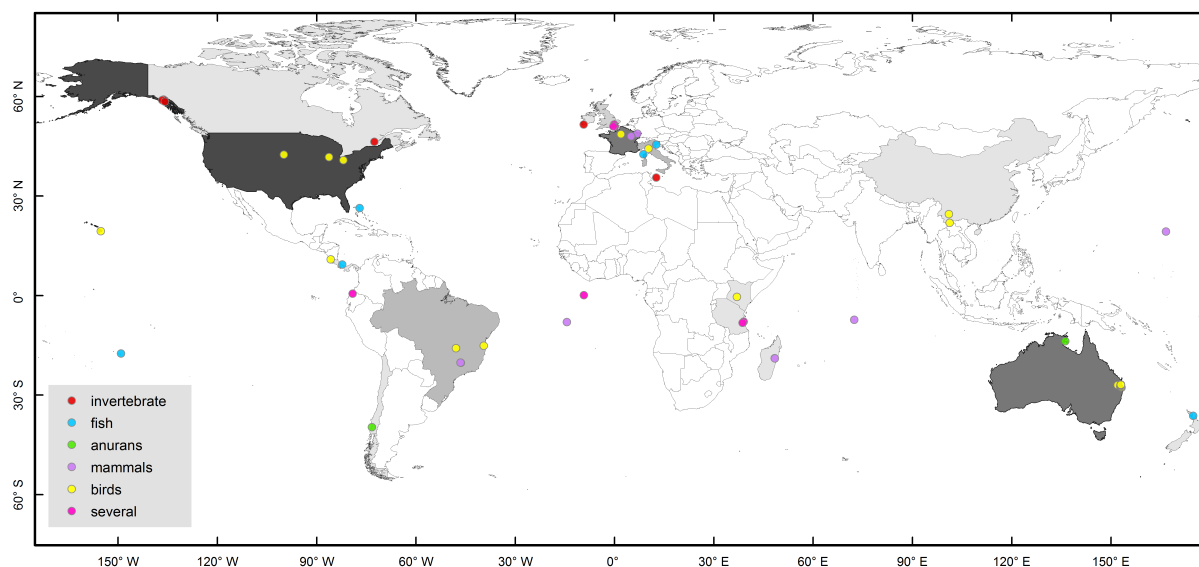
Supplementary Table 2: Variable descriptions for Supplementary Table 2. Available at <https://irene-alcocer.github.io/Acoustic-Indices/>

Supplementary Table 3: Number of effect sizes collected from each of the 34 studies included in the meta-analysis. ID corresponds to the study identification number in our dataset

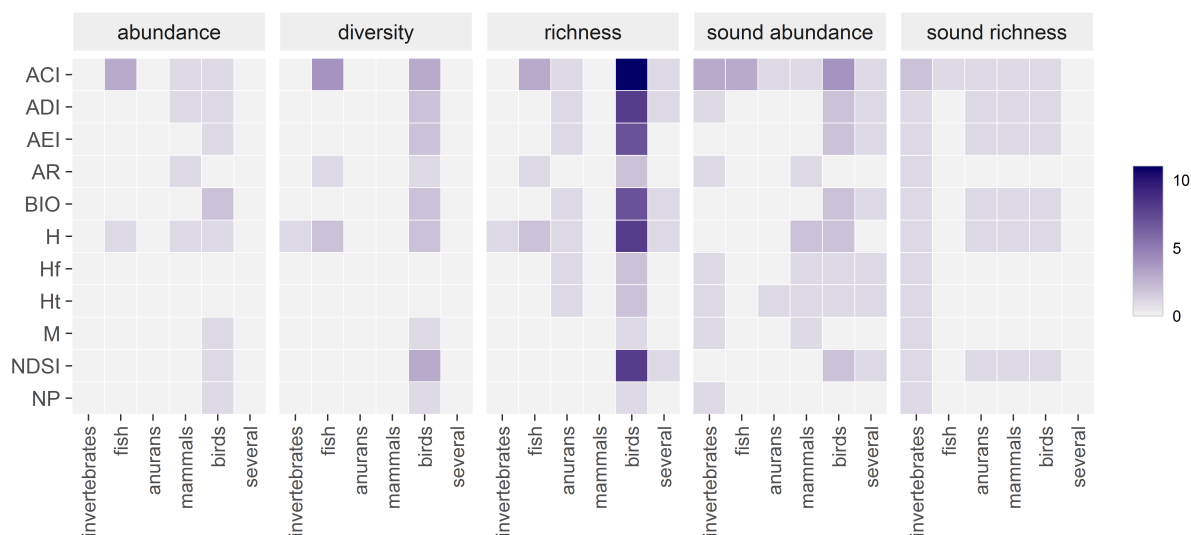
ID	Study	Effect_sizes
2740	Mammides et al. 2017	84
53	Moreno-Gomez 2019	42
87	Eldridge et al. 2018	28
80	Staaterman et al. 2017	24
90	Ferreira et al. 2018	24
96	Izaguirre et al. 2018	24
10	Buscaino et al. 2016	22
2	Desjonquères et al. 2015	12
11	Bertucci et al. 2016	12
89	Gage et al. 2017	12
2977	Jorge et al. 2018	12
70	Bolgan et al. 2018	11
9	Harris et al. 2016	6
86	Indraswari et al. 2018	6
427	Fuller et al. 2015	6
14	Wa Maina et al. 2016	4
60	Patrick Lyon et al. 2019	4
77	Fairbrass et al. 2017	4
92	Torti et al. 2018	4
15	Roca & Proulx 2016	3
45	McLaren 2012	3
13	McWilliam & Hawkin 2013	2
41	Paisley-Jones 2011	2
44	Machado et al. 2017	2
251	Buxton et al. 2016	2
4	Parks et al. 2014	1
6	Boelman et al. 2007	1
17	Zhang et al. 2015	1
37	Picciulin et al. 2016	1
1132	Depraetere et al. 2012	1
1177	Joo et al. 2011	1
1262	Pieretti et al. 2011	1
2745	Sueur et al. 2008	1
2986	Raynor et al. 2017	1

