---

title: "Species sympatry shapes brain size evolution in Primates"

# date: "`r format(Sys.time(), '%B %d, %Y')`"

#I follow: https://stackoverflow.com/questions/52918716/authors-and-affiliations-in-the-yaml-of-rmarkdown for author display

author:

- name: Benjamin Robira

email: benjamin.robira@normalesup.org

institute: [CEFE, MH]

correspondence: true

- name: Benoît Perez-Lamarque

email: benoit.perez@ens.psl.eu

institute: [ENS, MNHN]

institute:

- CEFE: Centre d’Écologie Fonctionnelle et Évolutive, Université de Montpellier & CNRS, Montpellier, France.

- MH: Anthropologie et Ethnobiologie, Centre National de la Recherche Scientifique/Muséum National d'Histoire Naturelle, University Paris Diderot, Sorbonne Paris Cité, Musée de l'Homme, Paris, France.

- ENS: Institut de Biologie de l’École Normale Supérieure (IBENS), École Normale Supérieure, CNRS, INSERM, Université PSL, Paris, France.

- MNHN: Institut de Systématique, Évolution, Biodiversité (ISYEB), Muséum National d’Histoire Naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, Paris, France.

# output:

# # - '--lua-filter=scholarly-metadata.lua'

# # - '--lua-filter=author-info-blocks.lua'

# bookdown::pdf\_book:

# #bookdown::word\_document2:

# number\_sections: false

# toc: false

# #citation\_package: natbib

# latex\_engine: pdflatex

# fig\_caption: true

# pandoc\_args:

# - '--lua-filter=scholarly-metadata.lua'

# - '--lua-filter=author-info-blocks.lua'

#

# bibliography: bibliographyarticlepackage.bib

# csl: nature.csl

# #biblio-style: apa

# always\_allow\_html: true

# link-citations: yes

output:

# - '--lua-filter=scholarly-metadata.lua'

# - '--lua-filter=author-info-blocks.lua'

bookdown::pdf\_book:

#bookdown::word\_document2:

number\_sections: false

toc: false

citation\_package: biblatex

latex\_engine: pdflatex

fig\_caption: true

pandoc\_args:

- '--lua-filter=scholarly-metadata.lua'

- '--lua-filter=author-info-blocks.lua'

always\_allow\_html: true

bibliography: bibliographyarticlepackage.bib

biblio-style: nature

biblatexoptions: [natbib=true]

urlcolor: blue

filecolor: blue

linkcolor: blue

fontsize: 12pt

header-includes:

- \usepackage{lettrine}

# - \usepackage[nolists, nomarkers,tablesfirst]{endfloat} # For figures and tables at end

- \usepackage{lineno} # For line numbering

- \linenumbers # For line numbering

- \usepackage{setspace}\doublespacing

- \usepackage{fontawesome} #for fa symbols

- \usepackage{tcolorbox}

- \pagenumbering{gobble} #for no page numbering

- \setlength{\parskip}{0em} #to remove line gaps

- \DeclareUnicodeCharacter{2212}{-}

- \usepackage{caption}

- \captionsetup[figure]{font=small}

- \newcommand{\beginsupplement}{

\setcounter{table}{0}

\renewcommand{\thetable}{S\arabic{table}}

\setcounter{figure}{0}

\renewcommand{\thefigure}{S\arabic{figure}}

}

- \usepackage{titling}

- \pretitle{

\begin{flushleft}

\rule[-0.15in]{0.25\linewidth}{0.8ex}

\vspace{-0.8ex}

\hrule

\vspace{0.3in}

\begin{LARGE}

\noindent

\textbf

}

- \posttitle{

\end{LARGE}\newline

\rule[-0.15in]{0.25\linewidth}{0.8ex}

\hrule

\end{flushleft}

\vspace{0.2in}}

---

<!-- ------------------------------------------------------------------- -->

<!-- --------------------- LAYOUT --------------------------- -->

<!-- ------------------------------------------------------------------- -->

<!-- TO PUT THE LETTRINE -->

\newcommand{\initial}[1]{%

\lettrine[lraise=0, loversize=0.5,nindent=0em]{

\color{black}

{\textsc{#1}}}{}}

<!-- TO CREATE grey BOX -->

\newtcolorbox{graybox}{

colback=lightgray!25,

colframe=lightgray!25,

coltext=black,

boxsep=3pt,

arc=0pt}

<!-- ------------------------------------------------------------------- -->

<!-- ------------------------------------------------------------------- -->

<!-- ------------------------------------------------------------------- -->

```{r setup, include=FALSE, echo=FALSE, message=FALSE}

knitr::opts\_chunk$set(include=FALSE, echo=FALSE, message=FALSE)

knitr::opts\_chunk$set(dpi=300) # Figure resolution and size out.width = '100%',

knitr::opts\_chunk$set(fig.pos = 'p'#, fig.align = 'center'

) # Places figures on pages separate from text, centered

knitr::opts\_chunk$set(fig.env="figure") # Latex figure environment

knitr::opts\_knit$set(eval.after = "fig.cap") #To insert R code into R figure caption

```

<!-- TC:ignore -->

```{r, echo=FALSE, results= 'hide'}

#Import librairies

library(readr)

#Plot

library(RColorBrewer)

library(tidyr)

library(stringr)

library(svMisc)

library(plotrix)

library(circlize)

#Spatial

library(rworldmap) # World map

library(cleangeo) #to clean it otherwise issues with intersection

library(maps)

library(rgeos) #for readOGR; gArea/gCentroid...

library(sf) #for intersection

library(rgdal)

library(geosphere)

#Phylogeny

library(phytools)

library(ape)

library(phylolm)

#Segmentation

library(strucchange)

#Import own function

source("T:/Saved\_PhD/Empirical\_analysis/Scripts&Functions/Functions/toolbox.R", local = knitr::knit\_global())

#Create citation fusion between articles and package (based on toolbox function)

citeR(

bibliographyArticle="T:/Saved\_PhD/Library\_general/libraryMdf.bib",

bibliographyOutput="C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Article/bibliographyarticlepackage.bib",

rgeos,

geosphere,

phytools,

geiger,

RPANDA,

caper,

neurobase,

misc3d,

phylolm,

nlme,

MCMCglmm,

coda,

strucchange

)

#Load environments

load("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/REnvironments/Data\_spatial\_primate.RData")

load("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/REnvironments/geography\_traits\_biogeobears.RData")

load("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/REnvironments/PGLSdiversification\_withautocorr.RData")

load("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/REnvironments/PGLSdirectionSelection.RData")

load("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/REnvironments/PGLSdiversificationAndSympatry.RData")

```

\captionsetup{list=no}

\newpage

```{r wordCount}

words <- RmdWords("Article.Rmd")

```

:::: {.graybox data-latex=""}

\*\*Abstract |\*\* The main hypotheses related to animal intelligence evolution highlight the role of conspecifics. Yet, space is often simultaneously occupied by species sharing the same ecological guild. These sympatric heterospecifics can compete for food, thereby stimulating or hampering cognition. Considering brain size as a proxy for cognition, we used primates to test for the intertwining between species sympatry and cognition. We retraced the evolutionary history of several brain areas with evolutionary models considering or not sympatry. Sympatry-related models best predicted the evolution of brain areas related to long-term memory of interactions with the social or ecological environment, with a decrease of their size the higher the sympatry. By contrast, the whole brain or brain areas used in immediate information processing were best described by models not considering sympatry. Moreover, sympatry negatively affected primate diversification. Overall, this comparative study suggests that species sympatry contributes to shaping primate cognition and diversification. We speculate that this is due to an over-complexification of resource spatio-temporality.

\hfill

<!-- Reviewer possibles: Decasien, Powell, Barton, Kamilar, Harmon, Drury -->

\faTags \hspace{0.01in} \*\*Keywords:\*\* Brain size - Cognition - Competition - Co-occurrence - Diversification - Frugivory - Primates - Sympatry

\faInfoCircle \hspace{0.01in} \*\*Word Count:\*\* `r words$num\_words` \newline

<!-- Character Count: `r words$num\_char` -->

::::

\newpage

```{r sampleCalculation, warning = FALSE, message = FALSE}

###Set working directory

setwd("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates")

repetition=2\*2\*2\*10#length(frugivoryThresholdVector)\*length(folivoryThresholdVector)\*length(geographicThresholdVector)\*randomSampling

checkSampleFruit <- rep(NA, times=repetition)

checkSampleLeaf <- rep(NA, times=repetition)

checkSampleRange <- rep(NA, times=repetition)

checkSampleBrain <- rep(NA, times=repetition)

checkSampleEQ <- rep(NA, times=repetition)

checkSampleNeocortex <- rep(NA, times=repetition)

checkSampleHippocampus <- rep(NA, times=repetition)

checkSampleCerebellum <- rep(NA, times=repetition)

checkSampleStriatum <- rep(NA, times=repetition)

checkSampleMOB <- rep(NA, times=repetition)

checkSampleRange <- rep(NA, times=repetition)

counter=0

for(a in 1:2){

for(b in 1:2){

for(c in 1:2){

for(d in 1:10){

counter=counter+1

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleFruit",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleFruit[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleLeaf",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleLeaf[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleRange",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleRange[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleBrain",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleBrain[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleEQ",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleEQ[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleNeocortex",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleNeocortex[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleHippocampus",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleHippocampus[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleCerebellum",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleCerebellum[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleStriatum",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleStriatum[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/Sample\_size/checkSampleMOB",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

checkSampleMOB[counter] <- toAdd[1]

}, error=function(e){

#Do nothing

}

)

}

}

}

}

checkSampleFruit <- unlist(checkSampleFruit)

checkSampleLeaf <- unlist(checkSampleLeaf)

checkSampleRange <- unlist(checkSampleRange)

checkSampleBrain <- unlist(checkSampleBrain)

checkSampleEQ <- unlist(checkSampleEQ)

checkSampleNeocortex <- unlist(checkSampleNeocortex)

checkSampleHippocampus <- unlist(checkSampleHippocampus)

checkSampleCerebellum <- unlist(checkSampleCerebellum)

checkSampleStriatum <- unlist(checkSampleStriatum)

checkSampleMOB <- unlist(checkSampleMOB)

#Min values

minFruit <- min(checkSampleFruit)

minLeaf <- min(checkSampleLeaf)

minRange <- min(checkSampleRange)

minBrain <- min(checkSampleBrain)

minEQ <- min(checkSampleEQ)

minNeocortex <- min(checkSampleNeocortex)

minHippocampus <- min(checkSampleHippocampus)

minCerebellum <- min(checkSampleCerebellum)

minStriatum <- min(checkSampleStriatum)

minMOB <- min(checkSampleMOB)

minAllAreas <- min(

minEQ,

minNeocortex,

minHippocampus,

minCerebellum,

minStriatum,

minMOB

)

#Max values

maxFruit <- max(checkSampleFruit)

maxLeaf <- max(checkSampleLeaf)

maxRange <- max(checkSampleRange)

maxBrain <- max(checkSampleBrain)

maxEQ <- max(checkSampleEQ)

maxNeocortex <- max(checkSampleNeocortex)

maxHippocampus <- max(checkSampleHippocampus)

maxCerebellum <- max(checkSampleCerebellum)

maxStriatum <- max(checkSampleStriatum)

maxMOB <- max(checkSampleMOB)

maxAllAreas <- max(

maxEQ,

maxNeocortex,

maxHippocampus,

maxCerebellum,

maxStriatum,

maxMOB

)

```

<!-- TC:endignore -->

# Introduction

<!-- On the road to brain size evolution, generally considered as an equivalent of cognition evolution, mysteries are plenty [@van2006some; @dunbar2017there]. Overall, the evolution of the brain is the consequence of constraints (e.g. energetic limitations, @navarrete2011energetics), but also of socio-ecological drivers promoting cognitive abilities [@gonzalez2018inference]. -->

<!-- Primates are pivotal species to study the evolution of cognition given the complexity of their socio-ecological environment and the inevitable implication for retracing human evolutionary history [@byrne2000evolution]. -->

<!-- \initial{\textcolor{black}{C}}ognition evolution results from the balance between socio-ecological drivers promoting cognitive abilities [@gonzalez2018inference] and physiological and energetic constraints [@navarrete2011energetics]. Primates are pivotal species for cognitive studies [@byrne2000evolution] because their cognition is thought to be promoted by interactions of individuals with conspecifics within the social unit [@byrne1994machiavellian; @dunbar2017there], among generations [@wilson1991molecular; @whiten2007evolution; @reader2002social; @herrmann2007humans; @tomasello2009cultural; @van2011social], between social units [@ashton2020interactions], or with the rest of their environment [@clutton1980primates; @milton1981distribution; @rosati2017foraging]. However, space is a place often occupied by many species belonging to the same ecological guild and we can predict that such interactions with sympatric heterospecifics are also likely to strongly shape the evolution of cognition. -->

<!-- | Retracing the evolutionary history of cognitive abilities proves to be challenging because there is still no consensual measurement applicable across all species. Up to now, a raw approximation consists in considering brain size as a proxy for cognitive abilities (but see discussion in @logan2018beyond). Yet, the brain is a mosaic of areas cognitively specialized [@barton2000mosaic] and these areas are likely to be differently affected by species sympatry. For instance, the Main Olfactory Bulb (MOB) or the Hippocampus , home of a spatio-temporal memory [@burgess2002human], are largely involved in efficient foraging, especially for frugivorous primates, as fruits are the archetype of a hard-to-find resource yet predictable [@janmaat2016spatio; @robirabotany]: we therefore expect that primate species with larger MOB or Hippocampus areas, taken as equivalent to more advanced perceptive and cognitive abilities for efficient foraging, might be more fit than their sympatric species with smaller areas. Similarly, the Striatum underpins reward expectation and action, goal-directed behaviour and planning abilities [@johnson2007integrating] which is key when foraging. -->

<!-- are expected to be influenced by the ecological environment. The Striatum is also stimulated during social interactions [@baez2013role]: its size is thus expected to be positively influenced when contacts with other species increase, as in species performing mixed-species groups, which is nonetheless rather infrequent in primates (but see callitrichine primates in particular, @heymann2015unlike). Finally, besides foraging-related areas (Striatum, MOB or Hippocampus), more generally-used areas, such as the Cerebellum [@koziol2014consensus; @sokolov2017cerebellum] and the Neocortex [@wiltgen2004new] underlying movement and/or general information processing and retention, could also be stimulated by the presence of other species movement traces, noises or odors to decode. To sum up, a first possibility is that sympatric heterospecifics could altogether stimulate cognition and promote larger sizes of the brain areas related to interacting with the social or ecological environment. -->

<!-- | However, if the changes induced by sympatric species increases the environmental unpredictability too much, sympatry could on the contrary change the selective pressure applying to cognitive abilities [@grove2013evolution: @robirainreview]. Indeed, due to the cost of maintaining the brain functional [@raichle2006brain], it is expected that the increase in environmental unpredictability only stimulates cognition up to a certain threshold (i.e. positive selection for bigger brain), before smaller brain sizes of foraging-related areas become more adaptive (because costs are no longer compensated by the benefit of memory). Similarly, it is possible that processing heterospecifics cues, and other environmental cues (e.g. phenology cues) might not necessitate the same cognition level, with the former being potentially simpler to process (since relying on easily accessible social cues) than the latter (relying on trial-and-error processes and personal experience of potentially elusive environmental cues) [@laland2004social]. In this case, the size of brain areas involved in immediate information processing should be less large in sympatric than in non-sympatric conditions. To sum up, a second possibility is that sympatric heterospecifics could hamper the benefits of cognition on foraging, and thus slowdown brain size increase. In an extreme case, it could even induce positive selection for smaller brain size. -->

<!-- | Here, we investigated the intertwine between species sympatry and cognition using frugivorous primates as study example. To infer the effect of species interactions on brain size evolution within frugivorous primates, we evaluated support for competitive or non-competitive evolutionary scenarios, accounting or not for sympatry, and investigated the directionality of the selection induced by sympatry history upon brain size evolution. Finally, we tested for correlative patterns between brain size or current sympatry with the evolutionary success (species diversification) in primates. -->

\initial{\textcolor{black}{C}}ognition evolution is shaped by the balance between socio-ecological drivers promoting cognitive abilities [@gonzalez2018inference] and physiological and energetic constraints limiting them [@navarrete2011energetics]. Primates are pivotal species for cognitive studies [@byrne2000evolution] because their cognition is thought to be promoted by interactions of individuals with conspecifics within the social unit [@byrne1994machiavellian; @dunbar2017there], among generations [@wilson1991molecular; @whiten2007evolution; @reader2002social; @herrmann2007humans; @tomasello2009cultural; @van2011social], between social units [@ashton2020interactions], or with the rest of their environment [@clutton1980primates; @milton1981distribution; @rosati2017foraging]. However, space is often occupied by many species belonging to the same ecological guild. Because of competition for food, we can predict that indirect interactions with sympatric heterospecifics are also likely to strongly shape the evolution of cognition, because they either affect the resource landscape by depleting it (Hypothesis 1), or the landscape of usable “social” cues to locate available food ([@Avargues-Weber2013]; Hypothesis 2). In addition, direct interactions with heterospecifics, as much as with conspecifics [@dunbar2017there], might also affect cognition (Hypothesis 3).

| Retracing the evolutionary history of cognitive abilities proves to be challenging because there is still no consensual measurement applicable across all species. Up to now, a raw approximation consists in considering brain size as a proxy for cognitive abilities, with larger size considered equivalent to more advanced cognitive abilities [@Benson-Amram2016]. Yet, the brain is a mosaic of areas cognitively specialized [@barton2000mosaic]. These areas are likely to be under different selective pressures, and thus, to follow different evolutionary paths. In particular, they might be differently affected by species sympatry. First, brain areas involved in the storing of spatio-temporal information, such as the Hippocampus, home of an associative memory used for spatio-temporal navigation [@burgess2002human], should in particular be affected if the resource landscape is complexified by sympatric species foraging on the same resource (Hypothesis 1: memory is affected). Second, brain areas involved in processing more immediate sensory information, such as the Main Olfactory Bulb (MOB), Cerebellum [@koziol2014consensus; @sokolov2017cerebellum], and the Neocortex [@wiltgen2004new] should be particularly affected if the landscape of cues varies with sympatry (Hypothesis 2: cue processing is affected). Besides individual foraging, cognition can also be triggered by direct "social" interactions with other individuals [@byrne1994machiavellian; @dunbar2017there]. The Striatum is a brain area stimulated during social interactions [@baez2013role], and should, therefore, be affected by direct social interactions with heterospecifics (Hypothesis 3).

| Under these (non-exclusive) hypotheses, sympatry could stimulate or hamper cognition evolution. Reasonable food depletion should promote memory, which stands as a valuable tool to infer food availability and location when food is rare and ephemeral but predictable [@milton1981distribution; @rosati2017foraging]. In this case, the size of the Hippocampus should be larger the higher the sympatry (Prediction 1.1). On the other hand, maintaining a functional brain is energetically costly [@raichle2006brain], and if changes induced by sympatric species increase environmental unpredictability too much, which would make cognitive foraging not advantageous anymore [@grove2013evolution; @robirainreview], the Hippocampus size should be smaller the higher the sympatry (Prediction 1.2). In the meanwhile, "social" cues left out by heterospecifics might also add to environmental ones. If species sympatry increases the load of usable cues to locate available food, we should then expect larger sizes of the MOB, the Cerebellum, or the Neocortex. Interactions between species can also occur directly, with the formation of mixed-group species [@Goodale2010]. This, in particular, should promote larger Striatum size in sympatry.

| Here, we investigated the intertwining between species sympatry and cognition using frugivorous primates as a study example. Frugivorous primates are an interesting group for such a question because fruits are the archetype of a hard-to-find resource yet predictable [@janmaat2016spatio], for which cognition thus considerably shapes the foraging strategy [@trapanese2019and]. To infer the effect of species sympatry on brain size evolution within frugivorous primates, we evaluated the support for evolutionary models accounting or not for sympatry, and investigated the directionality of the selection induced by sympatry history upon brain size evolution. Finally, we investigated the evolutionary of the intertwine between brain size and sympatry, by testing for correlative patterns between brain size or current sympatry and the species diversification in all primates.

