SUPPLEMENTARY INFORMATION

Song evolution in American Screech-owls

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SEQUENCE ALIGNMENT
------------------


Input data: 34 taxa with 6 partitions and 3917 total sites (13.8356%
missing data)


  ID  Name  Type  Seq   Site  Unique      Infor Invar Const
   1  CO1   DNA   32    376   144   118   239   238
   2  Cytb  DNA   34    1005  453   363   560   560
   3  ND2   DNA   30    1030  469   377   501   501
   4  CHD   DNA   25    346   37    9     312   312
   5  FGB   DNA   25    559   57    20    517   517
   6  MUSK  DNA   25    601   69    15    545   545

Column meanings:
  Unique: Number of unique site patterns
  Infor:  Number of parsimony-informative sites
  Invar:  Number of invariant sites
  Const:  Number of constant sites (can be subset of invariant sites)


ModelFinder
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Best-fit model according to BIC:
TVM+F+I+G4:CO1,TIM2+F+I+G4:Cytb,TIM2+F+I+G4:ND2,TPM3+F:CHD,TPM2u+F+I+G4:
FGB,HKY+F+G4:MUSK


List of best-fit models per partition:


  ID  Model             LogL          AIC      w-AIC      AICc     w-
AICc       BIC      w-BIC
   1  TVM+F+I+G4       -2754.4722   5528.9443 + 0.0000   5529.5471 +
0.0000   5568.2402 + 0.0000
   2  TIM2+F+I+G4      -8339.5903  16697.1806 + 0.0000  16697.3615 +
0.0000  16741.3953 + 0.0000
```

```
   3  TIM2+F+I+G4      -8093.2977  16204.5954 + 0.0000  16204.7719 +
0.0000  16249.0313 + 0.0000

   4  TPM3+F            -722.8403   1457.6805 + 0.0000   1457.9283 +
0.0000   1480.7591 + 0.0000

   5  TPM2u+F+I+G4     -1291.3080   2598.6160 + 0.0000   2598.8778 +
0.0000   2633.2252 + 0.0000

   6  HKY+F+G4         -1283.4963   2578.9925 + 0.0000   2579.1340 +
0.0000   2605.3841 + 0.0000


AIC, w-AIC   : Akaike information criterion scores and weights.

AICc, w-AICc : Corrected AIC scores and weights.

BIC, w-BIC   : Bayesian information criterion scores and weights.


Plus signs denote the 95% confidence sets.

Minus signs denote significant exclusion.


SUBSTITUTION PROCESS

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Edge-linked-proportional partition model but separate models between
partitions


  ID  Model           Speed  Parameters

   1  TVM+F+I+G4     1.5389
TVM{4.21435,50.3442,0.392673,0.0001}+F{0.265134,0.275127,0.186693,0.2730
45}+I{0.588598}+G4{1.08867}

   2  TIM2+F+I+G4    1.5768
TIM2{2.95432,60.1361,36.6835}+F{0.266515,0.353685,0.133657,0.246143}+I{0
.514309}+G4{1.43334}

   3  TIM2+F+I+G4    1.5293
TIM2{3.28709,71.9617,32.1286}+F{0.313025,0.356224,0.102305,0.228447}+I{0
.374617}+G4{1.19014}

   4  TPM3+F         0.0977
TPM3{5.73279,14.0276}+F{0.356171,0.118437,0.156988,0.368404}

   5  TPM2u+F+I+G4   0.1578
TPM2u{0.231745,0.890946}+F{0.325666,0.142783,0.213948,0.317603}+I{0.7862
51}+G4{0.455915}

   6  HKY+F+G4       0.0940
HKY{4.58523}+F{0.300833,0.172137,0.204679,0.322351}+G4{0.248534}
```

```
MAXIMUM LIKELIHOOD TREE
-----------------------


Log-likelihood of the tree: -22428.6914 (s.e. 438.7750)
Unconstrained log-likelihood (without tree): -13460.6277
Number of free parameters (#branches + #model parameters): 112
Akaike information criterion (AIC) score: 45081.3828
Corrected Akaike information criterion (AICc) score: 45088.0368
Bayesian information criterion (BIC) score: 45783.9679


Total tree length (sum of branch lengths): 1.7441
Sum of internal branch lengths: 0.3784 (21.6976% of tree length)


WARNING: 1 near-zero internal branches (<0.0003) should be treated with
caution
         Such branches are denoted by '**' in the figure below


NOTE: Tree is UNROOTED although outgroup taxon 'Megascops_alagoensis' is
drawn at root
Numbers in parentheses are SH-aLRT support (%) / ultrafast bootstrap
support (%)


+--Megascops_alagoensis
|
|     +--Megascops_ater
|  +--| (72.3/92)
|  |  |  +--Megascops_usta
|  |  +--| (82.9/94)
|  |     |                             +----Megascops_asio
|  |     |                          +--| (29.4/85)
|  |     |                          |  +----Megascops_kennicottii
|  |     |                       +--| (94.1/94)
|  |     |                       |  +-----Megascops_cooperi
|  |     |                    +--| (0.5/41)
|  |     |                    |  +----Megascops_sanctaecatarinae
```

```
|  |     |                 +--| (92.3/93)
|  |     |                 |  +-----Megascops_barbarus
|  |     |              +--| (90.4/58)
|  |     |              |  |         +------Megascops_albogularis
|  |     |              |  |      +--| (89.9/96)
|  |     |              |  |      |  |      +--Megascops_choliba
|  |     |              |  |      |  +------| (100/100)
|  |     |              |  |      |         +--Megascops_koepckeae
|  |     |              |  |   +--| (61.1/78)
|  |     |              |  |   |  |  +---Megascops_clarkii
|  |     |              |  |   |  +--| (98.5/99)
|  |     |              |  |   |     +-------Megascops_trichopsis
|  |     |              |  +---| (99.9/100)
|  |     |              |      |            +----------Megascops_nudipes
|  |     |              |      |      +-----| (100/100)
|  |     |              |      |      |     +----------
Psiloscops_flammeolus
|  |     |              |      +------| (100/100)
|  |     |              |             |              +------------
Lophostrix_cristata
|  |     |              |             |           +--| (95.5/92)
|  |     |              |             |           |  +-----------
Pulsatrix_koeniswaldiana
|  |     |              |             |        +**| (0/34)
|  |     |              |             |        |  +----------------
Strix_aluco
|  |     |              |             |     +--| (12.7/36)
|  |     |              |             |     |  +--------------Bubo_bubo
|  |     |              |             +-----| (100/99)
|  |     |              |                   |  +------------------------
-------Otus_megalotis
|  |     |              |                   +--| (91/52)
|  |     |              |                      +--------------------
Asio_otus
|  |     |           +--| (62.4/40)
|  |     |           |  |     +----Megascops_centralis
```

```
|  |     |           |  |  +--| (99.2/100)
|  |     |           |  |  |  +--Megascops_roraimae
|  |     |           |  +--| (100/99)
|  |     |           |     +--Megascops_guatemalae
|  |     |        +--| (81.2/85)
|  |     |        |  |     +--Megascops_colombianus
|  |     |        |  |  +--| (100/100)
|  |     |        |  |  |  +--Megascops_ingens
|  |     |        |  +--| (99.4/96)
|  |     |        |     |  +------Megascops_petersoni
|  |     |        |     +--| (82.1/88)
|  |     |        |        |  +---Megascops_hoyi
|  |     |        |        +--| (100/100)
|  |     |        |           +--Megascops_marshalli
|  |     |     +--| (88.2/95)
|  |     |     |  +----Megascops_gilesi
|  |     |  +--| (96/98)
|  |     |  |  +---Megascops_roboratus
|  |     +--| (100/100)
|  |        +---Megascops_watsonii
+--| (94.4/96)
|  +--Megascops_stangiae
|
+--Megascops_atricapilla


Tree in newick format:


(Megascops_alagoensis:0.0060363812,((Megascops_ater:0.0119403113,(Megasc
ops_usta:0.0118294354,(((((((((Megascops_asio:0.0316466320,Megascops_ke
nnicottii:0.0318025608)29.4/85:0.0027975721,Megascops_cooperi:0.03366240
09)94.1/94:0.0047458609,Megascops_sanctaecatarinae:0.0294976284)0.5/41:0
.0008168868,Megascops_barbarus:0.0350224363)92.3/93:0.0024705737,(((Mega
scops_albogularis:0.0405965166,(Megascops_choliba:0.0094780019,Megascops
_koepckeae:0.0125494733)100/100:0.0439570216)89.9/96:0.0065518214,(Megas
cops_clarkii:0.0249203267,Megascops_trichopsis:0.0484092785)98.5/99:0.01
47398940)61.1/78:0.0117073809,((Megascops_nudipes:0.0648357249,Psiloscop
s_flammeolus:0.0655354258)100/100:0.0347147611,((((Lophostrix_cristata:0
.0746288102,Pulsatrix_koeniswaldiana:0.0681479449)95.5/92:0.0216966093,S
```

```
trix_aluco:0.0993753528)0/34:0.0000020072,Bubo_bubo:0.0848272856)12.7/36
:0.0037654410,(Otus_megalotis:0.1825908162,Asio_otus:0.1224644719)91/52:
0.0145892693)100/99:0.0340241485)100/100:0.0409972157)99.9/100:0.0278978
664)90.4/58:0.0034424470,((Megascops_centralis:0.0293514430,Megascops_ro
raimae:0.0121522201)99.2/100:0.0106462944,Megascops_guatemalae:0.0180453
182)100/99:0.0180535492)62.4/40:0.0005076502,((Megascops_colombianus:0.0
143758196,Megascops_ingens:0.0194748582)100/100:0.0207569089,(Megascops_
petersoni:0.0439456977,(Megascops_hoyi:0.0268536480,Megascops_marshalli:
0.0179874441)100/100:0.0155154384)82.1/88:0.0028883894)99.4/96:0.0098277
265)81.2/85:0.0031082555,Megascops_gilesi:0.0285257268)88.2/95:0.0047134
332,Megascops_roboratus:0.0261273387)96/98:0.0060185813,Megascops_watson
ii:0.0269984848)100/100:0.0127958941)82.9/94:0.0014632010)72.3/92:0.0002
558407,Megascops_stangiae:0.0070014603)94.4/96:0.0029701086,Megascops_at
ricapilla:0.0050715443);


CONSENSUS TREE
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Consensus tree is constructed from 1000bootstrap trees
Log-likelihood of consensus tree: -22428.732611
Robinson-Foulds distance between ML tree and consensus tree: 2

Branches with support >0.000000% are kept (extended consensus)
Branch lengths are optimized by maximum likelihood on original alignment
Numbers in parentheses are bootstrap supports (%)

+--Megascops_alagoensis
|
|     +--Megascops_ater
|  +--| (92)
|  |  |  +--Megascops_usta
|  |  +--| (94)
|  |     |                             +----Megascops_asio
|  |     |                          +--| (85)
|  |     |                          |  +----Megascops_kennicottii
|  |     |                       +--| (94)
|  |     |                       |  +-----Megascops_cooperi
|  |     |                    +--| (56)
|  |     |                    |  +-----Megascops_barbarus
```

```
|  |     |                 +--| (93)
|  |     |                 |  +----Megascops_sanctaecatarinae
|  |     |              +--| (58)
|  |     |              |  |          +------Megascops_albogularis
|  |     |              |  |       +--| (96)
|  |     |              |  |       |  |      +--Megascops_choliba
|  |     |              |  |       |  +------| (100)
|  |     |              |  |       |         +--Megascops_koepckeae
|  |     |              |  |    +--| (78)
|  |     |              |  |    |  |  +---Megascops_clarkii
|  |     |              |  |    |  +--| (99)
|  |     |              |  |    |     +-------Megascops_trichopsis
|  |     |              |  +----| (100)
|  |     |              |       |            +----------
Megascops_nudipes
|  |     |              |       |      +-----| (100)
|  |     |              |       |      |     +----------
Psiloscops_flammeolus
|  |     |              |       +------| (100)
|  |     |              |              |              +------------
Lophostrix_cristata
|  |     |              |              |           +--| (92)
|  |     |              |              |           |  +-----------
Pulsatrix_koeniswaldiana
|  |     |              |              |        +--| (34)
|  |     |              |              |        |  +----------------
Strix_aluco
|  |     |              |              |     +--| (36)
|  |     |              |              |     |  +--------------Bubo_bubo
|  |     |              |              +-----| (99)
|  |     |              |                    |  +-----------------------
--------Otus_megalotis
|  |     |              |                    +--| (52)
|  |     |              |                       +--------------------
Asio_otus
|  |     |           +--| (40)
|  |     |           |  |     +----Megascops_centralis
```

```
|  |     |           |  |  +--| (100)
|  |     |           |  |  |  +--Megascops_roraimae
|  |     |           |  +--| (99)
|  |     |           |     +--Megascops_guatemalae
|  |     |        +--| (85)
|  |     |        |  |     +--Megascops_colombianus
|  |     |        |  |  +--| (100)
|  |     |        |  |  |  +--Megascops_ingens
|  |     |        |  +--| (96)
|  |     |        |     |  +------Megascops_petersoni
|  |     |        |     +--| (88)
|  |     |        |        |  +---Megascops_hoyi
|  |     |        |        +--| (100)
|  |     |        |           +--Megascops_marshalli
|  |     |     +--| (95)
|  |     |     |  +----Megascops_gilesi
|  |     |  +--| (98)
|  |     |  |  +---Megascops_roboratus
|  |     +--| (100)
|  |        +---Megascops_watsonii
+--| (96)
|  +--Megascops_stangiae
|
+--Megascops_atricapilla


Consensus tree in newick format:


(Megascops_alagoensis:0.0060376089,((Megascops_ater:0.0119433517,(Megasc
ops_usta:0.0118469004,(((((((((Megascops_asio:0.0319599191,Megascops_ke
nnicottii:0.0316606578)85:0.0027155192,Megascops_cooperi:0.0338790307)94
:0.0041248041,Megascops_barbarus:0.0344319438)56:0.0014576615,Megascops_
sanctaecatarinae:0.0296326389)93:0.0024399949,(((Megascops_albogularis:0
.0406406425,(Megascops_choliba:0.0094858673,Megascops_koepckeae:0.012553
6488)100:0.0440291417)96:0.0066156987,(Megascops_clarkii:0.0249163671,Me
gascops_trichopsis:0.0484692191)99:0.0146971009)78:0.0117980353,((Megasc
ops_nudipes:0.0648762668,Psiloscops_flammeolus:0.0655884147)100:0.034698
5667,((((Lophostrix_cristata:0.0746550125,Pulsatrix_koeniswaldiana:0.068
2004430)92:0.0217133954,Strix_aluco:0.0994393525)34:0.0000021257,Bubo_bu
```

```
bo:0.0848834096)36:0.0037684795,(Otus_megalotis:0.1827911999,Asio_otus:0
.1226043634)52:0.0145871129)99:0.0340531559)100:0.0409709302)100:0.02804
13603)58:0.0034074432,((Megascops_centralis:0.0293822461,Megascops_rorai
mae:0.0121710676)100:0.0107311306,Megascops_guatemalae:0.0179666828)99:0
.0181580744)40:0.0004066206,((Megascops_colombianus:0.0143604212,Megasco
ps_ingens:0.0195153564)100:0.0207444235,(Megascops_petersoni:0.044029736
4,(Megascops_hoyi:0.0268688751,Megascops_marshalli:0.0180068417)100:0.01
55282915)88:0.0029041593)96:0.0099440089)85:0.0031060468,Megascops_giles
i:0.0284552884)95:0.0046828004,Megascops_roboratus:0.0261733932)98:0.006
0041265,Megascops_watsonii:0.0269543585)100:0.0128621933)94:0.0014589026
)92:0.0002563955,Megascops_stangiae:0.0070019697)96:0.0029780856,Megasco
ps_atricapilla:0.0050739817);
```

Phylogenetic Comparative Analyses

Table. Correspondence between variable names used in the analysis scripts and their descriptive labels as presented in the main text. This table facilitates replication and cross-reference between the analytical dataset and the terminology used in the manuscript.

Variable_name	**Description of variable as in the text**
delta_freq_c_f	Frequency change (middle–final)
delta_freq_i_c	Frequency change (initial–middle)
Delta_Freq_m_nota_central	Mean bandwidth of the central notes
Delta_Freq_m_nota_final	Mean bandwidth of the final notes
Delta_Freq_m_nota_inicial	Mean bandwidth of the initial notes
Delta_Freq_medida_frase	Phrase bandwidth
delta_pace_c_f	Pace change (middle–final)
delta_pace_i_c	Pace change (initial–middle)
Delta_Time_m_interv._central	Mean interval duration of the central intervals
Delta_Time_m_interv._final	Mean interval duration of the final intervals
Delta_Time_m_interv._inicial	Mean interval duration of the initial intervals
Delta_Time_m_nota_central	Mean note duration of the central notes
Delta_Time_m_nota_final	Mean note duration of the final notes
Delta_Time_m_nota_inicial	Mean note duration of the initial notes
Delta_Time_medida_frase	Phrase duration
Freq_25_medida_frase	Frequency 25%
Freq_5_medida_frase	Frequency 5%
Freq_75_medida_frase	Frequency 75%
Freq_95_medida_frase	Frequency 95%
High_Freq_m_nota_central	Mean maximum frequency of the central notes
High_Freq_m_nota_final	Mean maximum frequency of the final notes
High_Freq_m_nota_inicial	Mean maximum frequency of the initial notes
High_Freq_medida_frase	Phrase maximum frequency
Low_Freq_m_nota_central	Mean minimum frequency of the central notes
Low_Freq_m_nota_final	Mean minimum frequency of the final notes
Low_Freq_m_nota_inicial	Mean minimum frequency of the initial notes
Low_Freq_medida_frase	Phrase minimum frequency
Max_Freq_m_nota_central	Mean dominant frequency of the central notes
Max_Freq_m_nota_final	Mean dominant frequency of the final notes
Max_Freq_m_nota_inicial	Mean dominant frequency of the initial notes
Max_Freq_medida_frase	Phrase dominant frequency
numero_de_notas	Number of notes
Pace	Overall pace
pace_central	Central pace
pace_final	Final pace
pace_inicial	Initial pace
Time_25_medida_frase	Time 25% relative
Time_5_medida_frase	Time 5% relative
Time_75_medida_frase	Time 75% relative
Time_95_medida_frase	Time 95% relative

R script

```
#########################################################################
#########################################################################
#########################################################################
########################################

Trabalho Corujas Luis Felipe#####################################


library(ape)

library(phytools)


setwd("")


# Criar nome automático do arquivo .txt

log_file <- paste0("console_log_", format(Sys.time(), "%Y%m%d_%H%M%S"),
".txt")


# Abrir log para saídas normais

#sink(log_file, split = TRUE)


# Abrir log também para mensagens (erros, avisos, etc.)

log_con <- file(log_file, open = "a")

#sink(log_con, type = "message")


cat("Log iniciado em", Sys.time(), "\n\n")


# Instalar treeio se necessário

if (!requireNamespace("treeio", quietly = TRUE)) {

  if (!requireNamespace("BiocManager", quietly = TRUE))

    install.packages("BiocManager")

  BiocManager::install("treeio")

}


# Carregar pacotes

library(treeio)

library(ape)


# === 1. Ler a árvore com metadados (formato BEAST/MrBayes)

tree_beast <- read.beast("infile.nex")  # Substitua pelo seu arquivo
```

```
# === 2. Converter para classe phylo
phylo_tree <- as.phylo(tree_beast)

# === 3. Identificar nós internos
n_tips <- length(phylo_tree$tip.label)
internal_node_ids <- (n_tips + 1):(n_tips + phylo_tree$Nnode)

# === 4. Extrair colunas relevantes do objeto treeio
data_nodes <- as.integer(tree_beast@data$node)
support_vals <- as.numeric(unlist(tree_beast@data$prob_percent))

# === 5. Selecionar os suportes que se referem a nós internos
internal_supports <- support_vals[data_nodes %in% internal_node_ids]

# === 6. Corrigir se estiver faltando o valor da raiz (BEAST costuma omitir)
if (length(internal_supports) == phylo_tree$Nnode - 1) {
  message("ℹ Adicionando suporte da raiz como 100 (valor default)")
  internal_supports <- c(internal_supports, 100)  # ou 1.0 se quiser proporção
}

# === 7. Verificação de consistência
if (length(internal_supports) != phylo_tree$Nnode) {
  stop(paste0("✖ Número de suportes (", length(internal_supports),
              ") não bate com número de nós internos (", phylo_tree$Nnode, ")"))
}

# === 8. Atribuir valores de suporte aos nós internos
phylo_tree$node.label <- internal_supports  # ou internal_supports / 100 para frações

# === 9. Exportar como Newick
write.tree(phylo_tree, file = "arvore_com_posterior.newick")
cat("✔ Árvore salva como 'arvore_com_posterior.newick'\n")
plot(phylo_tree)
tree<-phylo_tree
```

```
# tirando espécies com NA missing or inapplicable
#tree <- drop.tip(tree, "Megascops_choliba_duidae")

# vendo a árvore
plot(tree)
nodelabels(frame="circ",bg="white",cex=0.8)
tree$tip.label
tree$edge
tree$node.label

#outgroup <- 1:4 # may be several tips, numeric or tip labels
tree<-reroot(tree, node.number = 52)
is.rooted(tree) #check if tree is rooted
plot(tree) #to double check

# Usando método de Grafen (1989) para estimar comprimento de ramos (pacore ape)
#tree<-compute.brlen(tree, method = "Grafen", power = 1)

#plot(tree, main=expression(rho==1))

# lendo o data
data <- read.table("Medidas_mega(1).txt", header = TRUE, row.names=1)

## tranformando os dados (log)
data_quant <- data[,c(1,4:43)]
data_cat <- data[,1:3]

library(dplyr)
# Calcular a média de todas as colunas numéricas para cada espécie
medias <- data %>%
  group_by(Species) %>%
  summarise(across(where(is.numeric), mean, na.rm = TRUE))

# Adicionar as linhas de média ao conjunto de dados original
dados_com_medias <- bind_rows(data_quant, medias)

data_means <- dados_com_medias[158:193,]
```

```
data_means <- na.omit(data_means)

tree<-drop.tip(tree, "Otus_megalotis")

data_means2<-as.data.frame(scale(data_means[,2:41]))

# Conferindo o valor mínimo da escala
min(data_means2)

data.log_comp <- log10(data_means2 + 5)
rownames(data.log_comp)<-data_means$Species

## Tirei três variáveis com missing
#data <- data[, -c(4,5,9)]

# remove na in r - remove rows - na.omit function / option (removendo missing)
#data <- na.omit(data)

# tirando espécies com NA missing or inapplicable
#tree <- drop.tip(tree, c("Flec._pygmaeus", "G._pseustes"))

library("geiger")
namecheck<-name.check(tree, data_means, data.names = data_means$Species)

#pegando o vetor com os nomes que estão no dataset mas não na árvore
species2remove<-namecheck$data_not_tree
species2remove

#removendo do dataset os nomes que não estão na árvore
data.log_comp=data.log_comp[ !(rownames(data.log_comp) %in% species2remove), ]

#Isolando os nomes das espécies como vetor
library("tibble")
species<-rownames_to_column(data.log_comp)
species<-species[,1]
```

```
#mantendo apenas as mesmas espécies do dataset na árvore
library("ape")
tree<-keep.tip(tree, species)
plot(tree)

is.rooted(tree) #check if tree is rooted
is.ultrametric(tree)# ver se é ultramétrica

## ===========================

library(ape)
library(phytools)

# ============================================
# PREPARAÇÃO DA ÁRVORE
# ============================================

cat("=== PREPARANDO ÁRVORE ===\n\n")

# Tornar binária
if (!is.binary(tree)) {
  cat("Resolvendo politomias...\n")
  tree <- multi2di(tree, random = FALSE)
}

# Ajustar ramos muito pequenos
min_branch <- 1e-3
n_adjusted <- sum(tree$edge.length < min_branch)
tree$edge.length[tree$edge.length < min_branch] <- min_branch

cat("Ramos ajustados:", n_adjusted, "\n")
cat("Comprimento mínimo:", min(tree$edge.length), "\n\n")

# ============================================
# ULTRAMETRIZAÇÃO DIAGNÓSTICA (chronos)
# Escolhe o λ que melhor preserva as distâncias patristas da árvore original
```

```
# Requer: objeto 'tree' já enraizado e binário (feito na seção anterior)
# ============================================

library(ape)
library(phytools)

cat("=== ULTRAMETRIZAÇÃO DIAGNÓSTICA ===\n\n")