Supplementary Table 4: Number of effect sizes and studies per moderator levels.

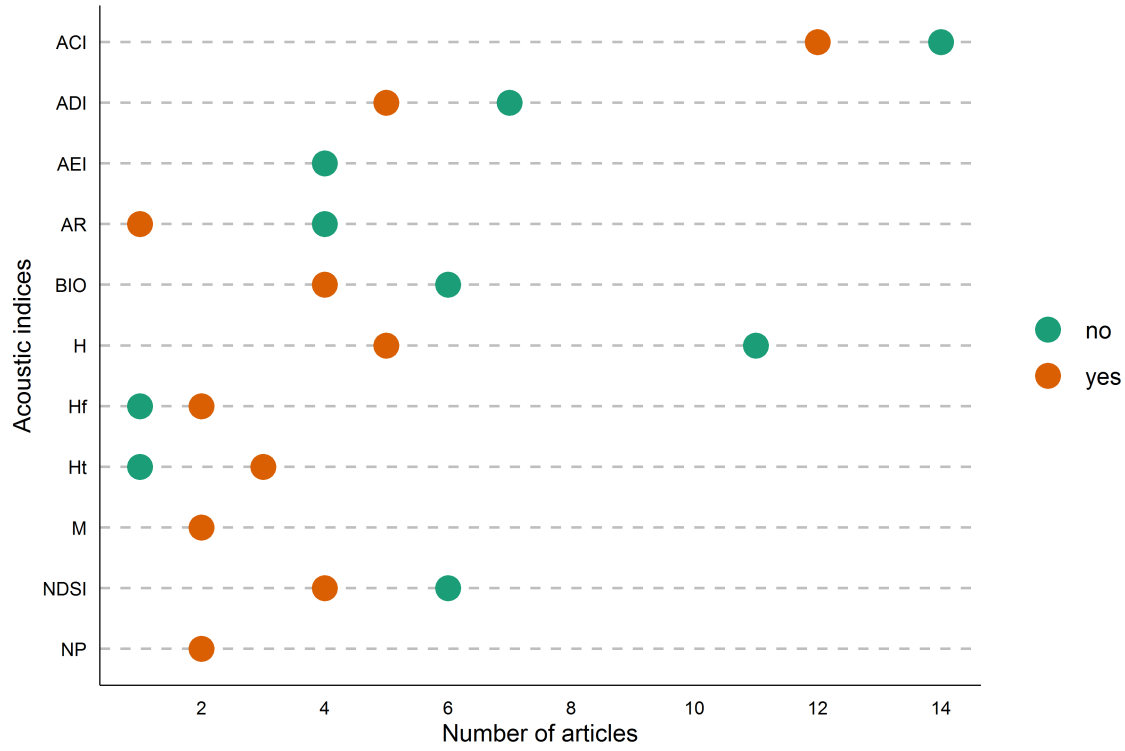
Moderator levels	Effect sizes	Studies
Acoustic indices		
ACI	113	25
ADI	38	12
AEI	34	8
AR	18	5
BIO	36	10
H	55	16
Hf	12	3
Ht	15	4
M	5	2
NDSI	33	10
NP	5	2
Biodiversity metrics		
Abundance	27	6
Diversity	49	9
Richness	187	21
Sound_abundance	66	11
Sound_richness	35	3
Diversity source		
Acoustic	200	26
No_acoustic	164	11
Environment		
Aquatic	95	10
Terrestrial	269	24



Supplementary Figure 2: The geographic distribution of the study sites corresponding to the 35 studies used in the literature review. The colouring of countries exhibits a white to black gradient relative to an increase in the number of studies contributed by each country. The coloured dots discriminate between different groups of studied taxa.



Supplementary Figure 3: Distribution of the 35 articles by biodiversity parameters, taxa and acoustic indices studied. The graph shows the number of articles for each biodiversity parameter and taxonomic group for each acoustic diversity index.



Supplementary Figure 4: Pseudoreplication summary. The data is representing the total number of articles for each index. Color orange represents number of pseudo-replicated studies and green non pseudo-replicated studies. The article (Papin et al., 2019b) was withdrawal from the pseudoreplication analysis due to impossibility of obtain the pseudoreplication data causing some variation on the total number of each acoustic index.