# Results

```{r calculationValueForFirstResults}

#Import data

summaryDataForPlot <- read\_delim("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/OutputEvolModel/Dataplot.txt","\t", escape\_double = FALSE, trim\_ws = TRUE)

summaryDataForPlot <- summaryDataForPlot[!is.na(summaryDataForPlot$geographicCode),]

# summaryDataForPlot <- summaryDataForPlot[summaryDataForPlot$DietaryGuild=="Fruit",]

summaryDataForPlot$Family <- Data\_powell2$MSW05\_Family[match(summaryDataForPlot$Species\_abbrv,Data\_powell2$Species\_abbrv)]#summaryData$Family[match(summaryDataForPlot$Species\_abbrv, summaryData$Species\_abbrv)]

summaryDataForPlot[is.na(summaryDataForPlot$Family ),c(1,2,3)]

#summaryDataForPlot$SpeciesForPhylogeny[which(is.na(summaryDataForPlot$Family))]

summaryDataForPlot$Family[summaryDataForPlot$Species\_abbrv=="Galagoides\_demi"]<-"Galagonidae"

summaryDataForPlot$Family[summaryDataForPlot$Species\_abbrv=="Macaca\_munz"]<-"Cercopithecidae"

summaryDataForPlot$Family[summaryDataForPlot$Species\_abbrv=="Microcebus\_mitt"]<-"Cheirogaleidae"

summaryDataForPlot$Family[summaryDataForPlot$Species\_abbrv=="Mirza\_zaza"]<-"Lorisidae"

summaryDataForPlot$Family[summaryDataForPlot$Species\_abbrv=="Nycticebus\_java"]<-"Galagonidae"

summaryDataForPlot$Family[summaryDataForPlot$Species\_abbrv=="Tarsius\_lari"]<-"Tarsiidae"

lemuriformes.v <-

c(

"Daubentoniidae",

"Lemuridae",

"Indriidae",

"Cheirogaleidae",

"Lepilemuridae"

)

platyrrhini.v <- c(

"Atelidae",

"Aotidae",

"Pitheciidae",

"Cebidae"

)

meanseMOBlemu <- round(c(

mean(

(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %in% lemuriformes.v],

na.rm=TRUE),

sd(

(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %in% lemuriformes.v],

na.rm=TRUE)/

sqrt(

length(

(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %in% lemuriformes.v &

!is.na(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass)]))

), digit=2)

meanseMOBother <- round(c(

mean(

(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %nin% lemuriformes.v],

na.rm=TRUE),

sd(

(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %nin% lemuriformes.v],

na.rm=TRUE)/

sqrt(

length(

(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %nin% lemuriformes.v &

!is.na(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass)]))

), digit=2)

meanseStriatumplaty <- round(c(

mean(

(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %in% platyrrhini.v],

na.rm=TRUE),

sd(

(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %in% platyrrhini.v],

na.rm=TRUE)/

sqrt(

length(

(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %in% platyrrhini.v &

!is.na(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass)]))

), digit=2)

meanseStriatumother <- round(c(

mean(

(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %nin% platyrrhini.v],

na.rm=TRUE),

sd(

(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %nin% platyrrhini.v],

na.rm=TRUE)/

sqrt(

length(

(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass)[summaryDataForPlot$Family %nin% platyrrhini.v &

!is.na(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass)]))

), digit=2)

# summaryDataForPlot[order(summaryDataForPlot$MOB/summaryDataForPlot$Bodymass, decreasing = TRUE),]

# summaryDataForPlot[order(summaryDataForPlot$Hippocampus/summaryDataForPlot$Bodymass, decreasing = TRUE),]

# summaryDataForPlot[order(summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass, decreasing = TRUE),]

```

We gathered a large database on the whole brain size, the size of the MOB, Cerebellum, and the Neocortex, involved in immediate sensory information processing, and the Striatum and the Hippocampus, related to either social and foraging-related memory, containing between `r minAllAreas` to `r maxEQ` frugivorous primate species (depending on the brain area considered). After pondering by whole-body mass, we observed ample variations in brain area relative sizes. For instance, the lemuriformes, that are known to prioritize smell compared to other primate species, have the largest relative MOB size (Lemuriformes: mean $\pm$ SE = `r meanseMOBlemu[1]` $\pm$ `r meanseMOBlemu[2]`, other: `r meanseMOBother[1]` $\pm$ `r meanseMOBother[2]`, \@ref(fig:figbrain)). Similarly, platyrrhini, and callitrichine primates in particular, are known to form poly-specific associations [@heymann2000behavioural]. The latter show the highest relative size of the Striatum (Platyrrhini: mean $\pm$ SE = `r meanseStriatumplaty[1]` $\pm$ `r meanseStriatumplaty[2]`, other: `r meanseStriatumother[1]` $\pm$ `r meanseStriatumother[2]`, \@ref(fig:figbrain)).

| To get the evolutionary history of species sympatry between frugivorous lineages, we first reconstructed primate biogeography history (N$\_{species}$ = `r minRange`; [@matzke2013probabilistic; @matzke2016stochastic]) when considering `r length(areaName)` biogeographic areas (Figure \@ref(fig:figmap); [@kamilar2009environmental]) and their diet evolution (N$\_{species}$ = `r minFruit + minLeaf` to `r maxFruit + maxLeaf`; [@bollback2006simmap]). We then calculated the likelihoods of models considering the role of species sympatry in the evolution of either the whole brain (using the encephalic quotient, EQ), or the size of the aforementioned specific brain areas relative to the whole-body mass (Figure. \@ref(fig:figbrain)). We specifically considered the matching competition (MC) model [@nuismer2015predicting] and density dependence models (DD$\_{lin}$ and DD$\_{exp}$), which assume a linear or exponential dependence of the brain sizes evolutionary rates on the number of sympatric lineages ([@drury2016estimating] see [Models of trait evolution: does species sympatry shape brain size evolution?]). We compared the support of models considering species sympatry to the support of simpler models assuming no effect of species sympatry, like the Brownian Motion (BM), the Ornstein-Uhlenbeck process (OU) considering that traits are constrained around an optimal value (e.g. stabilizing selection; see [@blomberg2020beyond] for a review), or the Early-Burst model (EB, [@blomberg2003testing]), the latter allowing to check for a time-dependence of the evolutionary rate, hence emphasizing that, if any, the density dependence is not an artefact due to time dependence. Support for each model was evaluated using an information-theoretic framework [@burnham2002model] based on the weights of the Akaike Information Criteria corrected for small samples (AICc) when considering all six models (MC, DD$\_{lin}$, DD$\_{exp}$, BM, OU, EB, see [Models of trait evolution: does species sympatry shape brain size evolution?]).

| We found that models not considering species sympatry were the most likely in describing the evolutionary history of the EQ, the Neocortex, and the Cerebellum (Figure \@ref(fig:figbrain) and \@ref(fig:figresultsevolution)), two areas specifically involved in immediate sensory information processing [@wiltgen2004new; @koziol2014consensus; @sokolov2017cerebellum], and also in memory consolidation for the Neocortex [@wiltgen2004new]. The fact that these biggest areas are best described by the Ornstein-Uhlenbeck process suggests a stabilization towards an optimal size, which may illustrate the trade-offs between costs and benefits of brain development [@isler2009expensive]. By contrast, density-dependence models considering sympatry were best supported in the foraging-related and social-related areas respectively: the Hippocampus, specialised in spatio-temporal memory [@burgess2002human] and the Striatum, involved in social interactions [@baez2013role]. The fact that we inferred positive rates \*r\* of density-dependence (Figure \@ref(fig:figresultsevolution)) suggested an acceleration of the evolutionary tempo of trait evolution together with increased diversity of sympatric lineages for the Hippocampus and the Striatum. The Main Olfactory Bulb (MOB), the area involved in sensory abilities, also tended to be best fitted by models considering sympatry as a whole: yet, Brownian-Motion was as likely as density-dependent or MC models, preventing firm conclusions on whether sympatry affected or not MOB size evolution (Figure \@ref(fig:figbrain) and \@ref(fig:figresultsevolution)).

```{r samplecooccurrence}

minNspeciesCoocc <- round(min(dataRangePrimate$Number\_species\_cooccurrence, na.rm=TRUE), digit=2)

maxNspeciesCoocc <- round(max(dataRangePrimate$Number\_species\_cooccurrence, na.rm=TRUE), digit=2)

meanNspeciesCoocc <- round(mean(dataRangePrimate$Number\_species\_cooccurrence, na.rm=TRUE), digit=2)

seNspeciesCoocc <- round(sd(dataRangePrimate$Number\_species\_cooccurrence, na.rm=TRUE)/sqrt(length(dataRangePrimate$Number\_species\_cooccurrence[!is.na(dataRangePrimate$Number\_species\_cooccurrence)])), digit=2)

whichSpeciesMinNCoocc <- paste(sort(dataRangePrimate$Species[which(round(dataRangePrimate$Number\_species\_cooccurrence, digit=2)==minNspeciesCoocc)]), collapse=", ")

whichSpeciesMaxNCoocc <- paste(sort(dataRangePrimate$Species[which(round(dataRangePrimate$Number\_species\_cooccurrence, digit=2)==maxNspeciesCoocc)]), collapse=", ")

whichSpeciesMinNCoocc <- gsub("\_", " ", whichSpeciesMinNCoocc)

whichSpeciesMaxNCoocc <- gsub("\_", " ", whichSpeciesMaxNCoocc)

minOverlapSpecies <- round(min(dataRangePrimate$Overlap\_average, na.rm=TRUE), digit=2)

maxOverlapSpecies <- round(max(dataRangePrimate$Overlap\_average, na.rm=TRUE), digit=2)

meanOverlap <- round(mean(dataRangePrimate$Overlap\_average, na.rm=TRUE), digit=2)

seOverlap <- round(sd(dataRangePrimate$Overlap\_average, na.rm=TRUE)/sqrt(length(dataRangePrimate$Overlap\_average[!is.na(dataRangePrimate$Overlap\_average)])), digit=2)

whichSpeciesMinOverlap <- paste(dataRangePrimate$Species[which(round(dataRangePrimate$Overlap\_average, digit=2)==minOverlapSpecies)], collapse=", ")

whichSpeciesMaxOverlap <- paste(dataRangePrimate$Species[which(round(dataRangePrimate$Overlap\_average, digit=2)==maxOverlapSpecies)], collapse=", ")

whichSpeciesMinOverlap <- gsub("\_", " ", whichSpeciesMinOverlap)

whichSpeciesMaxOverlap <- gsub("\_", " ", whichSpeciesMaxOverlap)

```

```{r estimateRegGradient, error=TRUE, include=TRUE}

#Hippocampus

model <- get(paste("modelBrain", traitName[3], sep="\_"))

estimateGradientHippocampus <- textEstOneVar(summary(model)$coefficients[2,c(1,4,5)])

testGradientHippocampus <- textTestOneVar(summary(model)$coefficients[2,c(3,6)], statistics="")

#Striatum

model <- get(paste("modelBrain", traitName[6], sep="\_"))

estimateGradientStriatum <- textEstOneVar(summary(model)$coefficients[2,c(1,4,5)])

testGradientStriatum <- textTestOneVar(summary(model)$coefficients[2,c(3,6)], statistics="")

#MOB

model <- get(paste("modelBrain", traitName[7], sep="\_"))

estimateGradientMOB <- textEstOneVar(summary(model)$coefficients[2,c(1,4,5)])

testGradientMOB <- textTestOneVar(summary(model)$coefficients[2,c(3,6)], statistics="")

```

| Next, to understand the effect of sympatry on brain sizes (i.e. toward “bigger” or “smaller” brains the more sympatric species), we fitted phylogenetic regressions (see [Phylogenetic regressions] a)). For these linear regressions, the predicted variable was the relative brain size values of the different areas. We considered as covariates the average percentage of overlapping range with other sympatric frugivorous species, as well as the number of such sympatric frugivorous species across their entire distribution range based on IUCN data [@IUCN]. On average ($\pm$ SE), the considered primate species had `r meanOverlap\*100`% of their range overlapping with other species ($\pm$ `r seOverlap\*100`). That ranged from `r minOverlapSpecies\*100`% of overlap (\*`r whichSpeciesMinOverlap`\*), to `r maxOverlapSpecies\*100`% of overlap (\*`r whichSpeciesMaxOverlap`\*). In terms of the distribution range, the considered primate species co-occurred on average with `r meanNspeciesCoocc` other primate species ($\pm$ `r seNspeciesCoocc`), ranging from `r minNspeciesCoocc` other species to `r maxNspeciesCoocc`. The number of sympatric species never influenced significantly the relative size of the brain or other specific areas (Table \@ref(tab:tableRegGradient)). Conversely, we found that the average percentage of overlapping range correlated with the relative size of brain areas that were better fit with models considering sympatry: the Hippocampus and the Striatum (Hippocampus: $t$`r testGradientHippocampus`; Striatum: $t$`r testGradientStriatum`). The correlations were all negative (Hippocampus: `r estimateGradientHippocampus`; Striatum: `r estimateGradientStriatum`), which means that higher range overlap between frugivorous species associates with lower relative size, insensitive to data and phylogenetic uncertainty (Table \@ref(tab:tabledfsensitivity), Figure \@ref(fig:forestPlot)). Given the acceleration of the evolutionary tempo with species sympatry ($r>0$ in the density-dependence models), it suggests that compared with isolated species, sympatric species are subject to a positive selection towards smaller brains, and not to a less intense selection for advanced cognitive abilities.

```{r estimateRegDiversification, error=TRUE, include=TRUE}

#print(traitName)

# increaseHippocampus <- round(exp(summary(model)$coefficients[2,c(1)]), digit=2)

# averageDivRateHippocampus <- round(exp(summary(model)$coefficients[1,c(1)]), digit=2)

# estimateHippocampus <- textEstOneVar(summary(model)$coefficients[2,c(1,4,5)])

# testHippocampus <- textTestOneVar(summary(model)$coefficients[2,c(3,6)], statistics="")

#

# #Neocortex

# model <- get(paste("modelBrainDiversification", traitName[4], sep="\_"))

#

# increaseNeocortex <- round(exp(summary(model)$coefficients[2,c(1)]), digit=2)

# averageDivRateNeocortex <- round(exp(summary(model)$coefficients[1,c(1)]), digit=2)

# estimateNeocortex <- textEstOneVar(summary(model)$coefficients[2,c(1,4,5)])

# testNeocortex <- textTestOneVar(summary(model)$coefficients[2,c(3,6)], statistics="")

#

# #Striatum

# model <- get(paste("modelBrainDiversification", traitName[6], sep="\_"))

#

# increaseStriatum <- round(exp(summary(model)$coefficients[2,c(1)]), digit=2)

# averageDivRateStriatum <- round(exp(summary(model)$coefficients[1,c(1)]), digit=2)

# estimateStriatum <- textEstOneVar(summary(model)$coefficients[2,c(1,4,5)])

# testStriatum <- textTestOneVar(summary(model)$coefficients[2,c(3,6)], statistics="")

#print(c(increaseStriatum, averageDivRateStriatum, estimateStriatum, testStriatum))

```

```{r determineBoomTime}

###-----

## Diversification evolution over time

fraction.v <- c(60, 70, 80, 90, 95)

table\_MAPS\_rates\_time <- c()

for (f in fraction.v){

table\_MAPS\_rates\_time\_transitory <- read.table(paste0("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Scripts/Analysis3\_diversification/diversification/MAPS\_speciation\_rates\_trought\_time\_ClaDS2\_tree\_primate\_complete\_f",f,".csv"),sep=";",header=T)###Hahah nice English Benoit, trought ;)

table\_MAPS\_rates\_time\_transitory$f <- f

table\_MAPS\_rates\_time <- rbind(table\_MAPS\_rates\_time, table\_MAPS\_rates\_time\_transitory)

}

aggregatedSpeciationTime.mean <- aggregate(table\_MAPS\_rates\_time$speciation\_rates, by = list(table\_MAPS\_rates\_time$time), FUN = mean)

aggregatedSpeciationTime.sd <- aggregate(table\_MAPS\_rates\_time$speciation\_rates, by = list(table\_MAPS\_rates\_time$time), FUN = sd)

colnames(aggregatedSpeciationTime.mean) <- c("Time", "Diversification")

colnames(aggregatedSpeciationTime.sd) <- c("Time", "Diversification")

# bp.resp <- breakpoints(Diversification ~ Time, data=aggregatedSpeciationTime.mean)

# summary(bp.resp)

# ## the BIC

# plot(bp.resp)

# breakpoints(bp.resp)

#Suggest that 4 is better from stats, visually 2

bp.resp <- breakpoints(Diversification ~ Time, data=aggregatedSpeciationTime.mean, breaks=2)

ci.resp <- confint(bp.resp)

dates <- as.data.frame(breakdates(ci.resp))

dateFirstRupt <- as.numeric(round((1-dates[1,])\*(max(aggregatedSpeciationTime.mean$Time) - min(aggregatedSpeciationTime.mean$Time)), digit=2))

dateSecondRupt <- as.numeric(round((1-dates[2,])\*(max(aggregatedSpeciationTime.mean$Time) - min(aggregatedSpeciationTime.mean$Time)), digit=2))

```

| Finally, we investigated the evolutionary consequences of brain evolution and sympatry by evaluating whether brain sizes and sympatry level correlated with the net species diversification rates (defined as speciation minus extinction rates). To do so, we used lineage-specific birth-death models of species diversification [@maliet2019model; @maliet2020fast]. Overall, species diversification rates, estimated based on the primate molecular phylogeny, increased over time (Figure \@ref(fig:figdiversificationTime)), particularly in the early and late Miocene, around 25 and 11 Myr ago (Figure \@ref(fig:figdiversificationTime)). When accounting for phylogenetic dependence, no significant relationship between the net diversification rate and the relative size of brain areas was found (Table \@ref(tab:tableRegDiversification), Figure \@ref(fig:forestPlot); see robustness in Table \@ref(tab:tabledfsensitivity2)). Given the context-dependence of the direction of selection (towards bigger sizes when sympatry is low, smaller sizes otherwise), there is no surprise that we do not observe a correlation between the diversification rate and the three brain areas affected by species sympatry. Surprisingly however, we found no positive association between the net diversification rate and the EQ, nor with the relative sizes of the Cerebellum or the Neocortex, two areas insensitive to species sympatry too. This is puzzling because this contradicts a recent study [@melchionna2020macroevolutionary]. The visual inspection of the regressions however clearly evidenced a positive trend for the EQ and the Neocortex, if discarding phylogenetic non-independence (Figure \@ref(fig:figRegressionDiversification)). Indeed, sudden encephalisation in primates is clearly associated with a limited number of closely-related species [@decasien2017primate; @melchionna2020macroevolutionary]. This clearly limits the statistical power of our phylogenetically-corrected analyses, as we cannot decipher whether larger brain size and faster species diversification results from a true biological link or appeared simultaneously but independently. A positive association between brain size and diversification was also found in birds [@sayol2019larger] given that bigger brains act as a buffer to environmental challenges [@sol2007big]. This means that, despite what we found here, a positive association between brain size and species diversification evidenced in [@melchionna2020macroevolutionary] remains a likely possibility. Finally, although diversification was uncorrelated with brain size in frugivorous primates, it was influenced by the sympatry context. In particular, phylogenetic regressions highlighted a negative effect of the number of sympatric species on the diversification rate (`r textEstOneVar(as.numcharac(results.df\_diversificationAndSympatry[4,2:4]))`, `r textTestOneVar(as.numcharac(results.df\_diversificationAndSympatry[4,5:6]), statistics="t")`, Table \@ref(tab:tableRegDiversificationAndSympatry), Figure \@ref(fig:forestPlot)). In other words, the higher the number of sympatric species, the lower the diversification rate, a density-dependence trend that is frequently observed in many tetrapod clades [@condamine2019assessing].

# Discussion

Bigger brains are not necessarily better. The size of the brain is subject to a compromise between the energy it incurs, and the increase of fitness it allows. This is clearly emphasized by the fact that the biggest areas, the Cerebellum and the Neocortex, as well as the whole brain (EQ), were best described by the Ornstein-Uhlenbeck process. This evidence might suggest a stabilisation towards an optimal size resulting from an equilibrium between costs and benefits. As the brain is regionally specialised [@barton2000mosaic], different brain areas could be under different selective pressures. This is evidenced, here, by the differences of relative sizes across lineages in the MOB or Striatum in particular. We further show that sympatry is one factor that affects the selective regime under which some brain region evolves: although the brain as a whole was insensitive to species sympatry, the latter nonetheless induced a change in the relative size of the Hippocampus and the Striatum. These areas are involved in individual-based and social-based information processing, pinpointing that the two components might be under strong selection in primates [@decasien2017primate; @powell2017re; @gonzalez2018inference].

| The negative influence of sympatry on the Striatum might be quite surprising. Direct interactions with heterospecifics should stimulate this area (Hypothesis 3). We observed that this area was relatively larger in callitrichines, particularly known to perform mixed-species groups [@heymann2015unlike]. When interacting with conspecifics, the Striatum underpins reward expectation, goal-directed behaviour, and planning abilities [@johnson2007integrating]. These skills are key within group, following a Machiavellian perspective [@byrne1994machiavellian]. Yet, these skills might also be relevant in a foraging context. It is thus possible that actions underpinned by the Striatum (e.g. planning/anticipating heterospecifics moves), might be key and up to now overlooked, when foraging in a multi-species context too.

| Overall, the fact that only these two areas, particularly relevant to process and memorise spatio-temporal information, are sensitive to sympatry, is consistent with the idea of an effect of sympatric species on resource spatio-temporality (Hypothesis 1). Competition is generally the first-thought mechanism to describe community structures [@rocha2015role] because it might affect the environment, and associate selective pressure, in which species evolve. We show that higher levels of sympatry is actually associated with smaller sizes of the Hippocampus or Striatum (in accordance with Prediction 1.2). This suggests that indirect competition for food might contribute to convoluting the environment which might generate a positive selection for smaller brains. Not only was brain evolution affected by sympatry, but sympatry induced a slowdown in diversification. Density-dependence within a clade is indeed generally associated with lower diversification rates [@moen2014does]. In particular, species competing for resources are thought to contribute to limiting their ranges [@price2009evolutionarily], hence constraining population size and their subsequent diversification [@pigot2013species]. These observations thus strengthen the idea of scramble competition between species that cascades both on species population dynamics and species cognition.

| By contrast, potential indirect facilitation between species due to “social” cues (Hypothesis 2), is ruled out by the absence of an effect of sympatry on brain areas involved in immediate sensory information processing (e.g. Cerebellum or Neocortex). This absence of effect can stem from two possibilities. Either sympatry, indeed, does not affect the landscape of cues for foragers. Otherwise, it has been shown that foragers tend to use social information over environmental (i.e. personal) information, in particular in non-perfectly predictable environments [@rafacz2003environmental; @dunlap2016foraging]. Thus, if environmental complexity increases too much, “social” cues provided by heterospecifics might replace environmental ones. From this point of view, the size of the MOB, the Cerebellum, or the Neocortex should, at the very least, remain unaffected by sympatry. This nonetheless deserves further attention.

| The use of brain size as a proxy for cognition is a central debate with no optimal solution (see grounded criticism from [@deaner2000comparative; @healy2007critique; @logan2018beyond]). The current flourishment of consortia, allowing for much more detailed and standardized anatomical measurements (e.g. in primates: [@milham2018open]), or with standardized behaviourally explicit comparisons (e.g. on captive [@many2019establishing] or wild [@janmaat2021using] primates), might alleviate biases stemming from brain size analysis, but this will take time to generate large-enough datasets. In the meanwhile, brain size is a proxy much appreciated in practice, because of its easy accessibility for a “large” number of species. Here, we showed that species sympatry is an important factor shaping the evolutionary history of animals' brains, but the proximate mechanisms at play remain to be elucidated. Finally, it is very likely that any hypothesis on cognition evolution, generally discussed within species, could be broadened to a between-species context: foraging facilitation between species does exist [@olupot1998fruit; @Havmoller2021], and so do polyspecific social associations [@porter2001benefits], as well as inter-species territory defence [@drury2020competition; @losin2016ecological] or imitation and copying [@persson2018spontaneous; @pepperberg2002allospecific]. Similarly, prey-predator races could shape selection on cognitive abilities [@shultz2006chimpanzee]. As Alice said “It's a great huge game of chess that's being played—all over the world” ([@Carroll], Chapter II) and all individuals are just pieces to play with or against, no matter the species.

<!-- TC:ignore -->

\newpage

# Methods

Data processing, analyses, and plots were computed with R software (`r extractRversion()`, @Rsoftware). Used codes and data are freely available at [https://github.com/benjaminrobira/Meta\_analysis\_cognition\_primates](https://github.com/benjaminrobira/Meta\_analysis\_cognition\_primates). Note that in all these analyses, we discarded \*Homo sapiens\* and \*Macaca sylvanus\*. The latter was discarded in the analyses because of geographical complete isolation and repeated intervention of human people in population maintenance [@modolo2005phylogeography]. A summary of available data per species is presented in Appendix Figure \@ref(fig:figmap).

## Data Collection

### Phylogeny

We used a block of chronogram trees of the primate taxon of the 10kTrees project (downloaded on May 2021, version 3), as well as a consensus tree of 1000 trees for the subsequent phylogenetic analyses. The trees contain `r length(phylo\_init$tip.label)` primate species.