# Cópia da árvore original para comparação
tree_orig <- tree

# Verificações importantes para o chronos
if (!is.rooted(tree)) {
  stop("A árvore precisa estar ENRAIZADA para usar chronos().")
}
if (any(tree$edge.length <= 0)) {
  # ramos não positivos podem quebrar o chronos
  min_pos <- min(tree$edge.length[tree$edge.length > 0])
  tree$edge.length[tree$edge.length <= 0] <- min_pos * 1e-3
  cat("Ajustei ramos com comprimento <= 0.\n")
}

# Função utilitária: correlação e RMSE entre distâncias patristas
score_vs_original <- function(tree0, tree1) {
  D0 <- cophenetic(tree0)
  D1 <- cophenetic(tree1)
  # alinhar pela ordem dos rótulos
  D1 <- D1[rownames(D0), colnames(D0)]
  x <- as.vector(D0[upper.tri(D0, diag = FALSE)])
  y <- as.vector(D1[upper.tri(D1, diag = FALSE)])
  r <- suppressWarnings(cor(x, y, method = "pearson"))
  rmse <- sqrt(mean((x - y)^2))
  c(r = r, rmse = rmse)
}

# Função segura para rodar chronos sem interromper por warnings/erros
chronos_safe <- function(tr, lambda) {
```

```
  suppressWarnings(
    tryCatch(
      chronos(tr, lambda = lambda, quiet = TRUE),
      error = function(e) NULL
    )
  )
}

# Grade de λ a testar (ajuste se quiser mais fino em torno do melhor)
lambdas <- c(0, 1e-3, 1e-2, 0.05, 0.1, 0.2, 0.4, 0.6, 0.8, 1.0)

# Tabelas de resultados e lista para armazenar árvores ultramétricas
results <- data.frame(lambda = lambdas, r = NA_real_, rmse = NA_real_,
ok = FALSE)
trees_ultra <- vector("list", length(lambdas))

cat("Testando λ em:", paste(lambdas, collapse = ", "), "\n")

# Loop principal
for (i in seq_along(lambdas)) {
  lam <- lambdas[i]
  tr1 <- chronos_safe(tree, lambda = lam)
  if (is.null(tr1)) {
    cat(sprintf("λ = %.5f -> chronos falhou.\n", lam))
    next
  }
  # chronos deve retornar ultramétrica; conferimos por garantia
  if (!is.ultrametric(tr1)) {
    cat(sprintf("λ = %.5f -> não ultramétrica (ignorado).\n", lam))
    next
  }
  sc <- score_vs_original(tree_orig, tr1)
  results$r[i]    <- sc["r"]
  results$rmse[i] <- sc["rmse"]
  results$ok[i]   <- TRUE
  trees_ultra[[i]] <- tr1
  cat(sprintf("λ = %.5f -> r = %.4f | RMSE = %.6f\n", lam, results$r[i],
results$rmse[i]))
```

```
}

# Seleção do λ: maior r; desempate por menor RMSE
if (!any(results$ok, na.rm = TRUE)) {
  warning("chronos falhou para todos os λ. Aplicando fallback force.ultrametric(method='extend').")
  tree_ultra <- force.ultrametric(tree_orig, method = "extend")
  best_lambda <- NA
} else {
  idx_rmax <- which(results$ok & results$r == max(results$r, na.rm = TRUE))
  best_idx <- if (length(idx_rmax) > 1) idx_rmax[ which.min(results$rmse[idx_rmax]) ] else idx_rmax
  best_lambda <- results$lambda[best_idx]
  tree_ultra <- trees_ultra[[best_idx]]
  cat(sprintf("\nλ escolhido = %.5f (r = %.4f; RMSE = %.6f)\n",
              best_lambda, results$r[best_idx], results$rmse[best_idx]))
}

# Relatório e salvamento dos resultados
cat("\nResumo dos λ testados:\n")
print(results)
write.csv(results, file = "ultrametrizacao_chronos_diagnostico.csv", row.names = FALSE)
cat("✔ Resultados salvos em ultrametrizacao_chronos_diagnostico.csv\n")

# Gráficos r vs λ e RMSE vs λ
op <- par(no.readonly = TRUE)
par(mfrow = c(1,2))
plot(results$lambda, results$r, type = "b", pch = 16,
     xlab = expression(lambda), ylab = "Correlação das distâncias (r)",
     main = "r vs λ")
plot(results$lambda, results$rmse, type = "b", pch = 16,
     xlab = expression(lambda), ylab = "RMSE das distâncias",
     main = "RMSE vs λ")
par(op)

# Histogramas de comprimentos de ramos (original vs melhor ultramétrica)
```

```
op <- par(no.readonly = TRUE)
par(mfrow = c(1,2))
hist(tree_orig$edge.length, main = "Original: comprimentos de ramos", xlab = "Comprimento")
ttl <- if (is.na(best_lambda)) "Ultramétrica (fallback)" else sprintf("Ultramétrica (λ = %.3f)", best_lambda)
hist(tree_ultra$edge.length, main = ttl, xlab = "Comprimento")
par(op)

# LTT comparativo
par(mfrow = c(1,1))
ltt.plot(tree_orig, log = "y", main = "LTT: original vs ultramétrica")
ltt.lines(tree_ultra, col = "red")
legend("topleft",
       legend = c("Original", if (is.na(best_lambda)) "Ultramétrica (fallback)" else sprintf("Ultramétrica λ=%.3f", best_lambda)),
       lty = 1, col = c("black", "red"), bty = "n")

# Salvar árvore ultramétrica escolhida
outfile <- if (is.na(best_lambda)) {
  "tree_ultrametric_fallback_extend.tre"
} else {
  sprintf("tree_ultrametric_lambda_%.3f.tre", best_lambda)
}
write.tree(tree_ultra, file = outfile)
cat("✔ Árvore ultramétrica salva em:", outfile, "\n")

# Objeto final para usar quando o método exigir ultrametria
tree_ultra_selected <- tree_ultra

tree<-tree_ultra_selected
#par(mfrow = c(1, 1))
plot(tree)

#Bloco para sinal filogenético das variáveis

# Atribuindo as variáveis
Low_Freq_m_nota_inicial      <- data.log_comp$Low_Freq_m_nota_inicial
```

```
High_Freq_m_nota_inicial     <- data.log_comp$High_Freq_m_nota_inicial
Delta_Freq_m_nota_inicial    <- data.log_comp$Delta_Freq_m_nota_inicial
Delta_Time_m_nota_inicial    <- data.log_comp$Delta_Time_m_nota_inicial
Max_Freq_m_nota_inicial      <- data.log_comp$Max_Freq_m_nota_inicial
Delta_Time_m_interv._inicial <-
data.log_comp$Delta_Time_m_interv._inicial
Low_Freq_m_nota_central      <- data.log_comp$Low_Freq_m_nota_central
High_Freq_m_nota_central     <- data.log_comp$High_Freq_m_nota_central

Delta_Freq_m_nota_central    <- data.log_comp$Delta_Freq_m_nota_central
Delta_Time_m_nota_central    <- data.log_comp$Delta_Time_m_nota_central
Max_Freq_m_nota_central      <- data.log_comp$Max_Freq_m_nota_central
Delta_Time_m_interv._central <-
data.log_comp$Delta_Time_m_interv._central
Low_Freq_m_nota_final        <- data.log_comp$Low_Freq_m_nota_final
High_Freq_m_nota_final       <- data.log_comp$High_Freq_m_nota_final
Delta_Freq_m_nota_final      <- data.log_comp$Delta_Freq_m_nota_final
Delta_Time_m_nota_final      <- data.log_comp$Delta_Time_m_nota_final
Max_Freq_m_nota_final        <- data.log_comp$Max_Freq_m_nota_final
Delta_Time_m_interv._final   <- data.log_comp$Delta_Time_m_interv._final
Low_Freq_medida_frase        <- data.log_comp$Low_Freq_medida_frase
High_Freq_medida_frase       <- data.log_comp$High_Freq_medida_frase
Delta_Freq_medida_frase      <- data.log_comp$Delta_Freq_medida_frase
Delta_Time_medida_frase      <- data.log_comp$Delta_Time_medida_frase
Max_Freq_medida_frase        <- data.log_comp$Max_Freq_medida_frase
Freq_25_medida_frase         <- data.log_comp$Freq_25_medida_frase
Freq_5_medida_frase          <- data.log_comp$Freq_5_medida_frase
Freq_75_medida_frase         <- data.log_comp$Freq_75_medida_frase
Freq_95_medida_frase         <- data.log_comp$Freq_95_medida_frase
Time_25_medida_frase         <- data.log_comp$Time_25_medida_frase
Time_5_medida_frase          <- data.log_comp$Time_5_medida_frase
Time_75_medida_frase         <- data.log_comp$Time_75_medida_frase
Time_95_medida_frase         <- data.log_comp$Time_95_medida_frase
pace_inicial               <- data.log_comp$pace_inicial
pace_central               <- data.log_comp$pace_central
pace_final                 <- data.log_comp$pace_final
delta_pace_i_c             <- data.log_comp$delta_pace_i_c
delta_pace_c_f             <- data.log_comp$delta_pace_c_f
```

```
delta_freq_i_c            <- data.log_comp$delta_freq_i_c
delta_freq_c_f            <- data.log_comp$delta_freq_c_f
numero_de_notas           <- data.log_comp$numero_de_notas
pace                      <- data.log_comp$pace

# Atribuindo os nomes das linhas para cada variável
names(Low_Freq_m_nota_inicial)      <- rownames(data.log_comp)
names(High_Freq_m_nota_inicial)     <- rownames(data.log_comp)
names(Delta_Freq_m_nota_inicial)    <- rownames(data.log_comp)
names(Delta_Time_m_nota_inicial)    <- rownames(data.log_comp)
names(Max_Freq_m_nota_inicial)      <- rownames(data.log_comp)
names(Delta_Time_m_interv._inicial) <- rownames(data.log_comp)
names(Low_Freq_m_nota_central)      <- rownames(data.log_comp)
names(High_Freq_m_nota_central)     <- rownames(data.log_comp)
names(Delta_Freq_m_nota_central)    <- rownames(data.log_comp)
names(Delta_Time_m_nota_central)    <- rownames(data.log_comp)
names(Max_Freq_m_nota_central)      <- rownames(data.log_comp)
names(Delta_Time_m_interv._central) <- rownames(data.log_comp)
names(Low_Freq_m_nota_final)        <- rownames(data.log_comp)
names(High_Freq_m_nota_final)       <- rownames(data.log_comp)
names(Delta_Freq_m_nota_final)      <- rownames(data.log_comp)
names(Delta_Time_m_nota_final)      <- rownames(data.log_comp)
names(Max_Freq_m_nota_final)        <- rownames(data.log_comp)
names(Delta_Time_m_interv._final)   <- rownames(data.log_comp)
names(Low_Freq_medida_frase)        <- rownames(data.log_comp)
names(High_Freq_medida_frase)       <- rownames(data.log_comp)
names(Delta_Freq_medida_frase)      <- rownames(data.log_comp)
names(Delta_Time_medida_frase)      <- rownames(data.log_comp)
names(Max_Freq_medida_frase)        <- rownames(data.log_comp)
names(Freq_25_medida_frase)         <- rownames(data.log_comp)
names(Freq_5_medida_frase)          <- rownames(data.log_comp)
names(Freq_75_medida_frase)         <- rownames(data.log_comp)
names(Freq_95_medida_frase)         <- rownames(data.log_comp)
names(Time_25_medida_frase)         <- rownames(data.log_comp)
names(Time_5_medida_frase)          <- rownames(data.log_comp)
names(Time_75_medida_frase)         <- rownames(data.log_comp)
names(Time_95_medida_frase)         <- rownames(data.log_comp)
```

```
names(pace_inicial)                 <- rownames(data.log_comp)

names(pace_central)                 <- rownames(data.log_comp)

names(pace_final)                   <- rownames(data.log_comp)

names(delta_pace_i_c)               <- rownames(data.log_comp)

names(delta_pace_c_f)               <- rownames(data.log_comp)

names(delta_freq_i_c)               <- rownames(data.log_comp)

names(delta_freq_c_f)               <- rownames(data.log_comp)

names(numero_de_notas)              <- rownames(data.log_comp)

names(pace)                         <- rownames(data.log_comp)


# Lista de variáveis a serem analisadas

variaveis <- c(

  "Low_Freq_medida_frase",

  "Delta_Time_medida_frase",

  "Time_25_medida_frase",

  "Time_5_medida_frase",

  "numero_de_notas"

)


# Criar um dataframe vazio para armazenar os resultados

resultados <- data.frame(Variavel = character(),

                         Metodo = character(),

                         Lambda_K = numeric(),

                         P_Valor = numeric(),

                         stringsAsFactors = FALSE)


# Loop para calcular phylosig para cada variável com os métodos "lambda"
e "K"

for (var in variaveis) {

  # Executa phylosig para o método "lambda"

  res_lambda <- phylosig(tree, get(var), method="lambda", test=TRUE,
nsim=1000)

  resultados <- rbind(resultados, data.frame(Variavel = var, Metodo =
"lambda",

                                             Lambda_K =
res_lambda$lambda,

                                             P_Valor = res_lambda$P))


  # Executa phylosig para o método "K"
```

```
  res_K <- phylosig(tree, get(var), method="K", test=TRUE, nsim=1000)
  resultados <- rbind(resultados, data.frame(Variavel = var, Metodo = 
"K",
                                             Lambda_K = res_K$K,
                                             P_Valor = res_K$P))
}


# Salvar os resultados em um arquivo CSV
write.csv(resultados, "resultados_phylosig.csv", row.names = FALSE)


########################################################################
###################


# mapear / otimizar caracteres


# Lista de variáveis a serem visualizadas
#variaveis2 <- c("Delta_Time_medida_frase", "Time_25_medida_frase", 
"Time_5_medida_frase", "numero_de_notas")


library(phytools)


for (var in variaveis) {


  # Cria o mapeamento contínuo sem plotar imediatamente
  trait_map <- contMap(tree, get(var), plot=FALSE)


  # Inverte a escala de cores
  trait_map <- setMap(trait_map, invert=TRUE)


  # Plota cada mapa
  plot(trait_map)
  plot(trait_map,type="fan", ftype="i")


  # Adiciona o nome da variável como título ao gráfico
  title(main = var)
}


# lendo o data com dados sobre massa e outros
```

```
dataBio <- read.table("Bio mega.txt", header = TRUE, row.names=1)

data.log_comp$Species <- rownames(data.log_comp)
dataBio$Species <- rownames(dataBio)

# Full join: todas as espécies de ambos os dataframes
comp_data <- full_join(data.log_comp, dataBio, by = "Species")
comp_data$Delta_Time_medida_frase2<-comp_data$Delta_Time_medida_frase

rownames(comp_data) <- comp_data$Species
#comp_data <- comp_data[,-41]

# Exportar árvore prunada em .tre
write.tree(tree, file = "arvore_podada.tre")

tree$node.label <- NULL

library(caper)
comp_data <- comparative.data(phy = tree, data = comp_data, names.col =
"Species", vcv = TRUE, na.omit = FALSE)

#######################
# Bloco para verificação do Intervalo de confiança das reconstruções de
estado ancestral

library(dplyr)
library(tidyr)
library(purrr)
# install.packages("openxlsx") # se precisar
library(openxlsx)

# função auxiliar: roda fastAnc com IC e devolve data.frame por variável
recon_var <- function(tree, x, varname) {
  if (is.null(names(x))) stop(paste0("A variável ", varname, " precisa
ter names = espécies."))
  comum <- intersect(tree$tip.label, names(x))
  if (length(comum) < length(tree$tip.label)) {
    tree_use <- drop.tip(tree, setdiff(tree$tip.label, comum))
```

```r
  } else {
    tree_use <- tree
  }
  x_use <- x[match(tree_use$tip.label, names(x))]

  fa <- phytools::fastAnc(tree_use, x_use, CI = TRUE, vars = TRUE)
  nT <- length(tree_use$tip.label)
  nN <- tree_use$Nnode
  nodes <- (nT + 1):(nT + nN)

  # suporte posterior (você já gravou em tree$node.label como porcentagem)
  node_label <- if (!is.null(tree_use$node.label)) tree_use$node.label else rep(NA_real_, nN)

  tibble(
    variavel  = varname,
    node      = nodes,
    node_label = node_label,
    estimate  = as.numeric(fa$ace),
    CI95_lo   = as.numeric(fa$CI95[, 1]),
    CI95_hi   = as.numeric(fa$CI95[, 2])
  )
}

# garantir que as variáveis existem no ambiente com names = espécies
stopifnot(all(variaveis %in% ls()))

# rodar para todas as variáveis
tabela_nos_long <- map_dfr(
  variaveis,
  ~ recon_var(tree, get(.x), .x)
) %>%
  arrange(variavel, node)

# versão larga com estimativa
tabela_nos_wide_est <- tabela_nos_long %>%
  dplyr::select(variavel, node, node_label, estimate) %>%
```

```r
  pivot_wider(names_from = variavel, values_from = estimate) %>%
  arrange(node)

# versão larga com IC em string
tabela_nos_wide_ic <- tabela_nos_long %>%
  mutate(estimate_ic = sprintf("%.6f [% .6f, % .6f]", estimate, CI95_lo, CI95_hi)) %>%
  dplyr::select(variavel, node, node_label, estimate_ic) %>%
  pivot_wider(names_from = variavel, values_from = estimate_ic) %>%
  arrange(node)

# exportar
write.csv(tabela_nos_long, "Reconstrucoes_nos_long.csv", row.names = FALSE)
write.csv(tabela_nos_wide_est, "Reconstrucoes_nos_wide_estimate.csv", row.names = FALSE)
write.csv(tabela_nos_wide_ic, "Reconstrucoes_nos_wide_estimate+IC.csv", row.names = FALSE)

wb <- createWorkbook()
addWorksheet(wb, "long")
addWorksheet(wb, "wide_estimate")
addWorksheet(wb, "wide_estimate+IC")
writeData(wb, "long", tabela_nos_long)
writeData(wb, "wide_estimate", tabela_nos_wide_est)
writeData(wb, "wide_estimate+IC", tabela_nos_wide_ic)
saveWorkbook(wb, file = "Reconstrucoes_nos.xlsx", overwrite = TRUE)

# opcional: incluir valores observados nos terminais (tips) em arquivo separado
# útil se quiser um pacote completo nós + tips
incluir_tips <- FALSE
if (incluir_tips) {
  tips_long <- map_dfr(
    variaveis,
    ~ tibble(variavel = .x, taxa = names(get(.x)), value_tip = as.numeric(get(.x)))
  )
  write.csv(tips_long, "Valores_tips_observados.csv", row.names = FALSE)
}
```

```
#
========================================================================
======
# 4. DEFINIÇÃO DOS MODELOS EVOLUTIVOS
#
========================================================================
======

cat("\n🚀 Rodando modelos evolutivos (isso pode levar alguns
segundos)...\n")

# --- Modelo 1: ER (Equal Rates) ---
# Assume que saltar de Aberto -> Fechado é tão fácil quanto Aberto ->
Misto
fit_ER <- fitDiscrete(tree, habitat_factor, model = "ER")

# --- Modelo 2: SYM (Symmetric) ---
# Taxas de ida e volta são iguais (A->B = B->A), mas A->B difere de A->C
fit_SYM <- fitDiscrete(tree, habitat_factor, model = "SYM")

# --- Modelo 3: ARD (All Rates Different) ---
# Modelo mais complexo, todas as transições têm taxas livres
fit_ARD <- fitDiscrete(tree, habitat_factor, model = "ARD")

# --- Modelo 4: ORDENADO (Step-wise / Customizado) ---
# Este é o modelo biologicamente esperado: Aberto <-> Misto <-> Fechado
# Transições diretas Aberto <-> Fechado são proibidas (taxa = 0)

# Criando a matriz base
model_matrix <- matrix(1, 3, 3)
rownames(model_matrix) <- colnames(model_matrix) <-
levels(habitat_factor)
diag(model_matrix) <- 0

# ZERAR AS TRANSIÇÕES DIRETAS ENTRE EXTREMOS
# Ajuste aqui os nomes exatos se o seu TXT estiver diferente!
# Estou assumindo: "Aberto", "Fechado" e alguma variação de
Misto/Generalista

# Identificando os nomes (ajuste strings se necessário)
idx_aberto <- grep("Aberto|Open", levels(habitat_factor), ignore.case =
TRUE)
idx_fechado <- grep("Fechado|Closed|Forest", levels(habitat_factor),
ignore.case = TRUE)

# Se encontrou ambos os extremos, zera a conexão entre eles
if(length(idx_aberto) > 0 & length(idx_fechado) > 0) {
# Zera Aberto -> Fechado
model_matrix[idx_aberto, idx_fechado] <- 0
# Zera Fechado -> Aberto
model_matrix[idx_fechado, idx_aberto] <- 0
cat("📌 Modelo Ordenado configurado: Transição direta entre",
levels(habitat_factor)[idx_aberto], "e",
levels(habitat_factor)[idx_fechado], "foi proíbida (0).\n")
} else {
warning("⚠ NÃO FOI POSSÍVEL CONFIGURAR

#testar colinearidade entre as variáveis

####################################################################
```

```
#Abaixoa matriz de correlação entre as variáveis numéricas — útil para detectar colinearidade de forma visual e complementar ao típico VIF que é melhor quadno é para GLMs etc.