Overall Effect Size

Model output

```
res_main <- rma.mv(z, var, random = ~1 | id/entry, data = df_tidy)
res_main

##
## Multivariate Meta-Analysis Model (k = 364; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed    factor
## sigma^2.1  0.0458  0.2139    34     no      id
## sigma^2.2  0.1755  0.4190   364     no  id/entry
##
## Test for Heterogeneity:
## Q(df = 363) = 2220.9097, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##  0.3461  0.0577  6.0014  <.0001  0.2331  0.4591  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

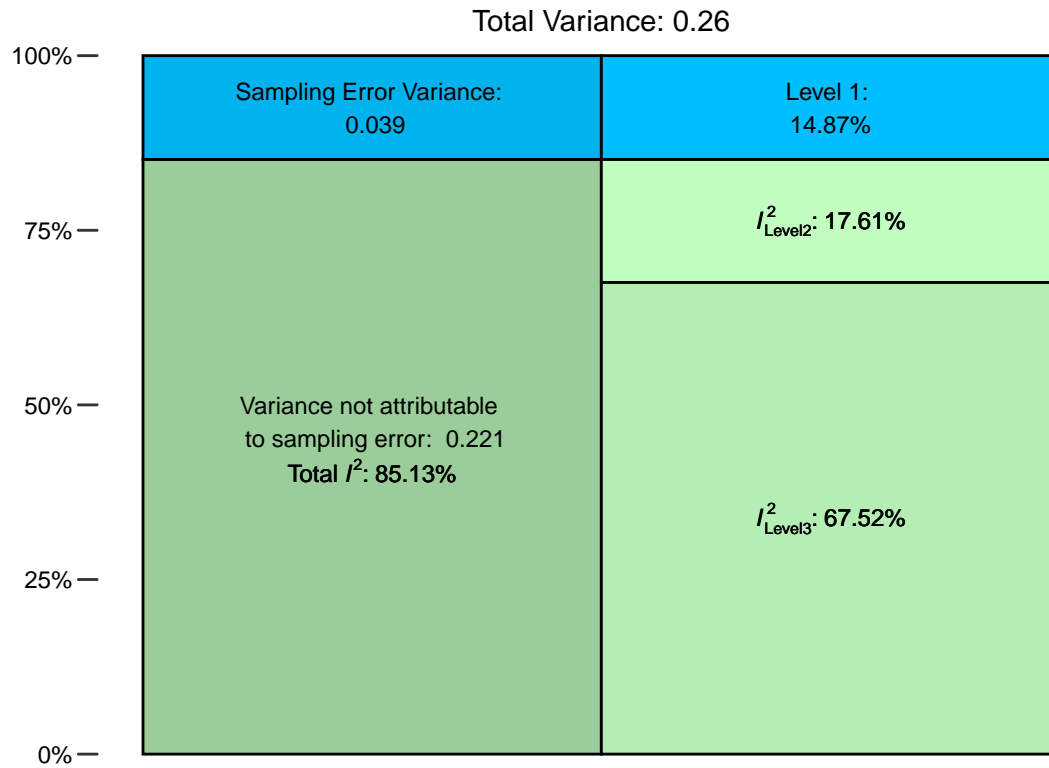
Supplementary Table 5: Resulting estimates from intercept-only model converted to Pearson's correlation. 'Estimate' is the Pearson's r summary effect size. 'CI.lb' and 'CI.ub' are the confidence intervals lower and upper bounds, respectively.

Parameter	Value
Estimate	0.33
CI.lb	0.23
CI.ub	0.43

Heterogeneity

Supplementary Table 6: Uncounted heterogeneity of the intercept-only model as measured by I^2 statistic. Within study heterogeneity (level 2) corresponds to the uncounted variation that is found on effect sizes within studies, and between study heterogeneity corresponds to the uncounted variation between studies (level 3).

	Within study	Between study
% Unexplained variation	17.61	67.52



Supplementary Figure 5: Visual representation of how variance was distributed over the multilevel structure of the intercept-only model. Within study heterogeneity (level 2) corresponds to the unaccounted variation that is found on effect sizes within studies, and between study heterogeneity corresponds to the unaccounted variation between studies (level 3).

Subgroup analysis

Model output

```
res_indices <- rma.mv(z, var, random = ~ 1 | id/entry, mods = ~ index - 1, data = df_indices)
res_indices

##
## Multivariate Meta-Analysis Model (k = 327; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed    factor
## sigma^2.1 0.0295  0.1716    34     no      id
## sigma^2.2 0.1710  0.4135   327     no  id/entry
##
## Test for Residual Heterogeneity:
## QE(df = 320) = 1876.0325, p-val < .0001
##
## Test of Moderators (coefficients 1:7):
## QM(df = 7) = 70.5454, p-val < .0001
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
## indexACI      0.3809 0.0685  5.5596 <.0001    0.2466    0.5152 ***
## indexADI      0.2493 0.0977  2.5506 0.0108    0.0577    0.4408  *
## indexAEI      0.0396 0.1048  0.3774 0.7059   -0.1658    0.2449
## indexAR       0.0780 0.1354  0.5756 0.5649   -0.1875    0.3434
## indexBIO      0.1950 0.1012  1.9266 0.0540   -0.0034    0.3934  .
## indexH        0.5511 0.0903  6.1036 <.0001    0.3742    0.7281 ***
## indexNDSI     0.4557 0.1037  4.3944 <.0001    0.2524    0.6589 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Supplementary Table 7: Resulting estimates from sub-group analysis. The 'Estimate' column is the Pearson correlation effect size; SE is the standard error and CI.lb and CI.up, the lower and upper bounds of the confidence intervals, respectively.