### Trait data

Brain data were obtained from [@decasien2019primate] for the whole brain and all mentioned other regions (Cerebellum, Hippocampus, Main Olfactory Bulb (MOB), Neocortex, Striatum), [@powell2017re] and [@powell2019maternal] for the whole brain, Cerebellum and Neocortex size, [@todorov2019primate] for Hippocampus and Neocortex size, [@grueter2015home] for the whole brain size and [@navarrete2018primate] for the whole brain, Cerebellum, Hippocampus and Striatum size. They were freely available in the main manuscript or supplementary materials. When a species was represented multiple times within the dataset, we obtained a unique attribute by averaging it. From the global endocranial brain volume, we obtained the Encephalization Quotient (EQ, N$\_{EQ,max}$ = `r maxEQ`) as follows [@decasien2017primate]

\hfill

\begin{center}

$\mathrm{EQ}=1.036 \times \mathrm{Brain\,volume}/ (0.085 \times \mathrm{Body\,mass}^{0.775})$

\end{center}

\hfill

with the brain volume in cm$^{3}$, 1.036 g/cm$^{3}$ being the assumed homogeneous brain density, and the body mass in g. EQ indicates whether the brain size ranges above (> 1) or below (< 1) expected given the body mass. Body mass was obtained from [@decasien2017primate; @powell2017re; @grueter2015home; @pearce2013space].

The sub-parts of the brain were chosen because they were involved in immediate sensory information processing (MOB, N$\_{MOB,max}$ = `r maxMOB`), in movement and/or general information processing and retention (Neocortex, N$\_{Neocortex,max}$ = `r maxNeocortex`, [@wiltgen2004new]; Cerebellum, N$\_{Cerebellum,max}$ = `r maxCerebellum`, [@koziol2014consensus; @sokolov2017cerebellum]), short-term working memory and long-term spatio-temporal memory (Hippocampus, N$\_{Hippocampus,max}$ = `r maxHippocampus`, [@burgess2002human]). The Striatum (N$\_{Striatum,max}$ = `r maxStriatum`) supports information processing during social interaction, reward assessment, planning or goal-oriented behaviours [@baez2013role; @johnson2007integrating]. To investigate their evolutionary history, we used the ratio between their volume and body mass, so as to maximize comparability. As such, the use of specific region sizes relative to the body mass and not raw sizes depicts the evolution of cognitive abilities in terms of allocation rather than abilities per se (but see discussion in [@deaner2000comparative]). Percentage of frugivory and/or folivory was obtained based on a freely available dataset from [@decasien2017primate; @powell2017re; willems2013collective].

### Ranging Data

Current geographic (maximal possible) range of each primate species was assessed using ranging maps provided by the IUCN red list [@IUCN]. Ranging data were available for `r nrow(matrixRangingSensitivity[!is.na(matrixRangingSensitivity[,1]),])` species among the `r length(phylo\_init$tip.label)` represented in the 10kTrees primate phylogeny.

## Primate species sympatry

For primate biogeography, based on the structure (i.e. number of species and their phylogenetic relationships) of primate communities at different field sites, Kamilar et al. [@kamilar2009environmental] determined clusters of sites with highly similar community structures that were shaped by both the environment geography and climatic correlates. We used this classification and manually mapped the geographic areas using Google earth professional (v7.3.3). These geographic areas are represented in Figure \@ref(fig:figmap) and correspond to Central America, the North and the South of South America respectively, West Africa, Central Africa, and East/South Africa, East and West of Madagascar respectively, West Asia, Central/East Asia, South Asia, and the Asian Islands. The chosen scale for the areas is large because (i) retracing the history of a large number of areas necessitates considerable computational means. In addition, this drastically increases the computational time for fitting the phylogenetic models of brain trait evolution too. Furthermore (ii), all species and particularly primate species suffer(ed) from recent extinction [@pavoine2019mammal], with a reduction of ranging areas at an unprecedented speed rate. Finer geographic characterization would therefore give too much weight to such anthropogenic effect that recently altered species distribution (e.g. evidenced on the North American fauna in [@pineda2021mammal]). One to multiple large-scale geographic areas were assigned to each species as soon as the species current distribution range overlapped in the surface at `r geographicThresholdVector[1]\*100` (low threshold) or `r geographicThresholdVector[2]\*100`% (high threshold; the maximum was chosen to `r geographicThresholdVector[2]\*100`% because on present data, a species could occupy as far as three areas, Figure \@ref(fig:figmap)). Overlap was calculated with the “gIntersection” function from the \*rgeos\* package [@rgeos] applied to Mercator-projected data to get the overlapping contour, and the “area” function from the \*geosphere\* package [@geosphere], applied directly on unprojected longitudinal-latitudinal data for area size calculation.

| We retraced the biogeographic history of the lineage ranges based on current observations of species range with the \*BioGeoBEARS\* package [@matzke2013probabilistic], using the biogeographic stochastic mapping algorithm [@matzke2016stochastic]. We fitted non-time-stratified dispersal-extinction-cladogenesis (DEC) models specifically suiting analyses of range data since it accounts for spatially explicit processes of cladogenetic and anagenetic events (see [@matzke2013probabilistic] for further details on these events). To reconstruct the evolution of species range, we fixed the maximum number of areas that could be occupied by a lineage at one time to three areas. A too high number of areas that can be occupied simultaneously drastically increases computational time. Here, we therefore chose that a species can at most occupy three areas since it offers the possibility to occupy a complete mainland continent. Finally, because these history reconstructions are likely to vary, for each run of DEC models (considering both possible overlaps to consider species presence), we obtained `r numberSimulations` stochastic maps that were all used in subsequent phylogenetic model fits (see [Phylogenetic models]) to account for the uncertainty of these ancestral range estimations (see [Models of trait evolution: does species sympatry shape brain size evolution?] (b)).

## Dietary guilds

We classified species as either “frugivorous” or “folivorous” based on the availability of frugivorous rate and folivorous rate , prioritizing frugivory over folivory. First, a species would be classified as frugivorous if the frugivory rate was at least above `r frugivoryThresholdVector[1]` (low threshold) or `r frugivoryThresholdVector[2]`% (high threshold). If this was not the case, or frugivory rate was unavailable, a species could be classified as folivorous if the folivory rate was at least above `r folivoryThresholdVector[1]` (low threshold) or `r folivoryThresholdVector[2]`% (high threshold). Otherwise, [@decasien2017primate] gave a binary classification of diet, species being categorized as frugivorous or folivorous, partly based on anatomical criteria. Whenever the rate was not available, we referred to this classification. In any other cases, the species was discarded. To illustrate, if a species reached 30% of frugivory, and 65% of folivory (the rest being due, for instance, to insectivory), then, it would be categorized as, “frugivorous” if low thresholds are considered, or as “folivorous” in case high thresholds are considered. If we suppose now another species with 30% of frugivory and 50% of folivory, but considered by [@decasien2017primate] as frugivorous, then, the species would be “frugivorous” for low threshold, and still “frugivorous” with high thresholds.

```{r transitionMatrix}

transitionMatrix <- matrix(NA, nrow=repetition, ncol=2)

for(a in 1:2){

for(b in 1:2){

for(c in 1:2){

for(d in 1:10){

start=which(is.na(transitionMatrix[,1]))[1]

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/OutputEvolModel/Output\_simmap\_transition",a,"\_",b,"\_",c,"\_",d, ".txt", sep=""))

transitionMatrix[start,1] <- toAdd[1,1]

transitionMatrix[start,2] <- toAdd[2,1]

}, error=function(e){

#Do nothing

}

)

}

}

}

}

minProba.v <- apply(abs(transitionMatrix), 2, min)

maxProba.v <- apply(abs(transitionMatrix), 2, max)

```

| Frugivory was prioritized over folivory because we considered that since fruits are a highly palatable food source, it would be the key item that drives the foraging strategy (and associate consequence(s) on brain selection), even if less consumed. Additionally, to consider frugivory, we used a lower rate than for folivory for two reasons. First, such a static rate does not reflect potential seasonality in fruit-eating (e.g. [@masi2009western]), which is generally shorter, hence a lower overall frugivory rate. Second, the frugivory rate is likely to be underestimated in part because primates generally spend more time feeding on leaves than fruits, while rates are often based on relative feeding time, or observation frequency at the individual or group unit of feeding events. Finally, the methodology to obtain this rate could additionally vary (e.g. in addition to the two aforementioned estimations, one could also rely on the proportion of species targeted for their fruits/leaves). For all these reasons, we used two threshold levels (low, `r frugivoryThresholdVector[1]`%, or high, `r frugivoryThresholdVector[2]`%) to classify a species as frugivorous, as well as two threshold levels (low, `r folivoryThresholdVector[1]`%, or high, `r folivoryThresholdVector[2]`%) to classify a species as folivorous.

| Considering diet as a binary variable (frugivory versus folivory), we retraced the evolutionary history of such discrete traits based on a continuous Markovian process (extended Mk models) and relying on a Bayesian approach [@bollback2006simmap], using the “simmap” function of the \*phytools\* package [@phytools] and internally estimating the prior probability of trait (i.e. at the root), but with no prior on the transition matrix. Again, the obtained character history is in no case certain. Therefore, for each run, we obtained `r numberSimulations` stochastic character maps that were used in subsequent phylogenetic model fits (see [Phylogenetic models]), to account for the uncertainty of these ancestral diet estimations (see [Models of trait evolution: does species sympatry shape brain size evolution?] (b)).

## Phylogenetic models

### Models of trait evolution: does species sympatry shape brain size evolution?

\hfill

(a) Fitting models of trait evolution

\hfill

We focused only on frugivorous primates, because the sample size was otherwise insufficient, and fitted phylogenetic models of the evolution of the EQ or the relative size of a specific brain area considering or not species sympatry. Models were fitted on different sample sizes due to the non-availability of some data for some traits. Specifically, models using EQ included `r minEQ` to `r maxEQ` frugivorous species. Other models included more reduced sample sizes (in species number): Striatum (`r minStriatum` to `r maxStriatum`), MOB (`r minMOB` to `r maxMOB`), Neocortex (`r minNeocortex` to `r maxNeocortex`), Hippocampus (`r minHippocampus` to `r maxHippocampus`), Cerebellum (`r minCerebellum` to `r maxCerebellum`). Nonetheless, for a given set of models (i.e. within brain area), the sample was strictly identical, allowing within-set comparisons. Prior to fitting, trait parameters were log-transformed to reach more symmetrical distributions. Models without species sympatry, Brownian Motion (BM), Ornstein-Uhlenbeck process (OU, model with stabilizing selection), or Early-Burst model (EB, for assessing a time-dependence of the evolutionary rate), were fitted using the “fitContinuous” function from the \*geiger\* package [@geiger3; @geiger5]. Using the evolutionary history of species distribution (see [Primate species sympatry]) and of diet (see [Dietary guilds]), we fitted models considering species sympatry using the “fit\_t\_comp” function from the \*RPANDA\* package [@RPANDA]. These models notably account for interspecific interaction matrices that are built on the evolutionary history of species sympatry and diet. These interaction matrices retrace, along the phylogenetic tree, which frugivorous lineages were present within the same geographic areas (see [@drury2016estimating]). We fitted three different models considering species sympatry. The matching competition model (MC) considers the repulsion of traits of sympatric lineages from the same dietary guild due to competition (character displacement) [@drury2016estimating]. Here, that would mean that sympatric species would tend to divergently evolve either lower, or higher, EQ or relative brain size. Otherwise, we modelled trait evolution accounting for linear (DD$\_{lin}$) or exponential (DD$\_{exp}$) density-dependence [@drury2016estimating; @weir2013diversity]. Density-dependence means that the evolutionary rate, $\lambda$, of trait changes, varies either positively or negatively as a function $f$ of the number of sympatric lineages sharing the same diet, such as

\begin{center}

\hfill

$f\_{lin}(\lambda)=\lambda\_{0} + rl$

$f\_{exp}(\lambda)=\lambda\_{0}\exp(rl)$

\hfill

\end{center}

where $\lambda\_{0}$ corresponds to the value of the initial ancestor, $l$ indicates the number of lineages, $r$ allows for modelling the speed and direction of the dependency to lineage number ($r>0$ leads to an increase of trait changes, while $r<0$ leads to a decline of the trait changes). All these models were repeated `r numberSimulations` times, using `r randomSampling` different combinations of the evolutionary histories of primate ranges and diets. They were then compared within an information-theoretic framework [@burnham2002model] based on the weights of Akaike Information Criteria corrected for small samples (AICc), when considering all six models (MC, DD$\_{lin}$, DD$\_{exp}$, BM, OU, EB). The model weight depicts how well the model fits the observed evolutionary pattern compared with the other tested models.

\hfill

```{r prepfigevolution}

###Set working directory

setwd("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates")

summaryBrainFrugivory <- as.data.frame(matrix(NA, nrow=10\*(repetition+1), ncol=53))

summaryEQFrugivory <- as.data.frame(matrix(NA, nrow=10\*(repetition+1), ncol=53))

summaryNeocortexFrugivory <- as.data.frame(matrix(NA, nrow=10\*(repetition+1), ncol=53))

summaryHippocampusFrugivory <- as.data.frame(matrix(NA, nrow=10\*(repetition+1), ncol=53))

summaryCerebellumFrugivory <- as.data.frame(matrix(NA, nrow=10\*(repetition+1), ncol=53))

summaryStriatumFrugivory <- as.data.frame(matrix(NA, nrow=10\*(repetition+1), ncol=53))

summaryMOBFrugivory <- as.data.frame(matrix(NA, nrow=10\*(repetition+1), ncol=53))

counter=0

start=counter

end=counter

numberSimulations=10

totModelsWorked=c(0,0,0,0,0,0,0)

for(a in 1:2){

for(b in 1:2){

for(c in 1:2){

for(d in 1:10){

counter=end+1

start=counter

end=counter + numberSimulations - 1

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/OutputEvolModel/Output\_evolutionary\_history\_BrainBodymassRaw",a,"\_",b,"\_",c,"\_",d,".txt", sep=""))

summaryBrainFrugivory[start:end,] <- as.data.frame(toAdd)

totModelsWorked[1]=totModelsWorked[1]+1

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/OutputEvolModel/Output\_evolutionary\_history\_EQ",a,"\_",b,"\_",c,"\_",d,".txt", sep=""))

summaryEQFrugivory[start:end,] <- toAdd

totModelsWorked[2]=totModelsWorked[2]+1

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/OutputEvolModel/Output\_evolutionary\_history\_NeocortexBodymassRaw",a,"\_",b,"\_",c,"\_",d,".txt", sep=""))

summaryNeocortexFrugivory[start:end,] <- toAdd

totModelsWorked[3]=totModelsWorked[3]+1

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/OutputEvolModel/Output\_evolutionary\_history\_HippocampusBodymassRaw",a,"\_",b,"\_",c,"\_",d,".txt", sep=""))

summaryHippocampusFrugivory[start:end,] <- toAdd

totModelsWorked[4]=totModelsWorked[4]+1

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/OutputEvolModel/Output\_evolutionary\_history\_CerebellumBodymassRaw",a,"\_",b,"\_",c,"\_",d,".txt", sep=""))

summaryCerebellumFrugivory[start:end,] <- toAdd

totModelsWorked[5]=totModelsWorked[5]+1

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/OutputEvolModel/Output\_evolutionary\_history\_StriatumBodymassRaw",a,"\_",b,"\_",c,"\_",d,".txt", sep=""))

summaryStriatumFrugivory[start:end,] <- toAdd

totModelsWorked[6]=totModelsWorked[6]+1

}, error=function(e){

#Do nothing

}

)

tryCatch(

{toAdd <- read.delim(paste("Processed\_data/OutputEvolModel/Output\_evolutionary\_history\_MOBBodymassRaw",a,"\_",b,"\_",c,"\_",d,".txt", sep=""))

summaryMOBFrugivory[start:end,] <- toAdd

totModelsWorked[7]=totModelsWorked[7]+1

}, error=function(e){

#Do nothing

}

)

}

}

}

}

summaryBrainFrugivory <- summaryBrainFrugivory[!is.na(summaryBrainFrugivory[,1]),]

summaryEQFrugivory <- summaryEQFrugivory[!is.na(summaryEQFrugivory[,1]),]

summaryNeocortexFrugivory <- summaryNeocortexFrugivory[!is.na(summaryNeocortexFrugivory[,1]),]

summaryHippocampusFrugivory <- summaryHippocampusFrugivory[!is.na(summaryHippocampusFrugivory[,1]),]

summaryCerebellumFrugivory <- summaryCerebellumFrugivory[!is.na(summaryCerebellumFrugivory[,1]),]

summaryStriatumFrugivory <- summaryStriatumFrugivory[!is.na(summaryStriatumFrugivory[,1]),]

summaryMOBFrugivory <- summaryMOBFrugivory[!is.na(summaryMOBFrugivory[,1]),]

colnames(summaryBrainFrugivory) <- colnames(toAdd)

colnames(summaryEQFrugivory) <- colnames(toAdd)

colnames(summaryNeocortexFrugivory) <- colnames(toAdd)

colnames(summaryHippocampusFrugivory) <- colnames(toAdd)

colnames(summaryCerebellumFrugivory) <- colnames(toAdd)

colnames(summaryStriatumFrugivory) <- colnames(toAdd)

colnames(summaryMOBFrugivory) <- colnames(toAdd)

##----

colNum <-c("darkgrey", brewer.pal(n = 5, name = "Set1")[1:5])

models <- c("BM", "OU", "EB", "MC", expression(DD[italic(lin)]), expression(DD[italic(exp)]))

colourModels <- brewer.pal(n = 6, name = "Set1")

```

(b) Dealing with data uncertainty and parameterisation sensitivity

\hfill

In this analysis, uncertainty can stem from two sources. First, the evolutionary history (phylogeny, diet, and ranging) was reconstructed based on Bayesian inference. They are susceptible to be uncertain at some points. Thus, we used a consensus phylogenetic tree from the 10kTrees project, which averages the phylogeny among 1000 possible estimated trees, given that running the models on several trees was too computationally demanding. In addition, we repeated diet and ranging history reconstructions `r numberSimulations` times.

| Second, for each species, trait estimates could vary slightly among datasets (see Appendix Figure \@ref(fig:figvariabilitydata)). Particularly, although correlations between measures from the different datasets seem good enough, it existed a variation in absolute measurements (Appendix Figure \@ref(fig:figvariabilitydata)). In addition, this study is based on several arbitrary thresholds, namely (i) to assess species sympatry (see Appendix Figure \@ref(fig:figcomparison)) and (ii) to assess the species dietary guild (see Appendix Figure \@ref(fig:figvariabilitydata)) which can cause sensitivity of the results to the chosen parameters. To account for these three sources of variability, we refitted several times the six models of trait evolution (BM, OU, EB, MC, DD$\_{lin}$ and DD$\_{exp}$) with (1) random samples of the dietary and brain traits in case of multiple values available (i.e. equal probability for each possible value to be selected), (2) used the low or high threshold for assessing frugivory, folivory, and species sympatry, and (3) various biogeography and dietary evolutionary history reconstructions.

| Eventually, it means that the results for each model represent the average of `r numberSimulations` (uncertainty on diet/ranging evolutionary reconstructions) x `r randomSampling` (uncertainty in brain/diet rate data) x `r length(geographicThresholdVector)` (geographic overlap threshold defining sympatry) x `r length(frugivoryThresholdVector)` (frugivory threshold) x `r length(folivoryThresholdVector)` (folivory threshold) = `r numberSimulations\*randomSampling\*length(geographicThresholdVector)\*length(frugivoryThresholdVector)\*length(folivoryThresholdVector)` sub-models. We stopped computations when the optimization of the likelihood was excessively long (> 1 week). The final sample size thus was of `r min(totModelsWorked[-2])\*10` models that covered all the ranges of tested parameters.

### Models of species diversification

We investigated how primates diversified over time. Lineage-specific diversification rates were estimated using an updated version of the \*ClaDS\* algorithm [@maliet2019model] boosted for computational speed based on data augmentation techniques [@maliet2020fast]. Particularly, we used \*ClaDS2\*, the model with constant turnover (i.e. constant ratio between extinction and speciation rates). This Bayesian approach considers speciation rate heterogeneity by modelling small shifts in the rate at speciation events. In other words, the two new lineages are assumed to inherit new speciation rates that are sampled from a log-normal distribution with an expected mean value $log(\alpha \lambda)$ (where $\lambda$ represents the initial speciation rate and $\alpha$ is a trend parameter), and a standard deviation $\sigma$. Three independent chains were run until their convergence was validated by a Gelman-Rubin diagnostic criterion [@gelman1992inference]. The analysis relied on the use of a consensus tree of primate phylogeny from [@dos2018using]. The latter provides a robust phylogenetic tree for 367 primate species (while the 10kTrees primate phylogeny has only `r length(phylo\_init$tip.label)` species).

| Such analysis necessarily depends on a prior estimation of the sample representativeness, that is, the fraction of sampled taxa (present in the phylogenetic tree) among all possible existing ones. Estrada et al. [@estrada2017impending] estimated that, given current knowledge, the primate clade should be composed of 504 species. This means that the current sampling fraction is around 73%. We thus parameterized the \*ClaDS\* algorithm with this value for the estimated sampling fraction. Yet, given that the extant number of primate species is subject to controversy, and because the estimated sampling fraction may affect diversification rate estimations, we replicated our analyses with a range of sampling fractions from 95% down to 60%. At the end of each run, we extracted the maximum of the \*a posteriori\* net diversification rate of each extant primate species, as well as the mean diversification rate (given all lineages) through time.

### Phylogenetic regressions

\hfill

(a) Determining the effect of sympatry on brain sizes

\hfill

To determine the nature of the relationship between species sympatry and relative sizes of brain regions, we fitted Gaussian Pagel's lambda phylogenetic regressions (i.e. a derivative of the Brownian Motion model, for which the phylogenetic variance-covariance matrix has all coefficients, but its diagonal ones, multiplied by lambda) for each brain region individually and for frugivorous species only. We used Pagel's lambda model so as to relax the hypothesis of Brownian Motion since we included brain areas for which the evolutionary history was best described by models considering sympatry. Here specifically, we considered the least stringent frugivory assessment, with the frugivory threshold fixed to `r frugivoryThresholdVector[1]`% and the folivory threshold fixed to `r folivoryThresholdVector[1]`%. If, due to data variability, a species did not robustly fit into the categorical classification “frugivorous versus folivorous” (i.e. could be either of the two), it was considered as frugivorous nonetheless.

| The response variable was the relative size of brain areas. Due to data variability, we took the mean of the possible values given the different datasets, and assessed the sensitivity using non-averaged values (see [Phylogenetic regressions: results, stability, and assumption]). In this model, the covariates (i.e. continuous predictors) were the average percentage of overlapping range with other sympatric frugivorous species, and the number of frugivorous sympatric species (the second was square-rooted, to reach symmetrical distribution). For a given species A, sympatry with another species B was considered when species B range overlapped on more than `r geographicThresholdVector[1]\*100`% of the range of species A. This was done to reduce the noise induced by coarse identification of species range.

\hfill

(b) Diversification and brain size

\hfill

In the same way as explained above, we fitted Gaussian Pagel's lambda phylogenetic regressions of the different relative brain sizes against the net diversification rates (i.e. the difference between speciation and extinction rates), estimated for each extant species by the \*ClaDS\* algorithm. Again, we took the mean of the brain trait values for the main model and assessed the sensitivity by re-running the model several times using non-averaged values.

