

Setup
Import Data
Create Functions
Plots & Analyses
Summaries
Multidimensional plots
Inter-subregional Correlations
Selective Regime Analysis
Tests
Save Results

Ecological Correlates of Hippocampal Subfield Volumes Across Primates

Code ▾

*Brian M. Schilder, Bioinformatician II
Raj Lab
Department of Neuroscience
Icahn School of Medicine at Mount Sinai
NYC, New York*

4/29/2017

Setup

Read comments in the setup section below for directions on install additional dependencies.

Hide

```
library(readxl)
library(dplyr)
library(pander)
library(reshape2)
library(shiny)
library(DT)

library(ggplot2) #devtools::install_github('cran/ggplot2')
library(gplots)
library(corrplot)
library(ggdendro)
library(ggrepel)
library(ggbiplot) #devtools::install_github("vqv/ggbiplot")
library(gridExtra)
library(grid)
library(cowplot)
library(plotly)
library(heatmaply)
#library(xlss) # For xlss, must first download JDK: https://www.oracle.com/technetwork/java/javase/downloads/jdk11-downloads-5066655.html

library(phytools)
library(caper)
library(ape)
# install.packages("https://cran.r-project.org/src/contrib/Archive/genlasso/genlasso_1.3.tar.gz", repos=NULL, method
#"libcurl")
# devtools::install_github("khabbazian/l lou")
library(l lou)

# For interactive 3D plotting
library(knitr)
library(rgl) # Macs need to download X11 first. Link here: http://xquartz.macosforge.org/trac/wiki
knitr::knit_hooks$set(webgl = hook_webgl)
knitr::opts_chunk$set(echo=T, warning=F, message=F)

thm <- knitr::knit_theme$get("solarized-dark")
knitr::knit_theme$set(thm)

sessionInfo()
```

```
## R version 3.5.1 (2018-07-02)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS 10.14.2
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] parallel  grid      stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
## [1] rgl_0.99.16      knitr_1.21       llou_1.41
## [4] genlasso_1.3    Matrix_1.2-15   magic_1.5-9
## [7] abind_1.4-5     grplasso_0.4-6 lars_1.2
## [10] phylolm_2.6    igraph_1.2.2   caper_1.0.1
## [13] mvtnorm_1.0-8   MASS_7.3-51.1 phytools_0.6-60
## [16] maps_3.3.0     ape_5.2        heatmaply_0.15.3
## [19] viridis_0.5.1  viridisLite_0.3.0 plotly_4.8.0
## [22] cowplot_0.9.3  gridExtra_2.3  ggbiplot_0.55
## [25] scales_1.0.0   plyr_1.8.4    ggrepel_0.8.0
## [28] ggdendro_0.1-20 corrplot_0.84  gplots_3.0.1
## [31] ggplot2_3.1.0  DT_0.5.1     shiny_1.2.0
## [34] reshape2_1.4.3  pander_0.6.3  dplyr_0.7.8
## [37] readxl_1.2.0
##
## loaded via a namespace (and not attached):
## [1] colorspace_1.3-2      class_7.3-14
## [3] modeltools_0.2-22    mclust_5.4.2
## [5] listenv_0.7.0        flexmix_2.3-14
## [7] codetools_0.2-16     mnormt_1.5-5
## [9] robustbase_0.93-3   jsonlite_1.6
## [11] cluster_2.0.7-1     kernlab_0.9-27
## [13] compiler_3.5.1      httr_1.4.0
## [15] assertthat_0.2.0     lazyeval_0.2.1
## [17] later_0.7.5         htmtools_0.3.6
## [19] tools_3.5.1         bindrcpp_0.2.2
## [21] coda_0.19-2         gtable_0.2.0
## [23] glue_1.3.0          clusterGeneration_1.3.4
## [25] fastmatch_1.1-0     Rcpp_1.0.0
## [27] cellranger_1.1.0    trimcluster_0.1-2.1
## [29] gdata_2.18.0        nlme_3.1-137
## [31] crosstalk_1.0.0     iterators_1.0.10
## [33] fpc_2.1-11.1        xfun_0.4
## [35] stringr_1.3.1       globals_0.12.4
## [37] miniUI_0.1.1.1      mime_0.6
## [39] phangorn_2.4.0       gtools_3.8.1
## [41] dendextend_1.9.0    future_1.10.0
## [43] DEoptimR_1.0-8       TSP_1.1-6
## [45] promises_1.0.1      expm_0.999-3
## [47] animation_2.6       RColorBrewer_1.1-2
## [49] yaml_2.2.0          stringi_1.2.4
## [51] gclus_1.3.1         foreach_1.4.4
## [53] plotrix_3.7-4       seriation_1.2-3
## [55] caTools_1.17.1.1    manipulateWidget_0.10.0
## [57] rlang_0.3.0.1       pkgconfig_2.0.2
## [59] prabclus_2.2-6      bitops_1.0-6
## [61] evaluate_0.12        lattice_0.20-38
## [63] purrr_0.2.5         bindr_0.1.1
## [65] htmlwidgets_1.3      tidyselect_0.2.5
## [67] magrittr_1.5          R6_2.3.0
## [69] combinat_0.0-8      pillar_1.3.1
## [71] whisker_0.3-2       withr_2.1.2
## [73] scatterplot3d_0.3-41 nnet_7.3-12
## [75] future.apply_1.0.1   tibble_2.0.0
## [77] crayon_1.3.4         KernSmooth_2.23-15
## [79] rmarkdown_1.11        data.table_1.11.8
## [81] digest_0.6.18        diptest_0.75-7
## [83] webshot_0.5.1        xtable_1.8-3
## [85] tidyr_0.8.2          httpuv_1.4.5.1
## [87] numDeriv_2016.8-1    stats4_3.5.1
```

```
## [89] munsell_0.5.0           registry_0.5
## [91] quadprog_1.5-5
```

Import Data

[Hide](#)

```
# Frahm HP-subfield data (1982) + Barger whole-HP & brain (2015) + Pantheria eco + ATWP eco
HP_orig <- as.data.frame(read_excel("Data/Frahm_HPsub_eco.xlsx", sheet = "Final_Data", na = "NA"))
# Apply filter to find variables with more than ##% of species missing that data, so that they can be excluded from the model (or have data added to them)
HP_filt <- HP_orig %>% dplyr:::select(which(colMeans(is.na(.)) < 0.25))

## Designate groups
HP_orig$Genus <- gsub(".*","",HP_orig$Species_10K)

HP_orig$Clade <-
  ifelse(grepl("Homo", HP_orig$Genus), "Homo sapiens",
         ifelse(grepl("Gorilla|Hylobates|Pan", HP_orig$Genus), "Apes",
                ifelse(grepl("Cercopithecus|Erythrocebus|Lophocebus|Miopithecus|Nasalis|Papio|Piliocolobus|Pygathrix", HP_orig$Genus), "Old World Monkeys",
                       ifelse(grepl("Alouatta|Aotus|Ateles|Callicebus|Callimico|Callithrix|Cebus|Lagothrix|Pithecia|Saguinus|Saimiri", HP_orig$Genus), "New World Monkeys",
                           ifelse(grepl("Tarsius", HP_orig$Genus), "Tarsiiformes",
                                  ifelse(grepl("Avahi|Cheirogaleus|Eulemur|Indri|Lepilemur|Microcebus|Propithecus|Varecia|Galago|Galagooides|Loris|Nycticebus|Otolemur|Perodicticus|Daubenton", HP_orig$Genus), "Strepsirrhines",
                                      "NA")))))
# Order Clade for plots
orderedClades <- c("Homo sapiens","Apes","Old World Monkeys","New World Monkeys","Tarsiiformes","Strepsirrhines")
HP_orig$Clade <- factor(HP_orig$Clade, labels=orderedClades, levels=orderedClades, ordered=T)

# Rename some variables
names(HP_orig)[names(HP_orig)== "HippocampusRetro"] <- "retroHP"
names(HP_orig)[names(HP_orig)== "FasciaDentata"] <- "FD"
names(HP_orig)[names(HP_orig)== "Subiculum"] <- "Sub"
names(HP_orig)[names(HP_orig)== "HP_HS_fibers"] <- "Fibers"
names(HP_orig)[names(HP_orig)== "Body"] <- "Body_Size"
names(HP_orig)[names(HP_orig)== "Schizocortex"] <- "EC" # switched from EC
names(HP_orig)[names(HP_orig)== "HR_filled"] <- "Home_Range"

# Log Neuroanatomical vars
#cols <- c("Body_Size","BrainVol","retroHP","FD","Hilus","CA3","CA2","CA1","Sub")
#HP_orig[cols] <- log(HP_orig[cols])

# Log Eco vars
HP_orig$PopulationDensity_n_km2 <- scales::rescale(log(HP_orig$PopulationDensity_n_km2),c(1,10))
HP_orig$GroupSize_filled <- scales::rescale(log(HP_orig$GroupSize_filled),c(1,10))
HP_orig$Home_Range <- scales::rescale(log(HP_orig$Home_Range),c(1,10))

# Add combined regions as variables
HP_orig$retroHP(EC <- HP_orig$retroHP + HP_orig$EC
HP_orig$DG <- HP_orig$FD + HP_orig$Hilus
HP_orig$CA2.3 <- HP_orig$CA2 + HP_orig$CA3

# Correct units of Barger (2015) data
HP_orig[,c("BrainVol","HPvol")] <- HP_orig[,c("BrainVol","HPvol")] * 1000

# Create retroHP minus each subregion
HP_orig$Body_Brain <- HP_orig$Body_Size - HP_orig$BrainMass
HP_orig$Brain_HP <- HP_orig$BrainVol - HP_orig$retroHP
HP_orig$Brain_EC <- HP_orig$BrainVol - HP_orig$EC
HP_orig$Brain_Fib <- HP_orig$BrainVol - HP_orig$Fibers

HP_orig$retroHP__DG <- HP_orig$retroHP - HP_orig$DG
HP_orig$retroHP__FD <- HP_orig$retroHP - HP_orig$FD
HP_orig$retroHP__Hil <- HP_orig$retroHP - HP_orig$Hilus
HP_orig$retroHP__CA2.3 <- HP_orig$retroHP - HP_orig$CA2.3
HP_orig$retroHP__CA3 <- HP_orig$retroHP - HP_orig$CA3
HP_orig$retroHP__CA2 <- HP_orig$retroHP - HP_orig$CA2
HP_orig$retroHP__CA1 <- HP_orig$retroHP - HP_orig$CA1
HP_orig$retroHP__Sub <- HP_orig$retroHP - HP_orig$Sub

colnames(HP_orig)
```

```

## [ 1] "Species_David"          "Sub"
## [ 3] "CA1"                     "CA2"
## [ 5] "CA3"                     "Hilus"
## [ 7] "FD"                      "Body_Size"
## [ 9] "HippocampusTotal"       "Fibers"
## [11] "retroHP"                 "Medulla"
## [13] "EC"                      "Nocturnality"
## [15] "Species_10K"             "Species_1981"
## [17] "BrainMass"                "BrainVol"
## [19] "HPvol"                   "Source"
## [21] "MSW93_Order"             "MSW93_Family"
## [23] "MSW93_Genus"              "MSW93_Species"
## [25] "MSW93_Binomial"           "ActivityCycle"
## [27] "AdultBodyMass_g"          "AdultForearmLen_mm"
## [29] "AdultHeadBodyLen_mm"      "AgeatEyeOpening_d"
## [31] "AgeatFirstBirth_d"        "BasalMetRate_mLO2hr"
## [33] "BasalMetRateMass_g"       "DietBreadth"
## [35] "DispersalAge_d"           "GestationLen_d"
## [37] "HabitatBreadth"           "HomeRange_km2"
## [39] "HomeRange_Indiv_km2"       "InterBirthInterval_d"
## [41] "LitterSize"                "LittersPerYear"
## [43] "MaxLongevity_m"           "NeonateBodyMass_g"
## [45] "NeonateHeadBodyLen_mm"     "PopulationDensity_n_km2"
## [47] "PopulationGrpSize"         "SexualMaturityAge_d"
## [49] "SocialGrpSize"             "TeatNumber"
## [51] "Terrestriality"            "TrophicLevel"
## [53] "WeaningAge_d"              "WeaningBodyMass_g"
## [55] "WeaningHeadBodyLen_mm"     "References"
## [57] "AdultBodyMass_g_EXT"       "LittersPerYear_EXT"
## [59] "NeonateBodyMass_g_EXT"      "WeaningBodyMass_g_EXT"
## [61] "GR_Area_km2"               "GR_MaxLat_dd"
## [63] "GR_MinLat_dd"              "GR_MRLat_dd"
## [65] "GR_MaxLong_dd"             "GR_MinLong_dd"
## [67] "GR_MRLong_dd"              "HuPopDen_Min_n/km2"
## [69] "HuPopDen_Mean_n/km2"       "HuPopDen_5p_n/km2"
## [71] "HuPopDen_Change"           "Precip_Mean_mm"
## [73] "Temp_Mean_01degC"          "AET_Mean_mm"
## [75] "PET_Mean_mm"                "ATWP_DR"
## [77] "ATWP_perForaging"          "ATWP_GroupSize"
## [79] "ATWP_HR"                    "ATWP_HR_km2"
## [81] "ATWP_perTravel"             "GroupSize_filled"
## [83] "Home_Range"                  "Population_Density"
## [85] "Genus"                       "Clade"
## [87] "retroHP.EC"                  "DG"
## [89] "CA2.3"                      "Body_Brain"
## [91] "Brain_HP"                   "Brain_EC"
## [93] "Brain_Fib"                  "retroHP_DG"
## [95] "retroHP_FD"                 "retroHP_Hil"
## [97] "retroHP_CA2.3"              "retroHP_CA3"
## [99] "retroHP_CA2"                 "retroHP_CA1"
## [101] "retroHP_Sub"

```

Hide

```

## Make shapes and colors consistent
shapes <- c(17,16,18,15,7,9)
names(shapes) <- levels(HP_orig$Clade)
#gg_color_hue <- function(n) { # ggplot default colors
  #hues = seq(15, 375, length=n+1)
  #hcl(h=hues, l=65, c=100)[1:n]
  #}
#colors <- gg_color_hue(6)
colors <- c("#C99800", "#F8766D", "#00BCD8", "#00BA38", "blue2", "#FD61D1")
# Remove human shape/color if humans were removed
if(!("Homo" %in% HP_orig$Genus)){colors<-colors[-1]; shapes<-shapes[-1]}
names(colors) <- names(shapes)

```

Hide

Tree & Comparative Files

Hide

```
# Primate tree from 10K Trees
tree10K <- read.nexus(file = "Data/Phylo/10k_Primates.nex")

## Rescale tree
# Need to rescale the tree due to errors with pgl's described here: http://blog.phytools.org/2011/12/error-message-fro
m-brownielite-and.html#
#scale <- 100
#tree10K$edge.length <- tree10K$edge.length/max(nodeHeights(tree10K)[,2])*scale

# Create comparative.data
HP <- comparative.data(phy=tree10K, data=HP_orig, names.col=Species_10K,
                         vcv=T, na.omit=F, warn.dropped=T)
```

Create Functions

PGLS residuals & plot function

[Hide](#)

```

pgls_function <- function(comp_data, response_var, predictor_var){
  HPres <- pgls(data=comp_data, log(eval(parse(text=response_var))) ~
    log(eval(parse(text=predictor_var))), lambda='ML')
  pgls_summary <- summary(HPres)
  print(pglis_summary)

  ## Get res
  res <- resid(HPres)
  res_name <- paste(response_var,"res",sep="_")
  ## Put back into comparative.data
  comp_data$data[res_name] <- as.vector(scales::rescale(res, c(1:2)))
  new_comp_data <- comp_data
  # Put into actual comparative.data in global environment
  comp_data$data[res_name] <- as.vector(scales::rescale(res, c(1:2)))
  assign('HP',comp_data,envir=.GlobalEnv)

  # Test if residuals are normally distributed
  #shapiro.test <- shapiro.test(x = comp_data$data[paste(response_var,"res",sep="_")])

  # Residuals XY Plot
  # radj <- as.numeric(pglis_summary$adj.r.squared)
  # p <- as.numeric(pglis_summary$coefficients[2,4])
  #title = title=paste(response_var,"vs.", predictor_var, paste("\n adj.R^2=", round(radj,4), ", p= ",round(p,4)))
  xy_plot_legend <- ggplot(comp_data$data, aes( y=log(eval(parse(text=response_var))),
    x=log(eval(parse(text=predictor_var))), fill=Clade, color=Clade, shape=Clade) ) +
    geom_abline(slope = pglis_summary$coefficients[2,1], intercept = pglis_summary$coefficients[1,1], color="black") +
    geom_point(size=3) +
    labs(y=paste(response_var,"vol (mm3)", x=paste(predictor_var,"vol (mm3)") ) +
    theme(plot.title = element_text(hjust=0.5, size=8)) +
    scale_shape_manual(values=shapes) + scale_color_manual(values=colors) + scale_fill_manual(values=colors)
  print(xy_plot_legend %>% ggplotly())

  xy_plot <- xy_plot_legend + theme(legend.position = "none")
  # + annotate("text",x=5, y=10, hjust=0, label =  paste("adj.R^2 =", round(radj,4), "; p = ", round(p,4)))

  # Plot fancy contMaps

  ## Absolute vols plot (not that informative since it's basically just tracking brain size)
  #HP_data <- as.matrix(comp_data$data[response_var])
  #names(HP_data) <- comp_data$phy$tip.label
  #phylo_plot <- contMap(comp_data$phy, HP_data, type="phylogram", plot=TRUE)
  ## Residuals plot
  HPres_data <- as.matrix(comp_data$data[res_name])
  names(HPres_data) <- comp_data$phy$tip.label
  res_phylo_plot <- contMap(comp_data$phy, HPres_data, type="phylogram",
    plot=FALSE, fsize=c(0.5, 1))
  plot(res_phylo_plot, leg.txt=paste(res_name),lwd=3, fsize=c(0.5, 1))

  # Use plot() to edit further
  #plot(res_phylo_plot)
  #par(cex.lab=.5)

  # Top residuals
  #res <- DG.HP_res$residuals
  res_data <- data.frame(species=row.names(res),res=res)

  print(paste("Top 5 Positive Residuals:", res_name))
  sort_res <- res_data[with(res_data, order(-res)), ]
  row.names(sort_res) <- NULL
  print(sort_res[1:5,])
  print("=====")
  print(paste("Top 5 Negative Residuals:", res_name))
  sort_res <- res_data[with(res_data, order(res)), ]
  row.names(sort_res) <- NULL
  print(sort_res[1:5,])
  # Output
  output <- list(response_var=response_var, predictor_var=predictor_var,
    pglis_summary=pglis_summary, residuals=res, sort_res=sort_res,
    xy_plot= xy_plot,
    res_phylo_plot=res_phylo_plot,
    new_comp_data=new_comp_data)
  return(output)
}