Index	Estimate	SE	CI.lb	CI.ub
ACI	0.363	0.068	0.242	0.474
ADI	0.244	0.097	0.058	0.414
AEI	0.040	0.104	-0.164	0.240
AR	0.078	0.135	-0.185	0.331
BIO	0.193	0.101	-0.003	0.374
H	0.501	0.090	0.358	0.622
NDSI	0.427	0.103	0.247	0.578

Meta-regression

Model output

```
res_full <- rma.mv(z, var, random = ~1 | id/entry,
                  mods = ~ index + bio + environ + diversity_source,
                  data = df_full)

res_full

##
## Multivariate Meta-Analysis Model (k = 296; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed    factor
## sigma^2.1  0.0355  0.1884    33     no      id
## sigma^2.2  0.1738  0.4168   296     no  id/entry
##
## Test for Residual Heterogeneity:
## QE(df = 284) = 1730.2577, p-val < .0001
##
## Test of Moderators (coefficients 2:12):
## QM(df = 11) = 27.4277, p-val = 0.0040
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt              0.3590  0.1416   2.5359  0.0112   0.0815   0.6365
## indexADI             -0.1294  0.1171  -1.1049  0.2692  -0.3590   0.1001
## indexAEI             -0.2916  0.1231  -2.3679  0.0179  -0.5329  -0.0502
## indexAR              -0.2735  0.1482  -1.8461  0.0649  -0.5639   0.0169
## indexBIO             -0.1449  0.1203  -1.2038  0.2287  -0.3807   0.0910
## indexH               0.1977  0.1092   1.8111  0.0701  -0.0162   0.4117
## indexNDSI            0.0840  0.1260   0.6667  0.5050  -0.1630   0.3310
## bioabundance         -0.0815  0.1589  -0.5133  0.6078  -0.3929   0.2298
## biodiversity         -0.0420  0.0950  -0.4423  0.6583  -0.2283   0.1442
## biosound_abundance    0.2600  0.1470   1.7690  0.0769  -0.0281   0.5480
## environA             -0.0656  0.1484  -0.4422  0.6583  -0.3565   0.2252
## diversity_sourceacoustic -0.0091  0.1464  -0.0623  0.9504  -0.2962   0.2779
##
## intrcpt              *
## indexADI
## indexAEI              *
## indexAR               .
## indexBIO
## indexH               .
## indexNDSI
## bioabundance
## biodiversity
## biosound_abundance   .
## environA
## diversity_sourceacoustic
##
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Collinearity

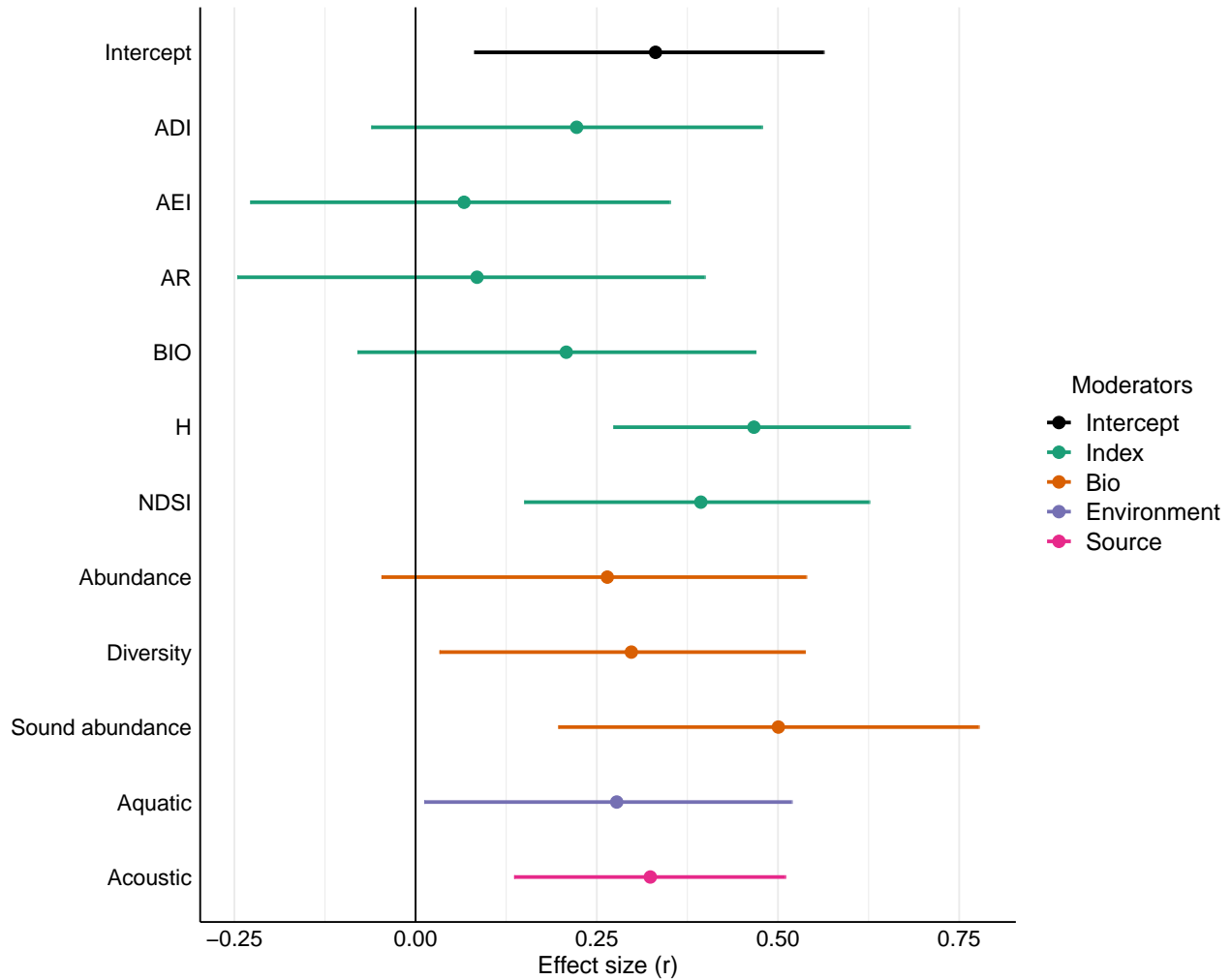
Supplementary Table 8: VIF values obtained for each moderator level.

Moderators	VIF
indexADI	1.4966
indexAEI	1.4504
indexAR	1.2503
indexBIO	1.4781
indexH	1.4722
indexNDSI	1.4375
bioabundance	1.2443
biodiversity	1.1561