# Remove a coluna de espécie (fator categórico) e qualquer variável com muitos NAs

dados_numericos <- data.log_comp[, sapply(data.log_comp, is.numeric)]

dados_numericos <- na.omit(dados_numericos)  # remove linhas com NAs


# Matriz de correlação entre variáveis numéricas

correlacao <- cor(dados_numericos)


# Exibe a matriz de correlação

print(round(correlacao, 2))


# Opcional: visualização com um heatmap

if (!require(corrplot)) install.packages("corrplot", dependencies = TRUE)

library(corrplot)


# Gera o gráfico

corrplot(correlacao, method = "color", type = "upper", tl.cex = 0.8, tl.col = "black", addCoef.col = "black")


#Removendo as variáveis dependentes (altamente correlacionadas)

data.log<- data.log_comp[,-c(24:27,1,2,5,7)]

#removendo mais variáveis dos removidos

data.log<- data.log[,-c(2,3,6,19,25,32)]

#removendo mais variáveis dos removidos

data.log<- data.log[,-c(1,2,3,4,5,6,7,9,10,16,19,20)]

#removendo mais variáveis dos removidos

data.log<- data.log[,-c(6)]


plot(tree)


is.rooted(tree) #check if tree is rooted


#para rodar a pPCA

# pPCA
```

```
datapPCA<-data.log[,1:12]
data_scaled <- scale(datapPCA)
ppca <- phyl.pca(tree, data_scaled, method = "lambda")

# Criar um biplot
biplot(ppca, main = "Biplot da pPCA")

# Extrair as pontuações das componentes principais
scores <- ppca$S

# Criar um gráfico de dispersão das duas primeiras componentes principais
plot(scores[,1], scores[,2],
     xlab = "Componente Principal 1",
     ylab = "Componente Principal 2",
     main = "Visualização da pPCA",
     pch = 19, col = "blue")

# Adicionar um título
text(scores[,1], scores[,2], labels = rownames(scores), pos = 4, cex = 0.7)

# verificar a variação de cada PC
prop_var <- ppca$Eval / sum(ppca$Eval)
round(prop_var * 100, 2)  # em porcentagem (%), com 2 casas decimais

#Extrair os scores da pPCA acima (PC1 a PC5) e usar esses valores para fazer teste de sinal filogenético
# Scores da pPCA
scores <- ppca$S[, 1:5]

# Testar o sinal filognético com lambda de pagel e k de blomberg

PC1<-scores[,1]
PC2<-scores[,2]
PC3<-scores[,3]
PC4<-scores[,4]
PC5<-scores[,5]
```

```
names(PC1)<-rownames(datapPCA)

names(PC2)<-rownames(datapPCA)

names(PC3)<-rownames(datapPCA)

names(PC4)<-rownames(datapPCA)

names(PC5)<-rownames(datapPCA)


phylosig(tree, PC1, method="lambda", test=TRUE, nsim=1000)

phylosig(tree, PC1, method="K", test=TRUE, nsim=1000)


phylosig(tree, PC2, method="lambda", test=TRUE, nsim=1000)

phylosig(tree, PC2, method="K", test=TRUE, nsim=1000)


phylosig(tree, PC3, method="lambda", test=TRUE, nsim=1000)

phylosig(tree, PC3, method="K", test=TRUE, nsim=1000)


phylosig(tree, PC4, method="lambda", test=TRUE, nsim=1000)

phylosig(tree, PC4, method="K", test=TRUE, nsim=1000)


phylosig(tree, PC5, method="lambda", test=TRUE, nsim=1000)

phylosig(tree, PC5, method="K", test=TRUE, nsim=1000)


# Extrair os loadings (cargas dos eixos)

loadings <- ppca$L[, 1:5]  # Apenas os 5 primeiros PCs


# Visualizar os loadings arredondados

print(round(loadings, 3))


# Salvar os loadings como .csv

write.csv(loadings, file = "pPCA_loadings_PC1_a_PC5.csv")


## fazer loadings plot para as duas primeiras PCs como em Hepp & Pombal
(2020)


library(ggplot2)

library(lattice)


sorted.loadings1 <- loadings[order(loadings[,1]),1]
```

```
# definimos o objeto que descreve o peso das variáveis para o PC1
Main = "Loadings Plot for PC1"; xlabs = "Variable Loadings"
# criamos objetos que descrevem o título e o eixo x da figura
load1 <- dotplot(sorted.loadings1, main=Main,
                 xlab=xlabs, cex=2, col="black", pch=16)
# para plotar um gráfico simples de pontos
load1

#mesmo procedimento para o PC2
sorted.loadings2 <- loadings[order(loadings[,2]),2]
Main="Loadings Plot for PC2"; xlabs="Variable Loadings"
load2<-dotplot(sorted.loadings2, main=Main,
               xlab=xlabs, cex=2, col="black", pch=16)
load2

#mesmo procedimento para o PC3
sorted.loadings3 <- loadings[order(loadings[,3]),3]
Main="Loadings Plot for PC3"; xlabs="Variable Loadings"
load3<-dotplot(sorted.loadings3, main=Main,
               xlab=xlabs, cex=2, col="black", pch=16)
load3

#mesmo procedimento para o PC4
sorted.loadings4 <- loadings[order(loadings[,4]),4]
Main="Loadings Plot for PC4"; xlabs="Variable Loadings"
load4<-dotplot(sorted.loadings4, main=Main,
               xlab=xlabs, cex=2, col="black", pch=16)
load4

#mesmo procedimento para o PC5
sorted.loadings5 <- loadings[order(loadings[,5]),5]
Main="Loadings Plot for PC5"; xlabs="Variable Loadings"
load5<-dotplot(sorted.loadings5, main=Main,
               xlab=xlabs, cex=2, col="black", pch=16)
load5
```

```
# Criar gráficos de barras para os 5 primeiros PCs (com nomes visíveis)
par(mfrow = c(2, 3), mar = c(8, 4, 3, 1))  # margens maiores inferior
for (i in 1:5) {
  barplot(loadings[, i],
          main = paste("Contribuição para PC", i),
          ylab = "Carga (loading)",
          names.arg = rownames(loadings),
          las = 2,              # rotaciona os nomes (vertical)
          cex.names = 0.7,      # diminui a fonte dos nomes
          col = "steelblue")
}
par(mfrow = c(1, 1))  # Reset layout


#mapear variáveis com sinal significativo para sinal filogenético k de
blomberg
# plotando na árvore (4)
PC3map <- contMap(tree,PC3, plot=F)
#invertendo as cores da escala do mapeamento no objeto
PC3map<-setMap(PC3map,invert=TRUE)
plot(PC3map, type="fan",outline=F, fsize=0.8, ftype="i",
lwd=6,leg.txt="PC2")
plot(PC3map, outline=F, fsize=0.8, ftype="i", lwd=6,leg.txt="PC2")


#para testar especificamente PCs com a Massa e Dimorfismo (que possuem
NA)
comp_data <- full_join(data.log_comp, dataBio, by = "Species")
rownames(comp_data) <- comp_data$Species
scores2<-as.data.frame(scores)
scores2$Species<-rownames(scores2)
comp_data2 <- full_join(comp_data, scores2, by = "Species")
rownames(comp_data2) <- comp_data2$Species


# PGLS
library(nlme)


# Bloco PC1


#Deixando apenas PC1, Habitat e Species
```

```
comp_data2$Habitat <- as.factor(comp_data2$Habitat)

comp_data5<-comp_data2[,c("PC1","Habitat","Species")]

comp_data5<-na.omit(comp_data5)

model_test<-gls(PC1~Habitat,data=comp_data5, correlation=corPagel(1,
tree, form = ~Species, fixed=F))

summary(model_test) # deu significativo!

plot(PC1~Habitat,data=comp_data5)

abline(a = coef(model_test)[1], b = coef(model_test)[2])

plot(model_test, abline=c(0,0))


ggplot(comp_data5, aes(x = Habitat, y = PC1, fill = Habitat)) +

  geom_boxplot(alpha = 0.7) +

  theme_minimal() +

  labs(

    title = "Distribuição de PC1 entre tipos de Habitat",

    x = "Habitat",

    y = "PC1"

  ) +

  theme(legend.position = "none")


#Deixando apenas PC1, Massa e Species

comp_data3<-comp_data2[,c("PC1","Mass","Species")]

comp_data3<-na.omit(comp_data3)

model_test<-gls(PC1~Mass,data=comp_data3, correlation=corPagel(1, tree,
form = ~Species, fixed=F))

summary(model_test) #não deu significativo


#Deixando apenas PC1, Dimorphism e Species

comp_data4<-comp_data2[,c("PC1","Dimorphism","Species")]

comp_data4<-na.omit(comp_data4)

model_test<-gls(PC1~Dimorphism,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))

summary(model_test) #não deu significativo


#Deixando apenas PC1, altitude1 e Species

comp_data4<-comp_data2[,c("PC1","Altitud_min","Species")]

comp_data4<-na.omit(comp_data4)

model_test<-gls(PC1~Altitud_min,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
```

```
summary(model_test) #não deu significativo

#Deixando apenas PC1, altitude2 e Species
comp_data4<-comp_data2[,c("PC1","Altitud_max","Species")]
comp_data4<-na.omit(comp_data4)
model_test<-gls(PC1~Altitud_max,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test) #não deu significativo

#Deixando apenas PC1, altitude3 e Species
comp_data4<-comp_data2[,c("PC1","Alt_range","Species")]
comp_data4<-na.omit(comp_data4)
model_test<-gls(PC1~Alt_range,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test) #não deu significativo

# Bloco PC2

#Deixando apenas PC2, Habitat e Species
comp_data5<-comp_data2[,c("PC2","Habitat","Species")]
comp_data5<-na.omit(comp_data5)
model_test<-gls(PC2~Habitat,data=comp_data5, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test)#não deu significativo

#Deixando apenas PC2, Massa e Species
comp_data3<-comp_data2[,c("PC2","Mass","Species")]
comp_data3<-na.omit(comp_data3)
model_test<-gls(PC2~Mass,data=comp_data3, correlation=corPagel(1, tree,
form = ~Species, fixed=F))
summary(model_test) #não deu significativo

#Deixando apenas PC2, Dimorphism e Species
comp_data4<-comp_data2[,c("PC2","Dimorphism","Species")]
comp_data4<-na.omit(comp_data4)
model_test<-gls(PC2~Dimorphism,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test) #não deu significativo
```

```
#Deixando apenas PC2, altitude1 e Species

comp_data4<-comp_data2[,c("PC2","Altitud_min","Species")]

comp_data4<-na.omit(comp_data4)

model_test<-gls(PC2~Altitud_min,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))

summary(model_test) #não deu significativo


#Deixando apenas PC2, altitude2 e Species

comp_data4<-comp_data2[,c("PC2","Altitud_max","Species")]

comp_data4<-na.omit(comp_data4)

model_test<-gls(PC2~Altitud_max,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))

summary(model_test) #não deu significativo


#Deixando apenas PC2, altitude3 e Species

comp_data4<-comp_data2[,c("PC2","Alt_range","Species")]

comp_data4<-na.omit(comp_data4)

model_test<-gls(PC2~Alt_range,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))

summary(model_test)


# Bloco PC3


#Deixando apenas PC3, Habitat e Species

comp_data5<-comp_data2[,c("PC3","Habitat","Species")]

comp_data5<-na.omit(comp_data5)

model_test<-gls(PC3~Habitat,data=comp_data5, correlation=corPagel(1,
tree, form = ~Species, fixed=F))

summary(model_test)#não deu por pouco para Generalista


#Deixando apenas PC3, Massa e Species

comp_data3<-comp_data2[,c("PC3","Mass","Species")]

comp_data3<-na.omit(comp_data3)

model_test<-gls(PC3~Mass,data=comp_data3, correlation=corPagel(1, tree,
form = ~Species, fixed=F))

summary(model_test) #não deu significativo


#Deixando apenas PC3, Dimorphism e Species

comp_data4<-comp_data2[,c("PC3","Dimorphism","Species")]
```

```
comp_data4<-na.omit(comp_data4)
model_test<-gls(PC3~Dimorphism,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test) # deu significativo!!
plot(PC3~Dimorphism,data=comp_data4)
abline(a = coef(model_test)[1], b = coef(model_test)[2])
plot(model_test, abline=c(0,0))


#Deixando apenas PC3, altitude1 e Species
comp_data4<-comp_data2[,c("PC3","Altitud_min","Species")]
comp_data4<-na.omit(comp_data4)
model_test<-gls(PC3~Altitud_min,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test)#não deu significativo


#Deixando apenas PC3, altitude2 e Species
comp_data4<-comp_data2[,c("PC3","Altitud_max","Species")]
comp_data4<-na.omit(comp_data4)
model_test<-gls(PC3~Altitud_max,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test)#não deu significativo


#Deixando apenas PC3, altitude3 e Species
comp_data4<-comp_data2[,c("PC3","Alt_range","Species")]
comp_data4<-na.omit(comp_data4)
model_test<-gls(PC3~Alt_range,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test)#não deu significativo


# Bloco PC4


#Deixando apenas PC4, Habitat e Species
comp_data5<-comp_data2[,c("PC4","Habitat","Species")]
comp_data5<-na.omit(comp_data5)
model_test<-gls(PC4~Habitat,data=comp_data5, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test) #deu muito significativo!!
plot(PC4~Habitat,data=comp_data5)
abline(a = coef(model_test)[1], b = coef(model_test)[2])
```

```
plot(model_test, abline=c(0,0))

summary(model_test)$tTable


library(ggplot2)

ggplot(comp_data5, aes(x = Habitat, y = PC4, fill = Habitat)) +

  geom_boxplot(alpha = 0.6) +

  geom_jitter(width = 0.1, alpha = 0.8) +

  theme_minimal() +

  labs(title = "Variação de PC4 entre habitats", y = "PC4", x =
"Habitat")


#Deixando apenas PC4, Massa e Species

comp_data3<-comp_data2[,c("PC4","Mass","Species")]

comp_data3<-na.omit(comp_data3)

model_test<-gls(PC4~Mass,data=comp_data3, correlation=corPagel(1, tree,
form = ~Species, fixed=F))

summary(model_test)


#Deixando apenas PC4, Dimorphism e Species

comp_data4<-comp_data2[,c("PC4","Dimorphism","Species")]

comp_data4<-na.omit(comp_data4)

model_test<-gls(PC4~Dimorphism,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))

summary(model_test)


#Deixando apenas PC4, altitude1 e Species

comp_data4<-comp_data2[,c("PC4","Altitud_min","Species")]

comp_data4<-na.omit(comp_data4)

model_test<-gls(PC4~Altitud_min,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))

summary(model_test) #deu significativo!!

plot(PC4~Altitud_min,data=comp_data4)

abline(a = coef(model_test)[1], b = coef(model_test)[2])

plot(model_test, abline=c(0,0))


#Deixando apenas PC4, altitude2 e Species

comp_data4<-comp_data2[,c("PC4","Altitud_max","Species")]

comp_data4<-na.omit(comp_data4)
```

```
model_test<-gls(PC4~Altitud_max,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test) #deu muito significativo!!
plot(PC4~Altitud_max,data=comp_data4)
abline(a = coef(model_test)[1], b = coef(model_test)[2])
plot(model_test, abline=c(0,0))

#Deixando apenas PC4, altitude3 e Species
comp_data4<-comp_data2[,c("PC4","Alt_range","Species")]
comp_data4<-na.omit(comp_data4)
model_test<-gls(PC4~Alt_range,data=comp_data4, correlation=corPagel(1,
tree, form = ~Species, fixed=F))
summary(model_test) #não deu significativo

# seguindo a recomendação da Odom et al. (2023)
#Testar através de PGLS se o Microhabitat explica as variáveis
acústicas: ENT    BW50  BW90  CentFreq    Deltatime   Freq25      Freq5
      Freq75      Freq95      MaxFreq
# PGLS com Microhabitat como explicador das variáveis acústicas

colnames(comp_data2)

library(nlme)   # gls()
library(ape)    # corPagel()

## -------- CONFIGURAÇÃO --------
# 1) data frame que contém TODAS as colunas
dat <- comp_data2        # ou comp_data, se for o que estiver usando

# 2) variáveis-resposta (que não são colineares)
resp_vars <- c(
  "Low_Freq_m_nota_inicial",
  "High_Freq_m_nota_inicial",
  "Delta_Freq_m_nota_inicial",
  "Delta_Time_m_nota_inicial",
  "Max_Freq_m_nota_inicial",
  "Delta_Time_m_interv._inicial",
  "Low_Freq_m_nota_central",
  "High_Freq_m_nota_central",
```

```
"Delta_Freq_m_nota_central",
"Delta_Time_m_nota_central",
"Max_Freq_m_nota_central",
"Delta_Time_m_interv._central",
"Low_Freq_m_nota_final",
"High_Freq_m_nota_final",
"Delta_Freq_m_nota_final",
"Delta_Time_m_nota_final",
"Max_Freq_m_nota_final",
"Delta_Time_m_interv._final",
"Low_Freq_medida_frase",
"High_Freq_medida_frase",
"Delta_Freq_medida_frase",
"Delta_Time_medida_frase",
"Max_Freq_medida_frase",
"Freq_25_medida_frase",
"Freq_5_medida_frase",
"Freq_75_medida_frase",
"Freq_95_medida_frase",
"Time_25_medida_frase",
"Time_5_medida_frase",
"Time_75_medida_frase",
"Time_95_medida_frase",
"pace_inicial",
"pace_central",
"pace_final",
"delta_pace_i_c",
"delta_pace_c_f",
"delta_freq_i_c",
"delta_freq_c_f",
"numero_de_notas",
"pace",
"PC1",
"PC2",
"PC3",
"PC4",
"PC5"
```

```r
)

# 3) preditores (um de cada vez, como você fazia manualmente)
pred_vars <- c("Habitat", "Mass", "Dimorphism", "Altitud_min", "Altitud_max", "Alt_range")

## -------- LOOP PRINCIPAL (com tratamento de falsa convergência) --------
results     <- list()      # modelos que convergiram
falhas_conv <- character() # combinações que deram "false convergence (8)"

for (y in resp_vars) {
  for (x in pred_vars) {

    df <- na.omit(dat[, c(y, x, "Species")])
    df <- df[df$Species %in% tree$tip.label, ]
    df <- df[is.finite(df[[y]]) & is.finite(df[[x]]), ]

    if(nrow(df) < 3) {
      message("⚠ Pulando ", y, "~", x, ": poucas linhas disponíveis")
      next
    }

    fml <- as.formula(paste0(y, " ~ ", x))

    tryCatch(
      {
        fit <- gls(
          fml,
          data        = df,
          method      = "REML",
          correlation = corPagel(1, tree, form = ~Species, fixed=F)
        )
        results[[paste(y, x, sep = "_")]] <- summary(fit)
      },
      error = function(e) {
        if (grepl("false convergence", e$message, fixed = TRUE)) {
```

```
          falhas_conv <<- c(falhas_conv, paste(y, x, sep = "_"))
          message("⚠ Pulando por falsa convergência: ", y, " ~ ", x)
        } else {
          message("❌ Erro inesperado: ", y, " ~ ", x, " -> ",
e$message)
        }
      }
    )
  }
}

## Exibe um resumo rápido ao final
cat("\nModelos que convergiram: ", length(results),
    "\nCombinações com falsa convergência: ", length(falhas_conv), "\n")

# Se quiser inspecionar:
# names(results)       # nomes dos modelos bem-sucedidos
# falhas_conv          # combinações problemáticas

saveRDS(results, "PGLS_results_ok.rds")
writeLines(falhas_conv, "PGLS_false_convergence.txt")

results

## ----- salvar os sumários em .txt -----

# (opcional) cria uma pasta só para os arquivos, se ainda não existir
dir.create("pgls_summaries", showWarnings = FALSE)

# 1) um arquivo por modelo ---------------------------------------------
--
for (nm in names(results)) {
  arq <- file.path("pgls_summaries", paste0(nm, ".txt"))
  capture.output(results[[nm]], file = arq)   # grava o sumário
}

# 2) um arquivo único, tudo empilhado ----------------------------------
--
```

```
arq_all <- "PGLS_all_summaries.txt"
cat("", file = arq_all)  # zera/ cria

for (nm in names(results)) {
  capture.output(
    {
      cat("\n\n===============================\n")
      cat("Modelo:", nm, "\n")
      cat("==============================\n")
      print(results[[nm]])
    },
    file = arq_all,
    append = TRUE
  )
}

# 3) combinações com falsa convergência ----------------------------------
writeLines(falhas_conv, "PGLS_false_convergence.txt")


cat("✅  Sumários gravados em 'pgls_summaries/' e também em 'PGLS_all_summaries.txt'.\n",
    "   Combinações sem convergência em 'PGLS_false_convergence.txt'.\n")

#########################################################
###Mapa do ambiente

# vendo a árvore
plot(tree)
nodelabels(frame="circ",bg="white",cex=0.8)
tree$tip.label
tree$edge
#pintar clados

#
# Carregar pacotes
# Carregar pacotes
```

```r
library(ape)
library(phytools)

# 1. Ler os dados
biomega <- read.table("Bio mega.txt", header = TRUE, row.names = 1, sep = "\t")

# 2. Obter vetor de estados (Habitat)
habitat_states <- biomega$Habitat
names(habitat_states) <- rownames(biomega)

# 3. Podar a árvore
tree_pruned <- keep.tip(tree, names(habitat_states))

# 4. Codificar estados como fator
habitat_factor <- as.factor(habitat_states[tree_pruned$tip.label])

# 5. Definir novas cores desejadas
states <- levels(habitat_factor)
cores <- setNames(c("forestgreen", "gold", "#8B4513"), states)  # Florestal, Generalista, Aberto

# 6. Criar vetor nomeado de estados
habitat_named <- setNames(as.character(habitat_factor), names(habitat_factor))

# 7. Simulação estocástica
set.seed(123)
tree_simmap <- make.simmap(tree_pruned, habitat_named, model = "ER", nsim = 1)

# Ajustar margens para abrir espaço à direita
par(mar = c(5, 4, 4, 8))  # margem direita aumentada (último número)

# Plotar árvore com simmap
plotSimmap(tree_simmap, fsize = 0.8, colors = cores, lwd = 2)
title("Reconstrução Ancestral do Habitat")

# Adicionar legenda fora da área da árvore (à direita)
```

```
legend("topright",
       inset = c(-0.25, 0),   # desloca para fora da área do gráfico
       legend = names(cores),
       fill = cores,
       border = "black",
       cex = 0.8,
       xpd = TRUE,            # permite desenhar fora da área do gráfico
       bty = "n")             # sem contorno

##########################################################
### Reconstrução ancestral de habitat (método ML - ace)

library(ape)
library(phytools)

# 1. Ler dados
biomega <- read.table("Bio mega.txt", header = TRUE, row.names = 1, sep = "\t")

# 2. Garantir correspondência
biomega <- biomega[tree$tip.label, , drop = FALSE]
habitat <- setNames(biomega$Habitat, rownames(biomega))

# 3. Codificar como fator numérico
habitat_factor <- as.factor(habitat)
habitat_num <- as.numeric(habitat_factor)

# 4. Reconstrução ancestral (modelo ER)
ace_res <- ace(habitat_num, tree, model = "ER", type = "discrete")

# 5. Definir cores
estados <- levels(habitat_factor)
cores <- setNames(c("forestgreen", "gold", "#8B4513")[seq_along(estados)], estados)

# 6. Plotar árvore colorindo os terminais e nós pelo estado mais provável
plot(tree, cex = 0.8)
```

```
tiplabels(pch = 21, bg = cores[habitat_factor], cex = 1.2)

# estado mais provável por nó
n_states <- apply(ace_res$lik.anc, 1, which.max)
n_col <- cores[estados[n_states]]
nodelabels(pch = 21, bg = n_col, cex = 1.2)

legend("topright",
       legend = estados,
       pt.bg = cores,
       pch = 21,
       cex = 0.8,
       bty = "n")

#title("Reconstrução Ancestral do Habitat (Máxima Verossimilhança)")

##########################################################################
########################

## fazendo um phylomorphospace plot

library("phytools")

# vendo a árvore
plot(tree)

nodelabels(frame="circ",bg="white",cex=0.8)

# vendo os números dos nós para definir os clados
plotTree(tree,ftype="i", type="fan")
nodelabels(frame="circ",bg="white",cex=0.8)

# definindo os clados
cladelabels(tree,c("0", "1", "2", "3", "4","5"), c(28, 50,46,43,39,32))
library(phytools)

# Inicializar objeto painted com a árvore original
painted <- tree
```

```
# Pintar os clados
painted <- paintSubTree(painted, node=28, state="0", anc.state="0")  # clado 0
painted <- paintSubTree(painted, node=50, state="1", anc.state="1")  # clado 1
painted <- paintSubTree(painted, node=46, state="2", anc.state="2")  # clado 2
painted <- paintSubTree(painted, node=43, state="3", anc.state="3")  # clado 3
painted <- paintSubTree(painted, node=39, state="4", anc.state="4")  # clado 4
painted <- paintSubTree(painted, node=32, state="5", anc.state="5")  # clado 5


# Visualizar
plotSimmap(painted, fsize=0.7, lwd=2)


# plotando a árvore pintada
plot(painted,lwd=3)


# label dos clades
cladelabels(painted,c("Clade 1", "Clade 2", "Clade 3", "Clade 4", "Clade 5"), c(50,46,43,39,32),wing.length=0.5,offset=0.5)


# rodando o phylomorphospace plot mesmo
# definindo o tipo de plot
par(bty="l")
# Salvado a versão completa
comp_data_comp<-comp_data2
#Usando a versão sem var colineares
comp_data2 <- full_join(data.log, dataBio, by = "Species")
rownames(comp_data2) <- comp_data2$Species
comp_data2 <- full_join(comp_data2, scores2, by = "Species")
rownames(comp_data2) <- comp_data2$Species


rownames(comp_data) <- comp_data$Species
comp_pm<-comp_data2[,21:22]
comp_pm2<-comp_data2[,c(22,24)]
comp_pm3<-comp_data2[,c(5,13)]
```

```
comp_pm4<-comp_data2[,c(6,13)]


phylomorphospace(painted,comp_pm3,bty="l",xlab="Amp de freq",
                 ylab="N notas",node.size=c(0,1))


# plotando o phylomorphospace plot pronto
par(bty="l")
phylomorphospace(painted,comp_pm4,bty="l",xlab="numero_de_notas",
                 ylab="Time_5_medida_frase",node.size=c(0,1.2),
label="horizontal", fsize=1, node.by.map=T)
legend(x="topright",legend=c("Clade 1", "Clade 2", "Clade 3", "Clade 4",
"Clade 5"),
       pch=21,pt.cex=1.5,pt.bg=palette()[2:5],bty="n")


## fazendo matriz de correlação entre variáveis considerando a filogenia
(lembrar de não padronizar os comprimentos de ramos para essa análise)
fancyTree(painted,type="scattergram",X=comp_pm4,label=F, fsize=0.4)
legend(x="left",legend=c("Clade 1", "Clade 2", "Clade 3", "Clade 4",
"Clade 5"),pch=21,pt.cex=1.5,pt.bg=palette()[2:5],bty="n")


######################################################################
#--- Comparando ajuste de modelos evolutivos
#Refiz o começo do script para não correr riscos de fazer besteira
library(geiger)
library(picante)
library(phytools)