```

Eco analyses function

NOTE: Some variables may not be appropriate to put in model together due to colinearity. To solve this, could:

* Remove certain variables *

Perform a stepwise regression: <http://blog.phytools.org/2014/06/performing-stepwise-phylogenetic.html>

(<http://blog.phytools.org/2014/06/performing-stepwise-phylogenetic.html>)

[Hide](#)

```
# MODEL HERE
# Analyze all eco variables in one model
run_eco <- function(pgls_function.out){
  # Run pgls
  HP.noHomo <- subset(pgls_function.out$new_comp_data, subset=! Genus=="Homo")
  pgls_eco_raw <- pgls(data=HP.noHomo, formula=
    eval(parse(text=paste(pgls_function.out$response_var,"res",sep="_"))))
  ~ DietBreadth + PopulationDensity_n_km2 +
    GroupSize_filled + Home_Range + Residual_HomeRange,
    lambda='ML')
  # + HR_filled + GroupSize_filled + ATWP_DR + ATWP_perForaging + ATWP_perTravel
  pgls_eco_summary <- summary(pgl_eco_raw)

  output <- list(pgl_eco_summary=pgls_eco_summary, pgl_eco_raw=pgls_eco_raw)
  return(output)
}
```

Eco plot functions

[Hide](#)

```

# Plot eco variable function
eco_plots <- function(pgls_function.out, eco_var, run_eco.out, figLabel=""){

  pgls_eco_sum <- run_eco.out$pgls_eco_summary
  response_var <- pgls_function.out$response_var
  data <- pgls_function.out$new_comp_data$data
  brain <- data[,paste(response_var,"res",sep="_")]
  eco_x <- data[,paste(eco_var)]
  slope <- as.numeric(pgls_eco_sum$coefficients[eco_var,1])
  p <- as.numeric(pgls_eco_sum$coefficients[eco_var,4])

  # Initialize plot
  eco_plot <- ggplot(data, aes(y=brain, x=eco_x, fill=Clade, color=Clade), shape=Clade) +
    theme_classic() + ggtitle(figLabel)

  # Conditionally add regression line
  if ( p<=0.05){
    eco_plot <- eco_plot +
      geom_smooth(na.rm=F, inherit.aes=F, method="lm", alpha = .15, data=data, aes(y=brain, x=eco_x))
  }

  # Conditionally add legend
  if (eco_var == "Residual_HomeRange"){
    eco_plot = eco_plot + theme(legend.position=c(1.75, 0.35), legend.background = element_rect(fill="whitesmoke"),
                                plot.title = element_text(hjust= -.3))
  } else{
    eco_plot = eco_plot + theme( legend.position="none",
                                plot.title = element_text(hjust= -.3))
  }

  # Add remaining features
  eco_plot <- eco_plot + geom_point(size=3, alpha=.7) +
    xlab(paste(eco_var,sep="")) + ylab(paste(response_var,"res",sep="_")) +
    scale_shape_manual(values=shapes) + scale_color_manual(values=colors) + scale_fill_manual(values=colors)

  #geom_abline(slope=SLOPE, intercept=INTERCEPT)
  #assign(paste("eco_plot",paste(response_var,"res",sep="_"), "vs", eco_var,sep=".") , eco_plot)
  #return(eco_plot) # %>% ggplotly()
}

# MAKE MORE FLEXIBLE (dependent on which model variables actually used)
all_eco_plots <- function(pgls_function.out){
  eco=run_eco(pgls_function.out)
  p_f.o <- pgls_function.out

  #e0 <- eco_plots(eco_var = "Nocturnality", run_eco.out=eco)
  e1 <- eco_plots(p_f.o, eco_var = "DietBreadth", run_eco.out=eco, figLabel="A")
  #e2 <- eco_plots(p_f.o, eco_var = "HomeRange_km2", run_eco.out=eco)
  #e3 <- eco_plots(p_f.o, eco_var = "HomeRange_Indiv_km2", run_eco.out=eco)
  e4 <- eco_plots(p_f.o, eco_var = "PopulationDensity_n_km2", run_eco.out=eco, figLabel="B")
  #e5 <- eco_plots(p_f.o, eco_var = "SocialGrpSize", run_eco.out=eco)
  #e6 <- eco_plots(p_f.o, eco_var = "ATWP_DR", run_eco.out=eco)
  #e7 <- eco_plots(p_f.o, eco_var = "ATWP_perForaging", run_eco.out=eco)
  #e8 <- eco_plots(p_f.o, eco_var = "ATWP_GroupSize", run_eco.out=eco)
  #e9 <- eco_plots(p_f.o, eco_var = "ATWP_HR", run_eco.out=eco)
  #e10 <- eco_plots(p_f.o, eco_var = "ATWP_perTravel", run_eco.out=eco)
  e11 <- eco_plots(p_f.o, eco_var = "GroupSize_filled", run_eco.out=eco, figLabel="C")
  e12 <- eco_plots(p_f.o, eco_var = "Home_Range", run_eco.out=eco, figLabel="D")
  e13 <- eco_plots(p_f.o, eco_var = "Residual_HomeRange", run_eco.out=eco, figLabel="E")

  gridExtra::grid.arrange(e1,e4,e11,e12,e13, ncol=3,
                         top = textGrob(paste("Ecological Plots:",
                                               paste(pgls_function.out$response_var,"res",sep="_"))),
                         gp=gpar(fontsize=18))

  #e6,e7,e10
  # mod_vars <- list(eco_vars=c("DietBreadth","PopulationDensity_n_km2","GroupSize_filled", "Home_Range", "Residual_HomeRange"))
  # subplot(e1,e4,e11,e12,e13, nrows = 2, shareY=F, shareX=F, titleX = T, titleY=T, margin = 0.1)

  # fluidPage(
  #   fluidRow( column(4, e1), column(4, e4), column(4, e11)),
  #   fluidRow( column(4, e12), column(8, e13) )
  # )

  #plot_grid( plotlist = list(e1,e4,e11,e12,e13), labels = list())
}

```

Plots & Analyses

Calculate Residual_HomeRange

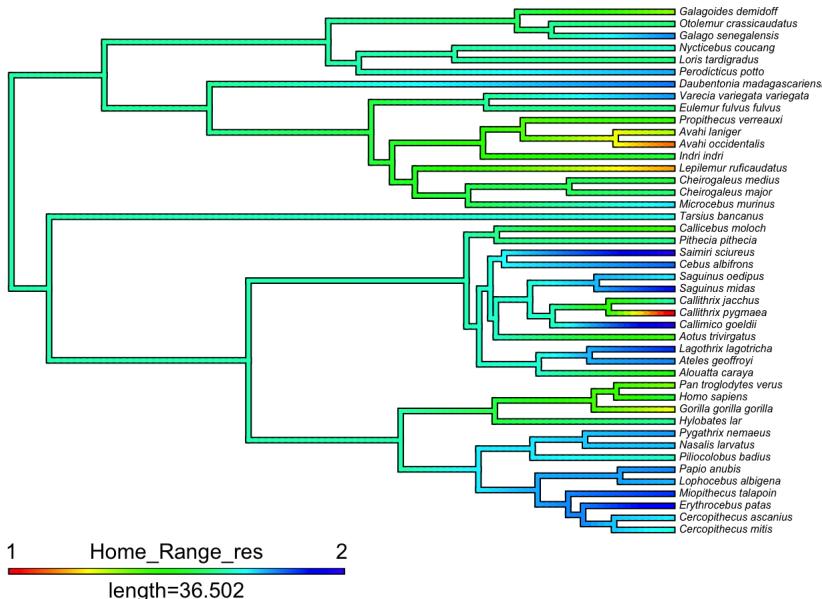
Hide

```
# We know HomeRange scales with BodySize, so perhaps using "extra" HR relative to body weight is a more relavent measure.
```

```
## Alternatively could include BodySize as covariate in eco model.
```

```
HR.body_res <- pgls_function(HP, "Home_Range", "Body_Size")
```

```
##  
## Call:  
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),  
##       data = comp_data, lambda = "ML")  
##  
## Residuals:  
##      Min        1Q     Median        3Q       Max  
## -0.09617 -0.02901 -0.00308  0.03024  0.13852  
##  
## Branch length transformations:  
##  
## kappa [Fix] : 1.000  
## lambda [ ML] : 0.128  
##   lower bound : 0.000, p = 0.49113  
##   upper bound : 1.000, p = 0.00165  
##  95.0% CI : (NA, 0.822)  
## delta [Fix] : 1.000  
##  
## Coefficients:  
##                               Estimate Std. Error t value  
## (Intercept)                 0.23158    0.28341  0.8171  
## log(eval(parse(text = predictor_var))) 0.16806    0.03717  4.5215  
##  
## (Intercept)                 0.4185  
## log(eval(parse(text = predictor_var))) 4.951e-05 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.04668 on 42 degrees of freedom  
## Multiple R-squared: 0.3274, Adjusted R-squared: 0.3114  
## F-statistic: 20.44 on 1 and 42 DF,  p-value: 4.951e-05
```



```

## [1] "Top 5 Positive Residuals: Home_Range_res"
##           species      res
## 1     Callimico_goeldii 0.6232619
## 2       Saimiri_sciureus 0.6146490
## 3   Erythrocebus_patas 0.5648503
## 4       Saguinus_midas 0.4677529
## 5 Miopithecus_talapoin 0.4263833
## [1] =====
## [1] "Top 5 Negative Residuals: Home_Range_res"
##           species      res
## 1     Callithrix_pygmaea -1.0361756
## 2       Avahi_occidentalis -0.8450562
## 3   Lepilemur_ruficaudatus -0.7604272
## 4 Gorilla_gorilla_gorilla -0.6303260
## 5       Avahi_laniger -0.5374609

```

[Hide](#)

```

# Put back into Comp.data
HP$data$Residual_HomeRange <- HR.body_res$residuals

```

Retrocommissural Hippocampus

retroHP vs. Total Brain Vol

[Hide](#)

```

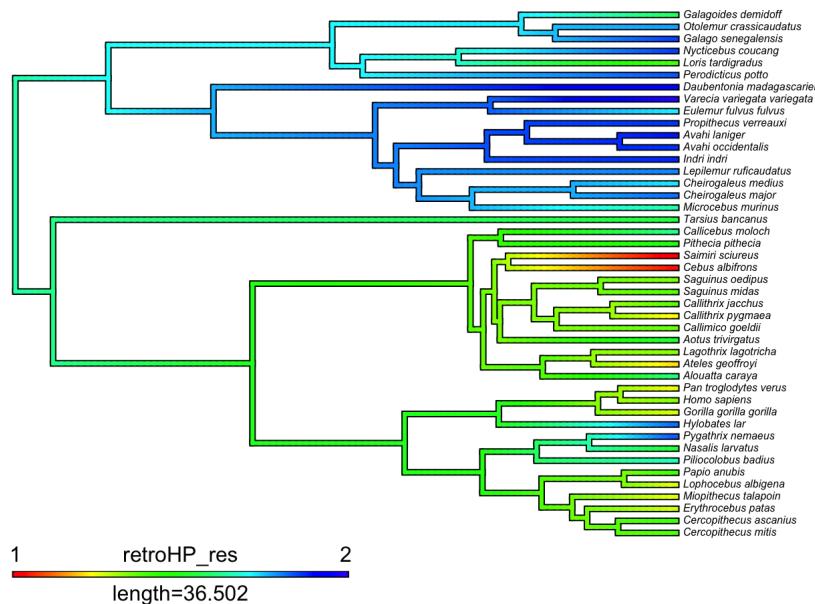
# HP vs. Brain
HP.Brain_res <- pgls_function(HP, "retroHP", "Brain__HP")

```

```

##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -0.088712 -0.031699  0.009512  0.030374  0.120211
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 1.000
## lower bound : 0.000, p = 1.8851e-06
## upper bound : 1.000, p = 1
## 95.0% CI : (0.461, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)             -0.917424   0.492829 -1.8615
## log(eval(parse(text = predictor_var))) 0.729459   0.046802 15.5860
##                               Pr(>|t|)
## (Intercept)                  0.06967 .
## log(eval(parse(text = predictor_var))) < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05227 on 42 degrees of freedom
## Multiple R-squared: 0.8526, Adjusted R-squared: 0.8491
## F-statistic: 242.9 on 1 and 42 DF, p-value: < 2.2e-16

```



```
## [1] "Top 5 Positive Residuals: retroHP_res"
##           species      res
## 1  Varecia_variegata_variegata 0.4870433
## 2  Daubentonia_madagascariensis 0.4276068
## 3          Avahi_laniger 0.3513009
## 4          Indri_indri 0.3339972
## 5  Avahi_occidentalis 0.3219001
## [1] "====="
## [1] "Top 5 Negative Residuals: retroHP_res"
##           species      res
## 1  Saimiri_sciureus -0.8912601
## 2  Cebus_albifrons -0.8418913
## 3  Ateles_geoffroyi -0.6007531
## 4  Callithrix_pygmaea -0.5751744
## 5  Pan_troglodytes_verus -0.5458775
```

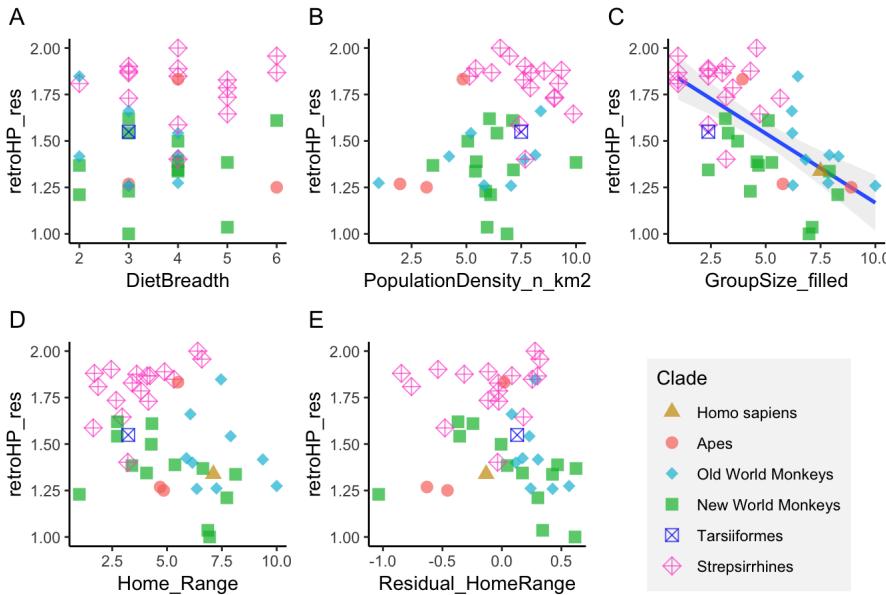
```
run_eco(HP.Brain_res); all_eco_plots(HP.Brain_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.040904 -0.015271 -0.001555  0.015806  0.055791 
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.623
## lower bound : 0.000, p = 0.0037727
## upper bound : 1.000, p = 0.048371
## 95.0% CI : (0.126, 0.999)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             1.418245  0.256011  5.5398 3.123e-06 ***
## DietBreadth            0.015049  0.022004  0.6839  0.4985    
## PopulationDensity_n_km2 0.029740  0.018422  1.6144  0.1154    
## GroupSize_filled        -0.074909 0.016777 -4.4650 7.978e-05 ***
## Home_Range              0.052285  0.032810  1.5936  0.1200    
## Residual_HomeRange     -0.114777 0.127411 -0.9008  0.3738    
## ---                     
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.02309 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.3836, Adjusted R-squared: 0.2956 
## F-statistic: 4.356 on 5 and 35 DF,  p-value: 0.003461
## 
## $pgls_eco_raw
## 
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
## 
## Coefficients:
## (Intercept)          DietBreadth PopulationDensity_n_km2
## 1.41825           0.01505          0.02974
## GroupSize_filled    Home_Range   Residual_HomeRange
## -0.07491           0.05228         -0.11478

```

Ecological Plots: retroHP_res



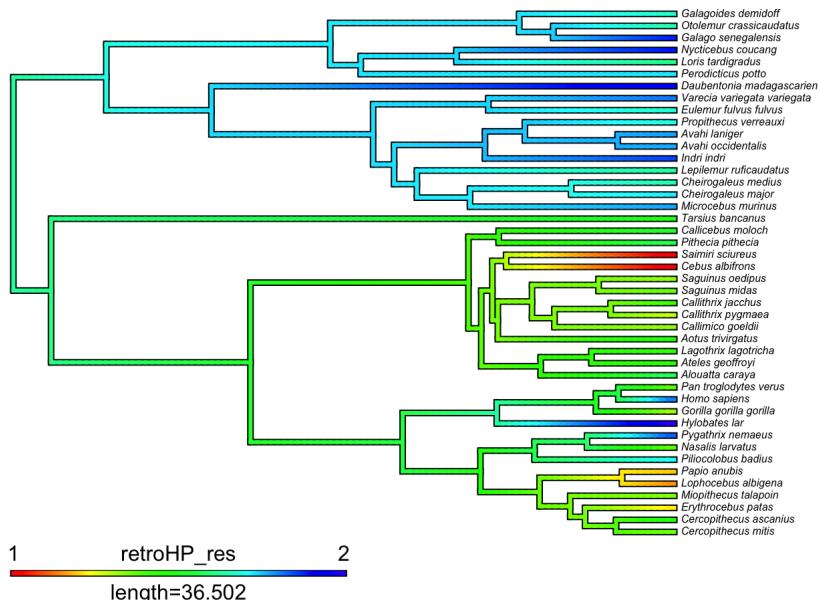
retroHP vs. Medulla ***

Result: No relationship

Hide

```
# HP vs. Medulla
HP.Med_res <- pgls_function(HP, "retroHP", "Medulla")

## 
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.083809 -0.020279  0.000924  0.021377  0.067852 
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.577
## lower bound : 0.000, p = 0.00019402
## upper bound : 1.000, p = 0.0090288
## 95.0% CI : (0.173, 0.947)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)             -0.103697  0.315499 -0.3287
## log(eval(parse(text = predictor_var))) 0.958138  0.045674 20.9776
## Pr(>|t|)                0.744
## (Intercept)             <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03239 on 42 degrees of freedom
## Multiple R-squared: 0.9129, Adjusted R-squared: 0.9108
## F-statistic: 440.1 on 1 and 42 DF,  p-value: < 2.2e-16
```



```

## [1] "Top 5 Positive Residuals: retroHP_res"
##           species      res
## 1       Hylobates_lar 0.4165238
## 2 Daubentonia_madagascariensis 0.3636936
## 3       Nycticebus_coucang 0.3090618
## 4       Galago_senegalensis 0.3006888
## 5       Indri_indri 0.2687092
## [1] "====="
## [1] "Top 5 Negative Residuals: retroHP_res"
##           species      res
## 1     Saimiri_sciureus -0.6878322
## 2     Cebus_albifrons -0.6874209
## 3 Lophocebus_albigena -0.5244967
## 4     Papio_anubis -0.4725856
## 5 Erythrocebus_patas -0.4463793