biosound_abundance	1.4543
environA	1.3931
diversity_sourceacoustic	1.6229

Visualization of results

Supplementary Table 9: Table used to plot Supplementary Figure 6. Each estimate corresponds to the additive effect when a moderator level is replaced in the intercept (e.g. ADI is the additive effect of ADI when ADI is put as intercept instead of ACI). The column 'Coefficients' lists the model intercept and the levels of each moderator. The column 'Estimate' is the estimated Pearson (r) correlation. 'SE' is the standard error of the estimate. 'CI' are the [lower] [upper] bounds of the confidence intervals.

Moderators	Coefficients	Estimate	SE	CI
Intercept	Intercept	0.344	0.141	[0.081] [0.563]
Index	ADI	0.226	0.147	[-0.061] [0.478]
Index	AEI	0.067	0.152	[-0.228] [0.351]
Index	AR	0.085	0.170	[-0.246] [0.399]
Index	BIO	0.211	0.149	[-0.08] [0.469]
Index	H	0.506	0.140	[0.273] [0.682]
Index	NDSI	0.416	0.148	[0.15] [0.626]
Bio	Abundance	0.271	0.164	[-0.047] [0.539]
Bio	Diversity	0.307	0.144	[0.033] [0.537]
Bio	Sound abundance	0.550	0.211	[0.197] [0.777]
Environment	Aquatic	0.285	0.142	[0.012] [0.519]
Source	Acoustic	0.336	0.108	[0.136] [0.51]



Supplementary Figure 6: Estimates (circles) and corresponding 95% confidence intervals (horizontal lines). Moderator are acoustic indices (Index), biodiversity metrics (Bio), environment (Environment) and acoustic source (Source). Each estimate corresponds to the additive effect when a moderator level is replaced in the intercept (e.g. ADI is the additive effect of ADI when ADI is put as intercept instead of ACI). Estimated effect sizes whose 95% confidence intervals do not overlap zero (black vertical line) indicate a positive correlation between acoustic indices and diversity if they are to the right of zero, or a negative correlation if they are to the left of zero.

Test of moderators

Supplementary Table 10: Wald-type tests for all moderators (first row), and for each moderator separately (remaining rows). 'Q' is the Wald statistic. 'df' are the degrees of freedom. 'p' is the probability that moderator estimates came from a chi-square distribution, where all estimates are equal to zero. So a p-value < 0.05 gives support against the null hypothesis that moderator levels estimates are equal to zero (i.e. they do not explain variation in effect sizes).