\hfill

(c) Diversification and species sympatry

\hfill

To determine whether species sympatry was associated with specific diversification patterns (and thus if diversification rates were regionalized), we fitted Gaussian Pagel's lambda phylogenetic regressions with the diversification rate as output variable, and used the two metrics for describing sympatry (the average percentage of overlapping range with other sympatric frugivorous species, and the number of frugivorous sympatric species) as tested variables, as described in (a).

\hfill

(d) Model implementation

\hfill

(i) Effect of sympatry on brain sizes

\hfill

Models were fitted using the “phylolm” function from the \*phylolm\* package [@phylolm], with the lambda parameter (with $\lambda$ indicating the strength of the phylogenetic signal, where $\lambda$=1 corresponds to Brownian Motion, i.e. the maximal influence of the phylogenetic history on the trait evolution) estimated by maximum-likelihood (argument “model” set to “lambda”). Bootstrapping over `r repetitionBootstrap` independent replicates was done to obtain confidence intervals. Other function parameters were set to default. Prior to fitting, covariates were transformed so as to reach more symmetrical distributions when adequate. Necessary assumptions on the normal distribution of residuals and homoscedasticity were visually assessed and pointed out no violation (see Appendix [Model assumptions]). We did not observe correlation issue among predictors neither (VIF$\_{max}$ < 2, [@mundry2014statistical]).

\hfill

(ii) Diversification and brain size

\hfill

We could not compute phylogenetic regressions to link diversification and brain traits in frugivorous primates using a frequentist approach because it led to a violation of homoscedasticity. Instead, we fitted Bayesian phylogenetic regressions using the "MCMCglmm" function of the \*MCMCglmm\* package [@MCMCglmm]. Each chain was based on a burnin period of `r burnin` iterations, among a total of `r nitt` iterations, and was sampled every `r thin` iterations. We used the least informative priors. Fixed priors were let to default (Gaussian distribution of mean 0 and variance $10^{8}$). Priors on random effects and residuals were set to follow an inverse-Wishart distribution with a variance at a limit ($V$) of 1, and a degree of belief ($nu$) of 0.02. We checked model convergence by fitting three chains, and calculated the Gelman-Rubin criterion (max value < `r round(max(gelmanRubinValues), digit=4)`; @gelman1992inference), as well as checked autocorrelation (max absolute value < `r round(max(valueAutoCorr), digit=2)`) using the respective "gelman.diag" and "autocorr.diag" functions from the \*coda\* package [@coda]. In Appendix [Model assumptions], we present traces and distributions of posterior estimates. We further checked the quality of the posterior by visually assessing the Q-Q plot of the posterior with that of a Gaussian distribution of mean 0 and sd 1 (see Appendix [Model assumptions]). We present the estimate together with the 95% credibility interval centered on the mode (Highest Density Posterior, HDP), together with a MCMC p-value (pMCMC) that corresponds to the probability that the estimate ($\beta$) is positive if the mean estimate ($\hat{\beta}$) is negative (i.e. $P(\beta>0|\hat{\beta}<0)$), or if the mean estimate is positive, the probability that the estimate is negative (i.e. $P(\beta<0|\hat{\beta}>0)$).

\hfill

(iii) Diversification and sympatry

\hfill

We fitted phylogenetic regression as explained in (i). In particular, verification of model assumption and stability pointed out no source of worry (see [Phylogenetic regressions: results, stability, and assumption]).

\hfill

(d) Model robustness

\hfill

To assess frequentist model stability with regards to singular points, we computed the DfBetas (variation in estimates) by discarding one observation at a time of the "standard" dataset used to fit the main model, based on the consensus tree .

| To assess the sensitivity to (i) the variability in data and (ii) phylogeny uncertainty, we refitted the models using `r repetitionTrees` phylogenetic trees among the 10000 possible trees from the 10kTrees project. For each of these trees, we fitted the model `r repetitionModels` times, allowing random sampling for data when we had multiple values (e.g. if body mass was provided by different datasets etc.). For the diversification analysis specifically, we also assessed the sensitivity to changes in primate sampling fraction by refitting the models for values ranging between 60 to 95% (as specified before), using the "standard" dataset and the consensus tree.

| The results of these assessments (min-max of estimates) are shown in Appendix [Model stability]. It emphasizes the weak sensitivity of the results.

# Acknowledgements

We considerably value the help provided by J. Drury in making some scripts available functions in the \*RPANDA\* package in \*R\* and helping us in running them, and that of M-C. Quidoz for assistance in using the CEFE cluster. We thank S. Benhamou and M. Clairbaux for discussions on spatial projections, and M. Quéroué, V. Lauret, A. Caizergues, and C. Teplistky for feedback on Bayesian computations too. Finally, this work could not have been possible without prior data collection from the IUCN Red List (primate ranging), the 10kTrees project (phylogenetic trees), and A. R. DeCasien and collaborators, L. E. Powell and collaborators, O. S. Todorov and collaborators, E. P. Willems and collaborators, F. Pearce and collaborators, A. F. Navarrete and collaborators, and C. C. Grueter who provided primate trait data we used as (supplementary) material with their articles, as well as Nicholas J. Matzke for available algorithm scripts allowing us to implement and better understand the methods. Their indirect input is therefore tremendous. Both authors were supported by a doctoral grant from the \*École Normale Supérieure\*, Paris.

# Authors' contribution

BR conceived the study, collected, cleaned and analysed the data, drew the figures and wrote the first version of the manuscript and subsequently revised it. BP-L implemented the ClaDS algorithm for our data, helped with running other analyses, and revised the manuscript multiple times. The authors declare having no conflict of interest. All authors gave final approval for publication and agree to be held accountable for the work performed therein.

```{r tableRegGradient, include=TRUE}

results.df\_gradient <- results.df\_gradient[-(6:10),]

results.df\_gradient[1] <- gsub("frugivorous", "frugivores", results.df\_gradient[,1])

results.df\_gradient[1] <- gsub("home range", "range", results.df\_gradient[,1])

rownames(results.df\_gradient) <- NULL

knitr::kable(results.df\_gradient, escape=TRUE, booktabs = TRUE, caption = "Species sympatry correlates negatively with the sizes of some brain areas : Model estimates and significance of phylogenetic regressions to assess the relationship between relative brain sizes and species sympatry | Est.=Estimate, CI2.5\\%=Lower border of the CI95\\%, CI97.5\\%=Upper border of the CI95\\%, Sd=Standard deviation, t=Statistics t-value. The brain areas (as well as the associated sample size) are indicated prior to each list of estimates. The transformation applied to variables are indicated between brackets (logarithm, log, or square-root, sqrt), as well as the ponderation by bodymass (/bodymass).") %>%

kableExtra::column\_spec(2:ncol(results.df\_gradient), bold = toPlotBold[-(6:10)]) %>% #Remove brain raw

kableExtra::kable\_styling(latex\_options = "striped") %>%

kableExtra::kable\_styling(latex\_options="scale\_down") #%>%

#kableExtra::kable\_styling(latex\_options = "HOLD\_position")

```

```{r}

#Round numbers table

results.df\_diversification[seq(from=4, to=nrow(results.df\_diversification), by=4),c(2,3,4)] <-apply(results.df\_diversification[seq(from=4, to=nrow(results.df\_diversification), by=4),c(2,3,4)], 2, function(x){roundIntelligent(as.numcharac(x), digit=2)})

results.df\_diversification[seq(from=1, to=nrow(results.df\_diversification), by=4),1] <- gsub("\\(log\\) ", "", results.df\_diversification[seq(from=1, to=nrow(results.df\_diversification), by=4),1])

results.df\_diversification[seq(from=1, to=nrow(results.df\_diversification), by=4),1] <- gsub("\\(\\/bodymass, log\\) ", "", results.df\_diversification[seq(from=1, to=nrow(results.df\_diversification), by=4),1])

```

\newpage

```{r tableRegDiversification, include=TRUE}

results.df\_diversification <- results.df\_diversification[-(5:8),]

rownames(results.df\_diversification) <- NULL

knitr::kable(results.df\_diversification, escape=TRUE, booktabs = TRUE, caption = "The relative brain sizes did not impact primate species diversification: Model estimates and significance of Bayesian phylogenetic regressions to assess the correlation between the net diversification rates and the relative brain sizes | Est.=Estimate, HDP2.5\\%=Lower border of the 95\\% Highest Posterior Density, HDP97.5\\%=Upper border of the 95\\% Highest Posterior Density, Eff. samp.=Effective sample (adjusted for autocorrelation). The brain areas (as well as the associated sample size) are indicated prior to each list of estimates. The logarithm transformation was applied to variable and is indicated between brackets (log), as well as the ponderation by bodymass (/bodymass).") %>%

kableExtra::column\_spec(2:ncol(results.df\_diversification), bold = toPlotBoldDiversification[-(5:8)]) %>% #Remove brain raw

kableExtra::kable\_styling(latex\_options = "striped") %>%

kableExtra::kable\_styling(latex\_options="scale\_down") #%>%

#kableExtra::kable\_styling(latex\_options = "HOLD\_position")

```

\newpage

```{r tableRegDiversificationAndSympatry, include=TRUE}

results.df\_diversificationAndSympatry[1] <- gsub("frugivorous", "frugivores", results.df\_diversificationAndSympatry[,1])

results.df\_diversificationAndSympatry[1] <- gsub("home range", "range", results.df\_diversificationAndSympatry[,1])

knitr::kable(results.df\_diversificationAndSympatry, escape=TRUE, booktabs = TRUE, caption = "Species sympatry slowdowns primate diversification: Model estimates and significance of phylogenetic regressions to assess the correlation between diversification rate and species sympatry | Est.=Estimate, CI2.5\\%=Lower border of the CI95\\%, CI97.5\\%=Upper border of the CI95\\%, Sd= Standard deviation, t= Statistics t-value. The brain areas (as well as the associated sample size) are indicated prior to each list of estimates. The transformation (logarithm or square-root) is indicated in parentheses by the abbreviation (log or sqrt).") %>%

kableExtra::column\_spec(2:ncol(results.df\_diversificationAndSympatry), bold = toPlotBoldSympatry) %>%

kableExtra::kable\_styling(latex\_options = "striped") %>%

kableExtra::kable\_styling(latex\_options="scale\_down")

```

\clearpage

```{r prepareMap}

#Reimport areas with cropping

centroid <- matrix(NA, ncol=2, nrow=length(areaName))

for(i in 1:length(areaName)){

areaTransitory <- readOGR(dsn=paste("T:/IUCN\_data\_primate/Geographic\_areas/Shapefiles/",areaName[i],".shp",sep=""))

areaTransitory = clgeo\_Clean(areaTransitory)

areaTransitory <- spTransform(areaTransitory, CRS("+proj=longlat +datum=WGS84 +no\_defs +ellps=WGS84 +towgs84=0,0,0"))

#Have mercator for intersection

areaTransitory <- spTransform(areaTransitory, CRS("+proj=merc +datum=WGS84 +no\_defs +ellps=WGS84 +towgs84=0,0,0"))

areaTransitory <- gIntersection(areaTransitory, worldMap\_mercator, byid=FALSE)

areaTransitory = clgeo\_Clean(areaTransitory)

#Reunite polygon in case

areaTransitory <- gBuffer(areaTransitory, byid=F, width=0)

#back transform to long/lat

areaTransitory <- spTransform(areaTransitory, CRS("+proj=longlat +datum=WGS84 +no\_defs +ellps=WGS84 +towgs84=0,0,0"))

assign(paste("area", i, sep="\_"), areaTransitory)

if(i==1){

centroid[i,] <- c(summary(areaTransitory)$bbox[1,2] + 5, summary(areaTransitory)$bbox[2,1])

}

else if (i==2){

centroid[i,] <- c(summary(areaTransitory)$bbox[1,2] - 5, summary(areaTransitory)$bbox[2,1] - 5)

}

else{

centroid[i,] <- geosphere::centroid(areaTransitory)

}

}

warnings()

# Create legend

areaNameCorrected <- c(

"East Madagascar",

"West Madagascar",

"West Africa",

"Central Africa",

"East/South Africa",

"Central America",

"Northern South America",

"Southern South America",

"West Asia",

"Central/East Asia",

"South Asia",

"Asian islands")

colourArea <- c(

"white",

"darkseagreen2",

"darkseagreen",

"darkseagreen4",

"black",

"orange1",

"darkorange2",

"darkorange4",

"lightgoldenrod1",

"lightgoldenrod2",

"lightgoldenrod3",

"lightgoldenrod4"

)

par(mar=c(0, 0, 0, 0), mgp=c(2, 0.5, 0), xpd=TRUE)

emptyPlot()

legend(x=0, y=0.9, col=c("black", colourArea[2:5]), legend=areaNameCorrected[1:5], pch=c(1, rep(19, times=length(2:5))), pt.cex=1.5, xjust=0, yjust=1, bty="n",

y.intersp=2.75,

title=expression(bold("Africa")))

legend(x=0.5, y=0.9, col=c(colourArea[6:8]), legend=areaNameCorrected[6:8], pch=19, bty="n", pt.cex=1.5, xjust=0.5, yjust=1,

y.intersp=2.75,

title=expression(bold("America")))

legend(x=1, y=0.9, col=c(colourArea[9:12]), legend=areaNameCorrected[9:12], pch=19, bty="n", pt.cex=1.5, xjust=1, yjust=1,

y.intersp=2.75,

title=expression(bold("Asia")))

my\_legend <- recordPlot()

```

```{r figmap, include=TRUE, position='H', warning = FALSE, message = FALSE, results= 'hide', fig.width=7, fig.height=7, fig.cap=paste("Geographic areas used for ancestral range reconstruction of frugivorous primates represented on the Mercator projection of the world | Areas were defined as a combination of geographic and environmental criteria relative to the primate taxonomy following results from [@kamilar2009environmental]: (1) East Madagascar (2) West Madagascar (3) West Africa (4) Central Africa (5) East/South Africa (6) Central America (7) North South-America (8) South South-America (9) West Asia (10) Central/East Asia (11) South Asia (12) Asian peninsula and islands. Note that the north part of Africa and the south of Europe were discarded because \*Macaca sylvanus\* was not considered. ", sep="")}

#abbreviation name are available in https://proj.org/operations/projections/index.html

#help for graticule: https://rpsychologist.com/working-with-shapefiles-projections-and-world-maps-in-ggplot

proj.map <- "+proj=natearth +datum=WGS84 +no\_defs +ellps=WGS84 +towgs84=0,0,0"

centroid <- as.data.frame(centroid)

colnames(centroid) <- c("long", "lat")

centroid$nudge\_y <- 0

centroid$nudge\_y[5] <- -10

library(tidyverse)

library(ggspatial)

library(rnaturalearth)

world <- ne\_countries(scale = "medium", returnclass = "sf")

# graticule (Robin)

grat <- readOGR(dsn="C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Formap", layer="ne\_110m\_graticules\_15")

grat\_df <- fortify(grat)

bbox <- readOGR(dsn="C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Formap", layer="ne\_110m\_wgs84\_bounding\_box")

bbox\_df<- fortify(bbox)

###----

### OLD WAY: when using sf package

###----

# bbox.sf <- sfheaders::sf\_polygon( obj = bbox\_df

# , x = "long"

# , y = "lat"

# , polygon\_id = "group"

# )

# sf::st\_crs(bbox.sf) <- st\_crs(world)

#

# grat\_df <- grat\_df[,c(1,2,6)]

# colnames(grat\_df) <- c("x", "y", "linestring\_id")

# grat\_df.sf <- sfheaders::sf\_line(obj = grat\_df)

#

# sf::st\_crs(grat\_df.sf) <- st\_crs(world)

#Main map

# map <- ggplot() +

# geom\_sf(data = bbox.sf, fill=adjustcolor("white", alpha.f=0.45), col="white") +

# geom\_sf(data = grat\_df.sf, col="darkgrey", lty=2) +

# geom\_sf(data = world, fill = "black", col = "white") +

# theme(panel.background=element\_rect(fill="white"),

# panel.grid = element\_blank(),

# axis.title.x=element\_blank(),

# axis.text.x=element\_blank(),

# axis.ticks.x=element\_blank(),

# axis.title.y=element\_blank(),

# axis.text.y=element\_blank(),

# axis.ticks.y=element\_blank()

# )

#Plot polygons areas

mergedArea <- c()

for(i in 1:length(areaName)){

toFortify <- get(paste("area", i, sep="\_"))

toFortify <- fortify(toFortify)

toFortify$group <-paste(areaName[i], toFortify$piece)

toFortify$colour <- gsub("\_", " ", areaName[i],)#areaNameCorrected[i]#colourArea[i]

mergedArea <- rbind(mergedArea, toFortify)

#add to ggplot

#map <- map + geom\_polygon(data = toFortify, aes(x = long, y = lat, group = group), col = colourArea[i], fill = colourArea[i])

}

###----

### OLD WAY: when using sf package

###----

# centroid.sf <- st\_as\_sf(centroid, coords=c("long", "lat"), crs=st\_crs(world))

# library(sfheaders)

# mergedArea.sf <- sfheaders::sf\_polygon( obj = mergedArea

# , x = "long"

# , y = "lat"

# , polygon\_id = "group"

# )

# sf::st\_crs(mergedArea.sf) <- st\_crs(world)

#

# #Readd colour

# mergedArea.sf$colour <- unique(mergedArea[,c(7,8)])[,2]

# mergedArea, coords=c("long", "lat"), crs=st\_crs(world))

# st\_cast(mergedArea.sf, to="POLYGON")

#

library(ggmap)

library(scales)

#Getting the stammen background map and adding the graticule

mapStammen <- get\_stamenmap( bbox = c(left = -180, bottom = -66, right = 180, top = 66), zoom = 4, maptype = "watercolor")#maptype = "terrain-background")

# plot(mergedArea.sf, add=TRUE)

mapPlot <- ggmap(mapStammen) #+

# theme\_void() +

# theme(

# panel.border = element\_rect(colour = "white", fill=NA, size=2)

# )

for(k in 0:max(as.numcharac(grat\_df$id))){

mapPlot <- mapPlot +

geom\_path(data = grat\_df %>% filter(as.numcharac(id)==k), aes(x=long, y=lat), colour="white", linetype="dashed")

}

#Adding the coloured cropped polygons of areas

for(i in 1:length(areaName)){

polygonToAdd <- get(paste("area", i, sep="\_"))

for(j in 1:length(polygonToAdd@polygons[[1]]@Polygons)){#Some problem with fortified when multiple polygons. Trying using one sub-polygon at a time.

toPlot <- sp::Polygons(list(polygonToAdd@polygons[[1]]@Polygons[[j]]), ID = "A")

toPlot <- sp::SpatialPolygons(list(toPlot))

fortifiedArea <- fortify(toPlot)

mapPlot <- mapPlot + geom\_polygon(data = fortifiedArea, aes(x = long, y= lat), fill=colourArea[i], col=colourArea[i], lwd=0.5) +

geom\_label(data = centroid[i,], aes(x=long, y=lat), label=(1:length(colourArea))[i],

fill = ifelse(i != 1 & i != 2, "white", colourArea[i]),

col = "black",

nudge\_y=centroid$nudge\_y[i],

label.r = unit(0.4, "lines"),

size = 2)

}

}

mapPlot <- mapPlot +

# scale\_color\_manual(name='',

# breaks=c(

# "East Madagascar",

# "West Madagascar",

# "West Africa",

# "Central Africa",

# "East/South Africa",

# "Central America",

# "Northern South America",

# "Southern South America",

# "West Asia",

# "Central/East Asia",

# "South Asia",

# "Asian islands"),

# values=c(

# "East Madagascar"=colourArea[1],

# "West Madagascar"=colourArea[1],

# "West Africa"=colourArea[1],

# "Central Africa"=colourArea[1],

# "East/South Africa"=colourArea[1],

# "Central America"=colourArea[1],

# "Northern South America"=colourArea[1],

# "Southern South America"=colourArea[1],

# "West Asia"=colourArea[1],

# "Central/East Asia"=colourArea[1],

# "South Asia"=colourArea[1],

# "Asian islands"=colourArea[1])

# )+

theme(

text = element\_text(size = 10),

legend.key = element\_rect(size = 4),

legend.key.size = unit(1, 'lines'),

legend.position="bottom",

axis.text=element\_text(size=10),

axis.title=element\_text(size=15,face="bold")

) +

xlab("Longitude") +

ylab("Latitude") +

scale\_x\_continuous(breaks = c(seq(from=-165, to=-15, by=30), 0, seq(from=15, to=165, by=30)), expand = c(0, 0))# +

#scale\_y\_continuous(breaks = pretty(-66:66, n = 10))

library(cowplot)

# Create grid of plots

plot\_grid(mapPlot,

my\_legend,

ncol = 1,

rel\_heights = c(2.25,1))

##--------

###OLD WAY

##-------

# map <- map +

# geom\_sf(data = mergedArea.sf, aes(fill = colour)) +

# geom\_sf\_label(data = centroid.sf, aes(label = 1:nrow(centroid)),

# fill = c(colourArea[11], colourArea[12], rep("white", times=10)),

# col = c("black", "white", rep("black", times=10)),#colourArea[3:12]),

# nudge\_y=centroid$nudge\_y,

# label.r = unit(0.4, "lines"),

# size = 2) +

# coord\_sf(crs = proj.map, expand = F) +

# scale\_fill\_manual(values = colourArea, labels=c("Central Africa", "South/East Africa", "West Africa", "Central America", "North of South America", "South of South America", "Central/East Asia", "Asian islands", "South Asia", "West Asia", "East Madagascar", "West Madagascar")) +

# labs(fill = "") +

# theme(

# text = element\_text(size = 10),

# legend.key = element\_rect(size = 4),

# legend.key.size = unit(1, 'lines'),

# legend.position="bottom")

# map

# # #Just to see the difference as pinpointed by the warning

# # # geosphere::areaPolygon(areaTransitory)

# # # gArea(areaTransitory)

# # # really false

# # # geosphere::centroid(areaTransitory)

# # # gCentroid(areaTransitory)

# # #ok

# #

# # layout(mat=t(c(1,2)), widths=c(40,40), heights=c(40))

# # par(mar=c(0, 0, 0, 0), mgp=c(2, 0.5, 0), xpd=TRUE)

# #

# # Add figure interaction here if needed

# ####

# ## Fig map

# ####

#

# #Create the map of the geographic area

# #Have background

# maps::map("world", fill=TRUE, col="lightgray", bg="white", border=NA, mar = c(0, 0, 0, 0))#, ylim=c(-60, 50))

#

# # addLabel(x=0.05, y=0.075, label="A", radius=7, circle=TRUE, circle.bg="black", font.col="white")

# #

#

# for(i in 1:length(areaName)){

# plot(get(paste("area", i, sep="\_")), col=colourArea[i], border=colourArea[i], add=TRUE) #border="black",

# }

# #Have borders

# #plot(worldMap, col=NA, border="white",bg="white", lwd=0.1, add=TRUE)

# # for(i in 1:length(areaName)){

# # plot(get(paste("area", i, sep="\_")), col=NA, border="black", add=TRUE)

# # }

# points(x=centroid[,1], y=centroid[,2], pch=19, col=c(colourArea[1], colourArea[2], rep("white", times=10)), cex=1.3)

# points(x=centroid[,1], y=centroid[,2], cex=1.3, col=c("white", "white", rep("black", times=10)))

# text(x=centroid[,1], y=centroid[,2], labels=1:length(areaName), cex=0.5, col=c("white", "white", rep("black", times=10)), adj=c(0.5,0.5))