#resolvendo as politomias com dicotomias de comprimento = zero
is.binary.tree(tree)
tree<-multi2di(tree)


is.ultrametric(tree)# ver se é ultramétrica


# 1. Crie uma lista com os dados que você quer testar
data_list <- list(
  Low_Freq_m_nota_inicial      = Low_Freq_m_nota_inicial,
  High_Freq_m_nota_inicial     = High_Freq_m_nota_inicial,
  Delta_Freq_m_nota_inicial    = Delta_Freq_m_nota_inicial,
  Delta_Time_m_nota_inicial    = Delta_Time_m_nota_inicial,
```

```
Max_Freq_m_nota_inicial      = Max_Freq_m_nota_inicial,
Delta_Time_m_interv._inicial = Delta_Time_m_interv._inicial,
Low_Freq_m_nota_central      = Low_Freq_m_nota_central,
High_Freq_m_nota_central     = High_Freq_m_nota_central,
Delta_Freq_m_nota_central    = Delta_Freq_m_nota_central,
Delta_Time_m_nota_central    = Delta_Time_m_nota_central,
Max_Freq_m_nota_central      = Max_Freq_m_nota_central,
Delta_Time_m_interv._central = Delta_Time_m_interv._central,
Low_Freq_m_nota_final        = Low_Freq_m_nota_final,
High_Freq_m_nota_final       = High_Freq_m_nota_final,
Delta_Freq_m_nota_final      = Delta_Freq_m_nota_final,
Delta_Time_m_nota_final      = Delta_Time_m_nota_final,
Max_Freq_m_nota_final        = Max_Freq_m_nota_final,
Delta_Time_m_interv._final   = Delta_Time_m_interv._final,
Low_Freq_medida_frase        = Low_Freq_medida_frase,
High_Freq_medida_frase       = High_Freq_medida_frase,
Delta_Freq_medida_frase      = Delta_Freq_medida_frase,
Delta_Time_medida_frase      = Delta_Time_medida_frase,
Max_Freq_medida_frase        = Max_Freq_medida_frase,
Freq_25_medida_frase         = Freq_25_medida_frase,
Freq_5_medida_frase          = Freq_5_medida_frase,
Freq_75_medida_frase         = Freq_75_medida_frase,
Freq_95_medida_frase         = Freq_95_medida_frase,
Time_25_medida_frase         = Time_25_medida_frase,
Time_5_medida_frase          = Time_5_medida_frase,
Time_75_medida_frase         = Time_75_medida_frase,
Time_95_medida_frase         = Time_95_medida_frase,
pace_inicial                 = pace_inicial,
pace_central                 = pace_central,
pace_final                   = pace_final,
delta_pace_i_c               = delta_pace_i_c,
delta_pace_c_f               = delta_pace_c_f,
delta_freq_i_c               = delta_freq_i_c,
delta_freq_c_f               = delta_freq_c_f,
numero_de_notas              = numero_de_notas,
pace                         = pace,
PC1                         = PC1,
```

```r
  PC2                         = PC2,
  PC3                         = PC3,
  PC4                         = PC4,
  PC5                         = PC5
)

# 2. Combine com a árvore em uma lista de pares phylo+data
cn_list <- lapply(data_list, function(x) picante::match.phylo.data(tree,
x))

# 3. Função auxiliar para ajustar modelos e calcular pesos de AICc
fit_models <- function(cn) {
  bm <- fitContinuous(cn$phy, cn$data)
  ou <- fitContinuous(cn$phy, cn$data, model = "OU")
  eb <- fitContinuous(cn$phy, cn$data, model = "EB")
  lb <- fitContinuous(cn$phy, cn$data, model = "lambda")
  dt <- fitContinuous(cn$phy, cn$data, model = "delta")
  kp <- fitContinuous(cn$phy, cn$data, model = "kappa")
  td <- fitContinuous(cn$phy, cn$data, model = "trend")
  df <- fitContinuous(cn$phy, cn$data, model = "drift")

  # --- adicionando white noise ---
  wn_data <- as.numeric(cn$data)
  wn_logL <- sum(dnorm(wn_data, mean = mean(wn_data), sd = sd(wn_data),
log = TRUE))
  wn_k <- 2  # parâmetros: média e variância
  wn_aic <- -2 * wn_logL + 2 * wn_k
  n <- length(wn_data)
  wn_aicc <- wn_aic + (2 * wn_k * (wn_k + 1)) / (n - wn_k - 1)
  # -------------------------------

  aicc <- c(BM = bm$opt$aicc, OU = ou$opt$aicc, EB = eb$opt$aicc, LB =
lb$opt$aicc,
            DT = dt$opt$aicc, KP = kp$opt$aicc, TD = td$opt$aicc, DF =
df$opt$aicc,
            WN = wn_aicc)

  aiccD <- aicc - min(aicc)
  aw <- exp(-0.5 * aiccD)
```

```
  aiccW <- aw / sum(aw)

  # --- extrair parâmetros de interesse ---
  lambda <- ifelse(!is.null(lb$opt$lambda), lb$opt$lambda, NA)
  delta  <- ifelse(!is.null(dt$opt$delta),  dt$opt$delta,  NA)
  kappa  <- ifelse(!is.null(kp$opt$kappa),  kp$opt$kappa,  NA)

  return(list(
    AICc = aicc,
    AICCd = aiccD,
    weights = aiccW,
    lambda = lambda,
    delta = delta,
    kappa = kappa
  ))
}

# 4. Aplicar a função a todos os conjuntos
results <- lapply(cn_list, fit_models)

# 5. (Opcional) Nomear a lista de resultados
names(results) <- names(data_list)

fit_results <- results
names(fit_results) <- names(data_list)

# 6. Visualizar os pesos de AICc de cada variável
aicc_weights <- lapply(results, function(x) x$weights)
aicc_delta <- lapply(results, function(x) x$AICCd)

# 7. Converter em data frame para inspeção e exportar
aicc_table1 <- do.call(rbind, lapply(aicc_weights, function(x)
as.data.frame(t(x))))
aicc_table1 <- cbind(Variable = names(aicc_weights), aicc_table1)

aicc_table2 <- do.call(rbind, lapply(aicc_delta, function(x)
as.data.frame(t(x))))
aicc_table2 <- cbind(Variable = names(aicc_delta), aicc_table2)
```

```
print(aicc_table1)

print(aicc_table2)


write.csv(aicc_table1, "AICc_model_weights.csv", row.names = FALSE)

write.csv(aicc_table2, "AICc_model_delta.csv", row.names = FALSE)


#  Extrair os valores dos parâmetros lambda, delta e kappa

params_table <- data.frame(

  Variable = names(results),

  lambda = sapply(results, function(x) x$lambda),

  delta  = sapply(results, function(x) x$delta),

  kappa  = sapply(results, function(x) x$kappa)

)


print(params_table)


# Salvar em CSV

write.csv(params_table, "Model_parameters_lambda_delta_kappa.csv",
row.names = FALSE)


### --- BLOCO ROBUSTO PARA PEGAR O MELHOR MODELO E EXTRair O PARÂMETRO -
-- ###


best_model <- apply(aicc_table1[, -1], 1, function(x)
names(x)[which.max(x)])

best_model_df <- data.frame(Variable = aicc_table1$Variable,

                            best_model = best_model,

                            stringsAsFactors = FALSE)


param_list <- lapply(seq_along(best_model_df$Variable), function(i) {

  var <- best_model_df$Variable[i]

  mod <- best_model_df$best_model[i]

  res <- fit_results[[var]]  # <- aqui fit_results é do fitContinuous


  lambda <- if (!is.null(res$lambda)) res$lambda else NA_real_

  delta  <- if (!is.null(res$delta))  res$delta  else NA_real_

  kappa  <- if (!is.null(res$kappa))  res$kappa  else NA_real_
```

```
  # Se o melhor modelo não é LB/DT/KP, zera tudo
  if (!(mod %in% c("LB","DT","KP"))) lambda <- delta <- kappa <-
NA_real_

  data.frame(Variable = var, lambda = lambda, delta = delta, kappa =
kappa,
             stringsAsFactors = FALSE)
})

best_params <- do.call(rbind, param_list)
best_params$best_model <- best_model_df$best_model
params_table <- best_params[,
c("Variable","best_model","lambda","delta","kappa")]

print(params_table)

# Salvar em CSV
write.csv(best_model_df, "Best models.csv", row.names = FALSE)

### --- fim do bloco --- ###

# fazendo PGLS as variáveis que o melhor modelo foi delta ou kappa
(lambda e BM dá na mesma na prática Whinte Noise não precisa)
# não colineares mais as 5 PCs da pPCA) usando a PGLS que
# permite usar os parâmetros lambda, delta, kappa

#Segundo os melhores modelos acima, 4 variáveis tiveram modelos
diferentes de BM e WN
#Delta_Time_medida_frase: KP
#Time_5_medida_frase: KP
#delta_freq_c_f: DT
#numero_de_notas: DT

library(caper)

# ---------- CONFIGURAÇÃO ----------

# Bloco Time_5_medida_frase kappa = 0.01
```

```
#Deixando apenas Time_5_medida_frase, Habitat e Species

caper1<-comp_data2[,c("Time_5_medida_frase", "Habitat", "Species")]

caper1<-na.omit(caper1)

caper1.1<-comparative.data(tree, caper1,names.col = "Species")

model_test<-pgls(Time_5_medida_frase~Habitat,data=caper1.1, kappa =
0.01)

summary(model_test) #não deu significativo


#Deixando apenas Time_5_medida_frase, Mass e Species

caper2<-comp_data2[,c("Time_5_medida_frase", "Mass", "Species")]

caper2<-na.omit(caper2)

caper2.1<-comparative.data(tree, caper2,names.col = "Species")

model_test<-pgls(Time_5_medida_frase~Mass,data=caper2.1, kappa = 0.01)

summary(model_test) #não deu significativo


#Deixando apenas Time_5_medida_frase, Dimorphism e Species

caper3<-comp_data2[,c("Time_5_medida_frase", "Dimorphism", "Species")]

caper3<-na.omit(caper3)

caper3.1<-comparative.data(tree, caper3,names.col = "Species")

model_test<-pgls(Time_5_medida_frase~Dimorphism,data=caper3.1, kappa =
0.01)

summary(model_test) #deu significativo!!!

plot(Time_5_medida_frase~Dimorphism,data=caper3)

abline(a = coef(model_test)[1], b = coef(model_test)[2])

plot(model_test, abline=c(0,0))


#Deixando apenas Time_5_medida_frase, Altitud_min e Species

caper4<-comp_data2[,c("Time_5_medida_frase", "Altitud_min", "Species")]

caper4<-na.omit(caper4)

caper4.1<-comparative.data(tree, caper4,names.col = "Species")

model_test<-pgls(Time_5_medida_frase~Altitud_min,data=caper4.1, kappa =
0.01)

summary(model_test) #não deu significativo


#Deixando apenas Time_5_medida_frase, Altitud_max e Species

caper5<-comp_data2[,c("Time_5_medida_frase", "Altitud_max", "Species")]

caper5<-na.omit(caper5)
```

```r
caper5.1<-comparative.data(tree, caper5,names.col = "Species")
model_test<-pgls(Time_5_medida_frase~Altitud_max,data=caper5.1, kappa = 0.01)
summary(model_test) #não deu significativo

#Deixando apenas Time_5_medida_frase, Alt_range e Species
caper6<-comp_data2[,c("Time_5_medida_frase", "Alt_range", "Species")]
caper6<-na.omit(caper6)
caper6.1<-comparative.data(tree, caper6,names.col = "Species")
model_test<-pgls(Time_5_medida_frase~Alt_range,data=caper6.1, kappa = 0.01)
summary(model_test) #não deu significativo

# Bloco Delta_Time_medida_frase kappa = 0.01

#Deixando apenas Delta_Time_medida_frase, Habitat e Species
caper1<-comp_data_comp[,c("Delta_Time_medida_frase", "Habitat", "Species")]
caper1<-na.omit(caper1)
caper1.1<-comparative.data(tree, caper1,names.col = "Species")
model_test<-pgls(Delta_Time_medida_frase~Habitat,data=caper1.1, kappa = 0.01)
summary(model_test) #não deu significativo por pouco

#Deixando apenas Delta_Time_medida_frase, Mass e Species
caper2<-comp_data_comp[,c("Delta_Time_medida_frase", "Mass", "Species")]
caper2<-na.omit(caper2)
caper2.1<-comparative.data(tree, caper2,names.col = "Species")
model_test<-pgls(Delta_Time_medida_frase~Mass,data=caper2.1, kappa = 0.01)
summary(model_test) #não deu significativo

#Deixando apenas Delta_Time_medida_frase, Dimorphism e Species
caper3<-comp_data_comp[,c("Delta_Time_medida_frase", "Dimorphism", "Species")]
caper3<-na.omit(caper3)
caper3.1<-comparative.data(tree, caper3,names.col = "Species")
model_test<-pgls(Delta_Time_medida_frase~Dimorphism,data=caper3.1, kappa = 0.01)
summary(model_test) # não deu significativo por pouco
```

```
#Deixando apenas Delta_Time_medida_frase, Altitud_min e Species
caper4<-comp_data_comp[,c("Delta_Time_medida_frase", "Altitud_min", "Species")]
caper4<-na.omit(caper4)
caper4.1<-comparative.data(tree, caper4,names.col = "Species")
model_test<-pgls(Delta_Time_medida_frase~Altitud_min,data=caper4.1, kappa = 0.01)
summary(model_test) #não deu significativo


#Deixando apenas Delta_Time_medida_frase, Altitud_max e Species
caper5<-comp_data_comp[,c("Delta_Time_medida_frase", "Altitud_max", "Species")]
caper5<-na.omit(caper5)
caper5.1<-comparative.data(tree, caper5,names.col = "Species")
model_test<-pgls(Delta_Time_medida_frase~Altitud_max,data=caper5.1, kappa = 0.01)
summary(model_test) #não deu significativo


#Deixando apenas Delta_Time_medida_frase, Alt_range e Species
caper6<-comp_data_comp[,c("Delta_Time_medida_frase", "Alt_range", "Species")]
caper6<-na.omit(caper6)
caper6.1<-comparative.data(tree, caper6,names.col = "Species")
model_test<-pgls(Delta_Time_medida_frase~Alt_range,data=caper6.1, kappa = 0.01)
summary(model_test) #não deu significativo


# Bloco para delta_pace_c_f com OU


library(ape)
library(nlme)
library("geiger")
library("tibble")


# estrutura de correlação tipo OU (modelo de Martins & Hansen, 1997)
cor_ou <- corMartins(value = 0.5, phy = tree,form = ~ Species, fixed = FALSE)


#Deixando apenas delta_pace_c_f, Habitat e Species
```

```
OUd1<-comp_data2[,c("delta_pace_c_f", "Habitat", "Species")]
OUd1$Habitat <- as.factor(OUd1$Habitat)
OUd1<-na.omit(OUd1)

model_test<-gls(delta_pace_c_f~Habitat,data=OUd1, correlation = cor_ou,
method = "ML")
summary(model_test) # deu significativo muito significativo

par(mfrow = c(1,1))
plot(delta_pace_c_f~Habitat,data=OUd1)
abline(a = coef(model_test)[1], b = coef(model_test)[2])
plot(model_test, abline=c(0,0))
summary(model_test)$tTable

library(ggplot2)
ggplot(OUd1, aes(x = Habitat, y = delta_pace_c_f, fill = Habitat)) +
  geom_boxplot(alpha = 0.6) +
  geom_jitter(width = 0.1, alpha = 0.8) +
  theme_minimal() +
  labs(title = "Variação de delta_pace_c_f entre habitats", y =
"delta_pace_c_f", x = "Habitat")

#Deixando apenas delta_pace_c_f, Mass e Species
OUd2<-comp_data2[,c("delta_pace_c_f", "Mass", "Species")]
OUd2<-na.omit(OUd2)

model_test<-gls(delta_pace_c_f~Mass,data=OUd2, correlation = cor_ou,
method = "ML")
summary(model_test) #não deu significativo

#Deixando apenas delta_pace_c_f, Dimorphism e Species
OUd3<-comp_data2[,c("delta_pace_c_f", "Dimorphism", "Species")]
OUd3<-na.omit(OUd3)

model_test<-gls(delta_pace_c_f~Dimorphism,data=OUd3, correlation =
cor_ou, method = "ML")
summary(model_test) # não deu significativo

#Deixando apenas delta_pace_c_f, Altitud_min e Species
```

```
OUd4<-comp_data2[,c("delta_pace_c_f", "Altitud_min", "Species")]

OUd4<-na.omit(OUd4)


model_test<-gls(delta_pace_c_f~Altitud_min,data=OUd4, correlation =
cor_ou, method = "ML")

summary(model_test) #não deu significativo


#Deixando apenas delta_pace_c_f, Altitud_max e Species

OUd5<-comp_data2[,c("delta_pace_c_f", "Altitud_max", "Species")]

OUd5<-na.omit(OUd5)


model_test<-gls(delta_pace_c_f~Altitud_max,data=OUd5, correlation =
cor_ou, method = "ML")

summary(model_test) #não deu significativo


#Deixando apenas delta_pace_c_f, Alt_range e Species

OUd6<-comp_data2[,c("delta_pace_c_f", "Alt_range", "Species")]

OUd6<-na.omit(OUd6)


model_test<-gls(delta_pace_c_f~Alt_range,data=OUd6, correlation =
cor_ou, method = "ML")

summary(model_test) #não deu significativo


# Bloco numero_de_notas com OU


#Deixando apenas numero_de_notas, Habitat e Species

OUd1<-comp_data2[,c("numero_de_notas", "Habitat", "Species")]

OUd1$Habitat <- as.factor(OUd1$Habitat)

OUd1<-na.omit(OUd1)


model_test<-gls(numero_de_notas~Habitat,data=OUd1, correlation = cor_ou,
method = "ML")

summary(model_test) # não deu significativo


#Deixando apenas numero_de_notas, Mass e Species

OUd2<-comp_data2[,c("numero_de_notas", "Mass", "Species")]

OUd2<-na.omit(OUd2)
```

```
model_test<-gls(numero_de_notas~Mass,data=OUd2, correlation = cor_ou,
method = "ML")
summary(model_test) #não deu significativo

#Deixando apenas numero_de_notas, Dimorphism e Species
OUd3<-comp_data2[,c("numero_de_notas", "Dimorphism", "Species")]
OUd3<-na.omit(OUd3)

model_test<-gls(numero_de_notas~Dimorphism,data=OUd3, correlation =
cor_ou, method = "ML")
summary(model_test) # não deu significativo

#Deixando apenas numero_de_notas, Altitud_min e Species
OUd4<-comp_data2[,c("numero_de_notas", "Altitud_min", "Species")]
OUd4<-na.omit(OUd4)

model_test<-gls(numero_de_notas~Altitud_min,data=OUd4, correlation =
cor_ou, method = "ML")
summary(model_test) #não deu significativo

#Deixando apenas numero_de_notas, Altitud_max e Species
OUd5<-comp_data2[,c("numero_de_notas", "Altitud_max", "Species")]
OUd5<-na.omit(OUd5)

model_test<-gls(numero_de_notas~Altitud_max,data=OUd5, correlation =
cor_ou, method = "ML")
summary(model_test) #não deu significativo por pouco!

#Deixando apenas numero_de_notas, Alt_range e Species
OUd6<-comp_data2[,c("numero_de_notas", "Alt_range", "Species")]
OUd6<-na.omit(OUd6)

model_test<-gls(numero_de_notas~Alt_range,data=OUd6, correlation =
cor_ou, method = "ML")
summary(model_test) # deu significativo
plot(numero_de_notas~Alt_range,data=OUd6)
abline(a = coef(model_test)[1], b = coef(model_test)[2])
plot(model_test, abline=c(0,0))
summary(model_test)$tTable
```

```
loadhistory(".Rhistory")
savehistory("meu_historico_comandos.txt")
```

Phylogenetic Principal Component Analysis (pPCA)

We retained 12 non-collinear variables for multivariate analysis: *Mean bandwidth of the final notes, Mean interval duration of the final intervals, Phrase minimum frequency, Phrase maximum frequency, Phrase bandwidth, Time 5% relative, Time 75% relative, Final pace, Pace change (initial–middle), Pace change (middle–final), Frequency change (initial–middle), Frequency change (middle–final),* and *Number of notes*.

Full results from PGLS using alternative evolutionary models "OU" and "Kappa"

```
Call:
pgls(formula = Time_5_medida_frase ~ Habitat, data = caper1.1,
   kappa = 0.01)

Residuals:
    Min       1Q   Median       3Q      Max
-0.08188 -0.01860  0.01479  0.03753  0.08758

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
                     Estimate Std. Error t value  Pr(>|t|)
(Intercept)          0.6069788  0.0462261 13.1306 1.896e-12
HabitatFlorestal     0.0068774  0.0344576  0.1996   0.84348
HabitatGeneralista -0.0633268  0.0367333 -1.7240   0.09757

(Intercept)        ***
HabitatFlorestal
```

```
HabitatGeneralista .
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.04415 on 24 degrees of freedom
Multiple R-squared: 0.1573,	Adjusted R-squared: 0.08711
F-statistic: 2.241 on 2 and 24 DF,  p-value: 0.1282
> #Deixando apenas Time_5_medida_frase, Mass e Species
> caper2<-comp_data2[,c("Time_5_medida_frase", "Mass", "Species")]
> caper2<-na.omit(caper2)
> caper2.1<-comparative.data(tree, caper2,names.col = "Species")
> model_test<-pgls(Time_5_medida_frase~Mass,data=caper2.1, kappa = 0.01)
> summary(model_test) #não deu significativo

Call:
pgls(formula = Time_5_medida_frase ~ Mass, data = caper2.1, kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max
-0.048399 -0.000663  0.016838  0.054321  0.121597

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
               Estimate  Std. Error t value  Pr(>|t|)
(Intercept)  0.54150740  0.07962835  6.8004 1.302e-06 ***
Mass        -0.00022247  0.00050365 -0.4417    0.6634
---
Signif. codes:
```

```
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.05447 on 20 degrees of freedom
Multiple R-squared: 0.01061,	Adjusted R-squared: -0.03886 
F-statistic: 0.2144 on 1 and 20 DF,  p-value: 0.6483
> #Deixando apenas Time_5_medida_frase, Dimorphism e Species
> caper3<-comp_data2[,c("Time_5_medida_frase", "Dimorphism", "Species")]
> caper3<-na.omit(caper3)
> caper3.1<-comparative.data(tree, caper3,names.col = "Species")
> model_test<-pgls(Time_5_medida_frase~Dimorphism,data=caper3.1, kappa = 0.01)
> summary(model_test) #deu significativo!!!