```

Hide

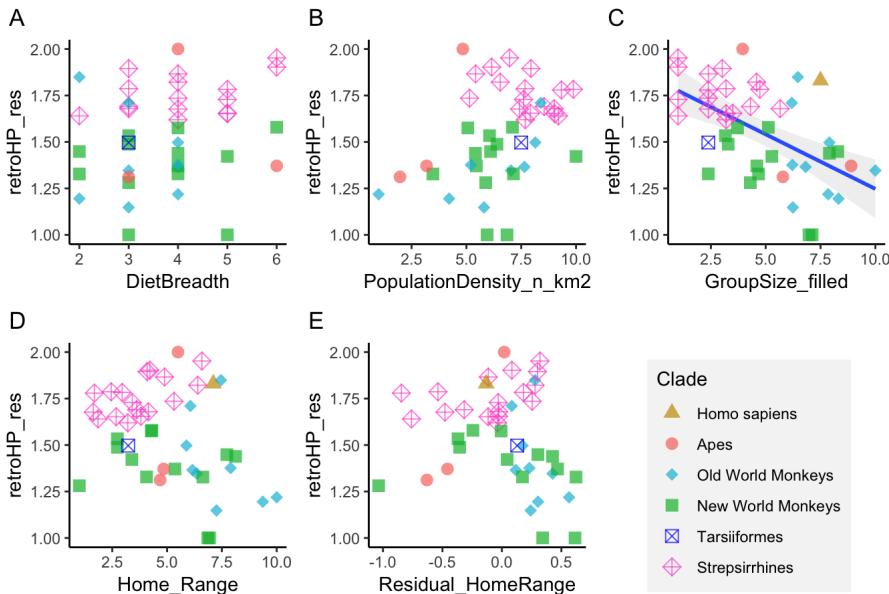
```
run_eco(HP.Med_res); all_eco_plots(HP.Med_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
##   "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
##   GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
##   lambda = "ML"))
##
## Residuals:
##      Min      1Q Median      3Q      Max 
## -0.06249 -0.02108  0.00045  0.01415  0.06815 
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.908
## lower bound : 0.000, p = 0.039497
## upper bound : 1.000, p = 0.51784
## 95.0% CI : (0.014, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)            1.642134   0.292771  5.6089 2.531e-06 ***
## DietBreadth            0.014168   0.022789  0.6217  0.53817    
## PopulationDensity_n_km2 0.019496   0.019805  0.9844  0.33167    
## GroupSize_filled        -0.044010  0.018240 -2.4128  0.02121 *  
## Home_Range              -0.010975  0.037213 -0.2949  0.76980    
## Residual_HomeRange      0.095746   0.140299  0.6824  0.49945    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03101 on 35 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared: 0.2385, Adjusted R-squared: 0.1297 
## F-statistic: 2.192 on 5 and 35 DF,  p-value: 0.07731
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
##   "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
##   GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
##   lambda = "ML"))
##
## Coefficients:
##             (Intercept) DietBreadth PopulationDensity_n_km2
##             1.64213            0.01417            0.01950
## GroupSize_filled          Home_Range      Residual_HomeRange
##             -0.04401            -0.01097            0.09575

```

Ecological Plots: retroHP_res



[Hide](#)

```
# Hyp: Relationship with overall brain vol?
#pgls_function(HP, "retroHP_res", "BrainVol")
```

retroHP.vs.Medulla Phenogram

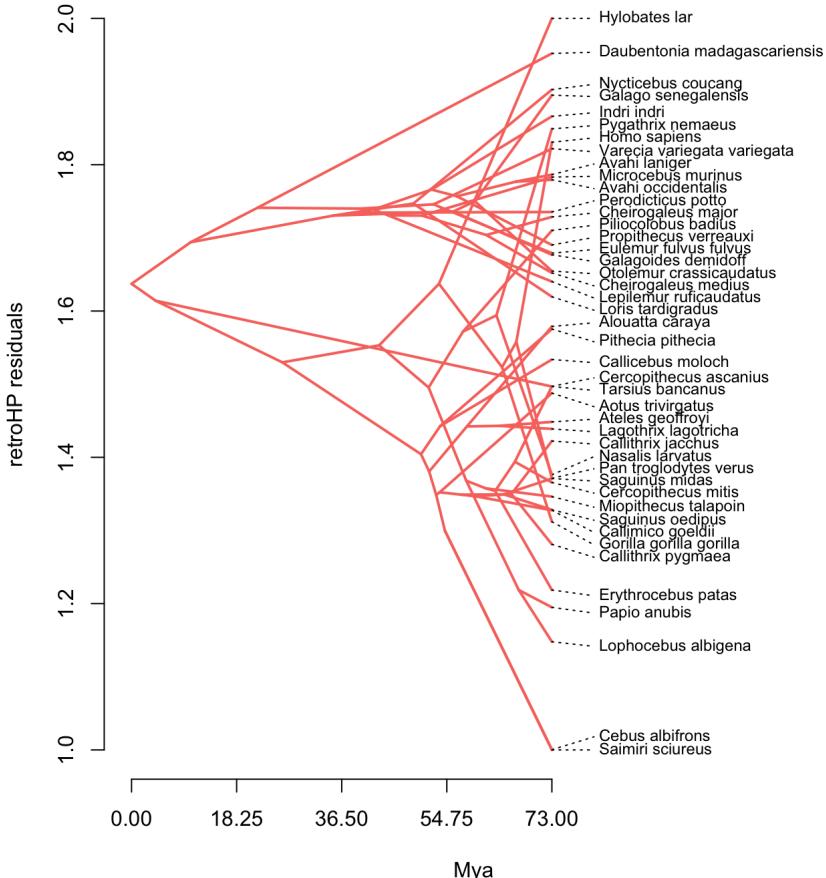
[Hide](#)

```
HPres <- HP.Med_res$new_comp_data$data$retroHP_res
names(HPres) <- HP.Med_res$new_comp_data$phy$tip.label
## Get colors from ggplot defaults
gg_color_hue <- function(n) {
  hues = seq(15, 375, length = n + 1)
  hcl(h = hues, l = 65, c = 100)[1:n]
}
colz = gg_color_hue(6)

phenogram(HP.Med_res$new_comp_data$phy, x=HPres, spread.labels=T,
          fsize=.75, colors=colz, axes=c(time, HPres),
          main="Phenogram:\n retroHP vs. medulla PGLS residuals",
          xlab="Mya", ylab="retroHP residuals") #spread.cost = c(1, 0)
```

```
## Optimizing the positions of the tip labels...
```

Phenogram:
retroHP vs. medulla PGLS residuals



Hide

```
## Color branches by clades??
```

retroHP_res vs. BrainVol

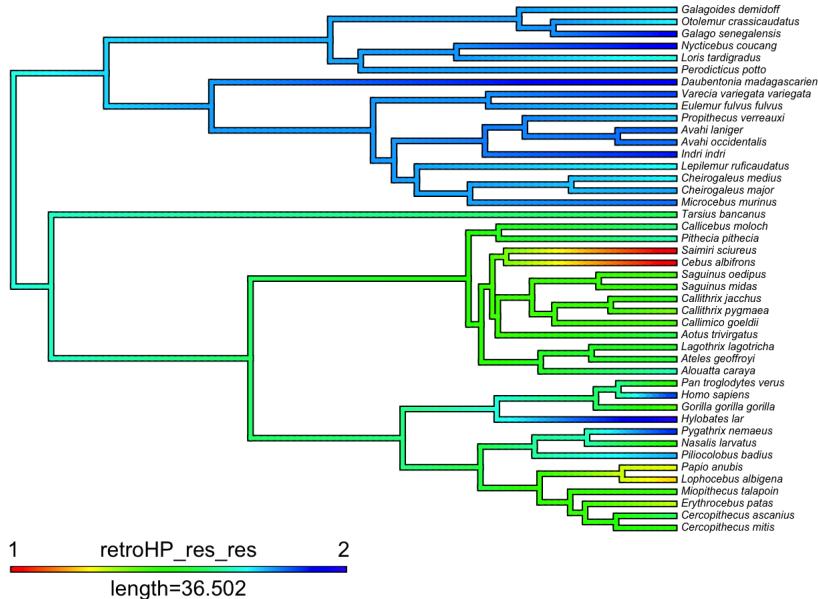
Hide

```
#Hyp: As brain size scales up, does retroHP_res becomes proportionally smaller?  
HPres.Brain_res <- pgls_function(HP, "retroHP_res", "Brain__HP")
```

```

## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.044786 -0.010563 -0.003388  0.014257  0.041070
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.567
## lower bound : 0.000, p = 0.00051585
## upper bound : 1.000, p = 0.01756
## 95.0% CI : (0.152, 0.964)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                0.4852431  0.2171933  2.2342
## log(eval(parse(text = predictor_var))) -0.0012756  0.0213581 -0.0597
##                               Pr(>|t|)
## (Intercept)                0.03085 *
## log(eval(parse(text = predictor_var)))  0.95266
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01998 on 42 degrees of freedom
## Multiple R-squared: 8.493e-05, Adjusted R-squared: -0.02372
## F-statistic: 0.003567 on 1 and 42 DF, p-value: 0.9527

```



```

## [1] "Top 5 Positive Residuals: retroHP_res_res"
##           species      res
## 1        Hylobates_lar 0.2225415
## 2 Daubentonia_madagascariensis 0.1972782
## 3     Nycticebus_coucang 0.1699622
## 4     Galago_senegalensis 0.1647316
## 5       Indri_indri 0.1520120
## [1] "=====
## [1] "Top 5 Negative Residuals: retroHP_res_res"
##           species      res
## 1 Saimiri_sciureus -0.4724358
## 2 Cebus_albifrons -0.4706772
## 3 Lophocebus_albigena -0.3326298
## 4     Papio_anubis -0.2916567
## 5 Erythrocebus_patas -0.2727841

```

Hide

```

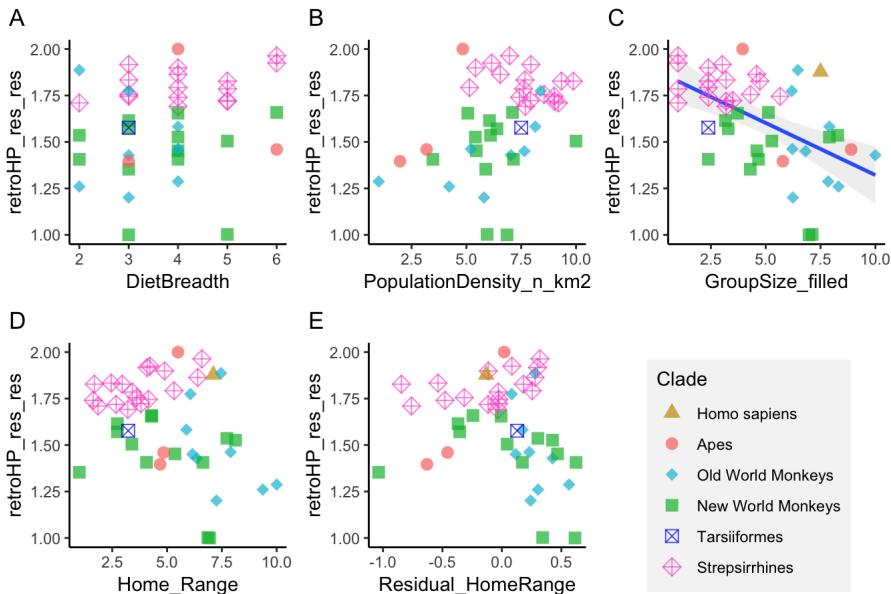
run_eco(HPres.Brain_res); all_eco_plots(HPres.Brain_res)

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.053831 -0.010347  0.003201  0.017669  0.054512
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.460
## lower bound : 0.000, p = 0.092216
## upper bound : 1.000, p = 0.54303
## 95.0% CI : (NA, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.5721486  0.2834565  5.5463 3.061e-06 ***
## DietBreadth          0.0225424  0.0252198  0.8938  0.37751
## PopulationDensity_n_km2 0.0220668  0.0207409  1.0639  0.29465
## GroupSize_filled     -0.0465959  0.0187597 -2.4838  0.01793 *
## Home_Range            0.0083041  0.0363120  0.2287  0.82044
## Residual_HomeRange   -0.0230984  0.1426419 -0.1619  0.87229
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02415 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.2414, Adjusted R-squared: 0.1331
## F-statistic: 2.228 on 5 and 35 DF, p-value: 0.07329
##
## $pgls_eco_raw
##

## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
##             (Intercept) DietBreadth PopulationDensity_n_km2
##             1.572149          0.022542          0.022067
## GroupSize_filled          Home_Range      Residual_HomeRange
##             -0.046596          0.008304         -0.023098

```

Ecological Plots: retroHP_res_res



[Hide](#)

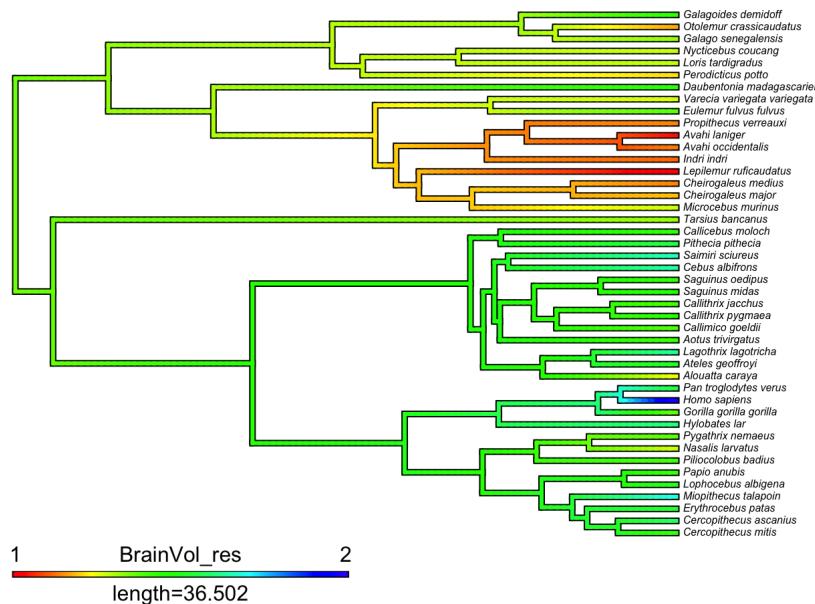
#Result: No relationship.

retroHP_res vs. Encephalization

[Hide](#)

```
#Hyp: As Encephalization scales up, does retroHP_res become proportionally smaller?
Enceph_res <- pgls_function(HP, "BrainVol", "Body_Brain")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -0.071675 -0.035637 -0.002602  0.017158  0.096395
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.542
## lower bound : 0.000, p = 7.9517e-05
## upper bound : 1.000, p = 0.00047895
## 95.0% CI : (0.185, 0.874)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                  4.789262   0.288205 16.618
## log(eval(parse(text = predictor_var))) 0.715537   0.036479 19.615
##                                     Pr(>|t|)
## (Intercept)                  < 2.2e-16 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04494 on 42 degrees of freedom
## Multiple R-squared: 0.9016, Adjusted R-squared: 0.8992
## F-statistic: 384.7 on 1 and 42 DF, p-value: < 2.2e-16
```



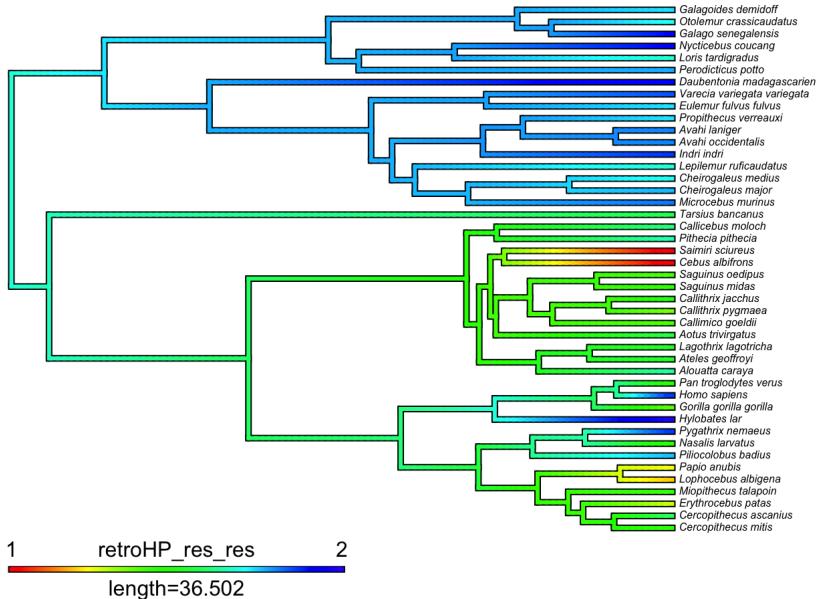
```
## [1] "Top 5 Positive Residuals: BrainVol_res"
##           species      res
## 1       Homo_sapiens 1.3611650
## 2 Miopithecus_talapoin 0.7230488
## 3     Saimiri_sciureus 0.6424171
## 4     Cebus_albifrons 0.6100275
## 5 Lagothrix_lagotricha 0.5898454
## [1] "=====
## [1] "Top 5 Negative Residuals: BrainVol_res"
##           species      res
## 1 Lepilemur_ruficaudatus -0.7613935
## 2     Avahi_laniger -0.6823231
## 3     Indri_indri -0.5210377
## 4     Avahi_occidentalis -0.4750168
## 5 Cheirogaleus_mediums -0.4638639
```

```
HPres.Enceph_res <- pgls_function(HP, "retroHP_res", "BrainVol_res")
```

```

## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.046638 -0.008408  0.004220  0.017394  0.040602
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.538
## lower bound : 0.000, p = 0.014627
## upper bound : 1.000, p = 0.071673
## 95.0% CI : (0.069, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                0.484757  0.084882  5.7110
## log(eval(parse(text = predictor_var))) -0.042656  0.208599 -0.2045
##                               Pr(>|t|)
## (Intercept)                 1.034e-06 ***
## log(eval(parse(text = predictor_var)))      0.839
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01971 on 42 degrees of freedom
## Multiple R-squared: 0.0009946, Adjusted R-squared: -0.02279
## F-statistic: 0.04182 on 1 and 42 DF, p-value: 0.839