Moderator	Q	df	p
All moderators	27.428	11	0.004
Acoustic indices	22.353	6	0.001
Biodiv. parameters	3.561	3	0.313
Environment	0.196	1	0.658
Diversity source	0.004	1	0.950

Contrasts between moderator levels

Contrasts between H and other acoustic indices

Supplementary Table 11: Wald-type tests for the contrasts between acoustic index H with all other acoustic indices. The column 'Compared' expresses the comparison, in this cases it is the difference between the estimate H and the estimate of each of the other acoustic indices. The column 'Estimate' is the estimate obtained from the difference expressed in the previous column. 'SE' is the standard error of the difference, and CI.lb, CI.up the confidence interval lower and upper bound, respectively. 'QM' is the Wald statistic. 'p' is the probability that the difference between estimates is equal to zero. Thus, a p-value < 0.05 gives support against the null hypothesis of no difference between the estimate of the H index and the estimate of the other index.

Compared	Estimate	SE	CI.lb	CI.up	QM	p
H - ADI	0.327	0.122	0.089	0.566	7.223	0.007
H - AEI	0.489	0.127	0.241	0.738	14.901	0.000
H - AR	0.471	0.152	0.173	0.769	9.623	0.002
H - BIO	0.343	0.124	0.099	0.586	7.591	0.006
H - ACI	0.198	0.109	-0.016	0.412	3.280	0.070
H - NDSI	0.114	0.130	-0.141	0.369	0.765	0.382

Contrasts between NDSI and other acoustic indices

Supplementary Table 12: Wald-type tests for the contrasts between acoustic index NDSI with all other acoustic indices. The column 'Compared' expresses the comparison, in this cases it is the difference between the estimate NDSI and the estimate of each of the other acoustic indices. The column 'Estimate' is the estimate obtained from the difference expressed in the previous column. 'SE' is the standard error of the difference, and CI.lb, CI.up the confidence interval lower and upper bound, respectively. 'QM' is the Wald statistic. 'p' is the probability that the difference between estimates is equal to zero. Thus, a p-value < 0.05 gives support against the null hypothesis of no difference between the estimate of the NDSI index and the estimate of the other index.

Compared	Estimate	SE	CI.lb	CI.up	QM	p
NDSI - ADI	0.213	0.133	-0.047	0.474	2.586	0.108
NDSI - AEI	0.376	0.138	0.106	0.645	7.442	0.006
NDSI - AR	0.358	0.161	0.041	0.674	4.914	0.027