Call:
pgls(formula = Time_5_medida_frase ~ Dimorphism, data = caper3.1, 
    kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max 
-0.061419 -0.034132  0.006174  0.050566  0.109182 

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
             Estimate Std. Error t value  Pr(>|t|)    
(Intercept)  0.726040   0.085658   8.476 2.071e-06 ***
Dimorphism  -0.287469   0.096240  -2.987   0.01134 *  
---
Signif. codes:  
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Residual standard error: 0.05501 on 12 degrees of freedom
Multiple R-squared: 0.3366,	Adjusted R-squared: 0.2813
F-statistic: 6.089 on 1 and 12 DF,  p-value: 0.02963
> plot(Time_5_medida_frase~Dimorphism,data=caper3)
> abline(a = coef(model_test)[1], b = coef(model_test)[2])
> plot(model_test, abline=c(0,0))
> #Deixando apenas Time_5_medida_frase, Altitud_min e Species
> caper4<-comp_data2[,c("Time_5_medida_frase", "Altitud_min", "Species")]
> caper4<-na.omit(caper4)
> caper4.1<-comparative.data(tree, caper4,names.col = "Species")
> model_test<-pgls(Time_5_medida_frase~Altitud_min,data=caper4.1, kappa = 0.01)
> summary(model_test) #não deu significativo

Call:
pgls(formula = Time_5_medida_frase ~ Altitud_min, data = caper4.1,
   kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max
-0.033980 -0.000543  0.021886  0.053618  0.129527

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
               Estimate  Std. Error t value  Pr(>|t|)
(Intercept)  5.0619e-01  4.6678e-02 10.8443 4.601e-10 ***
Altitud_min -1.8920e-05  2.4748e-05 -0.7645    0.4531
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Residual standard error: 0.0566 on 21 degrees of freedom
Multiple R-squared: 0.0376,	Adjusted R-squared: -0.008226
F-statistic: 0.8205 on 1 and 21 DF,  p-value: 0.3753
> #Deixando apenas Time_5_medida_frase, Altitud_max e Species
> caper5<-comp_data2[,c("Time_5_medida_frase", "Altitud_max", "Species")]
> caper5<-na.omit(caper5)
> caper5.1<-comparative.data(tree, caper5,names.col = "Species")
> model_test<-pgls(Time_5_medida_frase~Altitud_max,data=caper5.1, kappa = 0.01)
> summary(model_test) #não deu significativo

Call:
pgls(formula = Time_5_medida_frase ~ Altitud_max, data = caper5.1,
   kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max
-0.034833 -0.004563  0.015658  0.055594  0.128521

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
              Estimate  Std. Error t value  Pr(>|t|)
(Intercept)  5.1847e-01  6.0315e-02  8.5960 2.554e-08 ***
Altitud_max -1.1650e-05  2.4625e-05 -0.4731     0.641
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.057 on 21 degrees of freedom
```

```
Multiple R-squared: 0.02364,	Adjusted R-squared: -0.02285
F-statistic: 0.5085 on 1 and 21 DF,  p-value: 0.4837
> #Deixando apenas Time_5_medida_frase, Alt_range e Species
> caper6<-comp_data2[,c("Time_5_medida_frase", "Alt_range", "Species")]
> caper6<-na.omit(caper6)
> caper6.1<-comparative.data(tree, caper6,names.col = "Species")
> model_test<-pgls(Time_5_medida_frase~Alt_range,data=caper6.1, kappa = 0.01)
> summary(model_test) #não deu significativo

Call:
pgls(formula = Time_5_medida_frase ~ Alt_range, data = caper6.1, 
    kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max 
-0.052224  0.000397  0.016835  0.054391  0.132842 

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
              Estimate Std. Error t value  Pr(>|t|)    
(Intercept) 4.8370e-01 6.1717e-02  7.8374 1.143e-07 ***
Alt_range   1.1661e-05 3.2605e-05  0.3576    0.7242    
---
Signif. codes:  
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.0577 on 21 degrees of freedom
Multiple R-squared: -0.0004868,	Adjusted R-squared: -0.04813 
F-statistic: -0.01022 on 1 and 21 DF,  p-value: 1 
```

```
> #Deixando apenas Delta_Time_medida_frase, Habitat e Species
> caper1<-comp_data_comp[,c("Delta_Time_medida_frase", "Habitat", "Species")]
> caper1<-na.omit(caper1)
> caper1.1<-comparative.data(tree, caper1,names.col = "Species")
> model_test<-pgls(Delta_Time_medida_frase~Habitat,data=caper1.1, kappa = 0.01)
> summary(model_test) #não deu significativo por pouco

Call:
pgls(formula = Delta_Time_medida_frase ~ Habitat, data = caper1.1,
    kappa = 0.01)

Residuals:
     Min       1Q   Median       3Q      Max
-0.05115 -0.01860  0.00314  0.02837  0.10072

Branch length transformations:


kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
                   Estimate Std. Error t value  Pr(>|t|)
(Intercept)        0.585236   0.039582 14.7854 1.485e-13
HabitatFlorestal   0.054560   0.029505  1.8492   0.07679
HabitatGeneralista 0.039388   0.031454  1.2523   0.22254

(Intercept)        ***
HabitatFlorestal   .
HabitatGeneralista
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Residual standard error: 0.0378 on 24 degrees of freedom
Multiple R-squared: 0.1289,	Adjusted R-squared: 0.05628 
F-statistic: 1.775 on 2 and 24 DF,  p-value: 0.191
> #Deixando apenas Delta_Time_medida_frase, Mass e Species
> caper2<-comp_data_comp[,c("Delta_Time_medida_frase", "Mass", "Species")]
> caper2<-na.omit(caper2)
> caper2.1<-comparative.data(tree, caper2,names.col = "Species")
> model_test<-pgls(Delta_Time_medida_frase~Mass,data=caper2.1, kappa = 0.01)
> summary(model_test) #não deu significativo

Call:
pgls(formula = Delta_Time_medida_frase ~ Mass, data = caper2.1, 
    kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max 
-0.070926 -0.019307 -0.004768  0.020732  0.102102 

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
               Estimate  Std. Error t value  Pr(>|t|)    
(Intercept)  6.5398e-01  5.7027e-02 11.4678 3.018e-10 ***
Mass        -6.5708e-05  3.6070e-04 -0.1822    0.8573    
---
Signif. codes:  
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.03901 on 20 degrees of freedom
Multiple R-squared: 0.001462,	Adjusted R-squared: -0.04846 
```

```
F-statistic: 0.02928 on 1 and 20 DF,  p-value: 0.8658
> #Deixando apenas Delta_Time_medida_frase, Dimorphism e Species
> caper3<-comp_data_comp[,c("Delta_Time_medida_frase", "Dimorphism", "Species")]
> caper3<-na.omit(caper3)
> caper3.1<-comparative.data(tree, caper3,names.col = "Species")
> model_test<-pgls(Delta_Time_medida_frase~Dimorphism,data=caper3.1, kappa = 0.01)
> summary(model_test) # não deu significativo por pouco

Call:
pgls(formula = Delta_Time_medida_frase ~ Dimorphism, data = caper3.1,
    kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max
-0.041612 -0.026675 -0.001673  0.033940  0.085984

Branch length transformations:


kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
             Estimate Std. Error t value  Pr(>|t|)
(Intercept)  0.693909   0.061477 11.2873 9.538e-08 ***
Dimorphism  -0.139898   0.069072 -2.0254   0.06566 .
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.03948 on 12 degrees of freedom
Multiple R-squared: 0.1483,	Adjusted R-squared: 0.07738
F-statistic:  2.09 on 1 and 12 DF,  p-value: 0.1739
> #Deixando apenas Delta_Time_medida_frase, Altitud_min e Species
```

```
> caper4<-comp_data_comp[,c("Delta_Time_medida_frase", "Altitud_min", "Species")]
> caper4<-na.omit(caper4)
> caper4.1<-comparative.data(tree, caper4,names.col = "Species")
> model_test<-pgls(Delta_Time_medida_frase~Altitud_min,data=caper4.1, kappa = 0.01)
> summary(model_test) #não deu significativo

Call:
pgls(formula = Delta_Time_medida_frase ~ Altitud_min, data = caper4.1,
    kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max
-0.056505 -0.014158  0.003107  0.024050  0.107090

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
              Estimate Std. Error t value  Pr(>|t|)
(Intercept) 6.1716e-01 3.2070e-02 19.2439 7.994e-15 ***
Altitud_min 1.1961e-06 1.7003e-05  0.0703    0.9446
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.03888 on 21 degrees of freedom
Multiple R-squared: -6.78e-05,   Adjusted R-squared: -0.04769
F-statistic: -0.001424 on 1 and 21 DF,  p-value: 1
> #Deixando apenas Delta_Time_medida_frase, Altitud_max e Species
> caper5<-comp_data_comp[,c("Delta_Time_medida_frase", "Altitud_max", "Species")]
> caper5<-na.omit(caper5)
```

```
> caper5.1<-comparative.data(tree, caper5,names.col = "Species")
> model_test<-pgls(Delta_Time_medida_frase~Altitud_max,data=caper5.1, kappa = 0.01)
> summary(model_test) #não deu significativo

Call:
pgls(formula = Delta_Time_medida_frase ~ Altitud_max, data = caper5.1,
    kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max
-0.055172 -0.013684  0.004796  0.023359  0.106669

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
              Estimate  Std. Error t value  Pr(>|t|)
(Intercept)  6.3451e-01  4.0688e-02 15.5946 5.071e-13 ***
Altitud_max -1.0013e-05  1.6612e-05 -0.6028    0.5531
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.03845 on 21 degrees of freedom
Multiple R-squared: 0.02192,	Adjusted R-squared: -0.02466
F-statistic: 0.4706 on 1 and 21 DF,  p-value: 0.5002
> #Deixando apenas Delta_Time_medida_frase, Alt_range e Species
> caper6<-comp_data_comp[,c("Delta_Time_medida_frase", "Alt_range", "Species")]
> caper6<-na.omit(caper6)
> caper6.1<-comparative.data(tree, caper6,names.col = "Species")
> model_test<-pgls(Delta_Time_medida_frase~Alt_range,data=caper6.1, kappa = 0.01)
```

```
> summary(model_test) #não deu significativo

Call:
pgls(formula = Delta_Time_medida_frase ~ Alt_range, data = caper6.1,
    kappa = 0.01)

Residuals:
      Min        1Q    Median        3Q       Max
-0.053767 -0.010256  0.006618  0.030332  0.099252

Branch length transformations:

kappa  [Fix]  : 0.010
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
              Estimate  Std. Error t value  Pr(>|t|)
(Intercept)  6.4243e-01  4.0730e-02 15.7728 4.068e-13 ***
Alt_range   -1.9128e-05  2.1518e-05 -0.8889    0.3841
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.03808 on 21 degrees of freedom
Multiple R-squared: 0.04078,      Adjusted R-squared: -0.004895
F-statistic: 0.8928 on 1 and 21 DF,  p-value: 0.3555
> # Bloco para delta_pace_c_f com OU
>
> library(ape)
> library(nlme)
> library("geiger")
> library("tibble")
>
```

```
> # estrutura de correlação tipo OU (modelo de Martins & Hansen, 1997)
> cor_ou <- corMartins(value = 0.5, phy = tree,form = ~ Species, fixed = FALSE)
>
>
> #Deixando apenas delta_pace_c_f, Habitat e Species
> OUd1<-comp_data2[,c("delta_pace_c_f", "Habitat", "Species")]
> OUd1$Habitat <- as.factor(OUd1$Habitat)
> OUd1<-na.omit(OUd1)
>
> model_test<-gls(delta_pace_c_f~Habitat,data=OUd1, correlation = cor_ou, method = "ML")
> summary(model_test) # deu significativo muito significativo
Generalized least squares fit by maximum likelihood
  Model: delta_pace_c_f ~ Habitat
  Data: OUd1
        AIC       BIC   logLik
  -50.52675 -44.04757 30.26337

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
2.050165

Coefficients:
                       Value  Std.Error   t-value p-value
(Intercept)        0.5753800 0.05619443 10.239094  0.0000
HabitatFlorestal   0.1219567 0.04839822  2.519860  0.0188
HabitatGeneralista 0.1391985 0.04898600  2.841597  0.0090

 Correlation:
                   (Intr) HbttFl
HabitatFlorestal   -0.610
HabitatGeneralista -0.526  0.558
```

```
Standardized residuals:
        Min          Q1         Med          Q3         Max
-2.423052768 -0.194152702 -0.006194885  0.346990760  1.783527538

Residual standard error: 0.09458623
Degrees of freedom: 27 total; 24 residual
>
> par(mfrow = c(1,1))
> plot(delta_pace_c_f~Habitat,data=OUd1)
> abline(a = coef(model_test)[1], b = coef(model_test)[2])
> plot(model_test, abline=c(0,0))
> summary(model_test)$tTable
                        Value  Std.Error   t-value      p-value
(Intercept)        0.5753800 0.05619443 10.239094 3.092352e-10
HabitatFlorestal   0.1219567 0.04839822  2.519860 1.880291e-02
HabitatGeneralista 0.1391985 0.04898600  2.841597 9.012535e-03
>
> library(ggplot2)
> ggplot(OUd1, aes(x = Habitat, y = delta_pace_c_f, fill = Habitat)) +
+   geom_boxplot(alpha = 0.6) +
+   geom_jitter(width = 0.1, alpha = 0.8) +
+   theme_minimal() +
+   labs(title = "Variação de delta_pace_c_f entre habitats", y = "delta_pace_c_f", x = "Habitat")
>
>
>
>
> #Deixando apenas delta_pace_c_f, Mass e Species
> OUd2<-comp_data2[,c("delta_pace_c_f", "Mass", "Species")]
> OUd2<-na.omit(OUd2)
>
> model_test<-gls(delta_pace_c_f~Mass,data=OUd2, correlation = cor_ou, method = "ML")
> summary(model_test) #não deu significativo
Generalized least squares fit by maximum likelihood
```

```
  Model: delta_pace_c_f ~ Mass
  Data: OUd2
       AIC       BIC   logLik
  -31.15168 -26.78751 19.57584

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
  alpha
4.00249

Coefficients:
                Value  Std.Error  t-value p-value
(Intercept) 0.6075346 0.10557750 5.754394  0.0000
Mass        0.0005472 0.00073269 0.746809  0.4639

 Correlation:
     (Intr)
Mass -0.953

Standardized residuals:
       Min         Q1        Med         Q3        Max
-3.2356919 -0.1957814  0.2288657  0.4200242  1.6823596

Residual standard error: 0.1027525
Degrees of freedom: 22 total; 20 residual
>
>
>
> #Deixando apenas delta_pace_c_f, Dimorphism e Species
> OUd3<-comp_data2[,c("delta_pace_c_f", "Dimorphism", "Species")]
> OUd3<-na.omit(OUd3)
>
```

```
> model_test<-gls(delta_pace_c_f~Dimorphism,data=OUd3, correlation = cor_ou, method = "ML")
> summary(model_test) # não deu significativo
Generalized least squares fit by maximum likelihood
  Model: delta_pace_c_f ~ Dimorphism
  Data: OUd3
       AIC       BIC   logLik
  -18.80727 -16.25104 13.40364

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
39.14567

Coefficients:
                Value  Std.Error  t-value p-value
(Intercept) 0.6611086 0.04719765 14.00723  0.0000
Dimorphism  0.1379830 0.12587160  1.09622  0.2945

 Correlation:
           (Intr)
Dimorphism -0.823

Standardized residuals:
        Min          Q1         Med          Q3         Max
-1.88271835 -0.53750688  0.08644037  0.42234710  1.81989439

Residual standard error: 0.09288983
Degrees of freedom: 14 total; 12 residual
>
>
> #Deixando apenas delta_pace_c_f, Altitud_min e Species
> OUd4<-comp_data2[,c("delta_pace_c_f", "Altitud_min", "Species")]
```

```
> OUd4<-na.omit(OUd4)
>
> model_test<-gls(delta_pace_c_f~Altitud_min,data=OUd4, correlation = cor_ou, method = "ML")
> summary(model_test) #não deu significativo
Generalized least squares fit by maximum likelihood
  Model: delta_pace_c_f ~ Altitud_min
  Data: OUd4
       AIC       BIC   logLik
  -32.62662 -28.08464 20.31331

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
3.619772

Coefficients:
                Value  Std.Error   t-value p-value
(Intercept) 0.6724012 0.04003076 16.797115  0.0000
Altitud_min 0.0000132 0.00003097  0.425662  0.6747

 Correlation:
            (Intr)
Altitud_min -0.532

Standardized residuals:
       Min         Q1        Med         Q3        Max
-3.1332940 -0.2178520  0.1286494  0.4820868  1.9308426

Residual standard error: 0.1041104
Degrees of freedom: 23 total; 21 residual
>
> #Deixando apenas delta_pace_c_f, Altitud_max e Species
> OUd5<-comp_data2[,c("delta_pace_c_f", "Altitud_max", "Species")]
```

```
> OUd5<-na.omit(OUd5)
>
> model_test<-gls(delta_pace_c_f~Altitud_max,data=OUd5, correlation = cor_ou, method = "ML")
> summary(model_test) #não deu significativo
Generalized least squares fit by maximum likelihood
  Model: delta_pace_c_f ~ Altitud_max
  Data: OUd5
       AIC       BIC   logLik
  -32.49592 -27.95394 20.24796

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
4.648656

Coefficients:
                Value  Std.Error   t-value p-value
(Intercept)  0.6962807 0.06135209 11.348933  0.0000
Altitud_max -0.0000064 0.00002446 -0.259975  0.7974

 Correlation:
           (Intr)
Altitud_max -0.879

Standardized residuals:
       Min         Q1        Med         Q3        Max
-3.2310187 -0.2219347  0.1187435  0.4642716  1.8866142

Residual standard error: 0.1024482
Degrees of freedom: 23 total; 21 residual
>
> #Deixando apenas delta_pace_c_f, Alt_range e Species
> OUd6<-comp_data2[,c("delta_pace_c_f", "Alt_range", "Species")]
```

```
> OUd6<-na.omit(OUd6)
>
> model_test<-gls(delta_pace_c_f~Alt_range,data=OUd6, correlation = cor_ou, method = "ML")
> summary(model_test) #não deu significativo
Generalized least squares fit by maximum likelihood
  Model: delta_pace_c_f ~ Alt_range
  Data: OUd6
       AIC       BIC   logLik
  -32.99742 -28.45544 20.49871

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
5.545054

Coefficients:
                 Value  Std.Error   t-value p-value
(Intercept)  0.7223167 0.05492408 13.151185   0.000
Alt_range   -0.0000264 0.00003242 -0.815309   0.424

 Correlation:
          (Intr)
Alt_range -0.877

Standardized residuals:
        Min          Q1         Med          Q3         Max
-2.95342822 -0.39716546  0.06705496  0.45458617  2.06133404

Residual standard error: 0.1004993
Degrees of freedom: 23 total; 21 residual
>
>
> # Bloco numero_de_notas com OU
```

```
>
> #Deixando apenas numero_de_notas, Habitat e Species
> OUd1<-comp_data2[,c("numero_de_notas", "Habitat", "Species")]
> OUd1$Habitat <- as.factor(OUd1$Habitat)
> OUd1<-na.omit(OUd1)
>
> model_test<-gls(numero_de_notas~Habitat,data=OUd1, correlation = cor_ou, method = "ML")
> summary(model_test) # não deu significativo
Generalized least squares fit by maximum likelihood
  Model: numero_de_notas ~ Habitat
  Data: OUd1
        AIC       BIC   logLik
  -61.59262 -55.11344 35.79631

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
2.647123

Coefficients:
                        Value  Std.Error   t-value p-value
(Intercept)         0.6314435 0.04152282 15.207145  0.0000
HabitatFlorestal    0.0407117 0.03953833  1.029677  0.3134
HabitatGeneralista 0.0174409 0.04084089  0.427044  0.6732

 Correlation:
                   (Intr) HbttFl
HabitatFlorestal   -0.686
HabitatGeneralista -0.579  0.573

Standardized residuals:
       Min         Q1        Med         Q3        Max
-1.1220328 -0.3383655  0.5964616  1.1403650  2.3720655
```

```
Residual standard error: 0.07306062
Degrees of freedom: 27 total; 24 residual
>
>
> #Deixando apenas numero_de_notas, Mass e Species
> OUd2<-comp_data2[,c("numero_de_notas", "Mass", "Species")]
> OUd2<-na.omit(OUd2)
>
> model_test<-gls(numero_de_notas~Mass,data=OUd2, correlation = cor_ou, method = "ML")
> summary(model_test) #não deu significativo
Generalized least squares fit by maximum likelihood
  Model: numero_de_notas ~ Mass
  Data: OUd2
       AIC       BIC  logLik
  -50.20501 -45.84084 29.1025

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
2.194877

Coefficients:
                Value  Std.Error   t-value p-value
(Intercept)  0.711601 0.07115869 10.000198  0.0000
Mass        -0.000388 0.00046895 -0.827431  0.4178

 Correlation:
     (Intr)
Mass -0.899

Standardized residuals:
       Min         Q1        Med         Q3        Max
```

```
-1.0580958 -0.5145892  0.3148124  1.0577816  2.2452520

Residual standard error: 0.07211313
Degrees of freedom: 22 total; 20 residual
>
>
>
> #Deixando apenas numero_de_notas, Dimorphism e Species
> OUd3<-comp_data2[,c("numero_de_notas", "Dimorphism", "Species")]
> OUd3<-na.omit(OUd3)
>
> model_test<-gls(numero_de_notas~Dimorphism,data=OUd3, correlation = cor_ou, method =
"ML")
> summary(model_test) # não deu significativo
Generalized least squares fit by maximum likelihood
  Model: numero_de_notas ~ Dimorphism
  Data: OUd3
       AIC       BIC   logLik
  -25.41989 -22.86366 16.70994

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
3.570062

Coefficients:
                 Value  Std.Error  t-value p-value
(Intercept)  0.6831436 0.04335666 15.75637  0.0000
Dimorphism  -0.0488974 0.10091709 -0.48453  0.6367

 Correlation:
           (Intr)
Dimorphism -0.774
```

```
Standardized residuals:

       Min         Q1        Med         Q3        Max

-1.1721166 -0.7226736  0.2060927  0.5885165  1.9162896


Residual standard error: 0.07430755

Degrees of freedom: 14 total; 12 residual

>

>

> #Deixando apenas numero_de_notas, Altitud_min e Species

> OUd4<-comp_data2[,c("numero_de_notas", "Altitud_min", "Species")]

> OUd4<-na.omit(OUd4)

>

> model_test<-gls(numero_de_notas~Altitud_min,data=OUd4, correlation = cor_ou, method =
"ML")

> summary(model_test) #não deu significativo

Generalized least squares fit by maximum likelihood

  Model: numero_de_notas ~ Altitud_min

  Data: OUd4

        AIC      BIC   logLik

  -51.90248 -47.3605 29.95124


Correlation Structure: corMartins

 Formula: ~Species

 Parameter estimate(s):

   alpha

2.020761


Coefficients:

                 Value  Std.Error   t-value p-value

(Intercept)  0.6609720 0.03595001 18.385865  0.0000

Altitud_min -0.0000086 0.00001966 -0.439359  0.6649


 Correlation:
```

```
            (Intr)
Altitud_min -0.359

Standardized residuals:
       Min         Q1        Med         Q3        Max
-0.8444267 -0.5709146  0.2229663  0.9434724  2.1708611

Residual standard error: 0.07463126
Degrees of freedom: 23 total; 21 residual
>
> #Deixando apenas numero_de_notas, Altitud_max e Species
> OUd5<-comp_data2[,c("numero_de_notas", "Altitud_max", "Species")]
> OUd5<-na.omit(OUd5)
>
> model_test<-gls(numero_de_notas~Altitud_max,data=OUd5, correlation = cor_ou, method =
"ML")
> summary(model_test) #não deu significativo por pouco!
Generalized least squares fit by maximum likelihood
  Model: numero_de_notas ~ Altitud_max
  Data: OUd5
        AIC       BIC   logLik
  -54.61614 -50.07417 31.30807

Correlation Structure: corMartins
 Formula: ~Species
 Parameter estimate(s):
   alpha
3.732128

Coefficients:
                 Value  Std.Error   t-value p-value
(Intercept)  0.7320934 0.04028333 18.173609   0.000
Altitud_max -0.0000298 0.00001543 -1.931377   0.067
```

```
 Correlation: 
            (Intr)
Altitud_max -0.859

Standardized residuals:
        Min          Q1         Med          Q3         Max 
-1.17870506 -0.57218667  0.05273956  0.85665366  2.32836898 

Residual standard error: 0.06436595 
Degrees of freedom: 23 total; 21 residual
> 
> #Deixando apenas numero_de_notas, Alt_range e Species
> OUd6<-comp_data2[,c("numero_de_notas", "Alt_range", "Species")]
> OUd6<-na.omit(OUd6)
> 
> model_test<-gls(numero_de_notas~Alt_range,data=OUd6, correlation = cor_ou, method = "ML")
> summary(model_test) # deu significativo
Generalized least squares fit by maximum likelihood
  Model: numero_de_notas ~ Alt_range 
  Data: OUd6 
        AIC       BIC   logLik
  -56.64726 -52.10529 32.32363

Correlation Structure: corMartins
 Formula: ~Species 
 Parameter estimate(s):
   alpha 
23.11678 

Coefficients:
                 Value   Std.Error   t-value p-value
(Intercept)  0.7619603 0.028993158 26.280694   0.000
Alt_range   -0.0000560 0.000017885 -3.133234   0.005
```

```
 Correlation: 
          (Intr)
Alt_range -0.894

Standardized residuals:
        Min          Q1         Med          Q3         Max 
-1.56517738 -0.87985705  0.05183927  0.78045992  1.78723355 