```



```

## [1] "Top 5 Positive Residuals: retroHP_res_res"
##           species      res
## 1        Hylobates_lar 0.2286994
## 2 Daubentonia_madagascariensis 0.2004642
## 3      Nycticebus_coucang 0.1691135
## 4      Galago_senegalensis 0.1665564
## 5       Homo_sapiens 0.1495324
## [1] "===="
## [1] "Top 5 Negative Residuals: retroHP_res_res"
##           species      res
## 1     Cebus_albifrons -0.4631238
## 2 Saimiri_sciureus -0.4631026
## 3 Lophocebus_albigena -0.3293192
## 4     Papio_anubis -0.2915026
## 5 Erythrocebus_patas -0.2688949

```

Hide

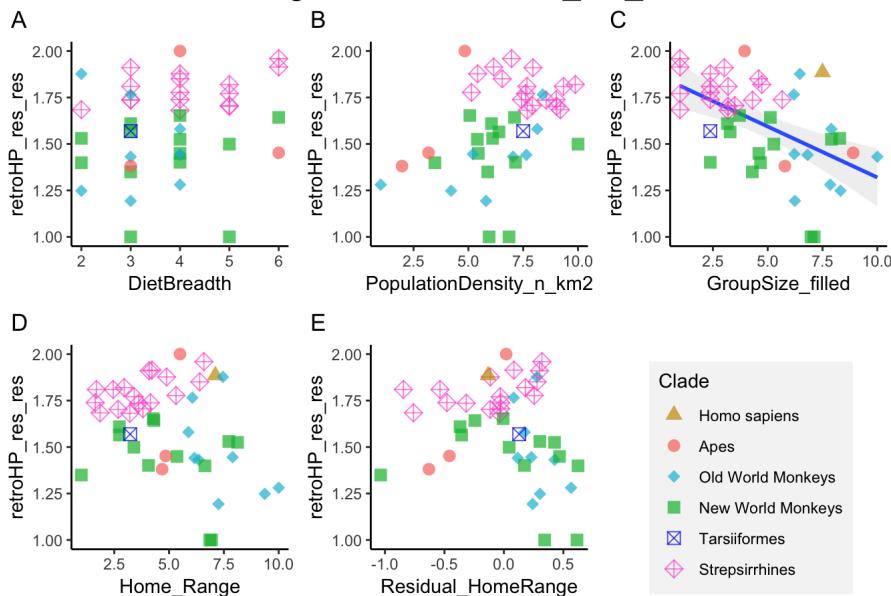
```

run_eco(HPres.Enceph_res); all_eco_plots(HPres.Enceph_res)

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")))) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.039518 -0.008095  0.005989  0.013945  0.052302
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.403
## lower bound : 0.000, p = 0.11914
## upper bound : 1.000, p = 0.50353
## 95.0% CI : (NA, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.5572932  0.2833048  5.4969 3.558e-06 ***
## DietBreadth          0.0237717  0.0254844  0.9328  0.35732
## PopulationDensity_n_km2 0.0220057  0.0208202  1.0569  0.29778
## GroupSize_filled     -0.0460671  0.0187780 -2.4532  0.01928 *
## Home_Range            0.0078726  0.0362749  0.2170  0.82945
## Residual_HomeRange    -0.0204486  0.1429990 -0.1430  0.88711
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02375 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.2431, Adjusted R-squared: 0.135
## F-statistic: 2.249 on 5 and 35 DF, p-value: 0.07106
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")))) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
##             (Intercept) DietBreadth PopulationDensity_n_km2
##             1.557293          0.023772          0.022006
## GroupSize_filled          Home_Range      Residual_HomeRange
##             -0.046067          0.007873         -0.020449

```

Ecological Plots: retroHP_res_res



Hide

#Result: No relationship.

Entorhinal Cortex*

- Entorhinal Cortex*: "Included are entorhinal, perirhinal, presubiculum and parasubiculum cortices and the underlying white matter. These cortices are characterized by the presence of one or several, almost cell-free layers of sublayers."
- Stephan, H. et al. (1981) New and revised data on volume of brain structures in insectivores and primates. *Folia primatol.* 35, 1–29

Entorhinal Cortex* vs. Medulla

NOTE: Using EC.med instead of EC.HP 1) flips the axes of the pPCA, and 2) gets rid of selective regime shift in human lineage. This is because humans are more divergent in EC.med (due to our massively enlarged neocortex, which EC is part of).

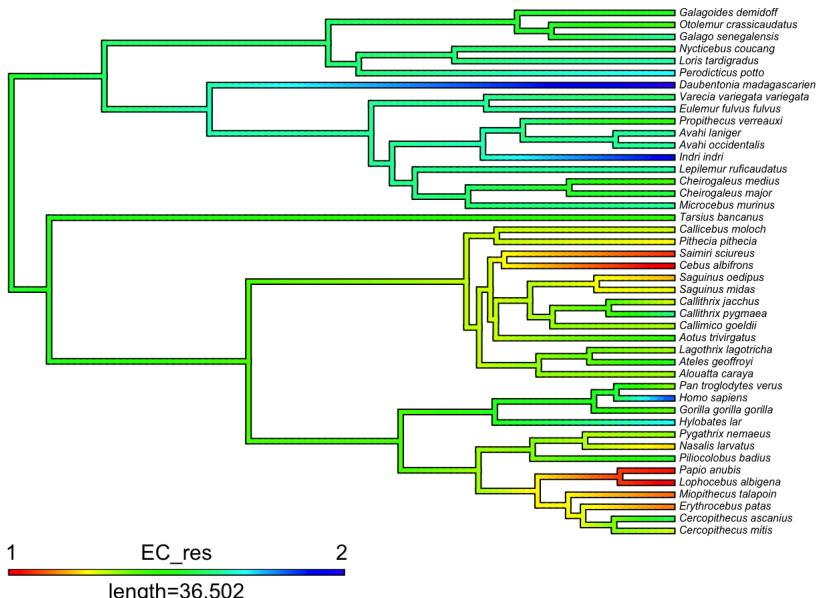
Hide

```
EC.Med_res <-pgls_function(HP, "EC", "Medulla")
```

```

## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.049098 -0.022767  0.000841  0.026473  0.071945
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.551
## lower bound : 0.000, p = 0.00052895
## upper bound : 1.000, p = 0.0010635
## 95.0% CI : (0.155, 0.897)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)             -1.260007  0.311501 -4.045
## log(eval(parse(text = predictor_var))) 1.045791  0.045156 23.160
##                               Pr(>|t|)
## (Intercept)          0.0002192 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03191 on 42 degrees of freedom
## Multiple R-squared: 0.9274, Adjusted R-squared: 0.9257
## F-statistic: 536.4 on 1 and 42 DF,  p-value: < 2.2e-16

```



```

## [1] "Top 5 Positive Residuals: EC_res"
##           species      res
## 1 Daubentonia_madagascariensis 0.5509330
## 2           Indri_indri 0.4711853
## 3        Homo_sapiens 0.3911152
## 4       Perodicticus_potto 0.2322718
## 5     Hylobates_lar 0.2226758
## [1] "=====
## [1] "Top 5 Negative Residuals: EC_res"
##           species      res
## 1      Cebus_albifrons -0.5759630
## 2 Lophocebus_albigena -0.5601726
## 3        Papio_anubis -0.5305268
## 4     SaimiriSciureus -0.4994545
## 5 Miopithecus_talapoin -0.4432129

```

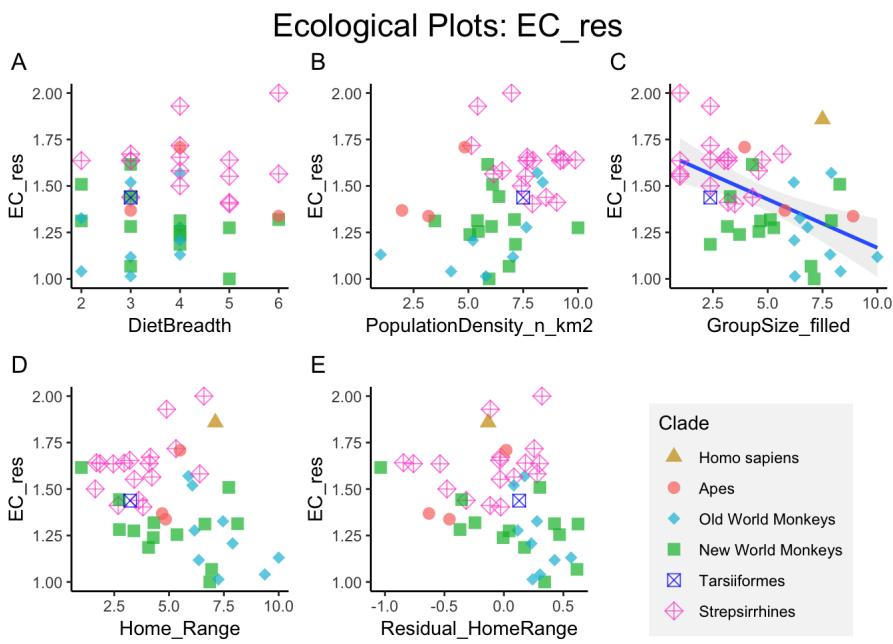
Hide

```

run_eco(EC.Med_res); all_eco_plots(EC.Med_res)

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")))) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.041054 -0.008587  0.003876  0.013826  0.055197
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.280
## lower bound : 0.000, p = 0.2419
## upper bound : 1.000, p = 0.029801
## 95.0% CI : (NA, 0.975)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.3972236  0.2928674  4.7708 3.199e-05 ***
## DietBreadth          0.0022403  0.0269587  0.0831  0.93424
## PopulationDensity_n_km2 0.0184299  0.0216737  0.8503  0.40092
## GroupSize_filled     -0.0436355  0.0194039 -2.2488  0.03092 *
## Home_Range            0.0293699  0.0374438  0.7844  0.43810
## Residual_HomeRange   -0.1753546  0.1486214 -1.1799  0.24601
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02385 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.1994, Adjusted R-squared: 0.08498
## F-statistic: 1.743 on 5 and 35 DF,  p-value: 0.1506
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")))) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
## (Intercept) DietBreadth PopulationDensity_n_km2
## 1.39722        0.00224        0.01843
## GroupSize_filled Home_Range Residual_HomeRange
## -0.04364       0.02937      -0.17535

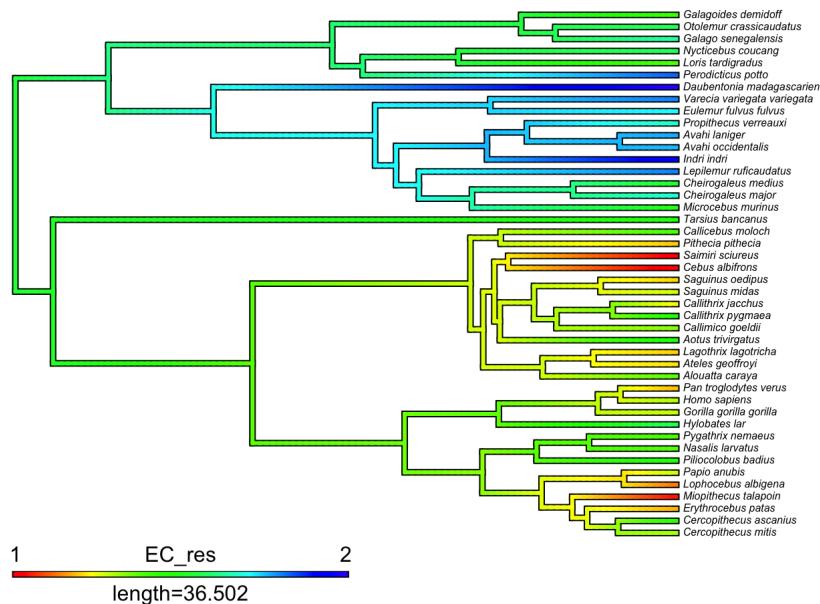
```



Entorhinal Cortex* vs. BrainVol

```
EC.Brain_res <- pgls_function(HP, "EC", "Brain_EC")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.105175 -0.030835 -0.005778  0.010862  0.064724
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.900
## lower bound : 0.000, p = 1.5716e-07
## upper bound : 1.000, p = 0.35433
## 95.0% CI : (0.461, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)             -2.195026  0.407268 -5.3896
## log(eval(parse(text = predictor_var))) 0.799761  0.039232 20.3852
##                               Pr(>|t|)
## (Intercept)            2.98e-06 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04014 on 42 degrees of freedom
## Multiple R-squared: 0.9082, Adjusted R-squared: 0.906
## F-statistic: 415.6 on 1 and 42 DF, p-value: < 2.2e-16
```



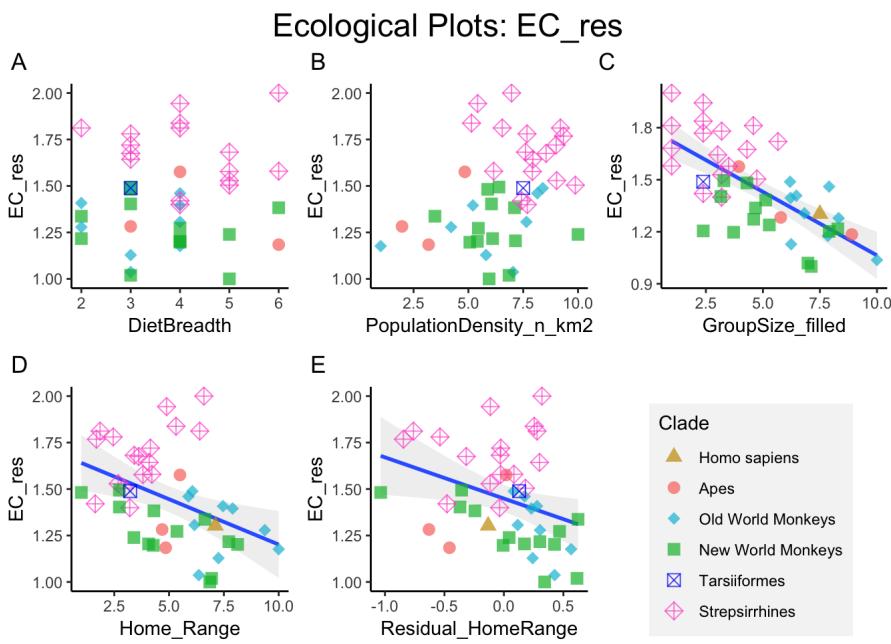
```
## [1] "Top 5 Positive Residuals: EC_res"
##           species      res
## 1 Daubentonia_madagascariensis 0.6219063
## 2           Indri_indri 0.5446920
## 3       Perodicticus_potto 0.4010237
## 4 Varecia_variegata_variegata 0.3658015
## 5 Lepilemur_ruficaudatus 0.3655613
## [1] "====="
## [1] "Top 5 Negative Residuals: EC_res"
##           species      res
## 1     Cebus_albifrons -0.7396199
## 2 Saimiri_sciureus -0.7132759
## 3 Miopithecus_talapoin -0.6892490
## 4 Lophocebus_albigena -0.5649179
## 5 Erythrocebus_patas -0.4994827
```

```
run_eco(EC.Brain_res); all_eco_plots(EC.Brain_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
##     "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
##     GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
##     lambda = "ML"))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.039334 -0.010057 -0.000811  0.013971  0.041542
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.619
## lower bound : 0.000, p = 0.001537
## upper bound : 1.000, p = 0.01499
## 95.0% CI : (0.168, 0.962)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.3623392  0.2311814  5.8929 1.068e-06 ***
## DietBreadth          -0.0097907  0.0198905 -0.4922  0.62563
##
## PopulationDensity_n_km2 0.0245033  0.0166442  1.4722  0.14991
## GroupSize_filled      -0.0668212  0.0151557 -4.4090 9.420e-05 ***
## Home_Range             0.0659861  0.0296283  2.2271  0.03247 *
## Residual_HomeRange    -0.2576751  0.1150949 -2.2388  0.03163 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02081 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.4054, Adjusted R-squared: 0.3205
## F-statistic: 4.773 on 5 and 35 DF,  p-value: 0.00198
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
##     "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
##     GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
##     lambda = "ML"))
##
## Coefficients:
## (Intercept) DietBreadth PopulationDensity_n_km2
## 1.362339    -0.009791    0.024503
## GroupSize_filled Home_Range Residual_HomeRange
## -0.066821     0.065986    -0.257675

```



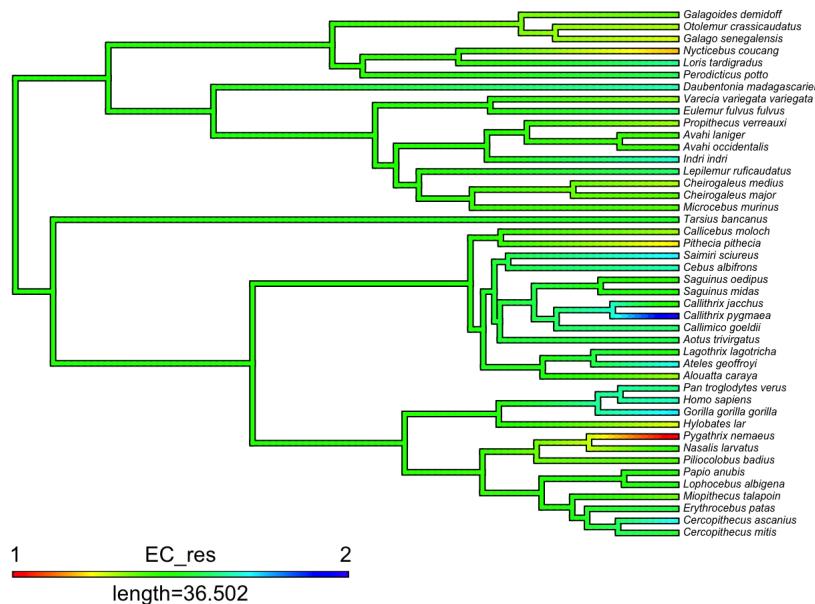
Entorhinal Cortex* vs. retroHP

Note:: Used as final EC

Result: No relationship

```
EC.HP_res <- pgls_function(HP, "EC", "retroHP")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -0.043789 -0.019876 -0.003536  0.008272  0.051459
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.00012483
## 95.0% CI   : (NA, 0.480)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)             -1.039620  0.173105 -6.0057
## log(eval(parse(text = predictor_var))) 1.075045  0.026845 40.0466
##                               Pr(>|t|)
## (Intercept)             3.898e-07 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02088 on 42 degrees of freedom
## Multiple R-squared: 0.9745, Adjusted R-squared: 0.9739
## F-statistic: 1604 on 1 and 42 DF, p-value: < 2.2e-16
```