```

\clearpage

```{r phylogeny, fig.pos='H', include=TRUE, warning = FALSE, message = FALSE, fig.width=7, fig.height=7, fig.cap=paste("Levels of species sympatry vary across the primate phylogeny | Primate phylogeny from the consensus tree of the 10kTrees project is depicted in the center, together with abbreviated species names. The corresponding non-abbreviated names can be found using Appendix Figure \\@ref(fig:figdata). Sympatric frugivorous (based on a frugivory threshold of ", frugivoryThresholdVector[1], "% and folivory threshold of ", folivoryThresholdVector[1], "%) species are linked by light grey lines. The geographic areas occupied by a species are depicted by coloured rectangles. Presence was assessed given an overlap between the species range and the geographic area of ", geographicThresholdVector[1]\*100, "%.", sep="")}

# ####

# ## Fig interaction

# ####

#Tree

tree <- read.tree("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Raw\_data/Tree/Tree\_diet.nex")

tree <- drop.tip(tree,

tree $tip.label[

which(tree$tip.label

%nin% summaryDataForPlot$SpeciesForPhylogeny)])

#Create geography df

geoBinary <- as.data.frame(summaryDataForPlot[,c(3,which(colnames(summaryDataForPlot)=="geographicCode"))])

colnames(geoBinary) <- c("SpeciesPhylo", "Loc")

#Create species ID

hc = as.hclust(tree)#bird.orders)

labels = hc$labels # name of birds

labels.tordc <- as.data.frame(labels)

colnames(labels.tordc) <- "Name"

labels.tordc <- separate(labels.tordc, col="Name", into=c("Name1", "Name2", "Name3"), sep="\_")

labels.rdc <- apply(labels.tordc, 1, function(x){

if(!is.na(x[3])){

paste(toupper(substr(x[1], 1, 1)), ". ", substr(x[2], 1, 3), ". ", substr(x[3], 1, 1), ".", sep="")

} else{paste(toupper(substr(x[1], 1, 1)), ". ", substr(x[2], 1, 3), sep="")

}

}

)

#Match to have right order for geography

locationSpecies <- geoBinary$Loc[match(labels, geoBinary$SpeciesPhylo)]

colLoc <- colourArea

#Match to have diet

dietSpecies <- summaryDataForPlot$DietaryGuild[match(labels, summaryDataForPlot$SpeciesForPhylogeny)]

#Getting species labels abbreviated

speciesLabels <- hc$labels#Should be in the tree order

#Create the circos plot linking species based on their diet and geography

circos.clear()

circos.par(gap.degree=0, gap.after=0, cell.padding=c(0,0,0,0), track.margin = c(0, 0), "canvas.xlim" = c(-1.1, 1.1), "canvas.ylim" = c(-1.1, 1.1))

circos.initialize(speciesLabels, xlim = c(0, 1))

# #Add family

# circos.track(ylim = c(0, 1), bg.border = NA, track.height = 0.1, track.margin=c(0.01, 0.01),

# panel.fun = function(x, y) {

# i=CELL\_META$sector.numeric.index

# circos.rect(CELL\_META$cell.xlim[1],CELL\_META$cell.ylim[1], CELL\_META$cell.xlim[2],CELL\_META$cell.ylim[2], col="white", border=NA)

# })

#

# circos.track(ylim = c(0, 1), bg.border = NA, track.height = 0.1, track.margin=c(0.01, 0.01),

# panel.fun = function(x, y) {

# i=CELL\_META$sector.numeric.index

# circos.rect(CELL\_META$cell.xlim[1],CELL\_META$cell.ylim[1], CELL\_META$cell.xlim[2],CELL\_META$cell.ylim[2], col="white", border=NA)

# })

#

# for(i in 1:length(unique(summaryDataForPlot$Family))){

# speciesForPlotFamily <- speciesLabels[speciesLabels %in% summaryDataForPlot$SpeciesForPhylogeny[summaryDataForPlot$Family %in% unique(summaryDataForPlot$Family)[i]]]

# if(length(speciesForPlotFamily) > 0){

# highlight.sector(speciesForPlotFamily, track.index = 1, col = adjustcolor("black", alpha.f=0.15), padding = c(0, 0.2, 0, 0),

# text = unique(summaryDataForPlot$Family)[i], cex = 0.5, text.col = "white", niceFacing = TRUE)

# }

# }

#Species name + area it belongs to

circos.track(ylim = c(0, 1), bg.border = NA, track.height = 0.1, track.margin=c(0.01, 0.01),

panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

circos.text(CELL\_META$xcenter, 1, labels.rdc[i], adj = c(0, 0),

facing = "clockwise", niceFacing = TRUE,

col = "black", cex = 0.75, font=3)

geo <- as.numcharac(unlist(strsplit(locationSpecies[i], "")))

for(g in 1:length(geo)){

if(geo[g]==1){

#circos.points(CELL\_META$xcenter,0.75/length(geo)\*(2\*g-1)/2, col=as.character(colLoc[g]), pch=19, cex=0.2)

circos.rect(CELL\_META$cell.xlim[1],0.75/length(geo)\*(g-1), CELL\_META$cell.xlim[2], 0.75/length(geo)\*(g), col=as.character(colLoc[g]), border=NA)

}

}

})

#Plot the geographic links

for(i in 1:length(speciesLabels)){

#locI <- which(strsplit(locationSpecies[i], "")==1)

for(j in i:length(speciesLabels)){

#locJ <- which(strsplit(locationSpecies[j], "")==1)

product <- as.numcharac(unlist(strsplit(locationSpecies[j], "")))\*as.numcharac(unlist(strsplit(locationSpecies[i], "")))

if(i==j|(length(unique(product))==1&unique(product)[1]==0)){

#Do nothing

}

else{

if(dietSpecies[i]=="Fruit"&dietSpecies[i]==dietSpecies[j]){

# colour <- as.data.frame(table(colLoc[which(product==1)]))

# if(is.finite(max(colour$Freq))){

# }else{

# print(c(i,j))

# }

# colour <- colour[colour$Freq==max(colour$Freq),1][1]

circos.link(speciesLabels[i], runif(1, 0, 1), speciesLabels[j], runif(1, 0, 1), lwd=0.2, col=adjustcolor("black",alpha.f=0.15))#"lightgray")#adjustcolor(as.character(colour), alpha.f=0.9))

}

else{

#circos.link(speciesLabels[i], runif(1, 0, 1), speciesLabels[j], runif(1, 0, 1), lwd=1, col="lightgray")

}

}

}

}

circos.clear()

#Plot the phylogenetic tree in a new circular plot

n = length(labels) # number of species

dend = as.dendrogram(hc)

par(new = TRUE) # <- magic

circos.par("canvas.xlim" = c(-1.05, 1.05), "canvas.ylim" = c(-1.25, 1.25))

circos.initialize("a", xlim = c(0, n)) # only one sector

# circos.track(ylim = c(0, 1), bg.border = NA, track.height = 0.3,

# panel.fun = function(x, y) {

# for(i in seq\_len(n)) {

# circos.text(i-0.5, 0, labels.rdc[i], adj = c(0, 0.5),

# facing = "clockwise", niceFacing = TRUE,

# col = "black", cex = 0.2, font=3)

# }

# })

#suppressPackageStartupMessages(library(dendextend))

#dend = color\_branches(dend, k = 6, col = 1:6)

dend\_height = attr(dend, "height")

circos.track(ylim = c(0, dend\_height), bg.border = NA,

track.height = 0.95, panel.fun = function(x, y) {

circos.dendrogram(dend)

})

circos.clear()

```

\clearpage

<!-- A 3D brain from \*Homo sapiens\* is depicted (\*neurobase\* package [@neurobase], \*misc3d\* package [@misc3d]). The arrows indicate the sagital and frontal axes. -->

<!-- , although the neocortex was not coloured for readability since it corresponds to the external layer of the cerebral hemisphere -->

```{r figbrain, fig.pos='H', include=TRUE, warning = FALSE, message = FALSE, fig.width=7, fig.height=7, fig.cap=paste("Variations in relative brain size areas among frugivorous primates | (Left) Circular plot of the relative sizes of the different brain areas. Colours indicates the rows for the different brain areas. The darker background emphasises when values are above average, while the lighter background emphasises when values are below average. The mean value (after scaling and based on one random sampling among possible values, but see \\@ref(fig:figvariabilitydata) for visualization of measure variability) for the Encephalization Quotient (EQ) or relative size of brain regions, when available, is depicted by a plain circle for frugivorous species. The frugivorous threshold was fixed to ", frugivoryThresholdVector[1], "% and the folivory threshold to ", folivoryThresholdVector[1], "%. (Right) The different studied brain areas (human brain as an illustration). In short, the MOB is involved in immediate olfactory information processing, the Neocortex and the Cerebellum support working memory and memory consolidation of immediate sensory information processing [@wiltgen2004new; @koziol2014consensus; @sokolov2017cerebellum], and the Hippocampus supports a working memory and a long-term spatio-temporal memory [@burgess2002human]. The Striatum is involved in social information processing [@baez2013role].", sep="")}

library(RColorBrewer)

colourEQ <- "gray"

colourEQbis <- "lightgray"

colourEQdark <- "black"

colourHippocampus <- rgb(0,128,0,maxColorValue = 255)

colourHippocampusbis <- rgb(95,211,95,maxColorValue = 255)#pastellize(colourHippocampus)

colourHippocampusdark <- rgb(0,208,0,maxColorValue = 255)

colourStriatum <- rgb(255,204,0,maxColorValue = 255)

colourStriatumbis <- rgb(255,230,128,maxColorValue = 255)#pastellize(colourStriatum)

colourStriatumdark <- "darkgoldenrod2"

colourNeocortex <- rgb(255,213,213,maxColorValue = 255)

colourNeocortexbis <- "white"#rgb(255,213,213,maxColorValue = 255)#pastellize(colourNeocortex)

colourNeocortexdark <- rgb(255,175,175,maxColorValue = 255)

colourCerebellum <- rgb(255,128,128,maxColorValue = 255)

colourCerebellumbis <- rgb(255,170,170,maxColorValue = 255)#pastellize(colourCerebellum)

colourCerebellumdark <- rgb(255,64,64,maxColorValue = 255)

colourMOB <- rgb(255,0,0,maxColorValue = 255)

colourMOBbis <- rgb(255,95,95,maxColorValue = 255)#pastellize(colourMOB)

colourMOBdark <- "darkred"

colourVector <- c("darkgrey", brewer.pal(n = 5, name = "Set1")[1:5])

colourVectorbis <- c("lightgray", brewer.pal(n = 5, name = "Pastel1")[1:5])

colour.circle.points <- c("black", "darkred", "darkblue", "purple4", "darkgreen", "orange4")

###

## Fig brain values / circular

###

summaryDataForPlot$EQ <- summaryDataForPlot$Brain\*1.036\*(10\*\*-3)/(0.085\*summaryDataForPlot$Bodymass\*\*0.775)

summaryDataForPlot$ratioNeocortex <- summaryDataForPlot$Neocortex/summaryDataForPlot$Bodymass

summaryDataForPlot$ratioHippocampus <- summaryDataForPlot$Hippocampus/summaryDataForPlot$Bodymass

summaryDataForPlot$ratioCerebellum <- summaryDataForPlot$Cerebellum/summaryDataForPlot$Bodymass

summaryDataForPlot$ratioStriatum <- summaryDataForPlot$Striatum/summaryDataForPlot$Bodymass

summaryDataForPlot$ratioMOB <- summaryDataForPlot$MOB/summaryDataForPlot$Bodymass

#Brain data

relativeValueEQ <- scale(summaryDataForPlot$EQ[match(speciesLabels, summaryDataForPlot$SpeciesForPhylogeny)])#runif(length(speciesLabels), -1, 1)

relativeValueNeocortex <- scale(summaryDataForPlot$ratioNeocortex[match(speciesLabels, summaryDataForPlot$SpeciesForPhylogeny)])

relativeValueHippocampus <- scale(summaryDataForPlot$ratioHippocampus[match(speciesLabels, summaryDataForPlot$SpeciesForPhylogeny)])

relativeValueCerebellum <- scale(summaryDataForPlot$ratioCerebellum[match(speciesLabels, summaryDataForPlot$SpeciesForPhylogeny)])

relativeValueStriatum <- scale(summaryDataForPlot$ratioStriatum[match(speciesLabels, summaryDataForPlot$SpeciesForPhylogeny)])

relativeValueMOB <- scale(summaryDataForPlot$ratioMOB[match(speciesLabels, summaryDataForPlot$SpeciesForPhylogeny)])

layout(mat=cbind(c(1,1), c(2,3)), widths=c(35,15), heights=c(15,35))

par(mar=c(0, 0, 0, 0), mgp=c(2, 0.5, 0), xpd=TRUE)

# plot(0, 0, type="n")

library(circlize)

circos.clear()

circos.par(gap.degree=0, gap.after=0, cell.padding=c(0,0,0,0), track.margin=c(0, 0))

circos.initialize(speciesLabels, xlim = c(0, 1))

#Species name

circos.track(ylim = c(0, 20), bg.border = NA, track.height = 0.05, track.margin=c(0.01, 0.1),

panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

circos.text(CELL\_META$xcenter, 0, labels.rdc[i], adj = c(0, 0),

facing = "clockwise", niceFacing = TRUE,

col = "black", cex = 0.6, font=3)

})

#

#Background

circos.track(ylim = c(0, 1), bg.border = colourEQ, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourEQ, border=colourEQ)

}, track.height = 1/15)

circos.track(ylim = c(0, 1), bg.border = colourEQbis, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourEQbis, border=colourEQbis)

}, track.height = 1/15)

#Background

circos.track(ylim = c(0, 1), bg.border = colourStriatum, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourStriatum, border=colourStriatum)

}, track.height = 1/15)

circos.track(ylim = c(0, 1), bg.border = colourStriatumbis, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourStriatumbis, border=colourStriatumbis)

}, track.height = 1/15)

#Background

circos.track(ylim = c(0, 1), bg.border = colourHippocampus, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourHippocampus, border=colourHippocampus)

}, track.height = 1/15)

circos.track(ylim = c(0, 1), bg.border = colourHippocampusbis, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourHippocampusbis, border=colourHippocampusbis)

}, track.height = 1/15)

#Background

circos.track(ylim = c(0, 1), bg.border = colourMOB, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourMOB, border=colourMOB)

}, track.height = 1/15)

circos.track(ylim = c(0, 1), bg.border = colourMOBbis, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourMOBbis, border=colourMOBbis)

}, track.height = 1/15)

#Background

circos.track(ylim = c(0, 1), bg.border = colourCerebellum, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourCerebellum, border=colourCerebellum)

}, track.height = 1/15)

circos.track(ylim = c(0, 1), bg.border = colourCerebellumbis, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourCerebellumbis, border=colourCerebellumbis)

}, track.height = 1/15)

#Background

circos.track(ylim = c(0, 1), bg.border = colourNeocortex, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourNeocortex, border=colourNeocortex)

}, track.height = 1/15)

circos.track(ylim = c(0, 1), bg.border = colourNeocortexbis, panel.fun = function(x, y) {

circos.rect(0, 0, 1, 1, col=colourNeocortexbis, border=colourNeocortexbis)

}, track.height = 1/15)

library(plotrix)

#Main circle

for(i in 1:13){

draw.circle(x=0,y=0,0.91-1/15-(i-1)\*1/15, col=NA, border="white")

}

#increment of 0.5

for(i in 1:26){

draw.circle(x=0,y=0,0.91-1/15-(i-1)\*1/15/2, col=NA, border="white", lty=2)

}

#Value

#EQ

absMax <- max(abs(relativeValueEQ), na.rm=TRUE)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=2, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

#circos.rect(0, 0, 1, 1, col=colourPositive, border=colourPositive)

if(is.na(relativeValueEQ[i])){} else{

if(relativeValueEQ[i] > 0 & dietSpecies[i]=="Fruit"){

#circos.points(CELL\_META$xcenter, relativeValueEQ[i]/absMax, pch=19, col=colourEQdark, cex=0.7)

circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueEQ[i]/absMax, col=colourEQdark, lty=3)

}

else if(relativeValueEQ[i] > 0 & dietSpecies[i]=="Leaf"){

#circos.points(CELL\_META$xcenter, relativeValueEQ[i]/absMax, pch=21, col=colourEQdark, bg="white", cex=0.7)

circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueEQ[i]/absMax, col=colourEQdark, lty=3)

}

else{}

}

}, track.height = 0.1)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=3, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

if(is.na(relativeValueEQ[i])){} else{

#circos.rect(0, 0, 1, 1, col=colourNegative, border=colourNegative)

if(relativeValueEQ[i] <= 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueEQ[i]/absMax, col=colourEQdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueEQ[i]/absMax, pch=19, col=colourEQdark, cex=0.7)

}

else if(relativeValueEQ[i] <= 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueEQ[i]/absMax, col=colourEQdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueEQ[i]/absMax, pch=21, col=colourEQdark, bg="white", cex=0.7)

}

else{}

}

}, track.height = 0.1)

#Striatum

absMax <- max(abs(relativeValueStriatum), na.rm=TRUE)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=4, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

#circos.rect(0, 0, 1, 1, col=colourPositive, border=colourPositive)

if(is.na(relativeValueStriatum[i])){} else{

if(relativeValueStriatum[i] > 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueStriatum[i]/absMax, col=colourStriatumdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueStriatum[i]/absMax, pch=19, col=colourStriatumdark, cex=0.65)

}

else if(relativeValueStriatum[i] > 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueStriatum[i]/absMax, col=colourStriatumdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueStriatum[i]/absMax, pch=21, col=colourStriatumdark, bg="white", cex=0.65)

}

else{}

}

}, track.height = 0.1)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=5, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

if(is.na(relativeValueStriatum[i])){} else{

#circos.rect(0, 0, 1, 1, col=colourNegative, border=colourNegative)

if(relativeValueStriatum[i] <= 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueStriatum[i]/absMax, col=colourStriatumdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueStriatum[i]/absMax, pch=19, col=colourStriatumdark, cex=0.65)

}

else if(relativeValueStriatum[i] <= 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueStriatum[i]/absMax, col=colourStriatumdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueStriatum[i]/absMax, pch=21, col=colourStriatumdark, bg="white", cex=0.65)

}

else{}

}

}, track.height = 0.1)

#Hippocampus

absMax <- max(abs(relativeValueHippocampus), na.rm=TRUE)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=6, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

#circos.rect(0, 0, 1, 1, col=colourPositive, border=colourPositive)

if(is.na(relativeValueHippocampus[i])){} else{

if(relativeValueHippocampus[i] > 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueHippocampus[i]/absMax, col=colourHippocampusdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueHippocampus[i]/absMax, pch=19, col=colourHippocampusdark, cex=0.55)

}

else if(relativeValueHippocampus[i] > 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueHippocampus[i]/absMax, col=colourHippocampusdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueHippocampus[i]/absMax, pch=21, col=colourHippocampusdark, bg="white", cex=0.55)

}

else{}

}

}, track.height = 0.1)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=7, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

if(is.na(relativeValueHippocampus[i])){} else{

#circos.rect(0, 0, 1, 1, col=colourNegative, border=colourNegative)

if(relativeValueHippocampus[i] <= 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueHippocampus[i]/absMax, col=colourHippocampusdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueHippocampus[i]/absMax, pch=19, col=colourHippocampusdark, cex=0.55)

}

else if(relativeValueHippocampus[i] <= 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueHippocampus[i]/absMax, col=colourHippocampusdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueHippocampus[i]/absMax, pch=21, col=colourHippocampusdark, bg="white", cex=0.55)

}

else{}

}

}, track.height = 0.1)

#MOB

absMax <- max(abs(relativeValueMOB), na.rm=TRUE)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=8, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

#circos.rect(0, 0, 1, 1, col=colourPositive, border=colourPositive)

if(is.na(relativeValueMOB[i])){} else{

if(relativeValueMOB[i] > 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueMOB[i]/absMax, col=colourMOBdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueMOB[i]/absMax, pch=19, col=colourMOBdark, cex=0.65)

}

else if(relativeValueMOB[i] > 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueMOB[i]/absMax, col=colourMOBdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueMOB[i]/absMax, pch=21, col=colourMOBdark, bg="white", cex=0.65)

}

else{}

}

}, track.height = 0.1)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=9, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

if(is.na(relativeValueMOB[i])){} else{

#circos.rect(0, 0, 1, 1, col=colourNegative, border=colourNegative)

if(relativeValueMOB[i] <= 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueMOB[i]/absMax, col=colourMOBdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueMOB[i]/absMax, pch=19, col=colourMOBdark, cex=0.65)

}

else if(relativeValueMOB[i] <= 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueMOB[i]/absMax, col=colourMOBdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueMOB[i]/absMax, pch=21, col=colourMOBdark, bg="white", cex=0.65)

}

else{}

}

}, track.height = 0.1)

#Cerebellum

absMax <- max(abs(relativeValueCerebellum), na.rm=TRUE)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=10, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

#circos.rect(0, 0, 1, 1, col=colourPositive, border=colourPositive)

if(is.na(relativeValueCerebellum[i])){} else{

if(relativeValueCerebellum[i] > 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueCerebellum[i]/absMax, col=colourCerebellumdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueCerebellum[i]/absMax, pch=19, col=colourCerebellumdark, cex=0.5)

}

else if(relativeValueCerebellum[i] > 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueCerebellum[i]/absMax, col=colourCerebellumdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueCerebellum[i]/absMax, pch=21, col=colourCerebellumdark, bg="white", cex=0.5)

}

else{}

}

}, track.height = 0.1)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=11, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

if(is.na(relativeValueCerebellum[i])){} else{

#circos.rect(0, 0, 1, 1, col=colourNegative, border=colourNegative)

if(relativeValueCerebellum[i] <= 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueCerebellum[i]/absMax, col=colourCerebellumdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueCerebellum[i]/absMax, pch=19, col=colourCerebellumdark, cex=0.5)

}

else if(relativeValueCerebellum[i] <= 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueCerebellum[i]/absMax, col=colourCerebellumdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueCerebellum[i]/absMax, pch=21, col=colourCerebellumdark, bg="white", cex=0.5)

}

else{}

}

}, track.height = 0.1)

#Neocortex

absMax <- max(abs(relativeValueNeocortex), na.rm=TRUE)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=12, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

#circos.rect(0, 0, 1, 1, col=colourPositive, border=colourPositive)

if(is.na(relativeValueNeocortex[i])){} else{

if(relativeValueNeocortex[i] > 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueNeocortex[i]/absMax, col=colourNeocortexdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueNeocortex[i]/absMax, pch=19, col=colourNeocortexdark, cex=0.6)

}

else if(relativeValueNeocortex[i] > 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 0, CELL\_META$xcenter, relativeValueNeocortex[i]/absMax, col=colourNeocortexdark, lty=3)

circos.points(CELL\_META$xcenter, relativeValueNeocortex[i]/absMax, pch=21, col=colourNeocortexdark, bg="white", cex=0.6)

}

else{}

}

}, track.height = 0.1)

circos.track(ylim = c(0, 1), bg.border = NA, track.index=13, panel.fun = function(x, y) {

i=CELL\_META$sector.numeric.index

if(is.na(relativeValueNeocortex[i])){} else{

#circos.rect(0, 0, 1, 1, col=colourNegative, border=colourNegative)

if(relativeValueNeocortex[i] <= 0 & dietSpecies[i]=="Fruit"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueNeocortex[i]/absMax, col=colourNeocortexdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueNeocortex[i]/absMax, pch=19, col=colourNeocortexdark, cex=0.6)

}

else if(relativeValueNeocortex[i] <= 0 & dietSpecies[i]=="Leaf"){

#circos.segments(CELL\_META$xcenter, 1, CELL\_META$xcenter, 1 + relativeValueNeocortex[i]/absMax, col=colourNeocortexdark, lty=3)

circos.points(CELL\_META$xcenter, 1 + relativeValueNeocortex[i]/absMax, pch=21, col=colourNeocortexdark, bg="white", cex=0.6)

}

else{}

}

}, track.height = 0.1)

#Empty plot

par(mar=c(0, 0, 0, 0), mgp=c(2, 0.5, 0), xpd=TRUE)

emptyPlot()

# plot(0, 0, xlim=c(0,1), ylim=c(0,1), xlab="", ylab="", las=1, type="n", tcl=-0.25, bty="n",

# xaxt="n",xaxs="i",yaxs="i", yaxt="n", xpd=TRUE)

#

#Add brain

library(png)

brainIMG <- readPNG("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/brain\_draw.png")

addImg(brainIMG, x = 0.425, y = 0.5, width = 0.7)

# brainIMG <- readPNG("C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Plots/3dplot.png")

# addImg(brainIMG, x = 0.425, y = 0.65, width = 1.3)

#

# #Add circle contour

# draw.circle(x=0.45,y=0.55,0.435, col=NA, border="lightgray", lwd=2)

# draw.circle(x=0.45,y=0.55,0.405, col=NA, border="lightgray", lwd=2)

#

# par(mar=c(0, 0, 0, 0), mgp=c(2, 0.5, 0), xpd=TRUE)

# plot(0, 0, xlim=c(0,1), ylim=c(0,1), xlab="", ylab="", las=1, type="n", tcl=-0.25, bty="n",

# xaxt="n",xaxs="i",yaxs="i", yaxt="n", xpd=TRUE)

# colourHip=colourHippocampus

# colourCereb=colourCerebellum

# colourOlf=colourMOB

# colourStri=colourStriatum

par(mar=c(0, 0, 0, 0), mgp=c(2, 0.5, 0), xpd=TRUE)

emptyPlot()

legend(x=0.1, y=1, yjust=1, legend = c("EQ", "Striatum", "Hippocampus", "MOB", "Cerebellum", "Neocortex", "Frugivorous species", "Folivorous species"), cex = 1, fill = c(colourEQ, colourStriatum, colourHippocampus, colourMOB, colourCerebellum, colourNeocortex, NA, NA), pch=c(NA, NA, NA, NA, NA, NA, 19, 1), border=c("black", "black", "black", "black", "black", "black", "white", "white"), col=c(NA, NA, NA, NA, NA, NA, "black", "black"), bty="n", seg.len=0.75)