Residual standard error: 0.05935046 
Degrees of freedom: 23 total; 21 residual
> plot(numero_de_notas~Alt_range,data=OUd6)
> abline(a = coef(model_test)[1], b = coef(model_test)[2])
> plot(model_test, abline=c(0,0))
> summary(model_test)$tTable
                    Value    Std.Error   t-value      p-value
(Intercept)  7.619603e-01 0.0289931580 26.280694 1.499474e-17
Alt_range   -5.603946e-05 0.0000178855 -3.133234 5.022823e-03
> 
```

Tables

Table S1. GenBank accession numbers for mitochondrial (COI, Cytb, ND2) and nuclear (FGB, CHD, MUSK) genes used in this study. A dash (–) indicates that no sequence was available for that gene in the given species. Outgroups are indicated at the bottom of the table.

Taxa	CO1	Cytb	ND2	FGB	CHD	MUSK
Megascops alagoensis	MW477402	MW560399	MW588835	-	MW588873	-
M. albogularis	KT799281	KT799236	KT799332	KT799377	KT799438	KT799476
M. asio	KT799283	KT799238	KT799334	KT799379	HQ593874	KT799479
M. ater	MW477399	MW560414	MW588833	MW479490	MW588870	MW475315
M. atricapilla	KT799284	KT799239	KT799335	KT799381	KT799440	KT799481
M. barbarus	KT799286	KT799241	KT799337	KT799384	KT799442	KT799484
M. centralis	KT799300	KT799255	KT799347	KT799404	-	KT799501
M. choliba	KT799294	KT799249	KT799345	KT799396	KT799451	KT799492
M. clarkii	KT799289	KT799244	KT799340	KT799388	KT799445	KT799486
M. colombianus	KT799291	KT799246	KT799342	KT799392	KT799447	KT799489
M. cooperi	KT799292	KT799247	KT799343	KT799394	KT799448	KT799490
M. gilesi	-	KT799280	-	-	-	-
M. guatemalae	KT799299	KT799254	KT799352	KT799403	KT799454	KT799499
M. hoyi	KT799302	KT799257	KT799353	KT799405	KT799456	KT799504
M. ingens	KT799304	KT799259	KT799356	KT799407	KT799458	KT799506
M. kennicottii	KT799308	KT799264	KT799359	KT799411	-	KT799509
M. koepckae	KT799309	KT799263	KT799360	KT799412	KT799461	-
M. marshalli	KT799310	KT799265	KT799361	KT799414	KT799462	KT799510
M. petersoni	KT799314	KT799270	KT799365	KT799421	KT799466	KT799515
M. roboratus	KT799315	KT799271	KT799366	-	KT799467	-
M. roraimae	KT799301	KT799256	KT799351	KT799429	KT799455	KT799503
M. sanctaecatarinae	KT799316	KT799272	KT799367	KT799423	KT799468	KT799517
M. stangiae	MW477406	MW560419	MW588839	MW479498	MW588877	MW475320
M. trichopsis	KT799319	KT799275	KT799370	KT799428	KT799469	KT799520
M. usta	MW477426	MW560440	MW588854	MW479509	MW588892	MW475330
M. watsonii	MW477388	MW560403	MW588822	KT799432;	MW588860	MW475304
Gymnasio nudipes	KT799312	KT799268	KT799363	KT799417	KT799464	KT799513
Otus megalotis	KT799325	KT799234	KT799330	-	KT799437	KT799474
Psiloscops flammeolus	KT799328	KT799235	KT799331	KT799375	DQ985272	KT799475
Strix aluco	NC_072569	NC_072569	NC_072569	-	-	-
Asio otus	NC_039736	NC_039736	NC_039736	-	-	-
Bubo bubo	OR756278	OR756278	OR756278	-	KR019949	-
Lophostrix cristata	KT799327	KT799233	-	-	KT799436	-

Table S2. Substitution models, rate variation, and number of bases used for each partition in *MrBayes* analysis.

Partition	**Genes / codon positions included**	**Substitution model**	**Rate variation**	**Γ categories**
1	COI pos1 (1–376\3); Cytb pos3 (379–1381\3); ND2 pos1 (1382–2411\3)	GTR + G	Gamma-distributed rates	4
2	COI pos2 (2–376\3); ND2 pos3 (1384–2411\3)	GTR + I + G	Invariable + Gamma	4
3	COI pos3 (3–376\3); Cytb pos2 (378–1381\3); CHD intron 18 (2412–2757); FGB intron 5 (2758–3316); MUSK intron 4 (3317–3917)	GTR + I + G	Invariable + Gamma	4
4	Cytb pos1 (377–1381\3); ND2 pos2 (1383–2411\3)	GTR + I + G	Invariable + Gamma	2

Table S3. Sound archives and commercial sources that provided recordings used in this study.

Source name	**Institution**	**Country**	**Notes**
Arquivo Sonoro Prof. Elias Coelho	Universidade Federal do Rio de Janeiro (UFRJ)	Brazil	Institutional archive
Fonoteca Neotropical Jacques Vielliard	Universidade Estadual de Campinas (Unicamp)	Brazil	Institutional archive
Macaulay Library	Cornell Lab of Ornithology, Cornell University	USA	Institutional archive, public online access
Borror Laboratory of Bioacoustics	Ohio State University	USA	Institutional archive
Bird Sound Collection	Florida Museum of Natural History, University of Florida	USA	Institutional archive
Animal Sound Archive	Museum für Naturkunde	Germany	Institutional archive
Fonoteca Zoológica	Museo Nacional de Ciencias Naturales (MNCN)	Spain	Institutional archive
Soundlibrary Archives	Muséum National d'Histoire Naturelle	France	Institutional archive
Colección de Sonidos Ambientales	Instituto de Investigación de Recursos Biológicos Alexander von Humboldt	Colombia	Institutional archive
Xeno-canto.org	—	Global	Public community database
Chants d'Oiseaux de Guyane	—	France / French Guiana	Commercial CD
Aves do Brasil	—	Brazil	Commercial CD
Birds of Costa Rica	—	Costa Rica	Commercial DVD

Table S4. Habitat descriptions for *Megascops* species and *Gymnasio nudipes* (outgroup) based on species accounts in Birds of the World (Billerman et al. 2022). Text excerpts correspond to the portions of each species account in which we based the classification of habitat types. Text in brackets refers to related taxa or account substitutions in BOW used to infer habitat information.

Taxa	**BOW (Birds of the World)**	**Classification**
	Habitat	
Gymnasio nudipes	The species inhabits forests and woodlands of all types, including within urban areas, and it occurs from the lowlands up to about 900 m above sea level. Humid lowland forest is the primary habitat, though they also occur in dry forest. Any small territory with available nest cavities is ideal for this species.	Generalist
Megascops albogularis	Humid montane evergreen forest and cloudforest, especially stunted alpine forest; mostly open forest and edge, and semi-open areas with scattered trees; habitat often rich in epiphytes and bamboo thickets, sometimes with glades or at least gaps in canopy. Occurs mostly from 2,000–3,000 m elevation, but locally down to 1,300 m (1) and as high as 3,700 m on eastern slope of the Peruvian Andes (14).	Forest-dependent
M. koepckeae	Koepcke's Screech-Owls inhabit wooded areas and arid forest patches on Andean slopes, as well as *Polypeis* woodland in the upper montane zone. The habitat preferences of Koepcke's Screech-Owl are geographically variable. Nominate koepckeae occupies high elevation evergreen forests, including Polylepis woods and exotic Eucalyptus; it is replaced at lower elevations, in drier forests, by Peruvian Screech-Owl (Megascops roboratus) and, locally in more humid forests, by White-throated Screech-Owl (Megascops albogularis) (Fjeldså et al. 2012). Subspecies hockingi, in the dry intermontane valleys of south central Peru, occurs in dry forest, primarily in Prosopis, but other tree species include Eriotheca and Bombax, and it also occurs in scrubby areas with groves of Eucalyptus (Fjeldså et al. 2012). Koecke's Screech-Owl presumably is a cavity nester, and so potentially is vulnerable to loss or degradation of forests throughout its range. Much of its range, however, already is seriously degraded, especially in south central Peru, yet this screech-owl survives and even can be common, "provided some trees remain for roosting and perching, and holes in trees or banks for nesting" (Fjeldså et al. 2012).	Generalist

M. choliba	Tropical Screech-Owls are found in a wide variety of habitats: "open woodland, streamside groves, coffee plantations, second growth, suburban areas with trees" (Stiles and Skutch 1989), and "dry to humid regions of lighter open woodland, tall second growth, terra firme and várzea forest borders, clearings with trees, and residential areas" (Hilty and Brown 1986). Does not occur in the interior of humid lowland forest. Usually does not occur in humid montane forest either, except for subspecies (or species?) *duidae*, of southern Venezuela; this poorly-known taxon has been found in "dense forest to *Brocchinia*/bamboo scrub to the high-elevation pitcher plant swamps" (Willard et al. 1991). The Tropical Screech-Owl does not occur in the interior of closed-canopy humd forest, but only at forest edge. In areas that are experiencing rapid deforestation, however, such as in eastern Ecuador, the distribution of this species is predicted to expand (Ridgely and Greenfield 2001). Deforestation is a potentially beneficial factor to this species because it provides clearings and secondary growth, which are suitable habitat.	Open-habitat
M. clarkii	The Bare-shanked Screech-Owl is found from Costa Rica to extreme northwest Colombia, although it is largely absent from most of Panama, except the far west and the extreme east of the country. It is generally found at altitudes of 900 to 3300 m, and the species is strongly dependent on dense montane forest. Cloudforest and humid, dense mountain forest and forest edge; sometimes occurs in thinner upland forest. From 900 m to c. 2350 m elevation, occasionally to 3300 m; nest in Costa Rica was at c. 2490 m (2). Needs at least patchy forest; in Costa Rica, habitat adversely affected by development of dairy industry. With restricted distribution in mountains in Middle America, and possible threats to habitat, conservation status of species should probably be reassessed.	Forest-dependent

M. trichopsis	The Whiskered Screech-Owl inhabits montane forests at 1,000–2,900 m elevation from southeastern Arizona and adjacent New Mexico south to northern Nicaragua. Unless unduly disturbed, the Whiskered Screech-Owl captures insects attracted to lights in suburbanized canyons and nest successfully along roads in campgrounds, near houses, and in coffee fincas. Montane; nests at 1,000–2,900 m in canyon riparian forest with a closed canopy and adjacent evergreen woodland and coniferous (pine) forest with partly open to closed canopy. Marginal in tropical dry (deciduous), mixed coniferous, and cloud forests. Pine–oak (Pinus–Quercus) woodland (Marshall 1957c) and Madrean evergreen woodland (Brown 1982b, Brown et al. 1998b) are equivalent to evergreen woodland (Gehlbach 1981), a name that admits the co-dominance of junipers (Juniperus), cypresses (Cupressus), other evergreens, and locales outside the Mexican Sierra Madres and is used herein.The Whiskered Screech-Owl is a temperate (montane) habitat indicator in tropical regions (Griscom 1932a) and identifies the Sierra Madrean Biotic Provinces of Mexico (Goldman 1951). It is an indicator species of evergreen woodland (Marshall 1957c, Brown 1982b), an important habitat because of high avian endemism (Pliego et al. 1993, Peterson et al. 1998) and diversity (Marshall 1957c, Balda 1969, Hutto 1987, Gram 1998). Nest sites are beside cabins, along roads, in campgrounds and parking lots, often < 3 m from structures, indicating considerable tolerance of human activity. Yet nest boxes (Marshall 1967, Hakes 1983) and woodpecker holes in utility poles are rarely used, in contrast to frequent use by coexisting Elf Owls. Acceptance of partly cultivated woodland-forest and sparse suburbanization reflects tolerance of humans, which is typical of screech-owls. As with other screech-owls, Whiskered Screech-Owl is preadapted to some urbanization (Gehlbach 1996, Marzluff et al. 1998), but its minimum habitat area is unknown.	Forest-dependent

M. barbarus	It inhabits temperate habitats from 1800-2500 m in elevation, in humid pine-oak and cloud forests. More recently, in Mexico it has been listed as in peril of extinction (DOF 2010). This conservation status was determined because it is an endemic and restricted-range species, and in view of the lack of ecological and biological knowledge, and because the habitat of the Bearded Screech-Owl has been severely fragmented. The Bearded Screech-Owl occupies montane forest with a temperate humid climate. Vegetation types where this owl lives are pine-oak humid forest, oak forest and cloud forest (del Hoyo et al. 1999, König and Weick 2008). This species has been listed as endangered in the Mexican Official Norm (DOF 2002) and Near-Threatened globally (Bird Life International 2009), due to the lack of ecological information, its restricted distribution, and the high rates of deforestation in regions where it occurs. Humid mountain forests (pine-oak and cloud) have been deforested and landscape matrix is in different successional stages. Currently, cloud and humid pine-oak forests in good condition are restricted in high slopes or high mountains that are of difficult access.	Forest-dependent
M. sanctaecatarinae	Long-tufted Screech-Owl inhabits semi-open forested areas, as well as adjacent farmland, and is found at elevations from approximately 300 m to 1000 m. Semi-open woodland, wooded pasture, upland moors with patches of Araucaria, and forest edge and secondary growth; locally, treesvideo and copses in and near villages and agricultural areas; avoids dense forest. Found mainly at elevations from 300–1000 m (1).	Open-habitat
M. roboratus	Mostly found below 1200 m, this screech-owl ranges locally to 2100 m in Peru, and is often common dry deciduous woodland (the larger and darker-crowned *Megascops roboratus roboratus*) or arid coastal scrub with many cacti (*Megascops roboratus pacificus*). Dry deciduous woodland with scattered bushes on mountain slopes and in hilly country, mostly at 500–1200 m, but occasionally as high as 1800 m in Ecuador and 2100 m in Peru (4, 5). Race pacificus inhabits arid coastal plains and foothills, generally below 500 m; habitats range from open, dry scrub of various shrubs, cacti, mesquite and various short trees, to dry deciduous forest of small to medium-sized trees and columnar cactus (Cereus); other typical species include Capparis, Acacia, Prosopis and Bombax. Although able to occupy very sparse woodland and scrub, at least for foraging, and probably to lesser extent for roosting, species may not be able to survive in such open habitat without trees of at least moderate stature that can provide nesting cavities. Nominate race reported to nest in tree cavity and perhaps in old nests of the Pale-legged Hornero (Furnarius leucopus)	Open-habitat

M. gilesi	Apparently confined to humid forest between 1,800 and 2,500 m elevation (3). The species potentially occurs higher than this, but at lower altitudes, and in drier habitat, *M. gilesi* is replaced by Tropical Screech-Owl (*M. choliba*), which is known to occur up to c. 1,425 m in the Santa Marta, and could range even higher than this in drier valleys (3). As only c. 15% of the mapped range is covered by original forest, it is thought that just c. 675 km^2 of suitable habitat remains within the range of M. gilesi. Habitat loss stemming from deforestation is the main threat, with forests in the Sierra Nevada de Santa Marta having been heavily logged and burnt since the 1950s, with the result that c. 85% of original forest cover has been converted to non-native tree plantations (primarily pine and eucalyptus), and livestock farming (5, 2). Both the range and population of M. gilesi are believed to be declining.	Forest-dependent
M. watsonii	Fairly common throughout its large range, Tawny-bellied Screech-Owl inhabits the interior of humid lowland forest. There, they are the most common screech-owl, as Tropical Screech-Owl (Megascops choliba) favors edges and second growth. Interior of lowland rainforest, especially old-growth primary forest and mature second growth; occasionally in clearings or at forest edge; usta also inhabits remnant forest along rivers and forest fragments near human settlements (5). Frequents lower storey of forest, usually found no more than 30 m above ground, often descending into undergrowth. Generally occurs at elevations not exceeding 600–700 m (6, 1). Since it seems to be restricted to forest, the major threat to its survival must surely be destruction of its habitat.	Forest-dependent
M. atricapilla	It is a forest-based species, preferring areas with a dense understory. Humid forest, especially extensive lowland rainforest; partial to thick viny forest with dense undergrowth, and forest edge; occasionally more open woodland, sometimes near villages and roads, and in younger secondary forest (4, 5). Study in S Brazil found present species frequented forests with many tall, large-diameter trees but also used stands with low canopy and sparse density of trees (6). Mainly in lowlands, to at least 600 m in N of range; generally lower in S, to 300 m in Argentina. It seems to require fairly large areas of forest in some areas, and it may not be able to survive in remnant forest reserves.	Forest-dependent

M. guatemalae	of lowland and lower montane forest. can sometimes be spotlighted on perches at relatively low levels and in dense vegetation. Humid lowland to semi-arid evergreen forest, semi-deciduous forest and thorn forest; also dense second growth and similar scrubby woodlands (6) and plantations. Humid tropical forest in lowlands and foothills, to c. 1200 m. Race roraimae inhabits rainforest on mountain slopes. Nocturnal hunter, using forest clearings and edge. Populations have probably declined as a result of forest destruction. Needs almost solid forest.	Generalist