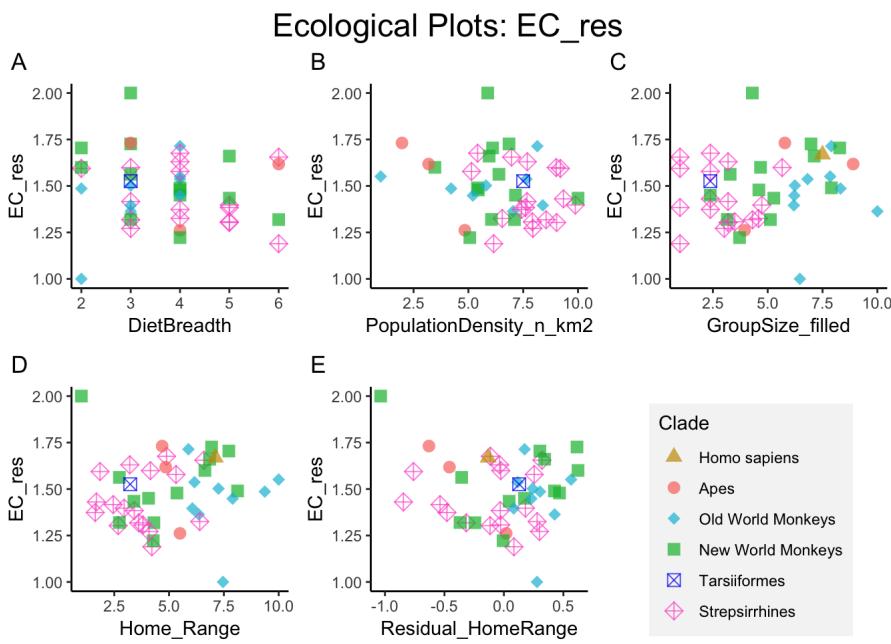
```
## [1] "Top 5 Positive Residuals: EC_res"
##           species      res
## 1   Callithrix_pygmaea 0.4985211
## 2 Gorilla_gorilla_gorilla 0.2398756
## 3   Saimiri_sciureus 0.2347544
## 4 Cercopithecus_ascanius 0.2231500
## 5   Ateles_geoffroyi 0.2139507
## [1] "=====
## [1] "Top 5 Negative Residuals: EC_res"
##           species      res
## 1 Pygathrix_nemaeus -0.4642726
## 2 Nycticebus_coucang -0.2819994
## 3 Pithecia_pithecia -0.2506530
## 4   Hylobates_lar -0.2124383
## 5 Galago_senegalensis -0.2030103
```

```
run_eco(EC.HP_res); all_eco_plots(EC.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.053811 -0.014170 -0.005918  0.004240  0.040923
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.0099063
## 95.0% CI : (NA, 0.650)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            1.572118   0.241729  6.5036 1.686e-07 ***
## DietBreadth          -0.029977   0.023896 -1.2545   0.2180
##
## PopulationDensity_n_km2 -0.012135   0.017825 -0.6808   0.5005
## GroupSize_filled        0.013815   0.015385  0.8980   0.3753
## Home_Range              0.010358   0.030771  0.3366   0.7384
## Residual_HomeRange     -0.137085   0.123989 -1.1056   0.2764
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01927 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.1877, Adjusted R-squared: 0.07162
## F-statistic: 1.617 on 5 and 35 DF,  p-value: 0.1812
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
##             (Intercept)      DietBreadth PopulationDensity_n_km2
##             1.57212           -0.02998           -0.01213
## GroupSize_filled      Home_Range      Residual_HomeRange
##             0.01382           0.01036           -0.13709

```



Hide

```
#pgls_function(HP, "EC_res", "BrainVol")
```

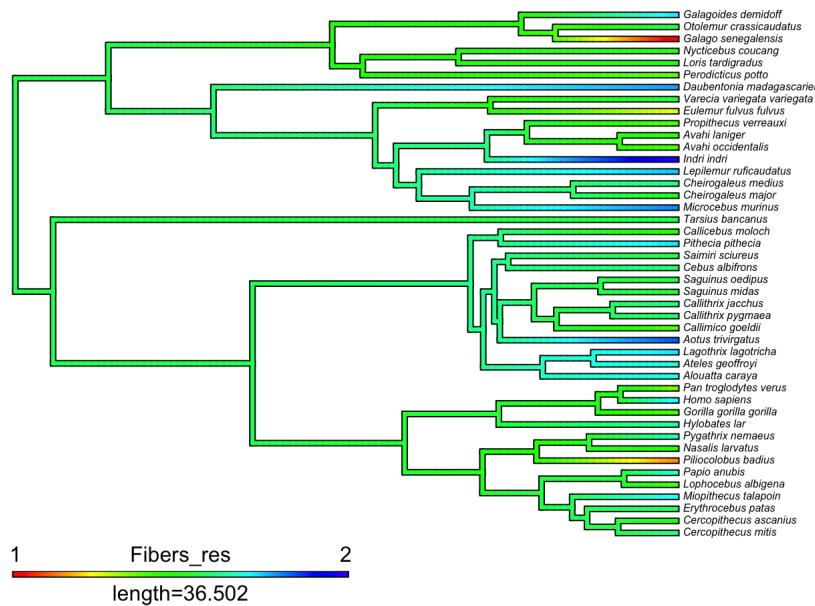
HP Fibers

HP Fibers vs. Medulla

Hide

```
fibers.Med_res <- pgls_function(HP, "Fibers", "Medulla")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.055341 -0.013059  0.003133  0.014117  0.054823
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 5.5998e-05
## 95.0% CI : (NA, 0.362)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                -3.322218  0.209037 -15.893
## log(eval(parse(text = predictor_var))) 1.209475  0.030218  40.026
##                               Pr(>|t|)    
## (Intercept)                < 2.2e-16 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.02487 on 42 degrees of freedom
## Multiple R-squared: 0.9745, Adjusted R-squared: 0.9738
## F-statistic: 1602 on 1 and 42 DF,  p-value: < 2.2e-16
```



```
## [1] "Top 5 Positive Residuals: Fibers_res"
##           species      res
## 1       Indri_indri 0.4938289
## 2       Aotus_trivirgatus 0.3173085
## 3       Microcebus_murinus 0.2793947
## 4 Daubentonia_madagascariensis 0.2570504
## 5       Lepilemur_ruficaudatus 0.2226778
## [1] "====="
## [1] "Top 5 Negative Residuals: Fibers_res"
##           species      res
## 1   Galago_senegalensis -0.6361491
## 2   Piliocolobus_badius -0.4740582
## 3 Eulemur_fulvus_fulvus -0.3480177
## 4   Pan_troglodytes_verus -0.2392978
## 5       Perodicticus_potto -0.2005770
```

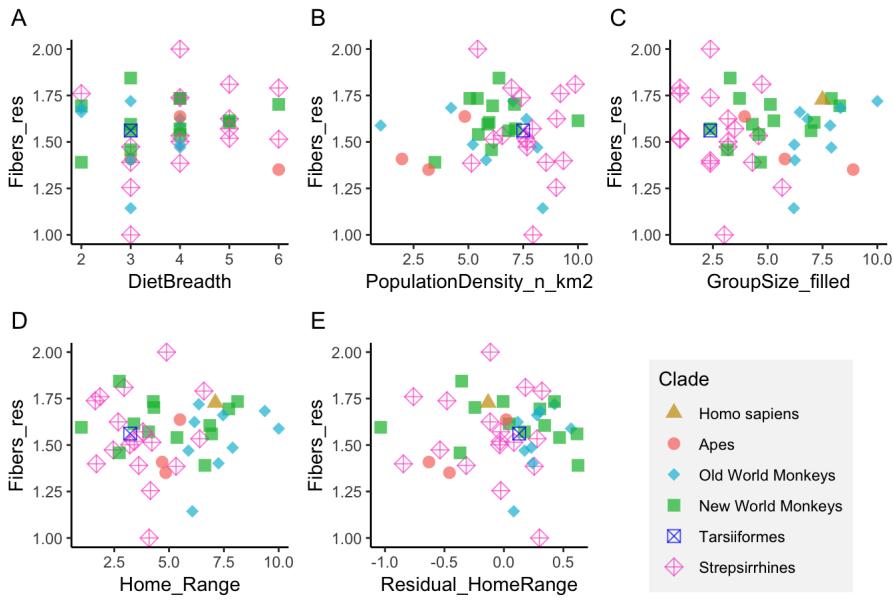
```
run_eco(fibers.Med_res); all_eco_plots(fibers.Med_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.044506 -0.012775 -0.002126  0.011611  0.052830
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.0023878
## 95.0% CI : (NA, 0.670)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.3384883  0.2880107  4.6474 4.632e-05 ***
## DietBreadth          0.0310582  0.0284712  1.0909   0.2828
## PopulationDensity_n_km2 0.0054009  0.0212372  0.2543   0.8007
## GroupSize_filled     -0.0108163  0.0183305 -0.5901   0.5589
## Home_Range            0.0247091  0.0366619  0.6740   0.5048
## Residual_HomeRange   -0.1109785  0.1477281 -0.7512   0.4575
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02296 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.05216, Adjusted R-squared: -0.08324
## F-statistic: 0.3852 on 5 and 35 DF,  p-value: 0.8555
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
## (Intercept)      DietBreadth PopulationDensity_n_km2
## 1.338488          0.031058          0.005401
## GroupSize_filled Home_Range    Residual_HomeRange
## -0.010816         0.024709        -0.110979

```

Ecological Plots: Fibers_res



Clade

- ▲ Homo sapiens
- Apes
- ◆ Old World Monkeys
- New World Monkeys
- ✖ Tarsiiformes
- ◇ Strepsirrhines

HP Fibers vs. BrainVol

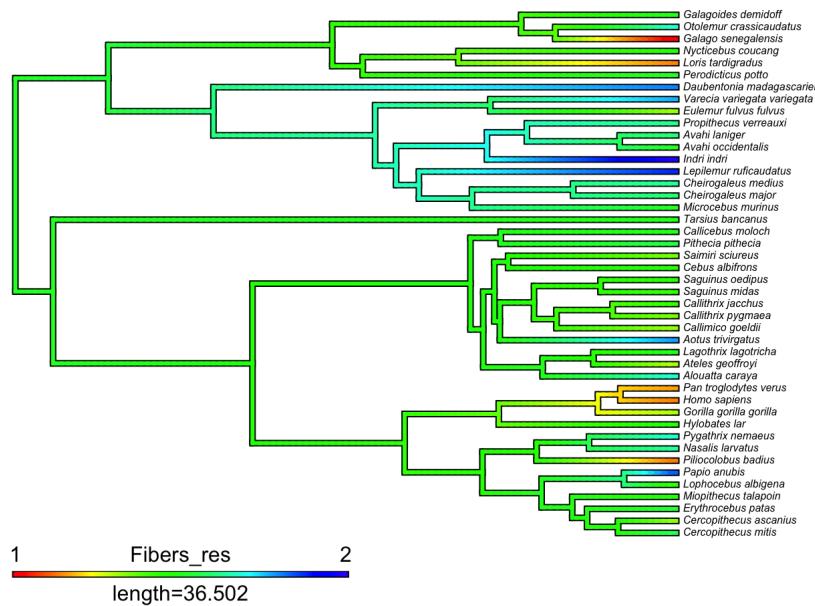
Hide

```
fibers.brain_res <- pgls_function(HP, "Fibers", "Brain_Fib")
```

```
## 
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
## 
## Residuals:
##      Min        1Q    Median        3Q       Max
## -0.073912 -0.009768  0.007488  0.030960  0.077741
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.229
##   lower bound : 0.000, p = 0.32324
##   upper bound : 1.000, p = 0.0027674
##  95.0% CI : (NA, 0.841)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)           -4.172607  0.353697 -11.797
## log(eval(parse(text = predictor_var)))  0.896683  0.034917  25.680
##                               Pr(>|t|)
## (Intercept)           6.439e-15 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---
```

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

```
## 
## Residual standard error: 0.03324 on 42 degrees of freedom
## Multiple R-squared: 0.9401, Adjusted R-squared: 0.9387
## F-statistic: 659.5 on 1 and 42 DF, p-value: < 2.2e-16
```



```
## [1] "Top 5 Positive Residuals: Fibers_res"
##           species      res
## 1       Indri_indri 0.6323122
## 2   Lepilemur_ruficaudatus 0.4868321
## 3       Papio_anubis 0.4455056
## 4 Daubentonia_madagascariensis 0.3943258
## 5       Aotus_trivirgatus 0.3655793
## [1] "=====
## [1] "Top 5 Negative Residuals: Fibers_res"
##           species      res
## 1   Galago_senegalensis -0.6537721
## 2   Piliocolobus_badius -0.4926383
## 3       Homo_sapiens -0.4811279
## 4       Loris_tardigradus -0.4771729
## 5 Pan_troglodytes_verus -0.4481332
```

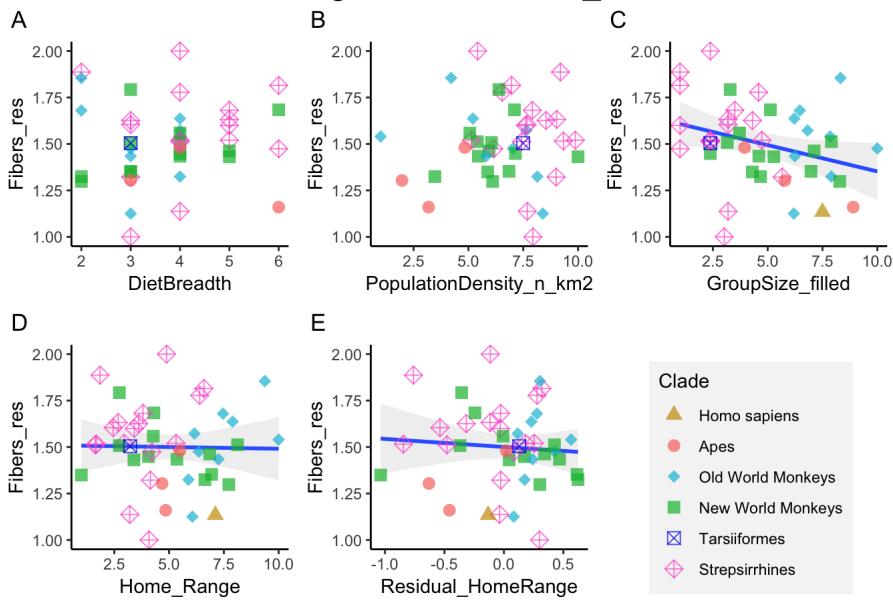
```
run_eco(fibers.brain_res); all_eco_plots(fibers.brain_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median      3Q     Max 
## -0.049496 -0.007407  0.000995  0.015324  0.046408
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.00035607
## 95.0% CI : (NA, 0.754)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)            0.944963  0.276933  3.4122 0.001642 **  
## DietBreadth           0.015458  0.027376  0.5647 0.575907    
## PopulationDensity_n_km2 0.035124  0.020420  1.7201 0.094253 .    
## GroupSize_filled      -0.061978  0.017625 -3.5164 0.001231 **  
## Home_Range             0.116240  0.035252  3.2974 0.002245 **  
## Residual_HomeRange    -0.389931  0.142046 -2.7451 0.009483 **  
## ---                
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02208 on 35 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared: 0.3122, Adjusted R-squared: 0.214  
## F-statistic: 3.178 on 5 and 35 DF,  p-value: 0.0181
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
## (Intercept)          DietBreadth  PopulationDensity_n_km2
## 0.94496             0.01546        0.03512
## GroupSize_filled     Home_Range    Residual_HomeRange
## -0.06198            0.11624        -0.38993

```

Ecological Plots: Fibers_res



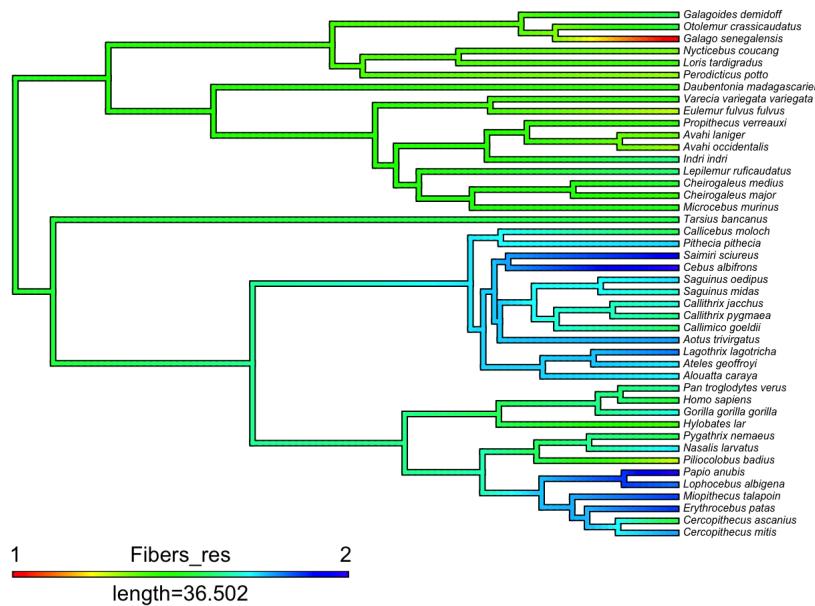
HP Fibers vs. retroHP + EC ***

Result: No relationship

Hide

```
fibers.HP_res <-pgls_function(HP, "Fibers", "retroHP.EC")
```

```
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -0.114213 -0.022447  0.004668  0.037841  0.065095
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.562
## lower bound : 0.000, p = 8.4659e-05
## upper bound : 1.000, p = 0.026958
## 95.0% CI   : (0.181, 0.972)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                 -3.02944   0.42170 -7.1839
## log(eval(parse(text = predictor_var))) 1.15218   0.06036 19.0885
##                               Pr(>|t|)
## (Intercept)                 7.943e-09 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04391 on 42 degrees of freedom
## Multiple R-squared: 0.8966, Adjusted R-squared: 0.8942
## F-statistic: 364.4 on 1 and 42 DF, p-value: < 2.2e-16
```



```
## [1] "Top 5 Positive Residuals: Fibers_res"
##           species      res
## 1   Cebus_albifrons 0.8586084
## 2     Papio_anubis 0.8490937
## 3   Saimiri_sciureus 0.7152923
## 4 Erythrocebus_patas 0.6314335
## 5 Miopithecus_talapoin 0.6179365
## [1] "====="
## [1] "Top 5 Negative Residuals: Fibers_res"
##           species      res
## 1   Galago_senegalensis -0.9886029
## 2 Piliocolobus_badius -0.4695262
## 3 Eulemur_fulvus_fulvus -0.4465302
## 4   Avahi_occidentalis -0.3898498
## 5 Perodicticus_potto -0.3852749
```