NDSI - BIO	0.229	0.135	-0.036	0.494	2.869	0.090
NDSI - H	-0.114	0.130	-0.369	0.141	0.765	0.382
NDSI - ACI	0.084	0.126	-0.163	0.331	0.444	0.505

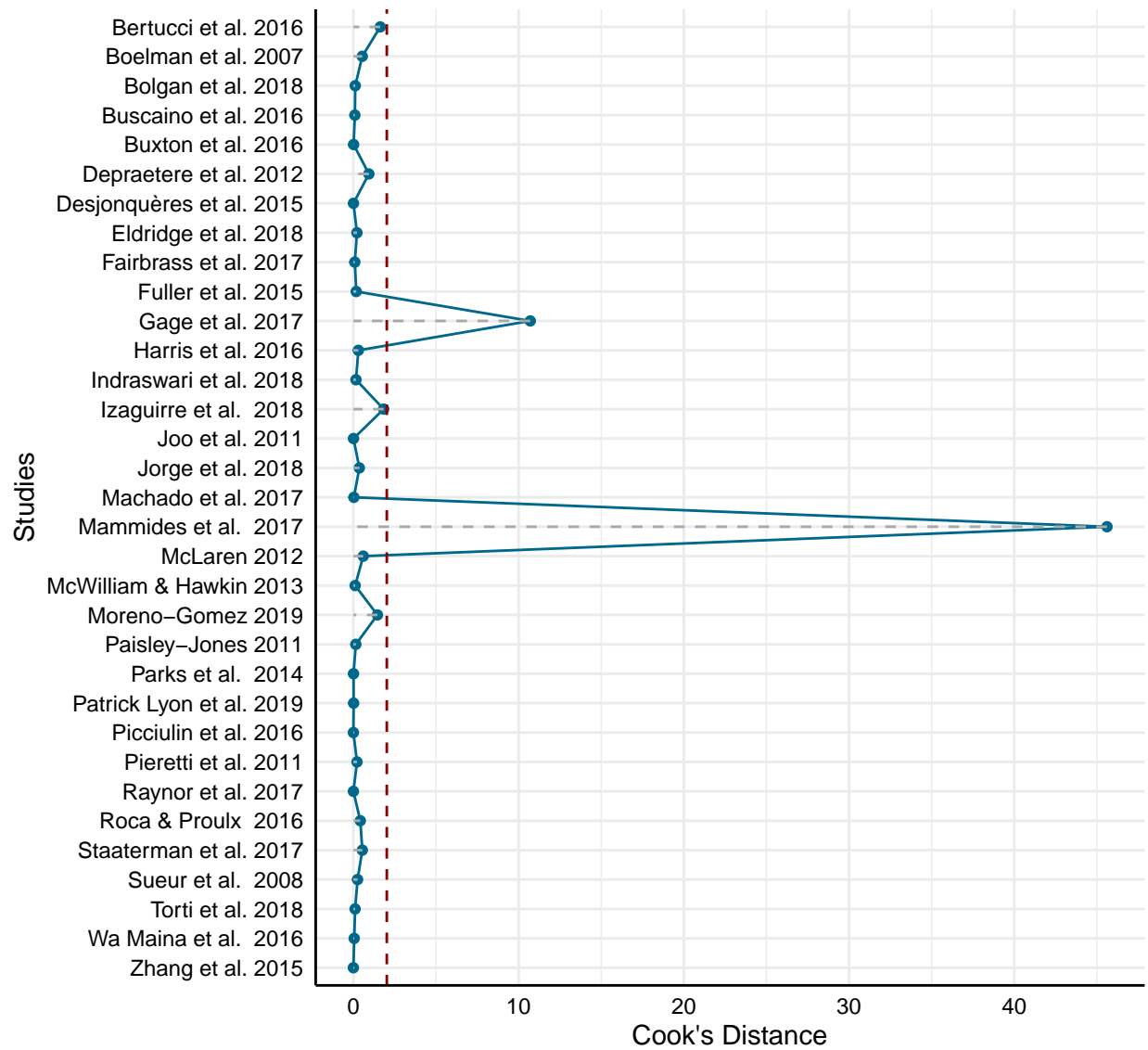
Contrasts between sound abundance and other biodiversity parameters

Supplementary Table 13: Wald-type tests for the contrasts between the biodiversity metric sound abundance with all other biodiversity parameters. The column 'Compared' expresses the comparison, in this cases it is the difference between the estimate sound abundance and the estimate of each of the other biodiversity metrics. The column 'Estimate' is the estimate obtained from the difference expressed in the previous column. 'SE' is the standard error of the difference, and CI.lb, CI.up the confidence interval lower and upper bound, respectively. 'QM' is the Wald statistic. 'p' is the probability that the difference between estimates is equal to zero. Thus, a p-value < 0.05 gives support against the null hypothesis of no difference between the estimate of the sound abundance metric and the estimate of the other metric.

Compared	Estimate	SE	CI.lb	CI.up	QM	p
sound_abundance - abundance	0.342	0.215	-0.079	0.762	2.530	0.112
sound_abundance - diversity	0.302	0.172	-0.035	0.639	3.087	0.079
sound_abundance - richness	0.260	0.147	-0.028	0.548	3.129	0.077

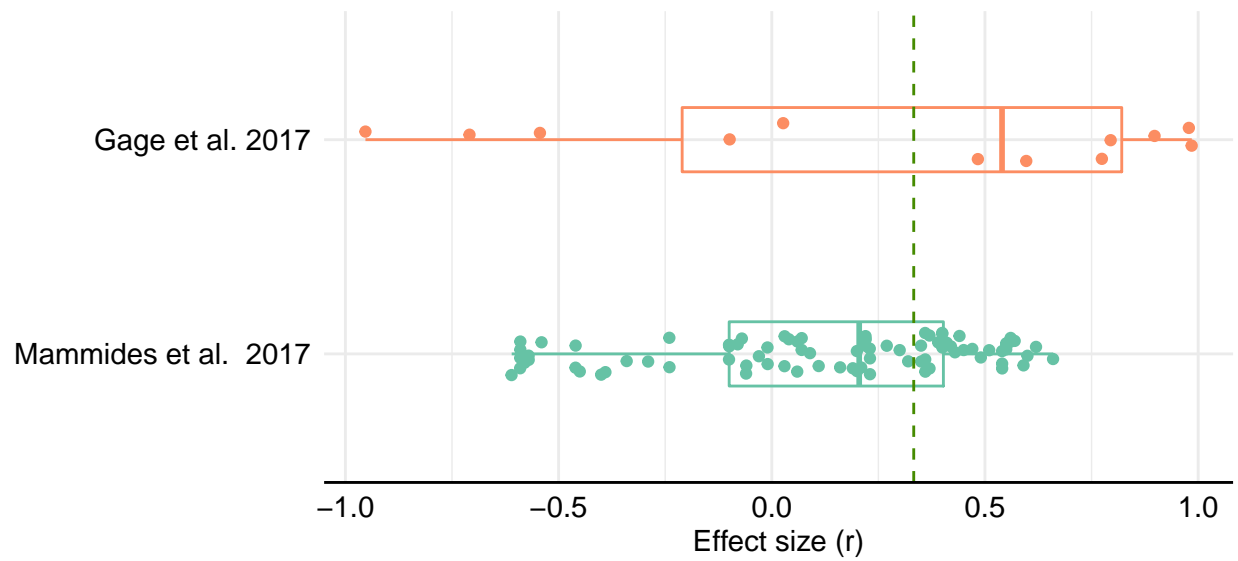
Sensibility analysis

Cook's distance



Supplementary Figure 7: Cook's distance values for each study (blue dots on the figure) and average Cook's distance over all studies indicated as a dashed vertical red line. The Cook's distance for a given study can be interpreted as the distance between the entire set of predicted values once with this study included and once with the this study excluded from the model fitting procedure. On the y-axis are the studies identified by first author and year. The x-axis corresponds to the Cook's distance values.

Inspection of outliers



Supplementary Figure 8: Boxplot and distribution of of effect size values (dots) of the two studies identified as outliers. The y-axis identifies the study, and the x-axis corresponds to the Pearson r effect size. The green vertical dashed line is the summary effect obtained in the intercept-only model.

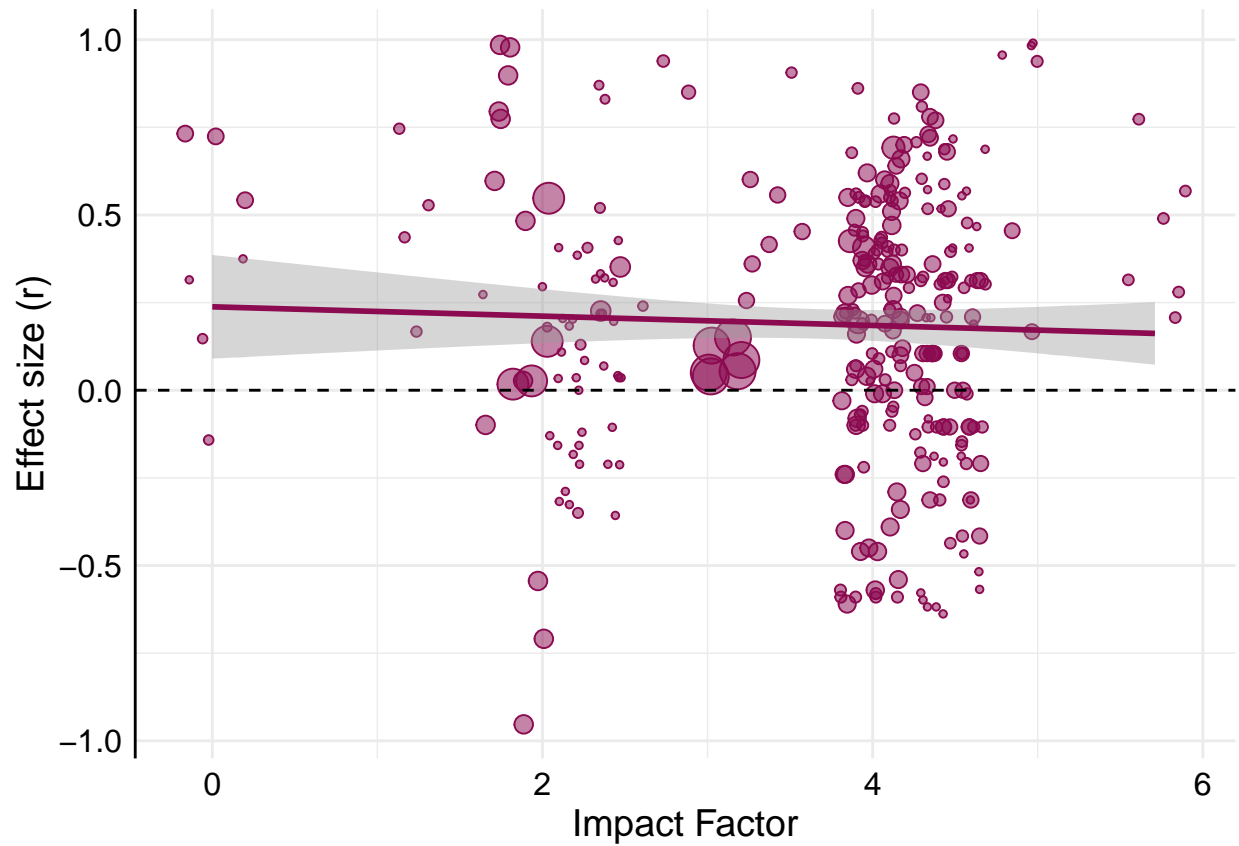
Model output without outliers