M. centralis	Owl of humid lowland and foothill forests. Humid lowland and foothill forests, forest borders, and secondary woodland (2, 28, 7, 3). A species mainly of forest mid-story, might descend to understory or emerge to forest edges presumably after prey. Inside forest, it has been seen in gaps and fairly open understory, presumably to facilitate prey location and seizure (Juan Freile, personal observation). appears to be somewhat tolerant of at least moderate habitat disturbance (2, 28, 7, 40). Nevertheless, although the Choco Screech-Owl may tolerate certain degree of forest fragmentation, it is a forest species that no longer persists in forest fragments surrounded by heavily degraded matrixes like the agricultural zone of central-west Ecuador (45).	Forest-dependent
M. roraimae	Dense, humid and wet rainforests, in the foothills and lower slopes of tepuis and mountains. Found above 250-300 m, up to around 1500 m, rarely to 1800 m. Specific habitat preferences not well-documented. Appears to prefer intact forest, but very little information available (14).	Forest-dependent
M. cooperi	Dry woodland, semi-open country, secondary vegetation and lakeside fields. Midstory and edges of dry and arid woodland and scrub, deciduous broadleaf forest (13), semi-open country (such as savannas) with scattered trees and bushes, palms, giant cardon and cacti, second growth and lakeside fields; also swamp-forest and edges of mangroves, and at the southernmost edge of the range is said to only inhabit the latter	Open-habitat

M. kennicottii	in low elevation woodlands and deserts. This owl occurs in a wide variety of wooded habitats ranging from arid woodland in southern areas to confer-dominated forests in the Pacific Northwest. The species reaches highest densities in riparian deciduous woodlands at low elevations. It is tolerant of humans and often nests and hunts in residential areas and suburban parks if suitable trees for nesting and roosting are available. The species is most associated with riparian habitats and deciduous trees over much of its range. Most habitat data come from Arizona deserts and woodland. The species occurs in high densities in velvet mesquite (Prosopis velutina) riparian zones in the Sonoran Desert. Marshall stated that "the Screech Owl is at home in any kind of woodland. . .	Generalist
M. asio	Tree-dominated landscapes of most types, natural and culturally modified, early successional to mature, mountain slopes to river valleys, mostly below 1,500 m. Has the broadest ecological niche of any owl in its range. Permanent residents of both rural and urban habitats from south of the Canadian boreal forest to near the Tropic of Cancer in Mexico. These owls nest in tree cavities in wooded environments below about 1,500 meters, occupying lowland forests to mountainside woodlands, both deciduous and evergreen. Urbanization and global warming may promote northward range expansion, and human settlement with tree planting may have increased interspecific and intraspecific contacts. Examples include northern and subtropical deciduous and mixed forest, riparian deciduous and southern pine (Pinus) forest, southwestern oak–juniper (Quercus–Juniperus) and subtropical thorn woodland, urban and suburban yards, parks, and green belts.	Generalist
M. petersoni	poorly known inhabitant of dense montane forests. Humid montane forest	Forest-dependent
M. marshalli	long thought to be restricted to humid montane forest of central and southern Peru. However, the species has also been recently discovered in western Bolivia. Humid, mossy cloud forest with epiphytes, ferns and dense undergrowth, generally at 1900–2600 m (1, 4), possibly higher;	Forest-dependent
M. hoyi	Montane forest and cloudforest, in more or less moist areas with tall, thick trees and epiphytes; in SE Salta (Argentina), found only a few km from dry bush and trees in closed forest. Occurs at 1000–2600 m, locally to 2800 m elevation.	Forest-dependent

M. [ingens] colombianus	This species primarily occurs in humid montane forest, primarily on the eastern slopes of the Andes; but one subspecies, *colombianus*, is found in similar habitat on the western Andes of Colombia and northwestern Ecuador. Rufescent Screech-Owl [ingens] occupies mature montane evergreen forest, secondary forest, thinned forests, forest edges and shrubs (9, 10, 17, S. Cordoba-Cordoba and O.H. Marín-Gómez, personal observations). It has also been observed in solitary tall trees in pastures and at forest edges, even at sites with extensive forests nearby (13). Apparently the species can use fragmented habitats, where some large forest patches remain. In some of these forests, however, White-throated Screech-Owl (Megascops albogularis) has been reported. White-throated Screech-Owl possibly is more tolerant of forest edges than is Colombian Screech-Owl. Rufescent Screech-Owl is vulnerable to deforestation, which is advancing throughout its range but perhaps especially in the western Andes (14), due to activities such as logging, human settlement, the cultivation of coca, and gold mining. In western Colombia this species already has lost 44% of its habitat (14).	Forest-dependent
M. ingens	This species primarily occurs in humid montane forest, primarily on the eastern slopes of the Andes; but one subspecies, *colombianus*, is found in similar habitat on the western Andes of Colombia and northwestern Ecuador. Rufescent Screech-Owl [ingens] occupies mature montane evergreen forest, secondary forest, thinned forests, forest edges and shrubs (9, 10, 17, S. Cordoba-Cordoba and O.H. Marín-Gómez, personal observations). It has also been observed in solitary tall trees in pastures and at forest edges, even at sites with extensive forests nearby (13). Apparently the species can use fragmented habitats, where some large forest patches remain. In some of these forests, however, White-throated Screech-Owl (Megascops albogularis) has been reported. White-throated Screech-Owl possibly is more tolerant of forest edges than is Colombian Screech-Owl. Rufescent Screech-Owl is vulnerable to deforestation, which is advancing throughout its range but perhaps especially in the western Andes (14), due to activities such as logging, human settlement, the cultivation of coca, and gold mining. In western Colombia this species already has lost 44% of its habitat (14).	Forest-dependent
M. alagoensis	NOT IN BOW [~*M. atricapilla*]	Forest-dependent

M. ater ["M. watsonii"]	[*M. watsonii*] Tawny-bellied Screech-Owl inhabits the interior of humid lowland forest. There, they are the most common screech-owl, as Tropical Screech-Owl (*Megascops choliba*) favors edges and second growth. Interior of lowland rainforest, especially old-growth primary forest and mature second growth; occasionally in clearings or at forest edge; usta also inhabits remnant forest along rivers and forest fragments near human settlements (5). Frequents lower storey of forest, usually found no more than 30 m above ground, often descending into undergrowth. Since it seems to be restricted to forest, the major threat to its survival must surely be destruction of its habitat.	Forest-dependent
M. stangiae ["M. watsonii"]	[*M. watsonii*] Tawny-bellied Screech-Owl inhabits the interior of humid lowland forest. There, they are the most common screech-owl, as Tropical Screech-Owl (*Megascops choliba*) favors edges and second growth. Interior of lowland rainforest, especially old-growth primary forest and mature second growth; occasionally in clearings or at forest edge; ustavideo also inhabits remnant forest along rivers and forest fragments near human settlements (5). Frequents lower storey of forest, usually found no more than 30 m above ground, often descending into undergrowth. Since it seems to be restricted to forest, the major threat to its survival must surely be destruction of its habitat.	Forest-dependent
M. usta ["M. watsonii"]	[*M. watsonii*] Tawny-bellied Screech-Owl inhabits the interior of humid lowland forest. There, they are the most common screech-owl, as Tropical Screech-Owl (*Megascops choliba*) favors edges and second growth. Interior of lowland rainforest, especially old-growth primary forest and mature second growth; occasionally in clearings or at forest edge; ustavideo also inhabits remnant forest along rivers and forest fragments near human settlements (5). Frequents lower storey of forest, usually found no more than 30 m above ground, often descending into undergrowth. Since it seems to be restricted to forest, the major threat to its survival must surely be destruction of its habitat.	Forest-dependent

Table S5. Morphological, ecological, and elevational data for *Megascops* species and *Gymnasio nudipes* (outgroup) included in the analyses. Habitat categories: Forest = forest-dependent, Open = open-habitat specialist, Generalist = habitat generalist, see table bellow. Elevational data were extracted from *Birds of the World* (Billerman 2022). Body mass compiled from König et al. (2008). Dimorphism (%) = 100 × [(female frequency - male frequency) / female frequency], when both were available in Krabbe 2017.

Species	**Mass (g)**	**Habitat**	**Dimorphism (%)**	**Elev. min (m)**	**Elev. max (m)**	**Elev. range (m)**
Gymnasio nudipes	128.5	Generalist	100.0	0	900	900
M. alagoensis	–	Forest	–	–	–	–
M. albogularis	157.5	Forest	26.0	1300	3700	2400
M. asio	187.5	Generalist	29.0	0	1500	1500
M. ater	–	Forest	–	–	–	–
M. atricapilla	137.5	Forest	11.0	0	600	600
M. barbarus	69.0	Forest	32.0	1800	2500	700
M. centralis	–	Forest	–	0	1575	1575
M. choliba	130.0	Open	–	0	3000	3000
M. clarkii	160.0	Forest	12.0	900	3300	2400
M. colombianus	180.0	Forest	–	1300	2100	800
M. cooperi	157.5	Open	23.0	0	1300	1300
M. gilesi	–	Forest	25.0	1800	2500	700
M. guatemalae	107.0	Generalist	–	0	1500	1500
M. hoyi	127.5	Forest	23.0	1000	2800	1800
M. ingens	178.5	Forest	22.0	700	2450	1750
M. kennicottii	170.0	Generalist	50.0	0	1750	1750
M. koepckeae	129.0	Generalist	17.0	1400	4500	3100
M. marshalli	111.0	Forest	–	1900	2600	700
M. petersoni	103.5	Forest	–	1650	2450	800
M. roboratus	153.0	Open	31.0	500	1800	1300
M. roraimae	105.0	Forest	31.0	250	1800	1550
M. sanctaecatarinae	183.0	Open	–	300	1000	700
M. stangiae	–	Forest	–	–	–	–
M. trichopsis	95.5	Forest	–	1000	2900	1900
M. usta	128.0	Forest	–	–	–	–
M. watsonii	134.5	Forest	–	0	700	700

Table S6. Pagel's λ and Blomberg's K values for all acoustic traits. Each trait appears twice, with one row for λ and one for K. mundo acha que é cocoλ and K quantify phylogenetic signal under Brownian Motion; $p < 0.05$ indicates significant phylogenetic structure.

Variable	Method	Lambda_K	P_Value
Central pace	lambda	7.70E-05	1
Central pace	K	0.399095079	0.172
Final pace	lambda	0.91139223	0.33294772
Final pace	K	0.480147194	0.066
Frequency 25%	lambda	7.70E-05	1
Frequency 25%	K	0.48450466	0.089
Frequency 5%	lambda	7.70E-05	1
Frequency 5%	K	0.531661079	0.064
Frequency 75%	lambda	7.70E-05	1
Frequency 75%	K	0.475506711	0.093
Frequency 95%	lambda	7.70E-05	1
Frequency 95%	K	0.468174751	0.088
Frequency change (initial–middle)	lambda	7.70E-05	1
Frequency change (initial–middle)	K	0.311392564	0.474
Frequency change (middle–final)	lambda	7.70E-05	1
Frequency change (middle–final)	K	0.363430915	0.416
Initial pace	lambda	7.70E-05	1
Initial pace	K	0.397734931	0.187
Mean bandwidth of the central notes	lambda	7.70E-05	1
Mean bandwidth of the central notes	K	0.262229273	0.691
Mean bandwidth of the final notes	lambda	7.70E-05	1
Mean bandwidth of the final notes	K	0.288460417	0.531
Mean bandwidth of the initial notes	lambda	0.62294909	0.229897369
Mean bandwidth of the initial notes	K	0.457518051	0.127
Mean dominant frequency of the central notes	lambda	7.70E-05	1
Mean dominant frequency of the central notes	K	0.395020945	0.258
Mean dominant frequency of the final notes	lambda	0.703083762	0.148879933
Mean dominant frequency of the final notes	K	0.44419545	0.118
Mean dominant frequency of the initial notes	lambda	7.70E-05	1
Mean dominant frequency of the initial notes	K	0.385885027	0.238
Mean interval duration of the central intervals	lambda	7.70E-05	1
Mean interval duration of the central intervals	K	0.409561042	0.146
Mean interval duration of the final intervals	lambda	7.70E-05	1
Mean interval duration of the final intervals	K	0.486667808	0.079
Mean interval duration of the initial intervals	lambda	7.70E-05	1
Mean interval duration of the initial intervals	K	0.406898602	0.197
Mean maximum frequency of the central notes	lambda	7.70E-05	1
Mean maximum frequency of the central notes	K	0.410733574	0.167
Mean maximum frequency of the final notes	lambda	7.70E-05	1
Mean maximum frequency of the final notes	K	0.395967571	0.207

Mean maximum frequency of the initial notes	lambda	7.70E-05	1
Mean maximum frequency of the initial notes	K	0.392600943	0.194
Mean minimum frequency of the central notes	lambda	7.70E-05	1
Mean minimum frequency of the central notes	K	0.54825584	0.059
Mean minimum frequency of the final notes	lambda	7.70E-05	1
Mean minimum frequency of the final notes	K	0.522472502	0.065
Mean minimum frequency of the initial notes	lambda	1.027792132	0.661932002
Mean minimum frequency of the initial notes	K	0.556722042	0.058
Mean note duration of the central notes	lambda	0.94406394	0.050556203
Mean note duration of the central notes	K	0.529280674	0.067
Mean note duration of the final notes	lambda	0.871817995	0.055266595
Mean note duration of the final notes	K	0.506408998	0.073
Mean note duration of the initial notes	lambda	0.914869422	0.057161013
Mean note duration of the initial notes	K	0.537650214	0.063
Number of notes	lambda	0.842614814	0.002881491
Number of notes	K	0.810565516	0.002
Overall pace	lambda	7.70E-05	1
Overall pace	K	0.424952159	0.141
Pace change (initial–middle)	lambda	7.70E-05	1
Pace change (initial–middle)	K	0.407448008	0.26
Pace change (middle–final)	lambda	0.933812627	0.080179678
Pace change (middle–final)	K	0.510492645	0.082
Phrase bandwidth	lambda	0.646680311	0.51581271
Phrase bandwidth	K	0.391055128	0.209
Phrase dominant frequency	lambda	7.70E-05	1
Phrase dominant frequency	K	0.505982655	0.071
Phrase duration	lambda	0.966183253	0.000210673
Phrase duration	K	1.091168796	0.001
Phrase maximum frequency	lambda	7.70E-05	1
Phrase maximum frequency	K	0.451188559	0.08
Phrase minimum frequency	lambda	1.032316935	0.4622581
Phrase minimum frequency	K	0.552303697	0.049
Time 25% relative	lambda	0.490416735	0.141101091
Time 25% relative	K	0.594590981	0.033
Time 5% relative	lambda	0.659441504	0.02809684
Time 5% relative	K	0.867210553	0.001
Time 75% relative	lambda	0.412272253	0.286181959
Time 75% relative	K	0.500004588	0.065
Time 95% relative	lambda	7.70E-05	1
Time 95% relative	K	0.448571232	0.1

Table S7. ΔAICc and Akaike weights (w_i) for all evolutionary models fitted to each acoustic variable. Models include Brownian Motion (BM), Ornstein–Uhlenbeck (OU), Early Burst (EB), Lambda (LB), Delta (DT), Kappa (KP), Time-Dependent (TD), Drift (DF), and White-Noise (WN). The lowest ΔAICc (0) indicates the best-supported model; model weights represent relative support among alternatives

Variable	**BM_DeltaAICc**	**BM_Weight**	**OU_DeltaAICc**	**OU_Weight**	**EB_DeltaAICc**	**EB_Weight**	**LB_DeltaAICc**	**LB_Weight**	**DT_DeltaAICc**	**DT_Weight**	**KP_DeltaAICc**	**KP_Weight**	**TD_DeltaAICc**	**TD_Weight**	**DF_DeltaAICc**	**DF_Weight**	**WN_DeltaAICc**	**WN_Weight**
Minimum frequency of the initial notes	0.0654	0.1830	0.2972	0.1630	2.6088	0.0513	2.5245	0.0535	0.4290	0.1526	2.6088	0.0513	1.1768	0.1050	2.6088	0.0513	0.0000	0.1891
maximum frequency of the initial notes	6.7723	0.0214	3.9393	0.0884	9.3158	0.0060	2.5245	0.1794	5.5688	0.0392	8.9757	0.0071	7.0578	0.0186	9.3158	0.0060	0.0000	0.6338
bandwidth of the initial notes	4.4777	0.0329	0.1032	0.2929	7.0212	0.0092	1.0830	0.1794	2.2449	0.1004	4.6819	0.0297	4.1883	0.0380	7.0212	0.0092	0.0000	0.3084
note duration of the initial notes	0.0000	0.2598	1.6070	0.1163	2.5435	0.0728	2.0381	0.0938	1.3248	0.1339	2.5241	0.0735	1.5000	0.1227	2.5435	0.0728	3.1315	0.0543
interval duration of the initial intervals	5.7965	0.0325	3.4558	0.1047	8.3400	0.0091	2.5245	0.1667	4.8368	0.0525	8.1636	0.0099	6.2054	0.0265	8.3400	0.0091	0.0000	0.5891
dominant frequency of the initial notes	5.1352	0.0421	3.1876	0.1116	7.6787	0.0118	2.5245	0.1555	4.3037	0.0639	6.6167	0.0201	5.5677	0.0339	7.6787	0.0118	0.0000	0.5493
minimum frequency of the central notes	0.5941	0.1712	0.8188	0.1530	3.1376	0.0480	2.5245	0.0652	1.0055	0.1394	3.1376	0.0480	1.7346	0.0968	3.1376	0.0480	0.0000	0.2304
maximum frequency of the central notes	8.3675	0.0106	5.0072	0.0568	10.9109	0.0030	2.5245	0.1964	7.0175	0.0208	9.4538	0.0061	8.5833	0.0095	10.9109	0.0030	0.0000	0.6939
bandwidth of the central notes	15.4480	0.0003	8.1183	0.0132	17.9915	0.0001	2.5245	0.2165	11.9466	0.0019	11.7465	0.0022	14.5374	0.0005	17.9915	0.0001	0.0000	0.7651
note duration of the central notes	0.0000	0.2777	1.9128	0.1067	2.5435	0.0778	2.2197	0.0915	1.6290	0.1230	2.5033	0.0794	1.7077	0.1182	2.5435	0.0778	3.5181	0.0478
interval duration of the central intervals	7.8849	0.0132	4.7257	0.0639	10.4284	0.0037	2.5245	0.1922	6.6287	0.0247	8.9337	0.0078	8.1433	0.0116	10.4284	0.0037	0.0000	0.6792