Hide

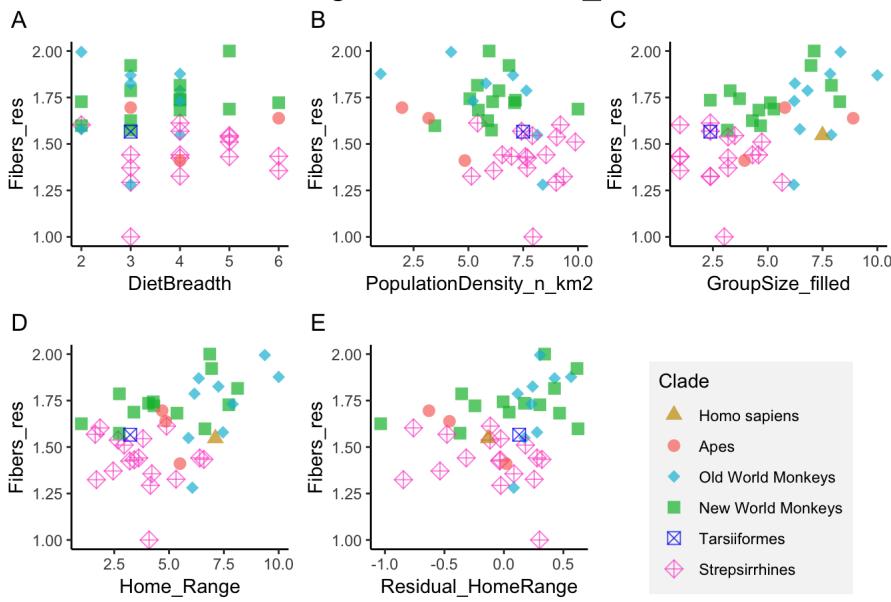
```
run_eco(fibers.HP_res); all_eco_plots(fibers.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
##     "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
##     GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
##     lambda = "ML"))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.047449 -0.014083 -0.000987  0.012054  0.029724
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.487
## lower bound : 0.000, p = 0.03058
## upper bound : 1.000, p = 0.035163
## 95.0% CI : (0.027, 0.984)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.322978  0.260265  5.0832 1.248e-05 ***
## DietBreadth          0.016960  0.023035  0.7363  0.4665
## PopulationDensity_n_km2 -0.011741  0.019001 -0.6179  0.5406
## GroupSize_filled      0.023917  0.017207  1.3899  0.1733
## Home_Range            0.030714  0.033347  0.9210  0.3633
## Residual_HomeRange    -0.122895  0.130769 -0.9398  0.3538
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02236 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.1907, Adjusted R-squared: 0.07513
## F-statistic: 1.65 on 5 and 35 DF,  p-value: 0.1727
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
##     "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
##     GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
##     lambda = "ML"))
##
## Coefficients:
##             (Intercept)      DietBreadth PopulationDensity_n_km2
##             1.32298          0.01696          -0.01174
## GroupSize_filled      Home_Range      Residual_HomeRange
##             0.02392          0.03071          -0.12289

```

Ecological Plots: Fibers_res



[Hide](#)

```
#pgls_function(HP, "Fibers_res", "BrainVol")
```

Subfields

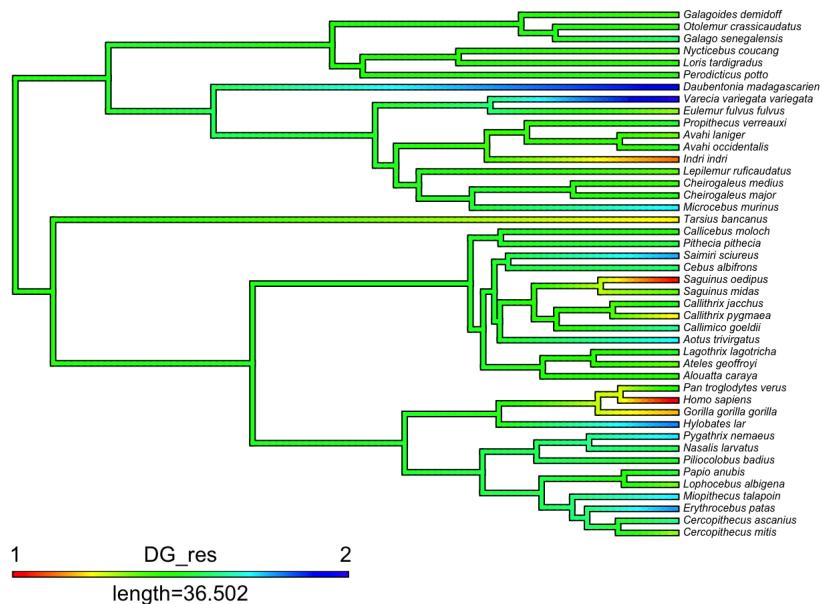
DentateGyrus vs. retroHP

Result: No relationship

[Hide](#)

```
DG.HP_res <- pgls_function(HP, "DG", "retroHP_DG")
```

```
## 
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
## 
## Residuals:
##      Min        1Q        Median        3Q        Max 
## -0.044758 -0.004895 -0.000280  0.011244  0.046333 
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ML] : 0.000
##   lower bound : 0.000, p = 1
##   upper bound : 1.000, p = 5.9368e-05
##   95.0% CI : (NA, 0.344)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)              -0.859271  0.135880 -6.3238
## log(eval(parse(text = predictor_var))) 0.951814  0.021998 43.2690
##                               Pr(>|t|)    
## (Intercept)              1.358e-07 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.01727 on 42 degrees of freedom
## Multiple R-squared: 0.9781, Adjusted R-squared: 0.9775
## F-statistic: 1872 on 1 and 42 DF,  p-value: < 2.2e-16
```



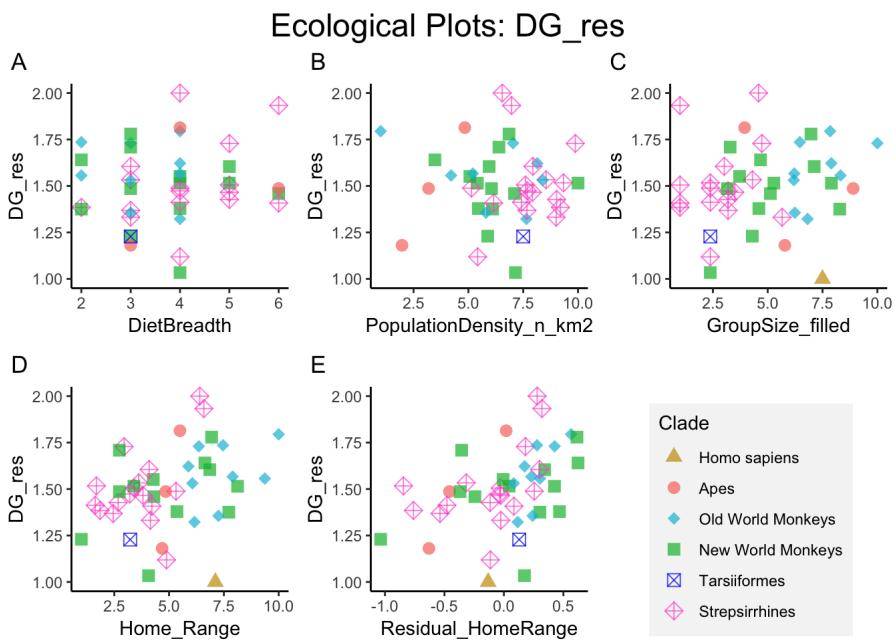
```
## [1] "Top 5 Positive Residuals: DG_res"
##           species      res
## 1 Varecia_variegata_variegata 0.3395355
## 2 Daubentonia_madagascariensis 0.2940967
## 3          Hylobates_lar 0.2136075
## 4      Erythrocebus_patas 0.2005716
## 5     Saimiri_sciureus 0.1902563
## [1] "====="
## [1] "Top 5 Negative Residuals: DG_res"
##           species      res
## 1       Homo_sapiens -0.3364611
## 2 Saguinus_oedipus -0.3135075
## 3      Indri_indri -0.2562227
## 4 Gorilla_gorilla_gorilla -0.2143917
## 5     Tarsius_bancaeus -0.1822520
```

```
run_eco(DG.HP_res); all_eco_plots(DG.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
##     "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
##     GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
##     lambda = "ML"))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.043611 -0.014098 -0.002317  0.014473  0.073599
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.0016392
## 95.0% CI : (NA, 0.312)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.1999917  0.2839819  4.2256 0.0001618 ***
## DietBreadth          0.0286114  0.0280730  1.0192 0.3151106
## PopulationDensity_n_km2 0.0107387  0.0209402  0.5128 0.6112922
## GroupSize_filled      0.0011407  0.0180741  0.0631 0.9500339
## Home_Range            0.0231376  0.0361491  0.6401 0.5263020
## Residual_HomeRange    0.1459805  0.1456616  1.0022 0.3231309
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02264 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.2277, Adjusted R-squared: 0.1173
## F-statistic: 2.063 on 5 and 35 DF, p-value: 0.09362
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
##     "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
##     GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
##     lambda = "ML"))
##
## Coefficients:
## (Intercept) DietBreadth PopulationDensity_n_km2
## 1.199992    0.028611    0.010739
## GroupSize_filled Home_Range Residual_HomeRange
## 0.001141    0.023138    0.145981

```



Hide

```
#pgls_function(HP, "DG_res", "BrainVol")
```

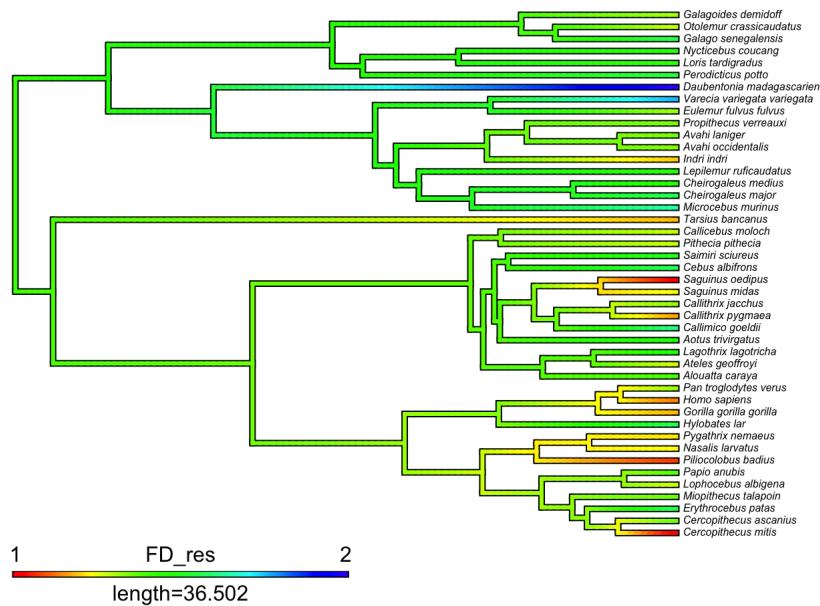
FasciaDentata vs. retroHP

Result: No relationship

Hide

```
FD.HP_res <- pgls_function(HP, "FD", "retroHP_FD")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.036482 -0.013993 -0.004226  0.008214  0.028007
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.250
## lower bound : 0.000, p = 0.27355
## upper bound : 1.000, p = 0.0050173
## 95.0% CI    : (NA, 0.905)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)              -0.845954  0.148924 -5.6804
## log(eval(parse(text = predictor_var))) 0.882871  0.023783 37.1217
##                               Pr(>|t|)    
## (Intercept)              1.143e-06 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.01704 on 42 degrees of freedom
## Multiple R-squared: 0.9704, Adjusted R-squared: 0.9697
## F-statistic: 1378 on 1 and 42 DF,  p-value: < 2.2e-16
```



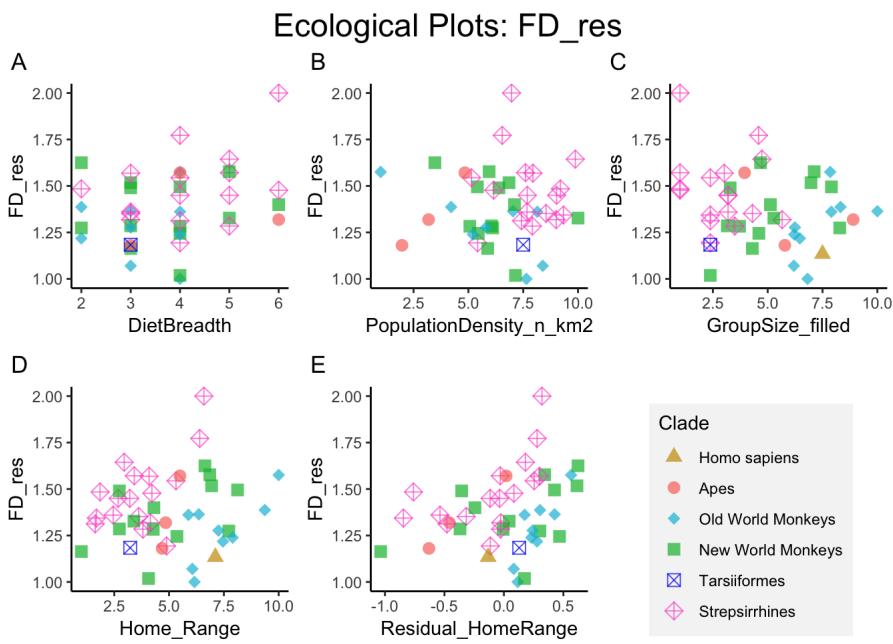
```
## [1] "Top 5 Positive Residuals: FD_res"
##           species      res
## 1 Daubentonia_madagascariensis 0.4270438
## 2 Varecia_variegata_variegata 0.2640871
## 3 Microcebus_murinus 0.1725792
## 4 Callimico_goeldii 0.1589197
## 5 Cebus_albifrons 0.1245981
## [1] "====="
## [1] "Top 5 Negative Residuals: FD_res"
##           species      res
## 1 Cercopithecus_mitis -0.2879172
## 2 Saguinus_oedipus -0.2745380
## 3 Piliocolobus_badius -0.2376205
## 4 Homo_sapiens -0.1918307
## 5 Callithrix_pygmaea -0.1709110
```

```
run_eco(FD.HP_res); all_eco_plots(FD.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.059296 -0.021073 -0.007653  0.009851  0.035367
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.400
## lower bound : 0.000, p = 0.34398
## upper bound : 1.000, p = 0.057737
## 95.0% CI : (NA, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.388253   0.275917  5.0314 1.459e-05 ***
## DietBreadth          0.028136   0.024835  1.1329   0.2650
## PopulationDensity_n_km2 -0.015576   0.020282 -0.7680   0.4477
## GroupSize_filled      -0.013237   0.018289 -0.7237   0.4740
## Home_Range            0.015263   0.035328  0.4320   0.6684
## Residual_HomeRange    0.166718   0.139292  1.1969   0.2394
## ---
##
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02311 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.2608, Adjusted R-squared: 0.1552
## F-statistic: 2.47 on 5 and 35 DF, p-value: 0.05113
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
## (Intercept)      DietBreadth PopulationDensity_n_km2
## 1.38825          0.02814        -0.01558
## GroupSize_filled Home_Range   Residual_HomeRange
## -0.01324         0.01526          0.16672

```



Hide

```
#pgls_function(HP, "FD_res", "BrainVol")
```

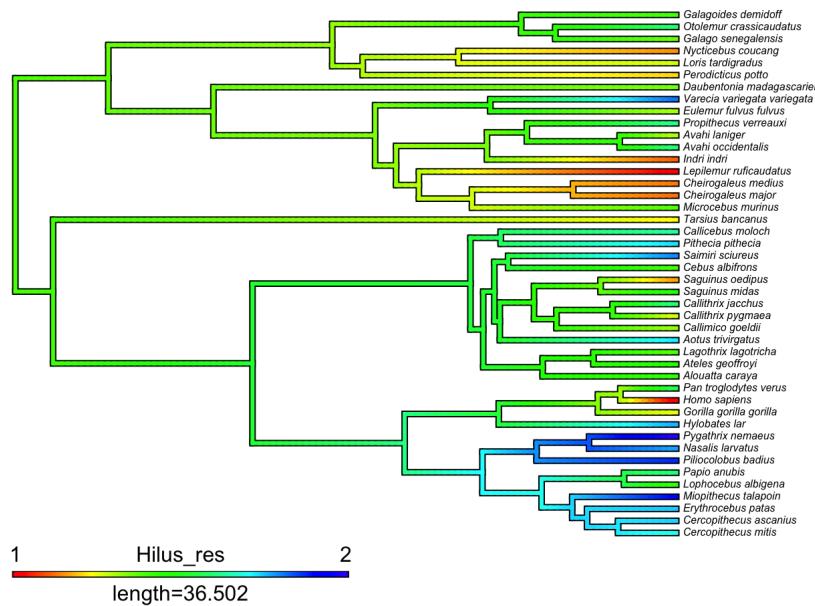
Hilus vs. retroHP

Result: No relationship

Hide

```
Hilus.HP_res <- pgls_function(HP, "Hilus", "retroHP__Hil")
```

```
## 
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.080351 -0.025964  0.004069  0.028502  0.056029
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.576
## lower bound : 0.000, p = 0.030443
## upper bound : 1.000, p = 0.005135
## 95.0% CI   : (0.025, 0.942)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)              -3.375794  0.327846 -10.297
## log(eval(parse(text = predictor_var))) 1.106491  0.050576  21.878
##                               Pr(>|t|)    
## (Intercept)               4.65e-13 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.03572 on 42 degrees of freedom
## Multiple R-squared: 0.9193, Adjusted R-squared: 0.9174
## F-statistic: 478.6 on 1 and 42 DF,  p-value: < 2.2e-16
```



```
## [1] "Top 5 Positive Residuals: Hilus_res"
##           species      res
## 1       Pygathrix_nemaeus 0.6250141
## 2       Miopithecus_talapoin 0.5358576
## 3       Piliocolobus_badius 0.5033657
## 4 Varecia_variegata_variegata 0.4421124
## 5       Saimiri_sciureus 0.4194780
## [1] "=====
## [1] "Top 5 Negative Residuals: Hilus_res"
##           species      res
## 1       Homo_sapiens -0.4420830
## 2 Lepilemur_ruficaudatus -0.4253741
## 3       Indri_indri -0.3277636
## 4       Cheirogaleus_major -0.3106372
## 5       Cheirogaleus_medium -0.3035452
```