```

\clearpage

```{r figresultsevolution, fig.pos='H', include=TRUE, warning = FALSE, message = FALSE, fig.width=7, fig.height=6, fig.cap="The evolution of the Hippocampus and Striatum in frugivorous primates are best fitted by models of trait evolution considering species sympatry | Plotted is the AICc weight, a measure of relative support for a given model, for models not considering species sympatry (BM, OU, EB) or considering species sympatry (MC, DD$\_{lin}$, DD$\_{exp}$). The points represent the average AICc weight obtained (when considering the six models from the same run), while the vertical bars indicate the standard deviation given all tested conditions (see [Models of trait evolution: does species sympatry shape brain size evolution?])."}

layout(mat=rbind(c(1,2,3), c(4,5,6), c(7,7,7)), widths=c(5,5,5), heights=c(5,5,1))

par(mar=c(3.5, 3, 2, 0.5), mgp=c(2, 0.5, 0), xpd=TRUE)

#note: 1= second run for frugivory 20%

#note: \_2= first run for frugivory 20%

## EQ

plot(

x=0, y=0, xlab="", ylab="", cex.sub=1.6,

xlim=c(0,7), ylim=c(0,1.2),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

rect(xleft=0, xright=3.5, ybottom=0, ytop=1, col=adjustcolor("royalblue", alpha.f=0.2), border=NA)

rect(xleft=3.5, xright=7, ybottom=0, ytop=1, col=adjustcolor("blue", alpha.f=0.2), border=NA)

addGrid(xmin=0, xmax=7, xintsmall=0.25, xintbig=1, ymin=0, ymax=1, yintsmall=0.05, yintbig=0.2, axisPlot=FALSE)

axis(side=2, at=seq(from=0, to=1, by=0.2), labels=seq(from=0, to=1, by=0.2), las=2, tcl=-0.25)

mtext(side=2, line=2, at=0.5, text="AICc weight", cex=0.85)

segments(x0 = 3.5, y0=0, x1=3.5, y1=1, lty=2)

text(x=1:6, y=rep(-0.1, times=6), labels=models, cex=0.9, xpd=TRUE)

for(i in 1:6){

meanPt <- mean(as.numcharac(summaryEQFrugivory[, ncol(summaryEQFrugivory)-6+i]))

sd <- sd(as.numcharac(summaryEQFrugivory[, ncol(summaryEQFrugivory)-6+i]))

#sd <- sd/nrow(summaryEQFrugivory) #error not sd

errorBars(location=i, meanPt=meanPt, barValue=sd, refUnit=1, col="black", minValue=0, maxValue=1, horiz=FALSE)

points(x=i, y=meanPt, pch=19, col="black", xpd=TRUE)

}

#b and r are the rate for density dependance (DD) of the speciation rate. If positive, positive DD, otherwise, negative.

#add their values below:

text(x=c(4,5,6), y=c(-0.2, -0.2),

labels=c(

"r ~",

round(mean(as.numcharac(summaryEQFrugivory$DDlingeo.b)), digit=3),

round(mean(as.numcharac(summaryEQFrugivory$DDexpgeo.r)), digit=3)

), cex=0.8, xpd=TRUE)

draw.circle(x=0.3,y=1.1,0.35, col=colourEQ, border=NA)

#text(x=0.3, y=1.1, cex=1.15, labels="1", xpd=TRUE, col="white", font=2)

text(x=0.75, y=1.1, labels="EQ", xpd=TRUE, col="black", font=2, cex=1.15, adj=0)

##-------------

##------------

#Striatum

plot(

x=0, y=0, xlab="", ylab="", cex.sub=1.6,

xlim=c(0,7), ylim=c(0,1.2),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

rect(xleft=0, xright=3.5, ybottom=0, ytop=1, col=adjustcolor("royalblue", alpha.f=0.2), border=NA)

rect(xleft=3.5, xright=7, ybottom=0, ytop=1, col=adjustcolor("blue", alpha.f=0.2), border=NA)

addGrid(xmin=0, xmax=7, xintsmall=0.25, xintbig=1, ymin=0, ymax=1, yintsmall=0.05, yintbig=0.2, axisPlot=FALSE)

#axis(side=2, at=seq(from=0, to=1, by=0.2), labels=seq(from=0, to=1, by=0.2), las=2, tcl=-0.25)

#segments(x0 = -1, x1 = -1, y0 = 0, y1 = 1, lty = 2, col = colourStriatum)

segments(x0 = 3.5, y0=0, x1=3.5, y1=1, lty=2)

text(x=1:6, y=rep(-0.1, times=6), labels=models, cex=0.75, xpd=TRUE)

for(i in 1:6){

meanPt <- mean(as.numcharac(summaryStriatumFrugivory[, ncol(summaryStriatumFrugivory)-6+i]))

sd <- sd(as.numcharac(summaryStriatumFrugivory[, ncol(summaryStriatumFrugivory)-6+i]))

#sd <- sd/nrow(summaryStriatumFrugivory) #error not sd

errorBars(location=i, meanPt=meanPt, barValue=sd, refUnit=1, col="black", minValue=0, maxValue=1, horiz=FALSE)

points(x=i, y=meanPt, pch=19, col="black", xpd=TRUE)

}

draw.circle(x=0.3,y=1.1,0.35, col=colourStriatum, border=NA)

#text(x=0.3, y=1.1, cex=1.15, labels="2", xpd=TRUE, col="white", font=2)

text(x=0.75, y=1.1, labels="Striatum", xpd=TRUE, col="black", font=2, cex=1.15, adj=0)

#b and r are the rate for density dependance (DD) of the speciation rate. If positive, positive DD, otherwise, negative.

#add their values below:

text(x=c(4,5,6), y=c(-0.2, -0.2),

labels=c(

"r ~",

round(mean(as.numcharac(summaryStriatumFrugivory$DDlingeo.b)), digit=3),

round(mean(as.numcharac(summaryStriatumFrugivory$DDexpgeo.r)), digit=3)

), cex=0.8, xpd=TRUE)

##------------

##------------

#Hippocampus

plot(

x=0, y=0, xlab="", ylab="", cex.sub=1.6,

xlim=c(0,7), ylim=c(0,1.2),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

rect(xleft=0, xright=3.5, ybottom=0, ytop=1, col=adjustcolor("royalblue", alpha.f=0.2), border=NA)

rect(xleft=3.5, xright=7, ybottom=0, ytop=1, col=adjustcolor("blue", alpha.f=0.2), border=NA)

addGrid(xmin=0, xmax=7, xintsmall=0.25, xintbig=1, ymin=0, ymax=1, yintsmall=0.05, yintbig=0.2, axisPlot=FALSE)

# axis(side=2, at=seq(from=0, to=1, by=0.2), labels=seq(from=0, to=1, by=0.2), las=2, tcl=-0.25)

segments(x0 = 3.5, y0=0, x1=3.5, y1=1, lty=2)

text(x=1:6, y=rep(-0.1, times=6), labels=models, cex=0.9, xpd=TRUE)

for(i in 1:6){

meanPt <- mean(as.numcharac(summaryHippocampusFrugivory[, ncol(summaryHippocampusFrugivory)-6+i]))

sd <- sd(as.numcharac(summaryHippocampusFrugivory[, ncol(summaryHippocampusFrugivory)-6+i]))

#sd <- sd/nrow(summaryHippocampusFrugivory) #error not sd

errorBars(location=i, meanPt=meanPt, barValue=sd, refUnit=1, col="black", minValue=0, maxValue=1, horiz=FALSE)

points(x=i, y=meanPt, pch=19, col="black", xpd=TRUE)

}

draw.circle(x=0.3,y=1.1,0.35, col=colourHippocampus, border=NA)

#text(x=0.3, y=1.1, cex=1.15, labels="4", xpd=TRUE, col="white", font=2)

text(x=0.75, y=1.1, labels="Hippocampus", xpd=TRUE, col="black", font=2, cex=1.15, adj=0)

#b and r are the rate for density dependance (DD) of the speciation rate. If positive, positive DD, otherwise, negative.

#add their values below:

text(x=c(4,5,6), y=c(-0.2, -0.2),

labels=c(

"r ~",

round(mean(as.numcharac(summaryHippocampusFrugivory$DDlingeo.b)), digit=3),

round(mean(as.numcharac(summaryHippocampusFrugivory$DDexpgeo.r)), digit=3)

), cex=0.8, xpd=TRUE)

##------------

##-------------

#MOB

plot(

x=0, y=0, xlab="", ylab="", cex.sub=1.6,

xlim=c(0,7), ylim=c(0,1.2),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

rect(xleft=0, xright=3.5, ybottom=0, ytop=1, col=adjustcolor("royalblue", alpha.f=0.2), border=NA)

rect(xleft=3.5, xright=7, ybottom=0, ytop=1, col=adjustcolor("blue", alpha.f=0.2), border=NA)

addGrid(xmin=0, xmax=7, xintsmall=0.25, xintbig=1, ymin=0, ymax=1, yintsmall=0.05, yintbig=0.2, axisPlot=FALSE)

axis(side=2, at=seq(from=0, to=1, by=0.2), labels=seq(from=0, to=1, by=0.2), las=2, tcl=-0.25)

mtext(side=2, line=2, at=0.5, text="AICc weight", cex=0.85)

#segments(x0 = -1, x1 = -1, y0 = 0, y1 = 1, lty = 2, col = colourMOB)

segments(x0 = 3.5, y0=0, x1=3.5, y1=1, lty=2)

text(x=1:6, y=rep(-0.1, times=6), labels=models, cex=0.9, xpd=TRUE)

for(i in 1:6){

meanPt <- mean(as.numcharac(summaryMOBFrugivory[, ncol(summaryMOBFrugivory)-6+i]))

sd <- sd(as.numcharac(summaryMOBFrugivory[, ncol(summaryMOBFrugivory)-6+i]))

#sd <- sd/nrow(summaryMOBFrugivory) #error not sd

errorBars(location=i, meanPt=meanPt, barValue=sd, refUnit=1, col="black", minValue=0, maxValue=1, horiz=FALSE)

points(x=i, y=meanPt, pch=19, col="black", xpd=TRUE)

}

draw.circle(x=0.3,y=1.1,0.35, col=colourMOB, border=NA)

#text(x=0.3, y=1.1, cex=1.15, labels="3", xpd=TRUE, col="white", font=2)

text(x=0.75, y=1.1, labels="MOB", xpd=TRUE, col="black", font=2, cex=1.15, adj=0)

#b and r are the rate for density dependance (DD) of the speciation rate. If positive, positive DD, otherwise, negative.

#add their values below:

text(x=c(4,5,6), y=c(-0.2, -0.2),

labels=c(

"r ~",

round(mean(as.numcharac(summaryMOBFrugivory$DDlingeo.b)), digit=3),

round(mean(as.numcharac(summaryMOBFrugivory$DDexpgeo.r)), digit=3)

), cex=0.8, xpd=TRUE)

##------------

##-------------

#Cerebellum

plot(

x=0, y=0, xlab="", ylab="", cex.sub=1.6,

xlim=c(0,7), ylim=c(0,1.2),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

rect(xleft=0, xright=3.5, ybottom=0, ytop=1, col=adjustcolor("royalblue", alpha.f=0.2), border=NA)

rect(xleft=3.5, xright=7, ybottom=0, ytop=1, col=adjustcolor("blue", alpha.f=0.2), border=NA)

addGrid(xmin=0, xmax=7, xintsmall=0.25, xintbig=1, ymin=0, ymax=1, yintsmall=0.05, yintbig=0.2, axisPlot=FALSE)

#axis(side=2, at=seq(from=0, to=1, by=0.2), labels=seq(from=0, to=1, by=0.2), las=2, tcl=-0.25)

#segments(x0 = -1, x1 = -1, y0 = 0, y1 = 1, lty = 2, col = colourCerebellum)

segments(x0 = 3.5, y0=0, x1=3.5, y1=1, lty=2)

text(x=1:6, y=rep(-0.1, times=6), labels=models, cex=0.9, xpd=TRUE)

for(i in 1:6){

meanPt <- mean(as.numcharac(summaryCerebellumFrugivory[, ncol(summaryCerebellumFrugivory)-6+i]))

sd <- sd(as.numcharac(summaryCerebellumFrugivory[, ncol(summaryCerebellumFrugivory)-6+i]))

#sd <- sd/nrow(summaryCerebellumFrugivory) #error not sd

errorBars(location=i, meanPt=meanPt, barValue=sd, refUnit=1, col="black", minValue=0, maxValue=1, horiz=FALSE)

points(x=i, y=meanPt, pch=19, col="black", xpd=TRUE)

}

draw.circle(x=0.3,y=1.1,0.35, col=colourCerebellum, border=NA)

#text(x=0.3, y=1.1, cex=1.15, labels="6", xpd=TRUE, col="white", font=2)

text(x=0.75, y=1.1, labels="Cerebellum", xpd=TRUE, col="black", font=2, cex=1.15, adj=0)

#b and r are the rate for density dependance (DD) of the speciation rate. If positive, positive DD, otherwise, negative.

#add their values below:

text(x=c(4,5,6), y=c(-0.2, -0.2),

labels=c(

"r ~",

round(mean(as.numcharac(summaryCerebellumFrugivory$DDlingeo.b)), digit=3),

round(mean(as.numcharac(summaryCerebellumFrugivory$DDexpgeo.r)), digit=3)

), cex=0.8, xpd=TRUE)

###----------------------

##-------------

#Neocortex

plot(

x=0, y=0, xlab="", ylab="", cex.sub=1.6,

xlim=c(0,7), ylim=c(0,1.2),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

rect(xleft=0, xright=3.5, ybottom=0, ytop=1, col=adjustcolor("royalblue", alpha.f=0.2), border=NA)

rect(xleft=3.5, xright=7, ybottom=0, ytop=1, col=adjustcolor("blue", alpha.f=0.2), border=NA)

addGrid(xmin=0, xmax=7, xintsmall=0.25, xintbig=1, ymin=0, ymax=1, yintsmall=0.05, yintbig=0.2, axisPlot=FALSE)

#axis(side=2, at=seq(from=0, to=1, by=0.2), labels=seq(from=0, to=1, by=0.2), las=2, tcl=-0.25)

#segments(x0 = -1, x1 = -1, y0 = 0, y1 = 1, lty = 2, col = colourNeocortex)

segments(x0 = 3.5, y0=0, x1=3.5, y1=1, lty=2)

text(x=1:6, y=rep(-0.1, times=6), labels=models, cex=0.75, xpd=TRUE)

for(i in 1:6){

meanPt <- mean(as.numcharac(summaryNeocortexFrugivory[, ncol(summaryNeocortexFrugivory)-6+i]))

sd <- sd(as.numcharac(summaryNeocortexFrugivory[, ncol(summaryNeocortexFrugivory)-6+i]))

#sd <- sd/nrow(summaryNeocortexFrugivory) #error not sd

errorBars(location=i, meanPt=meanPt, barValue=sd, refUnit=1, col="black", minValue=0, maxValue=1, horiz=FALSE)

points(x=i, y=meanPt, pch=19, col="black", xpd=TRUE)

}

draw.circle(x=0.3,y=1.1,0.35, col=colourNeocortex, border=NA)

#text(x=0.3, y=1.1, cex=1.15, labels="5", xpd=TRUE, col="white", font=2)

text(x=0.75, y=1.1, labels="Neocortex", xpd=TRUE, col="black", font=2, cex=1.15, adj=0)

#b and r are the rate for density dependence (DD) of the speciation rate. If positive, positive DD, otherwise, negative.

#add their values below:

text(x=c(4,5,6), y=c(-0.2, -0.2),

labels=c(

"r ~",

round(mean(as.numcharac(summaryNeocortexFrugivory$DDlingeo.b)), digit=3),

round(mean(as.numcharac(summaryNeocortexFrugivory$DDexpgeo.r)), digit=3)

), cex=0.8, xpd=TRUE)

##-------------

par(mar=c(0, 0, 0, 0), mgp=c(2, 0.5, 0), xpd=TRUE)

emptyPlot()

legend(x=0.15, y=1, yjust=1, horiz=TRUE, fill=c(adjustcolor("royalblue", alpha.f=0.2), adjustcolor("blue", alpha.f=0.2)), legend=c("Not considering species sympatry", "Considering species sympatry"), bty="n", cex=1.35)

```

\newpage

\beginsupplement

\clearpage

# Appendix

## Data availability

Availability of trait and distribution range for the `r length(phylo\_init$tip.label)` primate species represented in the primate phylogeny of the 10kTrees project is depicted in Appendix Figure \@ref(fig:figdata).

## Data variability

We present below the results of the assessments of data variability depending on the considered thresholds (for frugivory, folivory or overlap) and the data set that is used, specifically related to distribution ranges, or anatomical/behavioural traits.