dominant frequency of the central notes	4.5875	0.0514	2.9337	0.1175	7.1310	0.0144	2.5245	0.1442	3.8750	0.0734	5.4097	0.0341	5.0464	0.0409	7.1310	0.0144	0.0000	0.5096
minimum frequency of the final notes	2.3890	0.1112	1.8389	0.1464	4.9325	0.0312	2.5245	0.1039	2.4366	0.1086	4.9325	0.0312	3.3374	0.0692	4.9325	0.0312	0.0000	0.3672
maximum frequency of the final notes	10.9148	0.0032	6.4874	0.0289	13.4583	0.0009	2.5245	0.2096	9.1185	0.0078	9.9621	0.0051	10.8936	0.0032	13.4583	0.0009	0.0000	0.7406
bandwidth of the final notes	13.3046	0.0010	6.6331	0.0271	15.8481	0.0003	2.5245	0.2116	10.1435	0.0047	9.6813	0.0059	12.5580	0.0014	15.8481	0.0003	0.0000	0.7477
note duration of the final notes	0.0000	0.2323	1.4316	0.1135	2.5435	0.0651	1.1438	0.1311	1.2936	0.1216	1.9657	0.0869	1.4862	0.1105	2.5435	0.0651	2.2934	0.0738
interval duration of the final intervals	6.2580	0.0275	4.1229	0.0799	8.8015	0.0077	2.5245	0.1777	5.6862	0.0366	7.4945	0.0148	6.8753	0.0202	8.8015	0.0077	0.0000	0.6279
dominant frequency of the final notes	1.6475	0.1034	0.9257	0.1484	4.1910	0.0290	0.4408	0.1891	1.3668	0.1190	2.3796	0.0717	2.2987	0.0747	4.1910	0.0290	0.0000	0.2357
Phrase minimum frequency	0.0000	0.1922	0.4622	0.1525	2.5435	0.0539	2.5435	0.0539	0.5088	0.1490	2.5435	0.0539	1.1937	0.1058	2.5435	0.0539	0.0761	0.1850
Phrase maximum frequency	5.5876	0.0345	3.1590	0.1163	8.1311	0.0097	2.5245	0.1597	4.6859	0.0542	6.3241	0.0239	6.0312	0.0277	8.1311	0.0097	0.0000	0.5643

Phrase bandwidth	4.6701	0.0348	0.6771	0.2560	7.2135	0.0097	2.1022	0.1255	2.6854	0.0938	3.1648	0.0738	4.5155	0.0376	7.2135	0.0097	0.0000	0.3591
Phrase duration	3.0788	0.1130	3.7049	0.0826	5.6223	0.0317	5.2922	0.0374	3.2523	0.1036	0.0000	0.5267	3.9425	0.0734	5.6223	0.0317	16.5011	0.0001
Phrase dominant frequency	4.4800	0.0554	2.9894	0.1166	7.0234	0.0155	2.5245	0.1472	4.1874	0.0641	5.8426	0.0280	5.2471	0.0377	7.0234	0.0155	0.0000	0.5200
Frequency 25%	4.8056	0.0493	3.1979	0.1102	7.3491	0.0138	2.5245	0.1544	4.4001	0.0604	6.8262	0.0180	5.5130	0.0346	7.3491	0.0138	0.0000	0.5454
Frequency 5%	3.1286	0.0905	2.3690	0.1323	5.6720	0.0254	2.5245	0.1224	3.1547	0.0893	5.6240	0.0260	4.0685	0.0565	5.6720	0.0254	0.0000	0.4324
Frequency 75%	4.5492	0.0533	2.8821	0.1227	7.0927	0.0149	2.5245	0.1467	4.0966	0.0668	6.1128	0.0244	5.2284	0.0380	7.0927	0.0149	0.0000	0.5183
Frequency 95%	4.8583	0.0469	2.9576	0.1213	7.4018	0.0132	2.5245	0.1507	4.2723	0.0629	6.1216	0.0249	5.4675	0.0346	7.4018	0.0132	0.0000	0.5324
Time 25% relative	11.8608	0.0013	5.1609	0.0384	14.4043	0.0004	0.3586	0.4236	8.6578	0.0067	6.4169	0.0205	11.0497	0.0020	14.4043	0.0004	0.0000	0.5068
Time 5% relative	8.9500	0.0084	5.1229	0.0570	11.4935	0.0024	3.5971	0.1222	7.0398	0.0218	0.0000	0.7380	8.7637	0.0092	11.4935	0.0024	5.8948	0.0387
Time 75% relative	14.2223	0.0005	6.8441	0.0211	16.7658	0.0001	1.3870	0.3235	10.6843	0.0031	10.4594	0.0035	13.2482	0.0009	16.7658	0.0001	0.0000	0.6472
Time 95% relative	12.1435	0.0017	5.6571	0.0434	14.6870	0.0005	2.5245	0.2077	9.0525	0.0079	11.7417	0.0021	11.4283	0.0024	14.6870	0.0005	0.0000	0.7339
Initial pace	4.1982	0.0570	2.2325	0.1523	6.7417	0.0160	2.5245	0.1316	3.2683	0.0907	5.8914	0.0244	4.5762	0.0472	6.7417	0.0160	0.0000	0.4649
Central pace	4.2263	0.0567	2.2705	0.1507	6.7698	0.0159	2.5245	0.1327	3.3360	0.0884	5.9131	0.0244	4.6249	0.0464	6.7698	0.0159	0.0000	0.4689
Final pace	0.0000	0.1869	0.1542	0.1730	2.5435	0.0524	2.2422	0.0609	0.2001	0.1691	2.4443	0.0551	0.9617	0.1155	2.5435	0.0524	0.6551	0.1347
Pace change (i–m)	3.9208	0.0683	2.7791	0.1209	6.4643	0.0192	2.5245	0.1374	3.5270	0.0832	6.4643	0.0192	4.6578	0.0473	6.4643	0.0192	0.0000	0.4854
Pace change (m–f)	0.1958	0.1900	0.0000	0.2095	2.7393	0.0533	2.1141	0.0728	0.1927	0.1903	2.7393	0.0533	1.0817	0.1220	2.7393	0.0533	2.6509	0.0557
Frequency change (i–m)	14.7139	0.0005	8.4651	0.0111	17.2573	0.0001	2.5245	0.2171	11.8401	0.0021	13.0819	0.0011	14.1345	0.0007	17.2573	0.0001	0.0000	0.7672
Frequency change (m–f)	10.9659	0.0030	5.2142	0.0531	13.5094	0.0008	2.5245	0.2038	8.3163	0.0113	10.8081	0.0032	10.5058	0.0038	13.5094	0.0008	0.0000	0.7201
Number of notes	1.1800	0.1287	0.0000	0.2322	3.7235	0.0361	1.4697	0.1114	0.3587	0.1941	0.8902	0.1488	1.5299	0.1081	3.7235	0.0361	7.8263	0.0046
Overall pace	2.5318	0.0974	1.3696	0.1741	5.0753	0.0273	2.5245	0.0977	2.0446	0.1242	4.5910	0.0348	3.1355	0.0720	5.0753	0.0273	0.0000	0.3453
PC1	0.0000	0.2058	0.2115	0.1852	2.5435	0.0577	2.4964	0.0591	0.1511	0.1909	2.5435	0.0577	0.9635	0.1271	2.5435	0.0577	2.5064	0.0588
PC2	11.3389	0.0024	5.6052	0.0421	13.8824	0.0007	2.5245	0.1962	8.6133	0.0093	5.1751	0.0521	10.8162	0.0031	13.8824	0.0007	0.0000	0.6934
PC3	6.3170	0.0181	2.2617	0.1372	8.8605	0.0051	0.7001	0.2996	4.5724	0.0432	4.3488	0.0483	6.2806	0.0184	8.8605	0.0051	0.0000	0.4251
PC4	5.3846	0.0342	3.1029	0.1069	7.9280	0.0096	1.5979	0.2269	4.3748	0.0566	6.2222	0.0225	5.6751	0.0295	7.9280	0.0096	0.0000	0.5043
PC5	13.3348	0.0010	7.6225	0.0168	15.8783	0.0003	2.5245	0.2153	10.6609	0.0037	14.6575	0.0005	12.8715	0.0012	15.8783	0.0003	0.0000	0.7609

Table S8. Ancestral character state estimates (ACE) and 95% confidence intervals for internal nodes and treated measurements for terminal taxa of the *Megascops* phylogeny, based on three acoustic variables showing significant phylogenetic signal.

Variable	**node/terminal**	**estimate/measure**	**CI95_lo**	**CI95_hi**
N. of notes	28	0.648568089	0.499071199	0.79806498
N. of notes	29	0.647547828	0.560294034	0.734801622
N. of notes	30	0.694121791	0.643873321	0.744370262
N. of notes	31	0.70091348	0.654288812	0.747538148
N. of notes	32	0.726994655	0.671824495	0.782164815
N. of notes	33	0.753244749	0.696934828	0.80955467
N. of notes	34	0.779816179	0.741892099	0.817740259
N. of notes	35	0.790820347	0.757726647	0.823914046
N. of notes	36	0.811989153	0.779792799	0.844185507
N. of notes	37	0.790925709	0.757501842	0.824349576
N. of notes	38	0.700047705	0.653268755	0.746826654
N. of notes	39	0.705098344	0.652639952	0.757556737
N. of notes	40	0.728315716	0.676795137	0.779836295
N. of notes	41	0.703473344	0.64938164	0.757565048
N. of notes	42	0.707524818	0.653311451	0.761738185
N. of notes	43	0.692096941	0.638232567	0.745961316
N. of notes	44	0.691757215	0.636205459	0.747308971
N. of notes	45	0.676671731	0.626067895	0.727275567
N. of notes	46	0.692452596	0.640820301	0.74408489
N. of notes	47	0.692145437	0.639188538	0.745102335
N. of notes	48	0.676715684	0.620862126	0.732569243
N. of notes	49	0.672922583	0.614558256	0.73128691
N. of notes	50	0.628292037	0.548323929	0.708260145
N. of notes	51	0.622552719	0.540386588	0.704718849
N. of notes	52	0.610705272	0.56298197	0.658428575
N. of notes	53	0.612507262	0.529952076	0.695062447
N. of notes	*M. alagoensis*	0.840797667		
N. of notes	*M. albogularis*	0.600693159		
N. of notes	*M. asio*	0.696454549		
N. of notes	*M. ater*	0.845459827		
N. of notes	*M. atricapilla*	0.820159701		
N. of notes	*M. barbarus*	0.807441014		
N. of notes	*M. centralis*	0.642601083		
N. of notes	*M. choliba*	0.611555319		
N. of notes	*M. clarkii*	0.59017883		
N. of notes	*M. colombianus*	0.752478226		
N. of notes	*M. cooperi*	0.617474492		
N. of notes	*M. gilesi*	0.629838711		
N. of notes	*M. guatemalae*	0.735192973		
N. of notes	*M. hoyi*	0.767162427		
N. of notes	*M. ingens*	0.72153077		
N. of notes	*M. kennicottii*	0.607162738		
N. of notes	*M. koepckeae*	0.607162738		
N. of notes	*M. marshalli*	0.653197907		
N. of notes	*Gymnasio nudipes*	0.651026573		
N. of notes	*M. petersoni*	0.675364562		
N. of notes	*M. roboratus*	0.692185713		
N. of notes	*M. roraimae*	0.681833582		
N. of notes	*M. sanctaecatarinae*	0.675021403		
N. of notes	*M. stangiae*	0.737428799		
N. of notes	*M. trichopsis*	0.598242003		

N. of notes	*M. usta*	0.729476824		
N. of notes	*M. watsonii*	0.819667883		
Phrase Dur.	28	0.640677333	0.501895796	0.77945887
Phrase Dur.	29	0.645688345	0.564688562	0.726688127
Phrase Dur.	30	0.681778736	0.63513188	0.728425593
Phrase Dur.	31	0.693502223	0.65021943	0.736785017
Phrase Dur.	32	0.71491435	0.663698572	0.766130128
Phrase Dur.	33	0.747806261	0.695532415	0.800080107
Phrase Dur.	34	0.801583615	0.766377785	0.836789445
Phrase Dur.	35	0.801575333	0.77085366	0.832297005
Phrase Dur.	36	0.798118728	0.768230083	0.828007373
Phrase Dur.	37	0.802446785	0.77141861	0.83347496
Phrase Dur.	38	0.694197269	0.650771252	0.737623285
Phrase Dur.	39	0.722547851	0.673849472	0.771246231
Phrase Dur.	40	0.790239436	0.742411651	0.838067221
Phrase Dur.	41	0.722161936	0.671947315	0.772376558
Phrase Dur.	42	0.722658996	0.672331431	0.77298656
Phrase Dur.	43	0.682448504	0.632444917	0.73245209
Phrase Dur.	44	0.668548722	0.616978699	0.720118746
Phrase Dur.	45	0.652049799	0.605073049	0.69902655
Phrase Dur.	46	0.674687778	0.626756285	0.722619271
Phrase Dur.	47	0.67042729	0.621266136	0.719588445
Phrase Dur.	48	0.657576215	0.605726022	0.709426409
Phrase Dur.	49	0.653496015	0.599315015	0.707677015
Phrase Dur.	50	0.632151096	0.55791479	0.706387402
Phrase Dur.	51	0.626590051	0.550313268	0.702866834
Phrase Dur.	52	0.614830987	0.570528305	0.65913367
Phrase Dur.	53	0.624430903	0.547792951	0.701068855
Phrase Dur.	*M. alagoensis*	0.813361761		
Phrase Dur.	*M. albogularis*	0.605752658		
Phrase Dur.	*M. asio*	0.643070273		
Phrase Dur.	*M. ater*	0.848756715		
Phrase Dur.	*M. atricapilla*	0.776837472		
Phrase Dur.	*M. barbarus*	0.696098024		
Phrase Dur.	*M. centralis*	0.609883135		
Phrase Dur.	*M. choliba*	0.605039317		
Phrase Dur.	*M. clarkii*	0.618168494		
Phrase Dur.	*M. colombianus*	0.859519996		
Phrase Dur.	*M. cooperi*	0.619410148		
Phrase Dur.	*M. gilesi*	0.62587434		
Phrase Dur.	*M. guatemalae*	0.693813299		
Phrase Dur.	*M. hoyi*	0.748005083		
Phrase Dur.	*M. ingens*	0.771624167		
Phrase Dur.	*M. kennicottii*	0.61849766		
Phrase Dur.	*M. koepckeae*	0.621950257		
Phrase Dur.	*M. marshalli*	0.697964457		
Phrase Dur.	*Gymnasio nudipes*	0.628602496		
Phrase Dur.	*M. petersoni*	0.716561268		
Phrase Dur.	*M. roboratus*	0.626196886		
Phrase Dur.	*M. roraimae*	0.662599048		
Phrase Dur.	*M. sanctaecatarinae*	0.655519781		
Phrase Dur.	*M. stangiae*	0.764715606		
Phrase Dur.	*M. trichopsis*	0.612795662		
Phrase Dur.	*M. usta*	0.842023534		
Phrase Dur.	*M. watsonii*	0.795170358		

Time 5%	28	0.610400992	0.427311048	0.793490937
Time 5%	29	0.643199108	0.536338744	0.750059473
Time 5%	30	0.691936129	0.630396457	0.753475802
Time 5%	31	0.703263967	0.646162392	0.760365541
Time 5%	32	0.7006883	0.633120998	0.768255601
Time 5%	33	0.710968823	0.642005648	0.779931999
Time 5%	34	0.745139587	0.698693686	0.791585487
Time 5%	35	0.750781523	0.710251425	0.791311621
Time 5%	36	0.799783765	0.760352652	0.839214877
Time 5%	37	0.741172344	0.700237887	0.782106801
Time 5%	38	0.706093269	0.648802745	0.763383793
Time 5%	39	0.71926237	0.65501619	0.78350855
Time 5%	40	0.741990969	0.678893336	0.805088601
Time 5%	41	0.720298572	0.654052064	0.78654508
Time 5%	42	0.727733746	0.661338236	0.794129257
Time 5%	43	0.715472293	0.649504196	0.78144039
Time 5%	44	0.746205102	0.678170457	0.814239748
Time 5%	45	0.768695226	0.706720336	0.830670117
Time 5%	46	0.686401887	0.623167435	0.749636339
Time 5%	47	0.68181293	0.616956226	0.746669634
Time 5%	48	0.664253462	0.595849197	0.732657727
Time 5%	49	0.659101087	0.587621865	0.730580309
Time 5%	50	0.63112875	0.533191219	0.729066281
Time 5%	51	0.622407602	0.521778136	0.723037068
Time 5%	52	0.644026034	0.585578953	0.702473114
Time 5%	53	0.632570543	0.531464598	0.733676487
Time 5%	*M. alagoensis*	0.752062709		
Time 5%	*M. albogularis*	0.762944094		
Time 5%	*M. asio*	0.710118528		
Time 5%	*M. ater*	0.703832075		
Time 5%	*M. atricapilla*	0.753014732		
Time 5%	*M. barbarus*	0.765352003		
Time 5%	*M. centralis*	0.752377282		
Time 5%	*M. choliba*	0.676445795		
Time 5%	*M. clarkii*	0.691341036		
Time 5%	*M. colombianus*	0.75466125		
Time 5%	*M. cooperi*	0.445167134		
Time 5%	*M. gilesi*	0.783658711		
Time 5%	*M. guatemalae*	0.65988674		
Time 5%	*M. hoyi*	0.685111988		
Time 5%	*M. ingens*	0.772058563		
Time 5%	*M. kennicottii*	0.692425847		
Time 5%	*M. koepckeae*	0.802532716		
Time 5%	*M. marshalli*	0.687613267		
Time 5%	*Gymnasio nudipes*	0.554437233		
Time 5%	*M. petersoni*	0.649168961		
Time 5%	*M. roboratus*	0.577056402		
Time 5%	*M. roraimae*	0.801691154		
Time 5%	*M. sanctaecatarinae*	0.684746948		
Time 5%	*M. stangiae*	0.7090773		
Time 5%	*M. trichopsis*	0.757614654		
Time 5%	*M. usta*	0.647744199		
Time 5%	*M. watsonii*	0.665082891		

Table S9. Summary of associations between acoustic traits and body mass in *Megascops* species, based on Phylogenetic Generalized Least Squares (PGLS) models. None of the 40 vocal variables tested showed significant correlation with body mass, indicating that body size is not a primary driver of acoustic variation in the genus.

Variable	Estimate	Std_Error	T_value	P_value
Frequency change (middle–final)	0.0002221	0.00025558	0.868912	0.3952
Frequency change (initial–middle)	0.0003511	0.00050021	0.701938	0.4908
Mean bandwidth of the central notes	0.0002553	0.00034394	0.742198	0.4666
Mean bandwidth of the final notes	3.09E-05	3.06E-05	1.01154	0.3238
Mean bandwidth of the initial notes	0.000251	0.00022768	1.102231	0.2834
Phrase bandwidth	0.0002043	0.00029118	0.701719	0.4909
Pace change (middle–final)	0.0005044	0.0007094	0.711024	0.4853
Pace change (initial–middle)	-0.0001791	0.00089486	-0.200164	0.8434
Mean interval duration of the central intervals	0.0001078	0.000148433	0.726524	0.4759
Mean interval duration of the final intervals	8.90E-05	0.000176088	0.505542	0.6187
Mean interval duration of the initial intervals	0.0001134	0.000167721	0.676128	0.5067
Mean note duration of the central notes	0.0002119	0.00032337	0.655349	0.5197
Mean note duration of the final notes	0.0001893	0.0003853	0.49126	0.6286
Mean note duration of the initial notes	0.0002833	0.00028863	0.981433	0.3381
Phrase duration	-3.52E-05	0.00046224	-0.076102	0.9401
Frequency 25%	-0.0001769	0.00058452	-0.302565	0.7653
Frequency 5%	-0.0003019	0.00058609	-0.515032	0.6122
Frequency 75%	-0.0001064	0.00058068	-0.183171	0.8565
Frequency 95%	-6.86E-05	0.00058529	-0.117216	0.9079
Mean maximum frequency of the central notes	-0.0001085	0.00062662	-0.173187	0.8642
Mean maximum frequency of the final notes	-9.00E-07	5.85E-05	-0.01593	0.9874
Mean maximum frequency of the initial notes	-0.0002186	0.00051931	-0.420875	0.6783
Phrase maximum frequency	-0.0001207	0.00051852	-0.232698	0.8184
Mean minimum frequency of the central notes	-8.88E-05	0.00036573	-0.242777	0.8107
Mean minimum frequency of the final notes	-8.16E-05	0.00033355	-0.244494	0.8093
Mean minimum frequency of the initial notes	-0.0004564	0.00052793	-0.864496	0.3976
Phrase minimum frequency	-0.0004077	0.00050948	-0.800193	0.433
Mean dominant frequency of the central notes	-0.0001427	0.00057521	-0.248143	0.8066
Mean dominant frequency of the final notes	-6.91E-05	0.00059173	-0.116722	0.9082
Mean dominant frequency of the initial notes	-0.0003078	0.00056273	-0.547011	0.5904
Phrase dominant frequency	-7.28E-05	0.00057165	-0.127376	0.8999
Number of notes	-0.0004106	0.00043391	-0.946324	0.3553
Overall pace	-0.0003325	0.00054387	-0.611274	0.5479
Central pace	-0.0003693	0.00055901	-0.660605	0.5164
Final pace	-0.0001846	0.00053733	-0.343643	0.7347
Initial pace	-0.000329	0.00058338	-0.563994	0.579
Time 25% relative	-0.0005826	0.00062419	-0.933409	0.3617
Time 5% relative	-0.0004538	0.0004982	-0.910874	0.3732
Time 75% relative	-0.0004248	0.00055077	-0.771264	0.4496
Time 95% relative	-0.0001207	0.00025012	-0.48248	0.6347

Figures

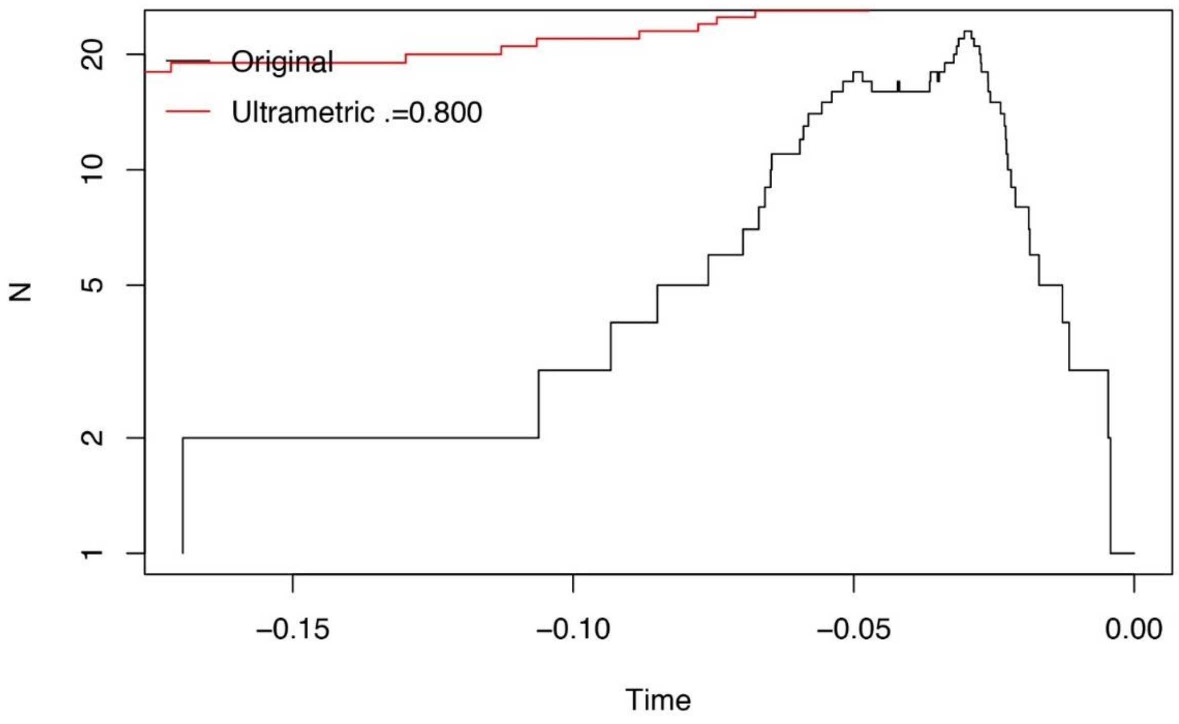

Figure S1. Lineage-through-time (LTT) plots comparing the original and ultrametric trees for the selected λ = 0.8.

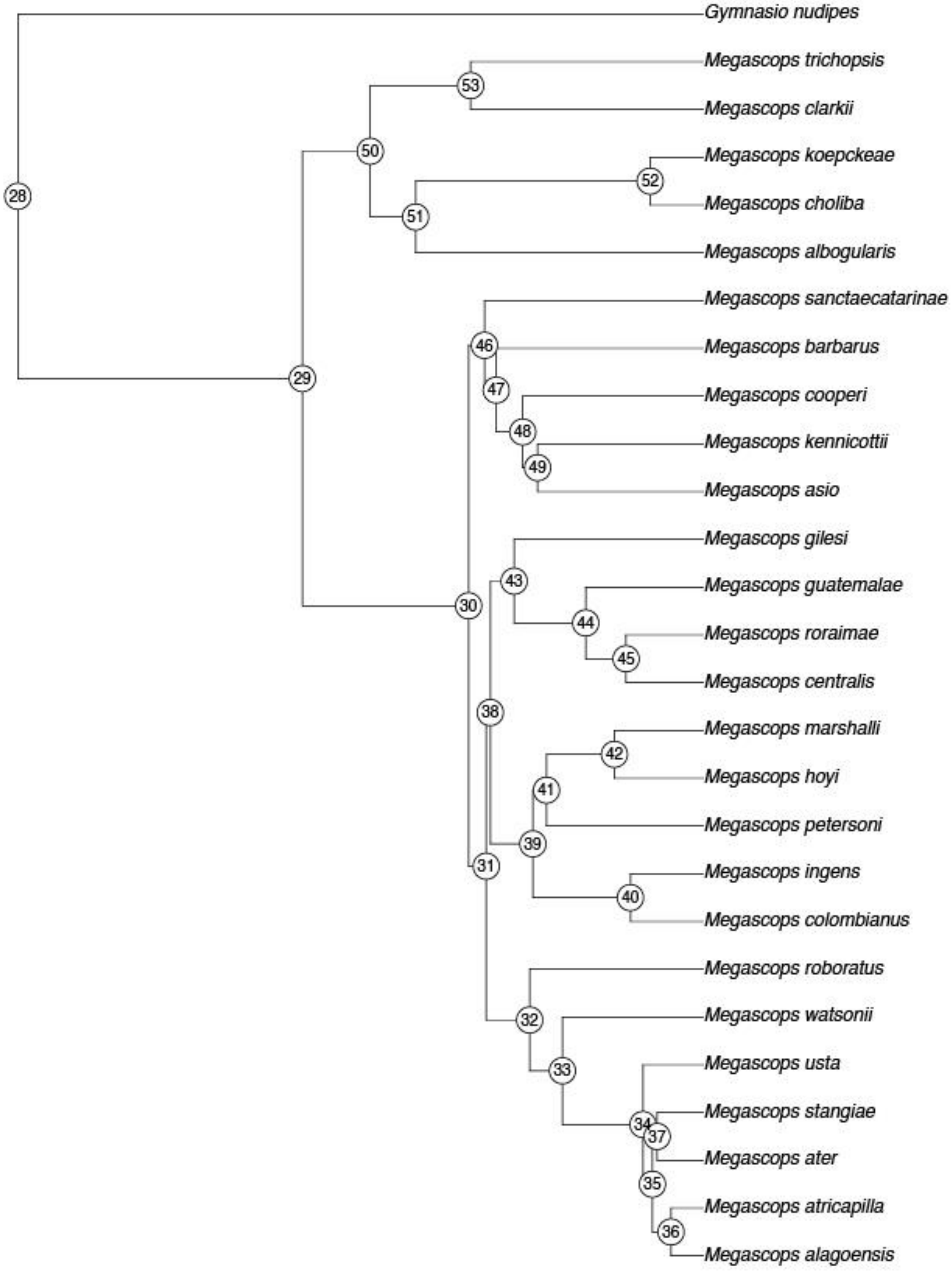

Figure S2. Phylogenetic tree of *Megascops* species showing node labels corresponding to the ancestral character estimation (ACE) results presented in Table S8. Terminal taxa represent extant species, while numbered circles indicate internal nodes used for ancestral state reconstruction.

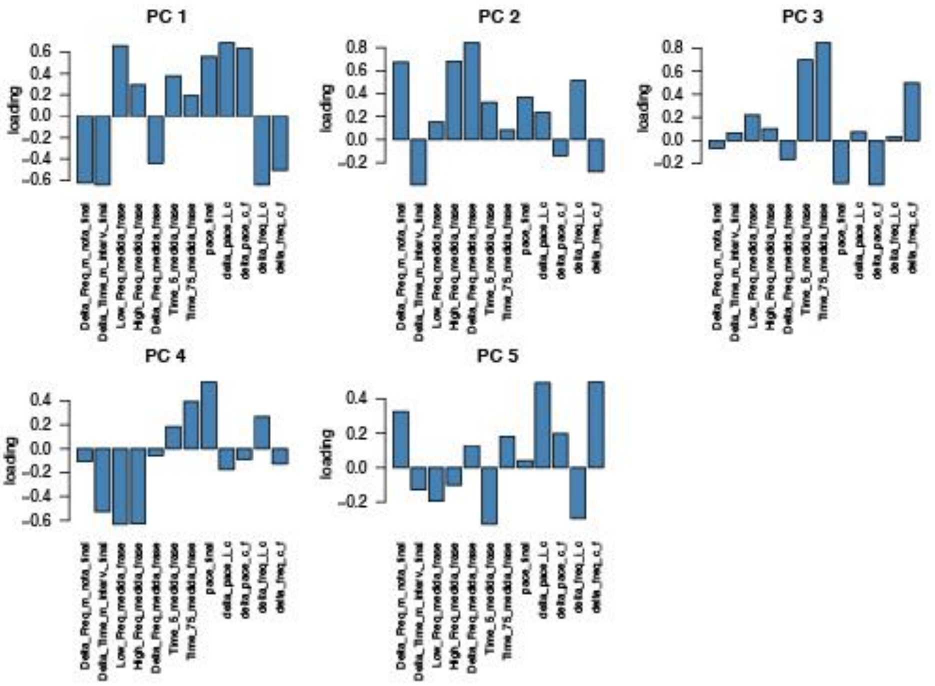

Figure S3. Loadings of the first five principal components from the phylogenetic Principal Component Analysis (pPCA). The pPCA was performed using the function *phyl.pca* in the *phytools* package with maximum-likelihood optimization of λ (Revell 2012). The first five components explained the majority of total variance.

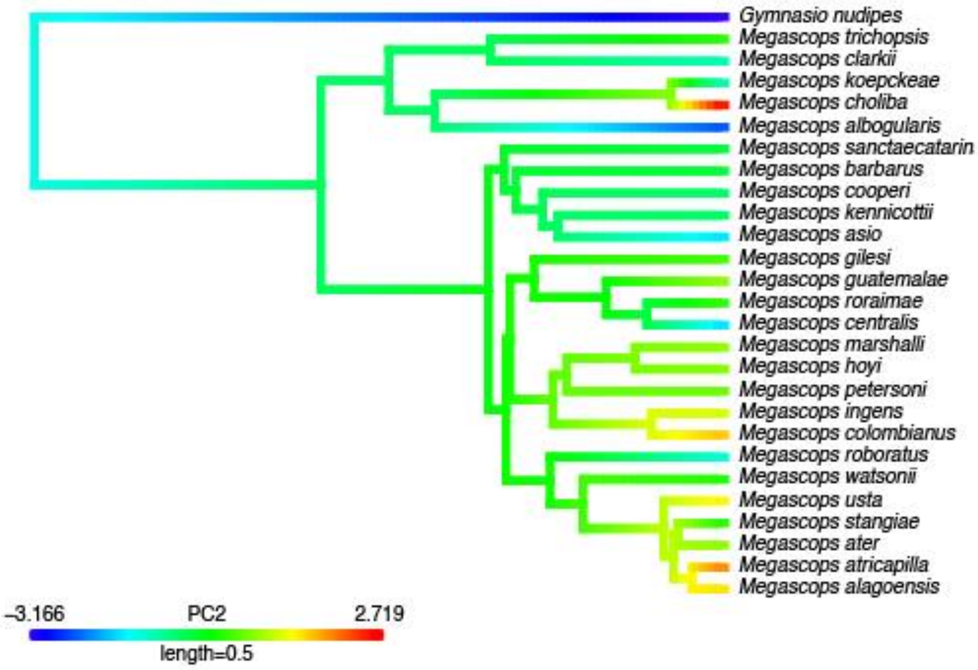

Figure S4. Phylogenetic reconstruction of PC2 scores from the phylogenetic Principal Component Analysis (pPCA) of *Megascops* primary-song traits. Branch colors represent ancestral state estimates of PC2, with warmer colors (yellow to red) indicating higher values and cooler colors (green to blue) indicating lower values. Phylogenetic reconstructions (PC2) revealed moderate structuring across *Megascops* clades

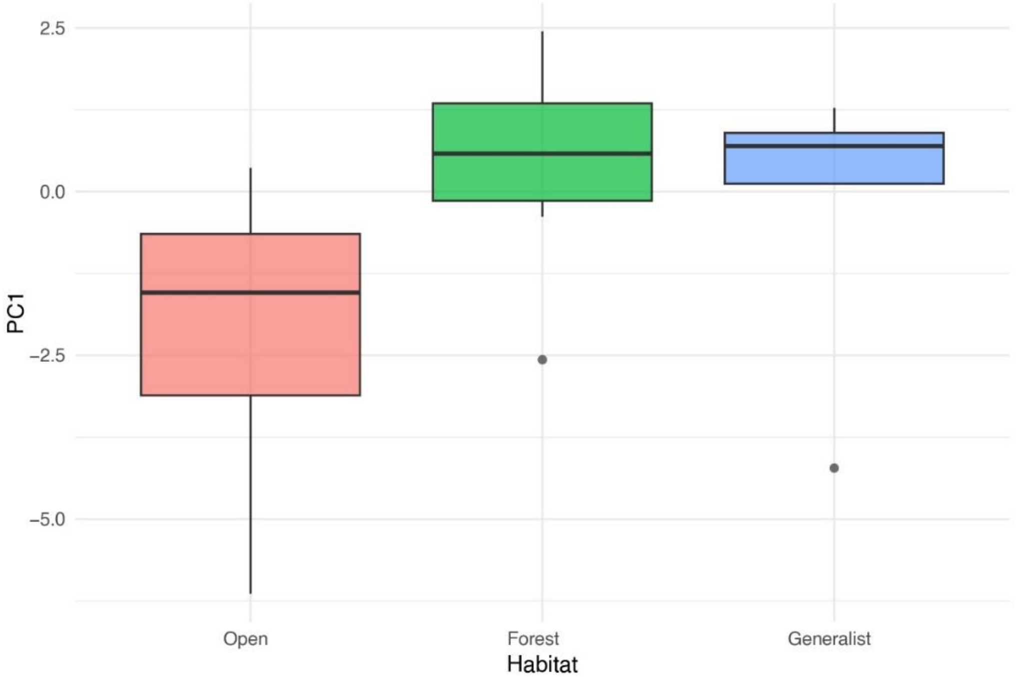

Figure S5. Variation in PC1 scores from the phylogenetic Principal Component Analysis (pPCA) of *Megascops* primary-song traits across habitat categories.

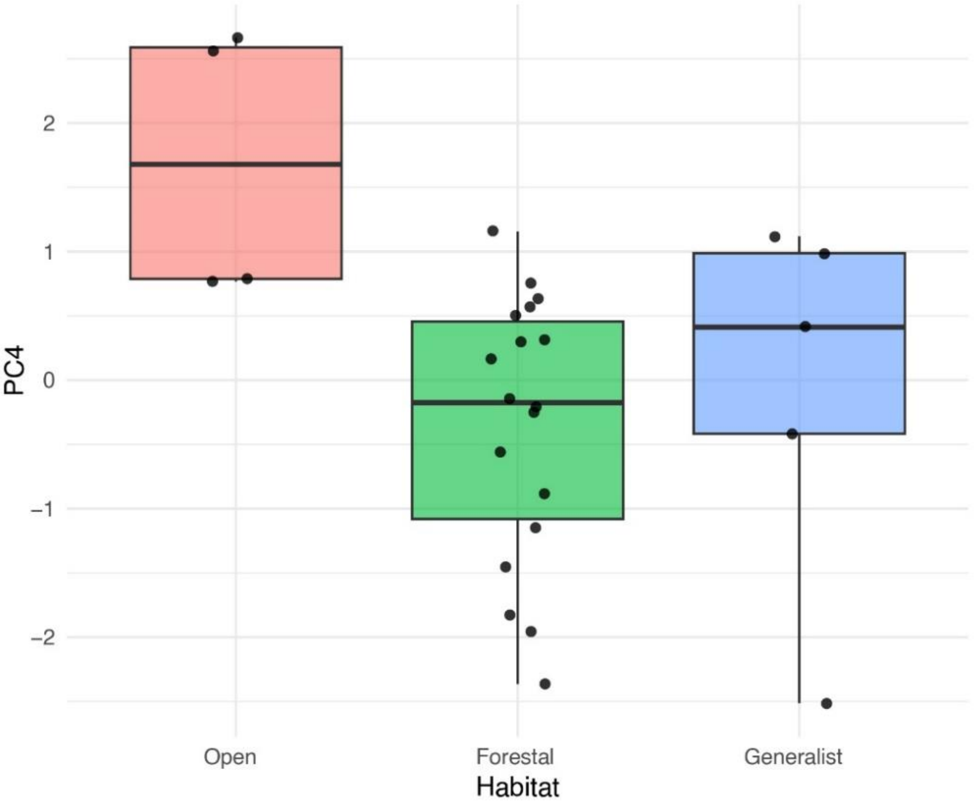

Figure S6. Variation in PC4 scores from the phylogenetic Principal Component Analysis (pPCA) of *Megascops* primary-song traits across habitat categories.