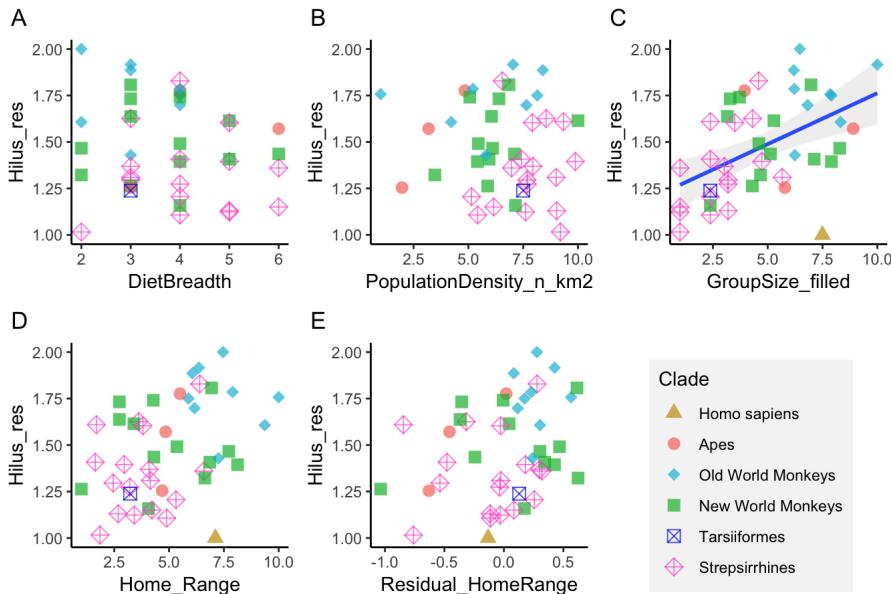
```
run_eco(Hilus.HP_res); all_eco_plots(Hilus.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.067811 -0.014365  0.002567  0.012040  0.070745
##
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.1339
## 95.0% CI : (NA, NA)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)           1.0719745  0.3059641  3.5036 0.001276 **  
## DietBreadth          0.0014501  0.0302460  0.0479 0.962034    
## PopulationDensity_n_km2 0.0118573  0.0225611  0.5256 0.602504    
## GroupSize_filled      0.0570350  0.0194731  2.9289 0.005949 **  
## Home_Range            0.0092176  0.0389473  0.2367 0.814293    
## Residual_HomeRange    0.0508184  0.1569368  0.3238 0.748006    
## ---                
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0244 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.3746, Adjusted R-squared: 0.2852
## F-statistic: 4.193 on 5 and 35 DF,  p-value: 0.004328
## 
## $pgls_eco_raw
## 
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
##             (Intercept)      DietBreadth  PopulationDensity_n_km2
##             1.071974        0.001450          0.011857
##             GroupSize_filled   Home_Range     Residual_HomeRange
##             0.057035        0.009218          0.050818

```

Ecological Plots: Hilus_res



Hide

```
#pgls_function(HP, "Hilus_res", "BrainVol")
```

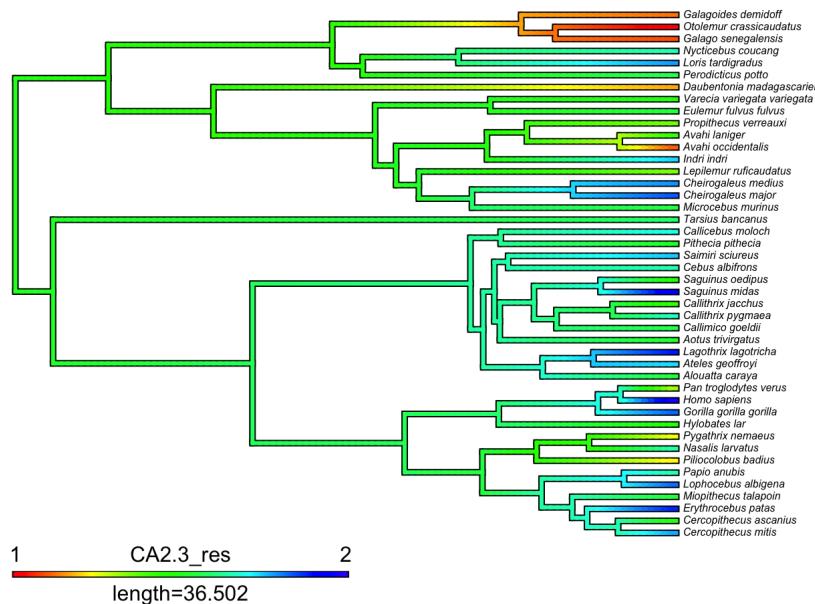
CA2/3 vs. retroHP

Result: Positive relationship between CA2.3_res and retroHP_res.

Hide

```
CA2.3.HP_res <- pgls_function(HP, "CA2.3", "retroHP__CA2.3")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.045949 -0.013998  0.001799  0.013998  0.039935 
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.335
## lower bound : 0.000, p = 0.16206
## upper bound : 1.000, p = 6.017e-05
## 95.0% CI    : (NA, 0.824)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)              -0.83386   0.17045 -4.8923
## log(eval(parse(text = predictor_var))) 0.98895   0.02779 35.5862
##                               Pr(>|t|)    
## (Intercept)              1.509e-05 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.01945 on 42 degrees of freedom
## Multiple R-squared: 0.9679, Adjusted R-squared: 0.9671
## F-statistic: 1266 on 1 and 42 DF,  p-value: < 2.2e-16
```



```
## [1] "Top 5 Positive Residuals: CA2.3_res"
##           species      res
## 1      Homo_sapiens 0.2999296
## 2     Saguinus_midas 0.2800443
## 3 Lagothrix_lagotricha 0.2397583
## 4   Erythrocebus_patas 0.2353949
## 5   Cheirogaleus_major 0.2050583
## [1] "=====
## [1] "Top 5 Negative Residuals: CA2.3_res"
##           species      res
## 1   Otolemur_crassicaudatus -0.3303920
## 2     Galago_senegalensis -0.2718822
## 3     Avahi_occidentalis -0.2700904
## 4     Galago demidoff -0.2511400
## 5 Daubentonia_madagascariensis -0.2241690
```

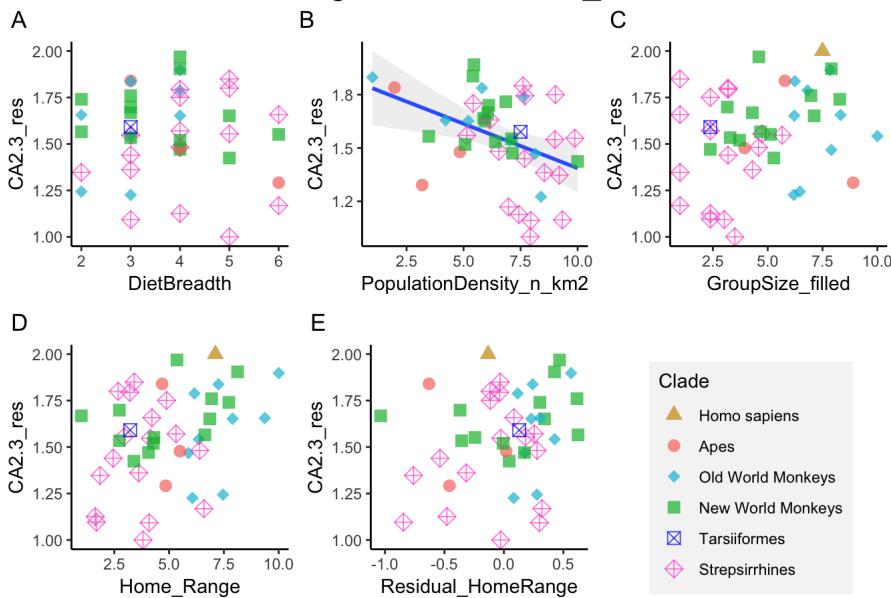
```
run_eco(CA2.3.HP_res); all_eco_plots(CA2.3.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.092909 -0.023585 -0.007841  0.006828  0.069768
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.664
## lower bound : 0.000, p = 0.076187
## upper bound : 1.000, p = 0.0090892
## 95.0% CI : (NA, 0.954)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.9651475  0.3358966  5.8505 1.215e-06 ***
## DietBreadth          -0.0118203  0.0285783 -0.4136  0.68168
## PopulationDensity_n_km2 -0.0512905  0.0240356 -2.1339  0.03993 *
## GroupSize_filled      0.0024482  0.0219247  0.1117  0.91173
## Home_Range            -0.0138896  0.0430395 -0.3227  0.74883
## Residual_HomeRange    0.1213689  0.1665732  0.7286  0.47108
## ---
##
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03082 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.1978, Adjusted R-squared: 0.08319
## F-statistic: 1.726 on 5 and 35 DF,  p-value: 0.1544
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
## (Intercept)      DietBreadth PopulationDensity_n_km2
## 1.965147      -0.011820      -0.051291
## GroupSize_filled Home_Range   Residual_HomeRange
## 0.002448      -0.013890      0.121369

```

Ecological Plots: CA2.3_res



Hide

```
#pgls_function(HP, "CA2.3_res", "BrainVol") # No relationship
#pgls_function(HP, "CA2.3_res", "retroHP") # No relationship
#pgls_function(HP, "CA2.3_res", "retroHP_res") # Significant***
```

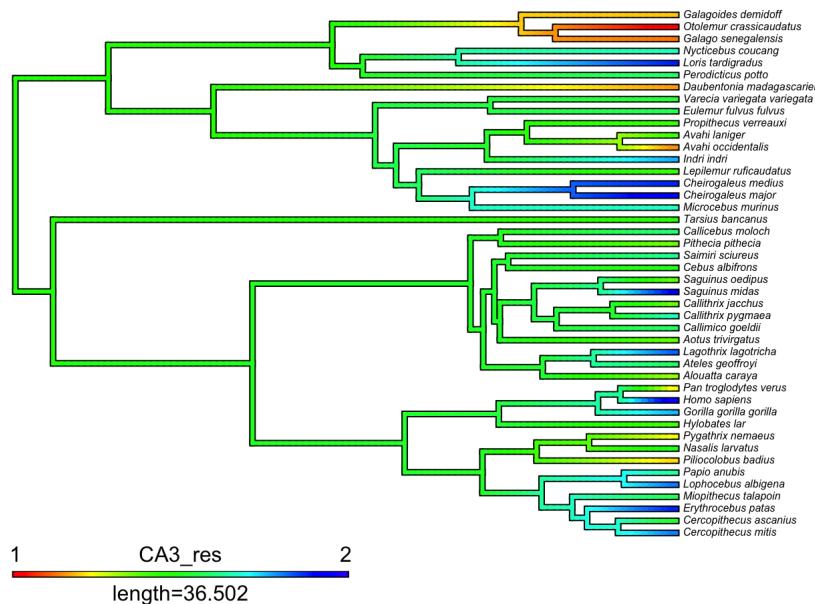
CA3 vs. retroHP

Result: CA3_res gets smaller as retroHP_res gets larger. Humans deviate drastically from this trend by having an unusually large CA3_res.

Hide

```
CA3.HP_res <- pgls_function(HP, "CA3", "retroHP__CA3")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.033300 -0.008370  0.000146  0.011557  0.038947
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 3.2297e-05
## 95.0% CI : (NA, 0.764)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)             -1.095813  0.141323 -7.754
## log(eval(parse(text = predictor_var))) 1.006628  0.022976 43.813
##                               Pr(>|t|)
## (Intercept)             1.238e-09 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01782 on 42 degrees of freedom
## Multiple R-squared: 0.9786, Adjusted R-squared: 0.9781
## F-statistic: 1920 on 1 and 42 DF, p-value: < 2.2e-16
```



```
## [1] "Top 5 Positive Residuals: CA3_res"
##           species      res
## 1       Homo_sapiens 0.2724025
## 2   Cheirogaleus_major 0.2464304
## 3     Saguinus_midas 0.2339498
## 4  Erythrocebus_patas 0.2135765
## 5    Loris_tardigradus 0.2122733
## [1] "=====
## [1] "Top 5 Negative Residuals: CA3_res"
##           species      res
## 1   Otolemur_crassicaudatus -0.3167509
## 2       Galago_senegalensis -0.2416518
## 3     Avahi_occidentalis -0.2346482
## 4 Daubentonia_madagascariensis -0.2244734
## 5       Galagoites_demidoff -0.2034281
```

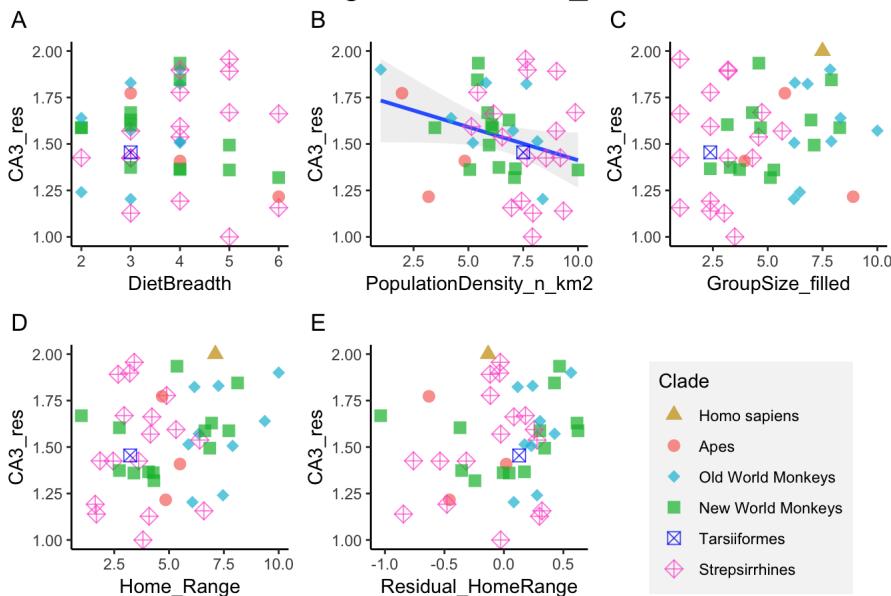
```
run_eco(CA3.HP_res); all_eco_plots(CA3.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.096477 -0.024839 -0.005344  0.021383  0.064294
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.695
## lower bound : 0.000, p = 0.075469
## upper bound : 1.000, p = 0.0135
## 95.0% CI : (NA, 0.965)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            2.0952809  0.3665149  5.7168 1.824e-06 ***
## DietBreadth          -0.0246618  0.0309309 -0.7973  0.43064
## PopulationDensity_n_km2 -0.0561902  0.0261055 -2.1524  0.03834 *
## GroupSize_filled        0.0077385  0.0238410  0.3246  0.74743
## Home_Range           -0.0339560  0.0469502 -0.7232  0.47434
## Residual_HomeRange     0.1945938  0.1812265  1.0738  0.29028
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0341 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.1851, Adjusted R-squared: 0.06864
## F-statistic: 1.59 on 5 and 35 DF, p-value: 0.1887
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
##             (Intercept)      DietBreadth PopulationDensity_n_km2
##             2.095281      -0.024662      -0.056190
##             GroupSize_filled   Home_Range   Residual_HomeRange
##             0.007738      -0.033956       0.194594

```

Ecological Plots: CA3_res



[Hide](#)

```
#pgls_function(HP, "CA3_res", "BrainVol")# No relationship
#pgls_function(HP, "CA3_res", "retroHP")# No relationship
#pgls_function(HP, "CA3_res", "retroHP_res") # Approaching sig **
```

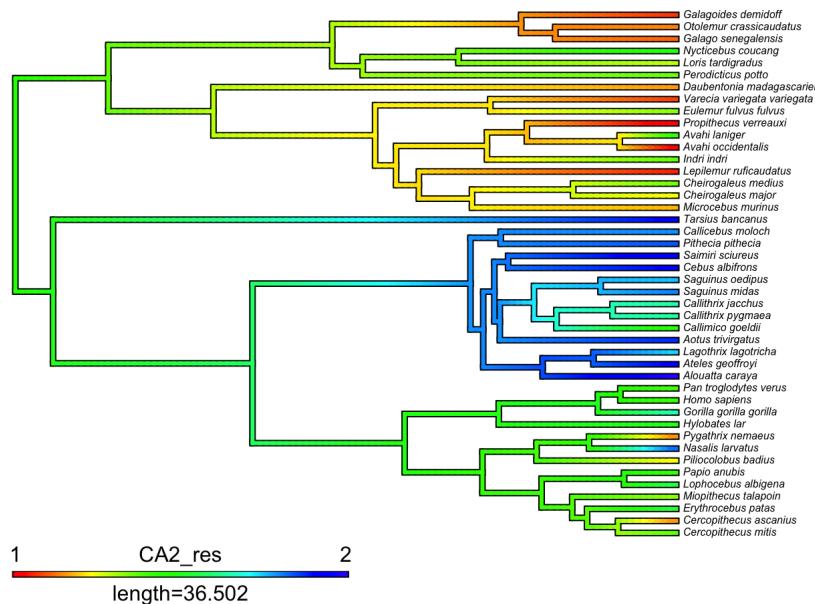
CA2 vs. retroHP

Result: CA2_res gets smaller has retroHP_res gets larger. Humans deviate from this by having somewhat larger CA2_res than expected.