```
res_no_outliers <- rma.mv(z, var, random = ~1 | id/entry,
  mods = ~ index + bio + environ + diversity_source,
  data = df_no_outliers)
res_no_outliers

##
## Multivariate Meta-Analysis Model (k = 200; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed    factor
## sigma^2.1  0.1225  0.3500    31     no      id
## sigma^2.2  0.0557  0.2360   200     no  id/entry
##
## Test for Residual Heterogeneity:
## QE(df = 188) = 472.4368, p-val < .0001
##
## Test of Moderators (coefficients 2:12):
## QM(df = 11) = 6.3074, p-val = 0.8521
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt              0.6457  0.1870   3.4522  0.0006   0.2791  1.0123
## indexADI             -0.2059  0.1118  -1.8412  0.0656  -0.4251  0.0133
## indexAEI             -0.0753  0.1260  -0.5977  0.5500  -0.3224  0.1717
## indexAR              -0.0770  0.2082  -0.3700  0.7114  -0.4850  0.3310
## indexBIO             -0.0992  0.1192  -0.8319  0.4054  -0.3328  0.1345
## indexH               -0.0357  0.1058  -0.3372  0.7360  -0.2430  0.1716
## indexNDSI            -0.0164  0.1406  -0.1165  0.9073  -0.2919  0.2591
## bioabundance         -0.1566  0.1512  -1.0355  0.3005  -0.4530  0.1398
## biodiversity         -0.1064  0.1298  -0.8199  0.4122  -0.3607  0.1479
## biosound_abundance    0.1597  0.2105   0.7587  0.4480  -0.2528  0.5722
## environA             -0.1907  0.2057  -0.9271  0.3539  -0.5939  0.2125
## diversity_sourceacoustic -0.1379  0.1909  -0.7226  0.4700  -0.5120  0.2362
##
## intrcpt              ***
## indexADI              .
## indexAEI
## indexAR
## indexBIO
## indexH
## indexNDSI
## bioabundance
## biodiversity
## biosound_abundance
## environA
## diversity_sourceacoustic
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Effect size tendencies

Relationship between effect size and journal impact factor



Supplementary Figure 9: Relation between effect size mean values (circles) and journal impact factor. Circle size indicates the relative sample size of each effect size. The fitted line is a simple least squares regression with the corresponding 95% confidence interval region in grey. The dashed horizontal line represents an effect size of 0. Effect size mean values are positioned along the impact factor axis with minor random noise to reduce overlapping.