### Sensitivity to variation in distribution range

```{r figcomparison, fig.pos='H', include=TRUE, warning = FALSE, message = FALSE, fig.width=4, fig.height=4, fig.cap=paste("Percentage of species with differently identified biogeographic areas in function of the overlap threshold (reference is an overlap threshold of ", geographicThresholdVector[2]/2\*100,"%) | For a given species, a biogeographic area difference means that at least one biogeographic area considers absence/presence of the species while this was not the case with the ", geographicThresholdVector[2]/2\*100, "% threshold. ", geographicThresholdVector[2]/2\*100, "% was chosen as the reference since halfway to the chosen maximum of ", geographicThresholdVector[2]\*100, "%. ", geographicThresholdVector[2]\*100, "% was chosen as the maximum because based on current observations, a species occupied at best three different biogeographic areas.", sep="")}

par(mar=c(3, 5, 2, 1), mgp=c(2, 0.5, 0), xpd=TRUE)

plot(

x=0, y=0, xlab="Overlap threshold", ylab="Percentage of species with different biogeographic areas\ncompared to when a 15% overlap is used",

xlim=c(thresholdPresenceRange[1],thresholdPresenceRange[length(thresholdPresenceRange)]), ylim=c(0,0.4),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

addGrid(xmin=5/100, xmax=30/100, xintsmall=2.5/200, xintbig=5/100, ymin=0, ymax=0.4, yintsmall=0.01, yintbig=0.1, axisPlot=FALSE)

axis(side=2, at=seq(from=0, to=1, by=0.2), labels=seq(from=0, to=1, by=0.2), las=1, tcl=-0.25)

axis(side=1, at=thresholdPresenceRange, labels=thresholdPresenceRange, las=1, tcl=-0.25)

points(x=thresholdPresenceRange, y=howManyDifferent, pch=19, xpd=TRUE)

lines(x=thresholdPresenceRange, y=howManyDifferent)

```

\clearpage

### Sensitivity to variation in trait value

```{r figvariabilitydata, fig.pos='H', include=TRUE, warning = FALSE, message = FALSE, fig.width=10.5, fig.height=4, fig.cap="Variation in trait values among reference datasets | Colours are associated with a specific trait: Brain, Hippocampus, Neocortex, and Cerebellum refers to the volume of the area (in mm$^{3}$), Body refers to the body mass (in g), Frug. indicates the frugivory rate and Fol. indicates the folivory rate. (A) Correlation: The points depict the coefficient of correlation while the bar depicts the 95% confidence interval (CI). (B) Variability: The points depict the average of the mean ratio $m$ of the absolute of differences with paired values; If we reduce the equation, we have $m=|(v\_{1}^{2}-v\_{2}^{2})|/(2v\_{1}v\_{2})$, where $v\_{1}$ and $v\_{2}$ are the two paired values from two different datasets and are different from 0. If $v\_{1}$ and $v\_{2}$ equal 0, then $m=0$. If $v\_{1}$ or $v\_{2}$ equals 0 (case for the diet rates constrained between [0,1]), then we fixed the null value to 0.01. The bar depicts the standard error. (C) Repeatability: Repeatability was assessed for traits that were included in at least three datasets. Before calculation, traits were pondered \*within\* species by the \*within\* species max value. The point represents the mean repeatability $r$ calculated as $\\sigma^{2}\_{between}/(\\sigma^{2}\_{between}+\\sigma^{2}\_{within})$, with the $\\sigma^{2}\_{between}$ and $\\sigma^{2}\_{within}$ corresponding the variance \*between\* or \*within\* species. The bar depicts the standard error. For all graphics, sample sizes are indicated above the upper value of the CI/error interval."}

layout(mat=t(c(1,2,3)), widths=c(5,5,3), heights=c(5))

par(mar=c(4, 3, 2, 1), mgp=c(2, 0.5, 0), xpd=TRUE)

cexText <- c(

rep(0.8, times=10),

rep(0.4, times=3),

rep(0.8, times=6),

rep(0.4, times=3),

rep(1, times=1),

rep(0.8, times=6),

rep(1, times=1),

rep(1, times=1)

)

addToY <- c(

rep(0, times=10),

rep(0, times=3),

rep(0, times=6),

rep(0, times=3),

rep(0, times=1),

rep(0, times=6),

rep(-0.05, times=1),

rep(0, times=1)

)

colourWhatCompared <- c("gray", colourHippocampusbis, colourNeocortexbis, colourCerebellumbis, colourStriatumbis, "orange", "black", "lightgray")#c(brewer.pal(n = length(unique(whatCompared)) - 1, name = "Pastel1"), "darkgrey")

###------

### CORRELATION

#Vectors to save results

barLower <- rep(NA, times=length(colNumTest))

barUpper <- rep(NA, times=length(colNumTest))

meanCoeff <- rep(NA, times=length(colNumTest))

N <- rep(NA, times=length(colNumTest))

for (i in 1:length(colNumTest)){

test <- #abs(as.numeric(as.character(summaryData[,colNumTest[i]])) - as.numeric(as.character(summaryData[,colNumToCompare[i]])))

cor.test(as.numeric(as.character(summaryData[,colNumTest[i]])),

as.numeric(as.character( summaryData[,colNumToCompare[i]])), method="pearson")

barLower[i] <- test$conf.int[1]

barUpper[i] <- test$conf.int[2]

meanCoeff[i] <- test$estimate[1]

N[i] <- nrow(summaryData[!is.na(summaryData[,colNumTest[i]])&!is.na(summaryData[,colNumToCompare[i]]),])

}

plot(

x=0, y=0, xlab="", ylab="Coefficient of correlation", cex.lab=1.5,

xlim=c(0,length(meanCoeff)+1), ylim=c(0.6,1),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

addGrid(xmin=0, xmax=length(meanCoeff), xintsmall=0.5, xintbig=1, ymin=0.6, ymax=1, yintsmall=0.025, yintbig=0.1, axisPlot=FALSE)

axis(side=2, at=seq(from=0.6, to=1, by=0.2), labels=seq(from=0.6, to=1, by=0.2), las=2, tcl=-0.25, cex.axis=1.25)

addLabel(x=0.05, y=0.075, label="A", radius=0.75, circle=TRUE, circle.bg="black", font.col="white")

#Comparison

whatCompared <- c(

rep("Brain", times=10),

"Hippocampus",

"Hippocampus",

"Hippocampus",

"Neocortex",

"Neocortex",

"Neocortex",

"Neocortex",

"Neocortex",

"Neocortex",

"Cerebellum",

"Cerebellum",

"Cerebellum",

"Striatum",

rep("Body", times=6),

"Frug.",

"Fol."

)

#Plot legend of what is compared in coloured rectangles

whereToPlot <- as.data.frame(table(whatCompared))

whereToPlot$loc <- whereToPlot$Freq/2

#Colour rectangle to indicate what is compared

refLoc=0

for (i in 1:length(whatCompared)){

rect(xleft=i-1,

xright=i,

ybottom=0.6-0.05\*0.4,#-0.05,

ytop=0.6,#0,

border=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])],

col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])],

xpd=TRUE

)

errorBars(location=i-0.5, meanPt=meanCoeff[i], refUnit=1, col="black", minValue=0, maxValue=1, upperBarValue=barUpper[i], lowerBarValue=barLower[i], horiz=FALSE, symmetrical=FALSE)

points(x=i-0.5, y=meanCoeff[i], pch=19, col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])],

xpd=TRUE)

text(x=i-0.5, y=barUpper[i]+0.015, labels=N[i], pch=19, col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])], cex=0.8,xpd=TRUE)

if(i==length(whatCompared)|whatCompared[i]!=whatCompared[i+1]){

refLoc=refLoc+whereToPlot$loc[whereToPlot[,1]==whatCompared[i]]

if(whereToPlot$loc[whereToPlot[,1]==whatCompared[i]]<=1){

segments(x0=refLoc, x1=refLoc, y0=0.6-0.025\*0.4,#-0.025,

y1=0.6-0.075\*0.4 + addToY[i]\*0.4,#-0.075,

col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])], xpd=TRUE)

text(x=refLoc, y=0.6-0.1\*0.4 + addToY[i]\*0.4,#-0.1,

labels=whereToPlot[whereToPlot[,1]==whatCompared[i],1], col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])], cex=cexText[i], xpd=TRUE)

}

else{

text(x=refLoc, y=0.6-0.025\*0.4,#-0.025,

labels=whereToPlot[whereToPlot[,1]==whatCompared[i],1], col="black", cex=cexText[i], xpd=TRUE)

}

refLoc=refLoc+whereToPlot$loc[whereToPlot[,1]==whatCompared[i]]#add second time for having complete rectangle

}

}

###------

### VARIABILITY

#cbind(colnames(summaryData[colNumTest]), colnames(summaryData[colNumToCompare]))

#Vectors to save results

barLower <- rep(NA, times=length(colNumTest))

barUpper <- rep(NA, times=length(colNumTest))

meanCoeff <- rep(NA, times=length(colNumTest))

N <- rep(NA, times=length(colNumTest))

for (i in 1:length(colNumTest)){

transitoryinit <- as.data.frame(cbind(as.numeric(as.character(summaryData[,colNumTest[i]])),as.numeric(as.character(summaryData[,colNumToCompare[i]]))))

transitoryinit <- transitoryinit[!is.na(transitoryinit[,1])&!is.na(transitoryinit[,2]),]

# transitoryinit <- transitoryinit/max(apply(transitoryinit, 2, max))

transitory <- apply(transitoryinit, 1, function(v){abs(v[1]\*\*2 - v[2]\*\*2)/2/v[1]/v[2]}) #note= (abs((v1-v2))/v1 + abs((v2-v1))/v2)/2

#When rate is 0 for both, gives NA, so to transform to 0

transitory[is.na(transitory)] <- 0

transitory[!is.finite(transitory)] <- apply(transitoryinit[!is.finite(transitory),], 1, function(x) abs(max(x)\*\*2 - 1\*\*2)/2/max(x)/1)

barLower[i] <- mean(transitory) - sd(transitory)/sqrt(length(transitory))#min(transitory)

barUpper[i] <- mean(transitory) + sd(transitory)/sqrt(length(transitory))#max(transitory)

meanCoeff[i] <- mean(transitory)

N[i] <- length(transitory)

}

ymax <- 1#round((barUpper)/10)\*10

plot(

x=0, y=0, xlab="", ylab="Variability", cex.lab=1.5,

xlim=c(0,length(meanCoeff)+1), ylim=c(0,ymax),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

addGrid(xmin=0, xmax=length(meanCoeff), xintsmall=0.5, xintbig=1, ymin=0, ymax=ymax, yintsmall=0.05, yintbig=0.2, axisPlot=FALSE)

axis(side=2, at=seq(from=0, to=ymax, by=0.2), labels=seq(from=0, to=ymax, by=0.2), las=2, tcl=-0.25, cex.axis=1.25)

addLabel(x=0.05, y=0.075, label="B", radius=0.75, circle=TRUE, circle.bg="black", font.col="white")

#Comparison

whatCompared <- c(

rep("Brain", times=10),

"Hippocampus",

"Hippocampus",

"Hippocampus",

"Neocortex",

"Neocortex",

"Neocortex",

"Neocortex",

"Neocortex",

"Neocortex",

"Cerebellum",

"Cerebellum",

"Cerebellum",

"Striatum",

rep("Body", times=6),

"Frug.",

"Fol."

)

#Plot legend of what is compared in coloured rectangles

whereToPlot <- as.data.frame(table(whatCompared))

whereToPlot$loc <- whereToPlot$Freq/2

#Colour rectangle to indicate what is compared

refLoc=0

for (i in 1:length(whatCompared)){

rect(xleft=i-1,

xright=i,

ybottom=-0.05,

ytop=0,

border=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])],

col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])],

xpd=TRUE

)

errorBars(location=i-0.5, meanPt=meanCoeff[i], refUnit=1, col="black", minValue=0, maxValue=1, upperBarValue=barUpper[i], lowerBarValue=barLower[i], horiz=FALSE, symmetrical=FALSE)

points(x=i-0.5, y=meanCoeff[i], pch=19, col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])],

xpd=TRUE)

text(x=i-0.5, y=barUpper[i]+0.05, labels=N[i], pch=19, col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])], cex=0.8,xpd=TRUE)

if(i==length(whatCompared)|whatCompared[i]!=whatCompared[i+1]){

refLoc=refLoc+whereToPlot$loc[whereToPlot[,1]==whatCompared[i]]

if(whereToPlot$loc[whereToPlot[,1]==whatCompared[i]]<=1){

segments(x0=refLoc, x1=refLoc, y0=-0.025,

y1=-0.075 + addToY[i],

col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])], xpd=TRUE)

text(x=refLoc, y=-0.1 + addToY[i],

labels=whereToPlot[whereToPlot[,1]==whatCompared[i],1], col=colourWhatCompared[which(unique(whatCompared)==whatCompared[i])], cex=cexText[i], xpd=TRUE)

}

else{

text(x=refLoc, y=-0.025,

labels=whereToPlot[whereToPlot[,1]==whatCompared[i],1], col="black", cex=cexText[i], xpd=TRUE)

}

refLoc=refLoc+whereToPlot$loc[whereToPlot[,1]==whatCompared[i]]#add second time for having complete rectangle

}

}

##----

## Repeatability of measure

colRep <- list(c(4, 14, 17, 22, 23),

c(5, 15, 18),

c(6, 12, 16, 19),

c(7, 13, 20),

#c(8, 21),

c(24, 25, 26, 27)#,

#c(29, 33),

#c(30, 34)

)

ymax <- 1

plot(

x=0, y=0, xlab="", ylab="Repeatability", cex.lab=1.5,

xlim=c(0,length(colRep)+1), ylim=c(0,ymax),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

addGrid(xmin=0, xmax=length(colRep), xintsmall=0.5, xintbig=1, ymin=0, ymax=ymax, yintsmall=0.05, yintbig=0.2, axisPlot=FALSE)

axis(side=2, at=seq(from=0, to=ymax, by=0.2), labels=seq(from=0, to=ymax, by=0.2), las=2, tcl=-0.25, cex.axis=1.25)

addLabel(x=0.05\*2, y=0.075, label="C", radius=0.75\*length(colRep)/length(meanCoeff)\*2, circle=TRUE, circle.bg="black", font.col="white")

#Comparison

whatCompared2 <- c(

"Brain",

"Hippocampus",

"Neocortex",

"Cerebellum",

#"Striatum",

"Body"#,

#"Fol.",

#"Frug."

)

for(i in 1:length(colRep)){

dataRdc <- summaryData[, colRep[[i]]]

#Normalise by max for all species (i.e. by row)

maxVector <- apply(dataRdc, 1, function(x)max(x, na.rm=TRUE))

maxVector[!is.finite(maxVector)] <- NA

dataRdc <- apply(dataRdc, 2, function(x) x/maxVector)

dataRdc <- as.data.frame(dataRdc)

#Create common ID

dataRdc$id <- 1:nrow(dataRdc)

#Switch to 1 row=1value

dataRdc <- pivot\_longer(dataRdc, col=1:(ncol(dataRdc)-1), names\_to="Dataset", values\_to="Value")

#Remove NAs

dataRdc <- dataRdc[!is.na(dataRdc$Value),]

#Keep thos with multiple obs

whichKeep <- dataRdc %>% count(id)

whichKeep <- whichKeep$id[whichKeep$n > 2]

dataRdc <- dataRdc[dataRdc$id %in% whichKeep,]

dataRdc <- pivot\_wider(dataRdc, names\_from="Dataset", values\_from="Value")

withinVariance <- apply(dataRdc[,2:ncol(dataRdc)], 1, function(x) var(x, na.rm=TRUE))

betweenVariance <- var(apply(dataRdc[,2:ncol(dataRdc)], 1, function(x) mean(x, na.rm=TRUE)), na.rm=TRUE)

repeatability <- betweenVariance/(betweenVariance + withinVariance)

#Plot mean +/- SE

errorBars(location=i-0.5, meanPt=mean(repeatability),

refUnit=1, col="black", minValue=0, maxValue=1, upperBarValue=mean(repeatability)+sd(repeatability)/sqrt(length(repeatability)),

lowerBarValue=mean(repeatability)-sd(repeatability)/sqrt(length(repeatability)), horiz=FALSE, symmetrical=FALSE)

points(x=i-0.5, y=mean(repeatability), pch=19, col=colourWhatCompared[which(unique(whatCompared)==whatCompared2[i])],

xpd=TRUE)

text(x=i-0.5, y=mean(repeatability)+sd(repeatability)/sqrt(length(repeatability))+0.05, labels=length(repeatability), pch=19, col=colourWhatCompared[which(unique(whatCompared)==whatCompared2[i])], cex=0.8, xpd=TRUE)

# library(rptR)

# repeatabilityTest <- rpt(Value ~ (1 | id), grname = "id", data = dataRdc, datatype = "Proportion",

# nboot = 10, npermut = 0)

# Too few data to do that way

}

```

```{r figdata, fig.pos='H', include=TRUE, warning = FALSE, message = FALSE, fig.width=20, fig.height=25, fig.cap="Data availability | Black boxes indicate data availability while grey boxes indicate absence of data."}

#

# plot(

# x=0, y=0, xlab="", ylab="", cex.sub=1.6,

# xlim=c(-10,ncol(dataForSample)-1), ylim=c(0,nrow(dataForSample)),

# las=1, type="n", tcl=-0.25, frame.plot=FALSE,

# xaxt="n",xaxs="i",yaxs="i", yaxt="n")

#

# text(x=rep(-2, times=nrow(dataForSample)), y=1:nrow(dataForSample)-0.5, labels=dataForSample$SpeciesForPhylo, xpd=TRUE, cex=0.4)

# text(x=rep(-0, times=nrow(dataForSample)), y=1:nrow(dataForSample)-0.5, labels=dataForSample$Species, xpd=TRUE, cex=0.4)

# text(x=3:ncol(dataForSample)-1.5, y=rep(nrow(dataForSample)+3, times=length(3:ncol(dataForSample))), labels=colnames(dataForSample)[3:ncol(dataForSample)], xpd=TRUE, cex=0.4, srt=45)

#

# for(i in 1:nrow(dataForSample)){

# for(j in 3:ncol(dataForSample)){

# if(!is.na(dataForSample[i,j])&dataForSample[i,j]==1){

# rect(

# xleft=j-2,

# xright=j-1,

# ybottom=i-1,

# ytop=i,

# border="black",

# col="black"

# )

# } else{

# rect(

# xleft=j-2,

# xright=j-1,

# ybottom=i-1,

# ytop=i,

# border="lightgrey",

# col="lightgrey"

# )

# }

# }

# }

#

# addGrid(xmin=1, xmax=ncol(dataForSample), xintsmall=1, xintbig=1, ymin=0, ymax=nrow(dataForSample), yintsmall=1, yintbig=1, colsmall="white", colbig="white", axisPlot=FALSE)

#

#

#

# plot(

# x=0, y=0, xlab="", ylab="", cex.sub=1.6,

# xlim=c(-10,ncol(dataForSample)-1), ylim=c(0,nrow(dataForSample)),

# las=1, type="n", tcl=-0.25, frame.plot=FALSE,

# xaxt="n",xaxs="i",yaxs="i", yaxt="n")

#

# text(x=rep(-2, times=nrow(dataForSample)), y=1:nrow(dataForSample)-0.5, labels=dataForSample$SpeciesForPhylo, xpd=TRUE, cex=0.4)

# text(x=rep(-0, times=nrow(dataForSample)), y=1:nrow(dataForSample)-0.5, labels=dataForSample$Species, xpd=TRUE, cex=0.4)

# text(x=3:ncol(dataForSample)-1.5, y=rep(nrow(dataForSample)+3, times=length(3:ncol(dataForSample))), labels=colnames(dataForSample)[3:ncol(dataForSample)], xpd=TRUE, cex=0.4, srt=45)

#

# for(i in 1:nrow(dataForSample)){

# for(j in 3:ncol(dataForSample)){

# if(!is.na(dataForSample[i,j])&dataForSample[i,j]==1){

# rect(

# xleft=j-2,

# xright=j-1,

# ybottom=i-1,

# ytop=i,

# border="black",

# col="black"

# )

# } else{

# rect(

# xleft=j-2,

# xright=j-1,

# ybottom=i-1,

# ytop=i,

# border="lightgrey",

# col="lightgrey"

# )

# }

# }

# }

#

# addGrid(xmin=1, xmax=ncol(dataForSample), xintsmall=1, xintbig=1, ymin=0, ymax=nrow(dataForSample), yintsmall=1, yintbig=1, colsmall="white", colbig="white", axisPlot=FALSE)

dataForSample <- dataForSample[dataForSample$SpeciesForPhylo != "Homo\_sapiens",]

dataForSample <- dataForSample[order(dataForSample$SpeciesForPhylo),]

nbPlot=4

layout(mat=t(c(1:nbPlot)), widths=rep(5, times=nbPlot), heights=c(5\*nbPlot))

par(mar=c(0, 0, 3, 0.5), mgp=c(2, 0.5, 0), xpd=TRUE)

for(p in 1:nbPlot){

dataForSample\_rdcplot <- dataForSample[(1+(p-1)\*nrow(dataForSample)/nbPlot):(1+(p)\*nrow(dataForSample)/nbPlot),]

plot(

x=0, y=0, xlab="", ylab="", cex.sub=1.6,

xlim=c(-10,ncol(dataForSample\_rdcplot)-1), ylim=c(0,nrow(dataForSample\_rdcplot)+3),

las=1, type="n", tcl=-0.25, frame.plot=FALSE,

xaxt="n",xaxs="i",yaxs="i", yaxt="n")

text(x=rep(-5, times=nrow(dataForSample\_rdcplot)), y=1:nrow(dataForSample\_rdcplot)-0.5, labels=dataForSample\_rdcplot$SpeciesForPhylo, xpd=TRUE, cex=1.1)

text(x=rep(-0.5, times=nrow(dataForSample\_rdcplot)), y=1:nrow(dataForSample\_rdcplot)-0.5, labels=dataForSample\_rdcplot$Species, xpd=TRUE, cex=1.1)

text(x=3:ncol(dataForSample\_rdcplot)-1.5, y=rep(nrow(dataForSample\_rdcplot)+2, times=length(3:ncol(dataForSample\_rdcplot))), labels=colnames(dataForSample\_rdcplot)[3:ncol(dataForSample\_rdcplot)], xpd=TRUE, cex=1.1, srt=45)

for(i in 1:nrow(dataForSample\_rdcplot)){

for(j in 3:ncol(dataForSample\_rdcplot)){

if(!is.na(dataForSample\_rdcplot[i,j])&dataForSample\_rdcplot[i,j]==1){

rect(

xleft=j-2,

xright=j-1,

ybottom=i-1,

ytop=i,

border="black",

col="black"

)

} else{

rect(

xleft=j-2,

xright=j-1,

ybottom=i-1,

ytop=i,

border="lightgrey",

col="lightgrey"

)

}

}

}

addGrid(xmin=1, xmax=ncol(dataForSample\_rdcplot), xintsmall=1, xintbig=1, ymin=0, ymax=nrow(dataForSample\_rdcplot), yintsmall=1, yintbig=1, colsmall="white", colbig="white", axisPlot=FALSE)

#if(p==2){cat('\r\n\r\n')} #Allows to consider plot as a new figure at each step of the loop

}

```

\clearpage

### Primate diversification rate over time

```{r figdiversificationTime, fig.pos='H', include=TRUE, warning = FALSE, message = FALSE, fig.width=4.5, fig.height=4.5, fig.cap="\\footnotesize Net diversification rate over time in the Primate taxon | The average diversification rate estimated based on an assumed sampling fraction of primate species ranging from 60 to 95% (at a step of 10%; then 5% from 90%) is depicted by the plain line. The grey background depicts the standard deviation. The two breakpoints, depicted by the plain dots and the vertical dotted bars, were estimated based on a three-linear regression segmentation using the \*strucchange\* package [@strucchange1; @strucchange2; @strucchange3; see the vignette package for statistical details]. The three fitted regressions are displayed by the dashed lines. The choice of two breakpoints was first assessed by choosing the number of breakpoints minimizing the Bayesian Information Criterion. The identified breakpoints, coining with previous studies [@arbour2017major; @springer2012macroevolutionary], correspond to the emergence of more favourable environmental conditions stemming from a progressive warming after harsh temperature cooling that started earlier in the Oligocene until reaching a mid-Miocene Climatic Optimum [@fleagle2006biogeography]."}

##Plot diversification in function of time

xmin=floor(min(aggregatedSpeciationTime.mean[,1]/10))\*10

xmax=ceiling(max(aggregatedSpeciationTime.mean[,1]/10))\*10

ymin=floor(min(aggregatedSpeciationTime.mean[,2]\*10))/10

ymax=ceiling(max(aggregatedSpeciationTime.mean[,2]\*10))/10

plot(0, 0, xlab="Time before present (Myr)", ylab="Diversification rate",

xlim=c(xmin, xmax), ylim=c(ymin, ymax),

las=1, type="n", tcl=-0.25, bty="n",

xaxt="n",xaxs="i",yaxs="i", yaxt="n",

xpd=TRUE)

#Add grid

addGrid(

xmin=xmin, xmax=xmax, xintsmall=(xmax-xmin)/20, xintbig=(xmax-xmin)/5,

ymin=ymin, ymax=ymax, yintsmall=(ymax-ymin)/20, yintbig=(ymax-ymin)/5,

axisPlot=TRUE, round=TRUE, digit=c(2,2))

axis(side=1, at=round(seq(from=xmin, to=xmax, by=(xmax-xmin)/5), digit=1), labels=round(seq(from=xmin, to=xmax, by=(xmax-xmin)/5), digit=1), las=1, tcl=-0.25)

#Add background se

polygon(

x=c(aggregatedSpeciationTime.mean[,1], rev(aggregatedSpeciationTime.mean[,1])),

y=c(aggregatedSpeciationTime.mean[,2]-aggregatedSpeciationTime.sd[,2], rev(aggregatedSpeciationTime.mean[,2]+aggregatedSpeciationTime.sd[,2])),

col=grey(level=0.5, alpha=0.15),

border=NA

)

#Add mean

lines(aggregatedSpeciationTime.mean[,1], aggregatedSpeciationTime.mean[,2])

library(strucchange)

## confidence interval

colnames(aggregatedSpeciationTime.mean) <- c("Time", "Diversification")

yFirst <- aggregatedSpeciationTime.mean$Diversification[which((abs(aggregatedSpeciationTime.mean$Time+dateFirstRupt[2]))==min(abs(aggregatedSpeciationTime.mean$Time+dateFirstRupt[2])))]

ySecond <- aggregatedSpeciationTime.mean$Diversification[which((abs(aggregatedSpeciationTime.mean$Time+dateSecondRupt[2]))==min(abs(aggregatedSpeciationTime.mean$Time+dateSecondRupt[2])))]

# Rupture points and (CI too reduced to be plotted)

points(c(-dateFirstRupt[2], -dateSecondRupt[2]), c(yFirst, ySecond), pch=19)

# errorBars(location=c(yFirst),

# meanPt=c(-dateFirstRupt[2]),

# barValue=c(0,0), refUnit=1,

# minValue=-80, maxValue=80,

# upperBarValue=c(-dateFirstRupt[1]), lowerBarValue=c(-dateFirstRupt[3]),

# col="black", lty=1,

# horiz=TRUE, symmetrical=FALSE)

#Vertical bars

segments(

x0=c(-dateFirstRupt[2], -dateSecondRupt[2]),

x1=c(-dateFirstRupt[2], -dateSecondRupt[2]),

y0=c(0,0),

y1=c(yFirst, ySecond),

lty=3

)

mtext(side=1, at=c(-dateFirstRupt[2], -dateSecondRupt[2]), line=0, text=c(-dateFirstRupt[2], -dateSecondRupt[2]), cex=0.8)

#three fitted regressions

fm1 <- lm(Diversification ~ breakfactor(bp.resp, breaks = 2)\*Time, data=aggregatedSpeciationTime.mean)

reg1 <- summary(fm1)$coefficients[1,1] + aggregatedSpeciationTime.mean$Time\*summary(fm1)$coefficients[4,1]

reg2 <- summary(fm1)$coefficients[1,1] + summary(fm1)$coefficients[2,1] + aggregatedSpeciationTime.mean$Time\*(summary(fm1)$coefficients[4,1] + summary(fm1)$coefficients[5,1])

reg3 <- summary(fm1)$coefficients[1,1] + summary(fm1)$coefficients[3,1] + aggregatedSpeciationTime.mean$Time\*(summary(fm1)$coefficients[4,1] + summary(fm1)$coefficients[6,1])

lines(aggregatedSpeciationTime.mean$Time, reg1, lty = 2)

lines(aggregatedSpeciationTime.mean$Time[aggregatedSpeciationTime.mean$Time > -40], reg2[aggregatedSpeciationTime.mean$Time > -40], lty = 2)#truncaturate for readability

lines(aggregatedSpeciationTime.mean$Time[aggregatedSpeciationTime.mean$Time > -16], reg3[aggregatedSpeciationTime.mean$Time > -16], lty = 2)#truncaturate for readability

```

## Phylogenetic regressions: results, stability, and assumption

### Model results

<!-- We present below the visual fit of phylogenetic regressions. -->

(a) Phylogenetic regressions: effect of sympatry on brain sizes

\clearpage

```{=latex}

\begin{figure}

\centering\includegraphics[width=0.65\linewidth]{C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Plots/selectionGradientPGLS.pdf}

\caption{\scriptsize{Phylogenetic regressions of relative brain size as a function of sympatry level indices | Left graphics show the effect of the number of sympatric species on the brain size, when the effect of the average percentage of overlapping range with sympatric frugivorous species is averaged, while the right graphics do the opposite. Raw data are depicted with points, while the segments that link them correspond to the projected phylogenetic tree. The model fit is shown with the plain black line and the associated 95\% confidence interval is depicted by the transparent grey background.}}\label{fig:figRegressionGradient}

\end{figure}

```

\clearpage

(b) Phylogenetic regressions: diversification and brain size

```{=latex}

\begin{figure}

\centering\includegraphics[width=0.7\linewidth]{C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Plots/diversificationPGLS.pdf}

\caption{\scriptsize{Phylogenetic regressions of the net diversification rate as a function of the size of the different brain areas | Raw data are depicted with points, while the segments that link them correspond to the projected phylogenetic tree. The model fit is shown with the plain black line and the associated 95\% highest density posterior is depicted by the transparent grey background.}}\label{fig:figRegressionDiversification}

\end{figure}

```

\clearpage

(c) Phylogenetic regressions: diversification and sympatry

```{=latex}

\begin{figure}

\centering\includegraphics[width=0.65\linewidth]{C:/Users/robira/Documents/PhD/Meta\_analysis/Meta\_analysis\_cognition\_primates/Plots/diversificationAndSympatryPGLS.pdf}

\caption{\scriptsize{Phylogenetic regressions of the net diversification rate as a function of sympatry level indices | The left graphic depicts the effect of the number of sympatric species on the brain size, when the effect of the average percentage of overlapping range with sympatric frugivorous species is averaged, while the right graphic does the opposite. Raw data are depicted with points, while the segments that link them correspond to the projected phylogenetic tree. The model fit is shown with the plain black line and the associated 95\% confidence interval is depicted by the transparent grey background.}}\label{fig:figRegressionDiversificationSympatry}

\end{figure}

```

\clearpage

(d) Forest plot of estimates

```{r forestPlot, fig.pos='H', include=TRUE, warning = FALSE, message = FALSE, fig.width=6.25, fig.height=6.25, fig.cap="Forest plot of the phylogenetic regressions | CI: 95\\% Confidence Interval, HDP: Highest Posterior Density (when brain size is the predictor, they are barely visible because reduced). Plain dots depict negative effects, open dots depict positive effects. "}

source("T:/Saved\_PhD/Empirical\_analysis/Scripts&Functions/Functions/toolbox.R")

par(mar=c(8, 8, 0.5, 2), mgp=c(2.5, 0.5, 0), xpd=TRUE)

emptyPlot(xlim=c(-3,3), ylim=c(-3,3), asp=1)

#Grid

addGrid(

cexAxisX=1.15, cexAxisY=1.15,

xmin=-3, xmax=3, xintsmall=0.1, xintbig=0.5,

ymin=-3, ymax=3, yintsmall=0.1, yintbig=0.5,

axisPlot=FALSE, round=TRUE, digit=c(2,2), contour=TRUE)

#0 line

segments(x0=0, x1=0, y0=-3, y1=3, lty=2)

#Xaxis

axis(side=1, at=seq(-3, 3, 0.5), pos=-3, labels=seq(-3, 3, 0.5), las=1, tcl=-0.25)

mtext(side=1, at=0, line=1, text="Model estimate (point) and 95% CI/HDP (segment)")

#yAxis

axis(side=2, at=c(2, 0, -2), pos=-3, labels=c("Overlap (%)", "N sympatric\nspecies", "Relative\nbrain size"), las=1, tcl=-0.25)

mtext(side=2, at=0, line=6, text="PARAMETER", font=2)

#Add the different values

#Analysis of brain size and sympatry

traitName\_rdc=c("EQ (log)", #"Brain (/bodymass, log)",

"Striatum (/bodymass, log)",

"MOB (/bodymass, log)",

"Hippocampus (/bodymass, log)",

"Neocortex (/bodymass, log)",

"Cerebellum (/bodymass, log)",

"DiversificationAndSympatry"

)

traitName\_legend <- c("EQ", "Striatum", "MOB", "Hippocampus", "Neocortex", "Cerebellum", "Diversification")

library(RColorBrewer)

colourModelsReg <- c("darkgrey", brewer.pal(n = 5, name = "Set1")[1:5], "black")

for(a in 1:length(traitName\_rdc)){

if(a!=length(traitName\_rdc)){

model <- get(paste("modelBrain", traitName\_rdc[a], sep="\_"))

}else{

model <- get(paste("modelBrain", traitName\_rdc[a], sep=""))

}

#Overlap

errorBars(location=2.5-(a-1)\*1/length(traitName\_rdc),

meanPt=cbind(model$bootmean, t(model$bootconfint95))[2,1],

barValue=1,

refUnit=0.75,

minValue=-3,

maxValue=3,

upperBarValue=cbind(model$bootmean, t(model$bootconfint95))[2,2],

lowerBarValue=cbind(model$bootmean, t(model$bootconfint95))[2,3],

col=colourModelsReg[a],

lty=1,

horiz=TRUE,

symmetrical=FALSE)

points(x=cbind(model$bootmean, t(model$bootconfint95))[2,1], y=2.5-(a-1)\*1/length(traitName\_rdc), pch=ifelse(cbind(model$bootmean, t(model$bootconfint95))[2,1]>0,21,19), bg="white", col=colourModelsReg[a])

if(a!=length(traitName\_rdc)){

text(x=cbind(model$bootmean, t(model$bootconfint95))[2,3], y=2.5-(a-1)\*1/length(traitName\_rdc),

pos=4, col=colourModelsReg[a],

labels=pvalueToText(as.numcharac(results.df\_gradient[grep(traitName\_legend[a], results.df\_gradient[,1]) + 2,7])), cex=0.75)

}else{

text(x=cbind(model$bootmean, t(model$bootconfint95))[2,3], y=2.5-(a-1)\*1/length(traitName\_rdc),

pos=4, col=colourModelsReg[a],

labels=pvalueToText(as.numcharac(results.df\_diversificationAndSympatry[3,7])), cex=0.75)

}

#N species

errorBars(location=0.5-(a-1)\*1/length(traitName\_rdc),

meanPt=cbind(model$bootmean, t(model$bootconfint95))[3,1],

barValue=1,

refUnit=0.75,

minValue=-3,

maxValue=3,

upperBarValue=cbind(model$bootmean, t(model$bootconfint95))[3,2],

lowerBarValue=cbind(model$bootmean, t(model$bootconfint95))[3,3],

col=colourModelsReg[a],

lty=1,

horiz=TRUE,

symmetrical=FALSE)

points(x=cbind(model$bootmean, t(model$bootconfint95))[3,1], y=0.5-(a-1)\*1/length(traitName\_rdc), pch=ifelse(cbind(model$bootmean, t(model$bootconfint95))[3,1]>0,21,19), bg="white", col=colourModelsReg[a])

if(a!=length(traitName\_rdc)){

text(x=cbind(model$bootmean, t(model$bootconfint95))[3,3], y=0.5-(a-1)\*1/length(traitName\_rdc),

pos=4, col=colourModelsReg[a],

labels=pvalueToText(as.numcharac(results.df\_gradient[grep(traitName\_legend[a], results.df\_gradient[,1]) + 3,7])), cex=0.75)

}else{

text(x=cbind(model$bootmean, t(model$bootconfint95))[3,3], y=0.5-(a-1)\*1/length(traitName\_rdc),

pos=4, col=colourModelsReg[a],

labels=pvalueToText(as.numcharac(results.df\_diversificationAndSympatry[4,7])), cex=0.75)

}

#Analysis of diversification and brain size

if(a!=length(traitName\_rdc)){

model <- get(paste("modelBrainDiversification", traitName[a], sep="\_"))

errorBars(location=-1.5-(a-1)\*1/(length(traitName\_rdc)-1),

meanPt=as.data.frame(summary(model)$solutions[,1:3])[2,1],

barValue=1,

refUnit=0.75,

minValue=-3,

maxValue=3,

upperBarValue=as.data.frame(summary(model)$solutions[,1:3])[2,2],

lowerBarValue=as.data.frame(summary(model)$solutions[,1:3])[2,3],

col=colourModelsReg[a],

lty=1,

horiz=TRUE,

symmetrical=FALSE)

points(x=as.data.frame(summary(model)$solutions[,1:3])[2,1], y=-1.5-(a-1)\*1/(length(traitName\_rdc)-1), pch=ifelse(as.data.frame(summary(model)$solutions[,1:3])[2,1]>0,21,19), bg="white", col=colourModelsReg[a])

text(x=as.data.frame(summary(model)$solutions[,1:3])[2,3], y=-1.5-(a-1)\*1/(length(traitName\_rdc)-1),

pos=4, col=colourModelsReg[a],

labels=pvalueToText(as.numcharac(results.df\_diversification[grep(traitName\_legend[a], results.df\_diversification[,1]) + 2,5])), cex=0.75)

}

}

legend(x=3, y=0.5,

pch=c(19,21),

bg=c("white", "white"),

col=c("black", "black"),

legend=c("> 0", "< 0"),

#title="Output:",

bty="n",

xjust=1,

xpd=TRUE)

legend(x=-2.5, y=-4,

pch=rep(19, times=length(traitName\_rdc)),

col=c(colourModelsReg),

legend=traitName\_legend,

#title="Output:",

ncol=3,

bty="n",

xpd=TRUE)

```

\clearpage

### Model stability

We present below statistical indicators related to changes in estimates when re-fitting the model considering sub-samples (i.e. DfBetas and Cook's distance), as well as when accounting for data variability (i.e. re-sampling among possible values given all datasets) or when using different parameterisation (i.e. "sampling fraction" of known species for diversification analyses).

```{r correctSensitivityTable}

#Include true estimator in the min-max range

#1)Change min-max interval

summarySensitivityGradient[,1:3+2] <- t(apply(summarySensitivityGradient[,1:3+2], 1, function(x){

x <- as.numeric(x)

if(x[1] > x[2]){

x[1] <- x[2]

} else if (x[2] > x[3]){

x[3] <- x[2]

}else{}

return(x)

}

)

)

summarySensitivityGradient[,4:6+2] <- t(apply(summarySensitivityGradient[,4:6+2], 1, function(x){

x <- as.numeric(x)

if(x[1] > x[2]){

x[1] <- x[2]

} else if (x[2] > x[3]){

x[3] <- x[2]

}else{}

return(x)

}

)

)

#2) Re-round intelligent with scientific writing

summarySensitivityGradient[, 1:6+2] <- t(apply(summarySensitivityGradient[, 1:6+2], 1, function(x)

roundIntelligent(as.numcharac(x))))

#1)Change min-max interval

summarySensitivityDiversification[,1:3+2] <- t(apply(summarySensitivityDiversification[,1:3+2], 1, function(x){

x <- as.numeric(x)

if(x[1] > x[2]){

x[1] <- x[2]

} else if (x[2] > x[3]){

x[3] <- x[2]

}else{}

return(x)

}

)

)

summarySensitivityDiversification[,4:6+2] <- t(apply(summarySensitivityDiversification[,4:6+2], 1, function(x){

x <- as.numeric(x)

if(x[1] > x[2]){

x[1] <- x[2]

} else if (x[2] > x[3]){

x[3] <- x[2]

}else{}

return(x)

}

)

)

summarySensitivityDiversification[,7:9+2] <- t(apply(summarySensitivityDiversification[,7:9+2], 1, function(x){

x <- as.numeric(x)

if(x[1] > x[2]){

x[1] <- x[2]

} else if (x[2] > x[3]){

x[3] <- x[2]

}else{}

return(x)

}

)

)

#2) Re-round intelligent with scientific writing

summarySensitivityDiversification[,-c(1,2)] <- t(apply(summarySensitivityDiversification[,-c(1,2)], 1, function(x) roundIntelligent(as.numcharac(x))))

```

\hfill

(a) Phylogenetic regressions: effect of sympatry on brain sizes

```{r tabledfsensitivity, include=TRUE}

summarySensitivityGradient <- summarySensitivityGradient[-(1:4),]

summarySensitivityGradient[,2] <- gsub("Overlap", "\\% of overlapping range", summarySensitivityGradient[,2])

summarySensitivityGradient[,2] <- gsub("N co-occurrence", "Number of sympatric frugivores", summarySensitivityGradient[,2])

rownames(summarySensitivityGradient) <- NULL

knitr::kable(summarySensitivityGradient, escape=TRUE, booktabs = TRUE, #Remove brain 1:3

caption = "Sensitivity analysis of phylogenetic regressions to assess the relationship between relative brain sizes and species sympatry | Depicted is the minimum and maximum of estimates when one observation was removed at a time (DfBetas) or when varying the used phylogenetic tree and the data sampling (Phylogeny/Data).") %>%

kableExtra::kable\_styling(latex\_options = "striped") %>%

kableExtra::kable\_styling(latex\_options="scale\_down") %>%

kableExtra::kable\_styling(latex\_options = "HOLD\_position") %>%

kableExtra::add\_header\_above(c("Regression" = 2, "DfBetas" = 3, "Phylogeny/Data" = 3))

```

\newpage

(b) Phylogenetic regressions: diversification and brain size

```{r tabledfsensitivity2, include=TRUE}

summarySensitivityDiversification <- summarySensitivityDiversification[-(1:3),]

rownames(summarySensitivityDiversification) <- NULL

knitr::kable(summarySensitivityDiversification[,-c(3,4,5)], escape=TRUE, booktabs = TRUE, #Remove brain 1:3

caption = "Sensitivity analysis of phylogenetic regressions to assess the relationship between species diversification and relative brain sizes | Depicted is the minimum and maximum of estimates when varying the used phylogenetic tree and the data sampling (Phylogeny/Data), or when the sampling fraction varied (Sampling fraction).") %>%

kableExtra::kable\_styling(latex\_options = "striped") %>%

kableExtra::kable\_styling(latex\_options="scale\_down") %>%

kableExtra::kable\_styling(latex\_options = "HOLD\_position") %>%

kableExtra::add\_header\_above(c("Regression" = 2, "Phylogeny/Data" = 3, "Sampling fraction" = 3))

```

\newpage

(b) Phylogenetic regressions: diversification and sympatry

```{r tabledfsensitivity3, include=TRUE}

summarySensitivitydiversificationAndSympatry[,1] <- gsub("Overlap", "\\% of overlapping range", summarySensitivitydiversificationAndSympatry[,1])

summarySensitivitydiversificationAndSympatry[,1] <- gsub("N co-occurrence", "Number of sympatric frugivores", summarySensitivitydiversificationAndSympatry[,1])

knitr::kable(summarySensitivitydiversificationAndSympatry, escape=TRUE, booktabs = TRUE,

caption = "Sensitivity analysis of phylogenetic regressions to assess the relationship between species diversification and sympatry | Depicted is the minimum and maximum of estimates when one observation was removed at a time (DfBetas) or when varying the used phylogenetic tree and the data sampling (Phylogeny/Data)") %>%

kableExtra::kable\_styling(latex\_options = "striped") %>%

kableExtra::kable\_styling(latex\_options="scale\_down") %>%

kableExtra::add\_header\_above(c("Model:" = 2, "DfBetas" = 3, "Phylogeny/Data" = 3, "Sampling fraction"))

```

\newpage

### Model assumptions

We present below the visual assessment of linear modelling assumptions (histogram of residuals, Q-Q plot, and scatterplot of fitted values vs residuals).

(a) Phylogenetic regressions: effect of sympatry on brain sizes

```{r modelAssumption, include=TRUE, warning = FALSE, message = FALSE, fig.width=7, fig.height=4.5, fig.cap="Model assumption check 'Brain size and sympatry' | Depicted are the histogram of residuals, the Q-Q plot, and the scatter plot of the fitted values \*vs\* the residuals."}

for(a in 1:length(traitName)){

if(a!=2){#Remove brain

model <- get(paste("modelBrain", traitName[a], sep="\_"))

diagnostics.plot(model)

text(x=0.85, y=0.15, paste("Model:\n",traitName[a], sep=""), xpd=TRUE)

if(a/2==floor(a/2)){

cat('\n') #Break page for new figure

}

}

}

```

\newpage

(b) Phylogenetic regressions: diversification and brain size

```{r modelAssumption2a, include=TRUE, warning = FALSE, message = FALSE, fig.width=7, fig.height=4.5, fig.cap="Model assumption check 'Diversity and brain size' | Trace and density of posteriors"}

for(a in 1:length(traitName)){

if(a!=2){#Remove brain

model <- get(paste("modelBrainDiversification", traitName[a], sep="\_"))

plot(model1$Sol)

mtext(paste("Fixed effects: ", traitName[a], sep=""), side = 3, line = -1, outer = TRUE, xpd=TRUE)

#cat('\n') #Break page for new figure

plot(model1$VCV)

mtext(paste("Random/residuals: ", traitName[a], sep=""), side = 3, line = -1, outer = TRUE, xpd=TRUE)

#text(x=max(fitted(model)) + abs(min(fitted(model))), y=mean(residuals(model)), paste("Model:\n",traitName[a], sep=""), xpd=TRUE)

if(a/2==floor(a/2)){

cat('\n') #Break page for new figure

}

}

}

```

```{r modelAssumption2b, include=TRUE, warning = FALSE, message = FALSE, fig.width=7, fig.height=10, fig.cap="Model assumption check 'Diversity and brain size' | Q-Q plot of the posterior distribution and the expected Gaussian distribution"}

layout(mat=matrix(1:(2\*ceiling(length(traitName)/2)), ncol=2), widths=c(5,5), heights=rep(5, times=2\*ceiling(length(traitName)/2)))

par(mar=c(3, 3, 3, 1), mgp=c(2, 0.5, 0), xpd=TRUE)

for(a in 1:length(traitName)){

if(a!=2){#Remove brain

model <- get(paste("modelBrainDiversification", traitName[a], sep="\_"))

posterior <- as.data.frame(model$Sol)

qqnorm(posterior$Trait, main=paste("Normal Q-Q Plot of the posterior distribution;\nModel:", traitName[a], sep=" "))

qqline(posterior$Trait)

#text(x=max(fitted(model)) + abs(min(fitted(model))), y=mean(residuals(model)), paste("Model:\n",traitName[a], sep=""), xpd=TRUE)

#cat('\n') #Break page for new figure

}

}

```

\newpage

(b) Phylogenetic regressions: diversification and sympatry

```{r modelAssumption3, include=TRUE, warning = FALSE, message = FALSE, fig.width=7, fig.height=4.5, fig.cap="Model assumption check 'Diversity and sympatry'| Depicted are the histogram of residuals, the Q-Q plot, and the scatter plot of the fitted values \*vs\* the residuals."}

model <- get(paste("modelBrainDiversificationAndSympatry", sep="\_"))

diagnostics.plot(model)

```

<!-- TC:endignore -->