[Hide](#)

```
CA2.HP_res <- pgls_function(HP, "CA2", "retroHP__CA2")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))), 
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.097534 -0.018477 -0.004084  0.015518  0.069596
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.703
## lower bound : 0.000, p = 6.6201e-08
## upper bound : 1.000, p = 0.0034411
## 95.0% CI   : (0.381, 0.933)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)              -3.238098  0.289909 -11.169
## log(eval(parse(text = predictor_var))) 0.980048  0.044041  22.253
##                               Pr(>|t|)
## (Intercept)                3.73e-14 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03224 on 42 degrees of freedom
## Multiple R-squared:  0.9218, Adjusted R-squared:  0.92
## F-statistic: 495.2 on 1 and 42 DF,  p-value: < 2.2e-16
```



```
## [1] "Top 5 Positive Residuals: CA2_res"
##           species      res
## 1   Alouatta_caraya 0.5561585
## 2   Saimiri_sciureus 0.5061737
## 3   Tarsius_bancanus 0.4733092
## 4   Ateles_geoffroyi 0.4719987
## 5   Cebus_albifrons 0.4715802
## [1] "=====
## [1] "Top 5 Negative Residuals: CA2_res"
##           species      res
## 1   Propithecus_verreauxi -0.4593405
## 2   Avahi_occidentalis -0.4471756
## 3   Lepilemur_ruficaudatus -0.4060374
## 4   Galago demidoff -0.3875900
## 5   Varecia_variegata_variegata -0.3790072
```

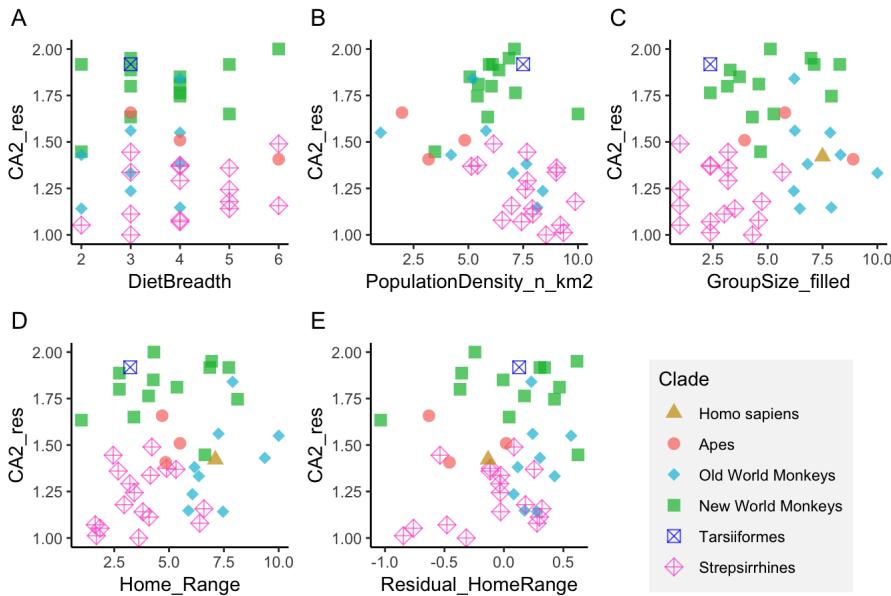
```
run_eco(CA2.HP_res); all_eco_plots(CA2.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median      3Q     Max 
## -0.08601 -0.01938 -0.00339  0.01853  0.05048
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.880
## lower bound : 0.000, p = 3.3236e-07
## upper bound : 1.000, p = 0.27323
## 95.0% CI : (0.519, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)           1.528399   0.329064  4.6447 4.67e-05 ***
## DietBreadth          0.022694   0.025981  0.8735  0.3884    
## PopulationDensity_n_km2 -0.021040   0.022477 -0.9361  0.3556    
## GroupSize_filled      -0.014328   0.020678 -0.6929  0.4930    
## Home_Range            0.011367   0.041914  0.2712  0.7878    
## Residual_HomeRange    -0.033605   0.158607 -0.2119  0.8334    
## ---                
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03411 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.09329, Adjusted R-squared: -0.03624
## F-statistic: 0.7202 on 5 and 35 DF,  p-value: 0.6127
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
##             (Intercept)      DietBreadth PopulationDensity_n_km2
##             1.52840          0.02269          -0.02104
## GroupSize_filled      Home_Range      Residual_HomeRange
##             -0.01433          0.01137          -0.03360

```

Ecological Plots: CA2_res



Hide

```
#pgls_function(HP, "CA2_res", "BrainVol")# No relationship
#pgls_function(HP, "CA2_res", "retroHP")# No relationship
#pgls_function(HP, "CA2_res", "retroHP_res") # Significant ***
```

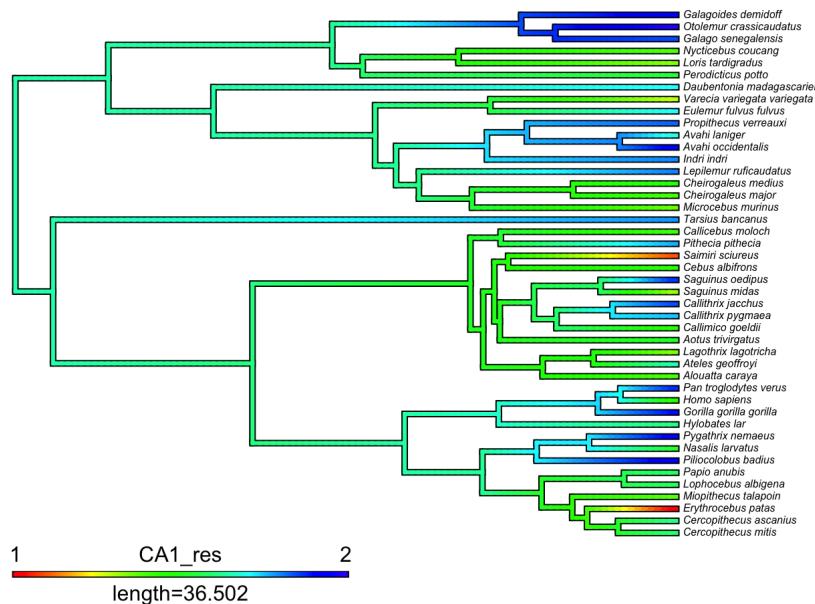
CA1 vs. retroHP

Result: No relationship.

Hide

```
CA1.HP_res <- pgls_function(HP, "CA1", "retroHP__CA1")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))), 
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.029571 -0.013796 -0.004069  0.007239  0.025376 
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.0002539
## 95.0% CI : (NA, 0.661)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                 -0.602976  0.108344 -5.5654
## log(eval(parse(text = predictor_var))) 1.020812  0.018148 56.2499
##                               Pr(>|t|)    
## (Intercept)                 1.671e-06 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.01399 on 42 degrees of freedom
## Multiple R-squared:  0.9869, Adjusted R-squared:  0.9866 
## F-statistic:  3164 on 1 and 42 DF,  p-value: < 2.2e-16
```



```
## [1] "Top 5 Positive Residuals: CA1_res"
##           species      res
## 1   Otolemur_crassicaudatus 0.1872592
## 2     Piliocolobus_badius 0.1603810
## 3     Avahi_occidentalis 0.1584400
## 4     Pygathrix_nemaeus 0.1567484
## 5   Galagooides_demidoff 0.1550986
## [1] "=====
## [1] "Top 5 Negative Residuals: CA1_res"
##           species      res
## 1     Erythrocebus_patas -0.2961636
## 2     Saimiri_sciureus -0.2512538
## 3 Varecia_variegata_variegata -0.1578039
## 4     Saguinus_midas -0.1456304
## 5     Loris_tardigradus -0.1323010
```

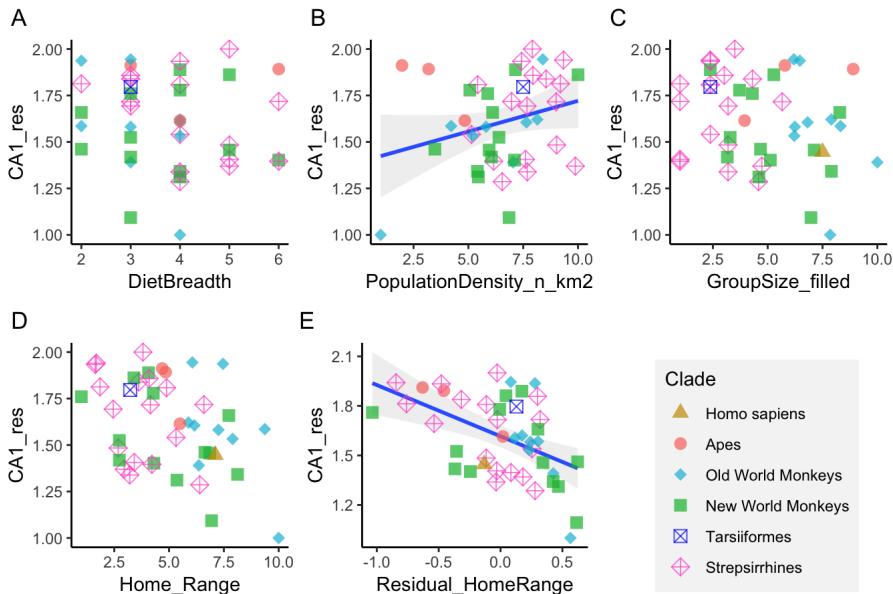
```
run_eco(CA1.HP_res); all_eco_plots(CA1.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.054667 -0.030028 -0.002221  0.016259  0.080860
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.789
## lower bound : 0.000, p = 0.57092
## upper bound : 1.000, p = 0.50835
## 95.0% CI : (NA, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.185496  0.334316  3.5460 0.001134 **
## DietBreadth            -0.022582  0.027399 -0.8242 0.415408
## PopulationDensity_n_km2 0.062626  0.023396  2.6768 0.011235 *
## GroupSize_filled        -0.021502  0.021445 -1.0027 0.322896
## Home_Range              0.047083  0.042752  1.1013 0.278281
## Residual_HomeRange     -0.397477  0.163510 -2.4309 0.020324 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03265 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.38, Adjusted R-squared:  0.2914
## F-statistic:  4.29 on 5 and 35 DF,  p-value: 0.003789
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
## (Intercept)          DietBreadth  PopulationDensity_n_km2
## 1.18550           -0.02258          0.06263
## GroupSize_filled    Home_Range    Residual_HomeRange
## -0.02150           0.04708          -0.39748

```

Ecological Plots: CA1_res



Hide

```
#pgls_function(HP, "CA1_res", "BrainVol")
```

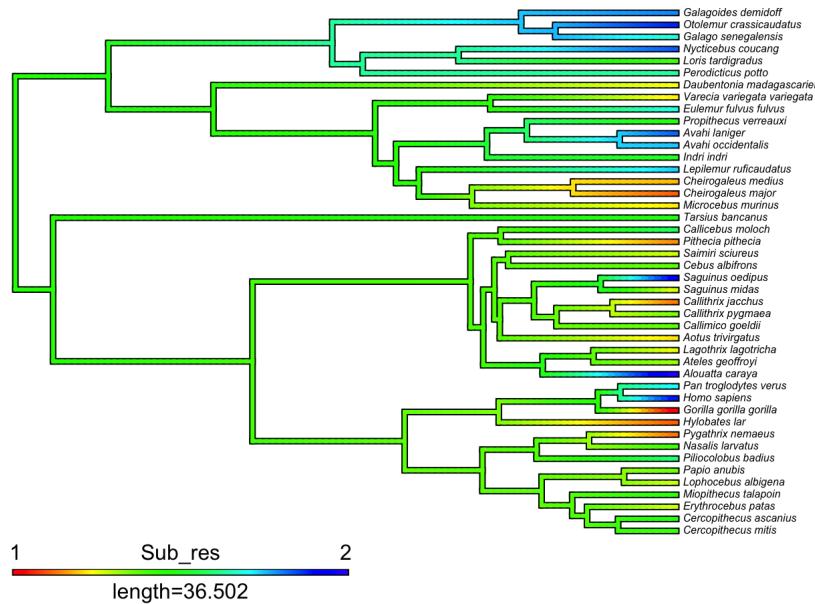
Subiculum vs. retroHP

Result: No relationship

Hide

```
Sub.HP_res <- pgls_function(HP, "Sub", "retroHP__Sub")
```

```
##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.046040 -0.014179  0.002727  0.021980  0.056048
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.073
## lower bound : 0.000, p = 0.66177
## upper bound : 1.000, p = 8.6846e-05
## 95.0% CI    : (NA, 0.627)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)              -2.422625  0.209220 -11.579
## log(eval(parse(text = predictor_var))) 0.999710  0.033004  30.291
##                               Pr(>|t|)    
## (Intercept)          1.177e-14 ***
## log(eval(parse(text = predictor_var))) < 2.2e-16 ***
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.02436 on 42 degrees of freedom
## Multiple R-squared: 0.9562, Adjusted R-squared: 0.9552
## F-statistic: 917.5 on 1 and 42 DF,  p-value: < 2.2e-16
```



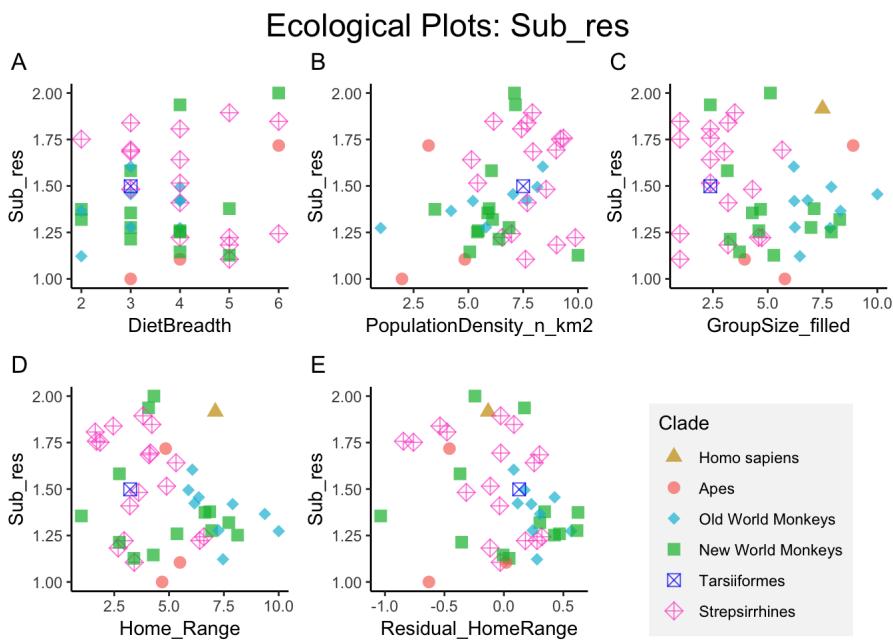
```
## [1] "Top 5 Positive Residuals: Sub_res"
##           species      res
## 1       Alouatta_caraya 0.4045345
## 2       Saguinus_oedipus 0.3557424
## 3       Homo_sapiens 0.3400115
## 4   Otolemur_crassicaudatus 0.3230059
## 5 Nycticebus_coucang 0.2871852
## [1] "=====
## [1] "Top 5 Negative Residuals: Sub_res"
##           species      res
## 1 Gorilla_gorilla_gorilla -0.3626834
## 2       Hylobates_lar -0.2820896
## 3 Cheirogaleus_major -0.2815960
## 4 Pygathrix_nemaeus -0.2691712
## 5 Callithrix_jacchus -0.2652362
```

```
run_eco(Sub.HP_res); all_eco_plots(Sub.HP_res)
```

```

## $pgls_eco_summary
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.056521 -0.024009 -0.006645  0.013166  0.050108
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.00070551
## 95.0% CI : (NA, 0.741)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.2296039  0.3815433  3.2227 0.002746 ***
## DietBreadth          0.0165116  0.0377174  0.4378 0.664242
## PopulationDensity_n_km2 0.0264608  0.0281341  0.9405 0.353395
## GroupSize_filled     -0.0100524  0.0242834 -0.4140 0.681428
## Home_Range            0.0070089  0.0485681  0.1443 0.886083
## Residual_HomeRange    -0.1516971  0.1957033 -0.7751 0.443464
## ---
##
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03042 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.1114, Adjusted R-squared: -0.01555
## F-statistic: 0.8775 on 5 and 35 DF,  p-value: 0.5062
##
## $pgls_eco_raw
##
## Call:
## pgls(formula = eval(parse(text = paste(pgls_function.out$response_var,
## "res", sep = "_")) ~ DietBreadth + PopulationDensity_n_km2 +
## GroupSize_filled + Home_Range + Residual_HomeRange, data = HP.noHomo,
## lambda = "ML")
##
## Coefficients:
##             (Intercept)      DietBreadth PopulationDensity_n_km2
##             1.229604          0.016512          0.026461
## GroupSize_filled      Home_Range      Residual_HomeRange
##             -0.010052          0.007009         -0.151697

```



Hide

```
#pgls_function(HP, "Sub_res", "BrainVol")
```

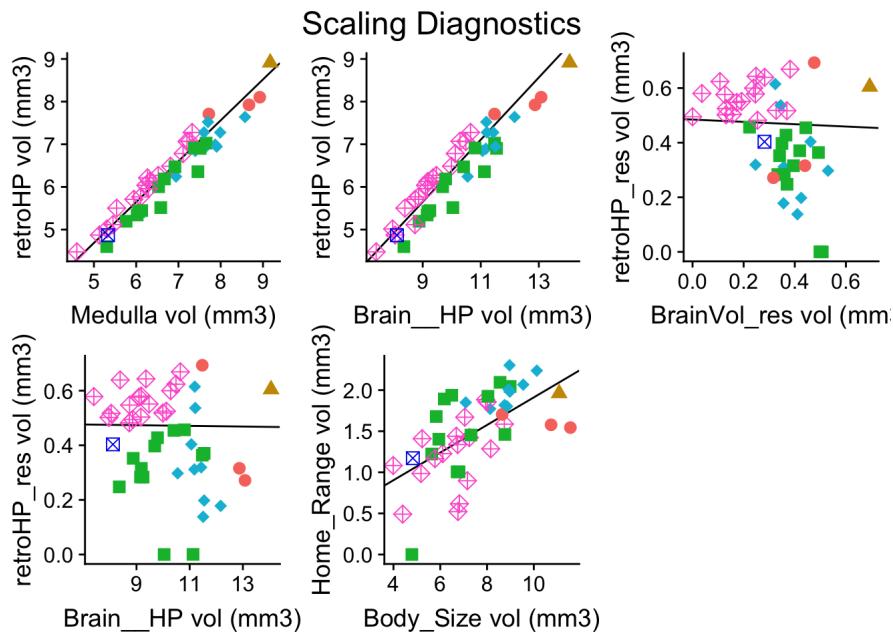
Summaries

All neuroanatomical regression plots

Scaling diagnostic multiplots

Hide

```
grid.arrange(HP.Med_res$xy_plot, HP.Brain_res$xy_plot, HPres.Enceph_res$xy_plot,
            HPres.Brain_res$xy_plot, HR.body_res$xy_plot,
            ncol = 3, top = textGrob("Scaling Diagnostics", gp=gpar(fontsize=18)))
```

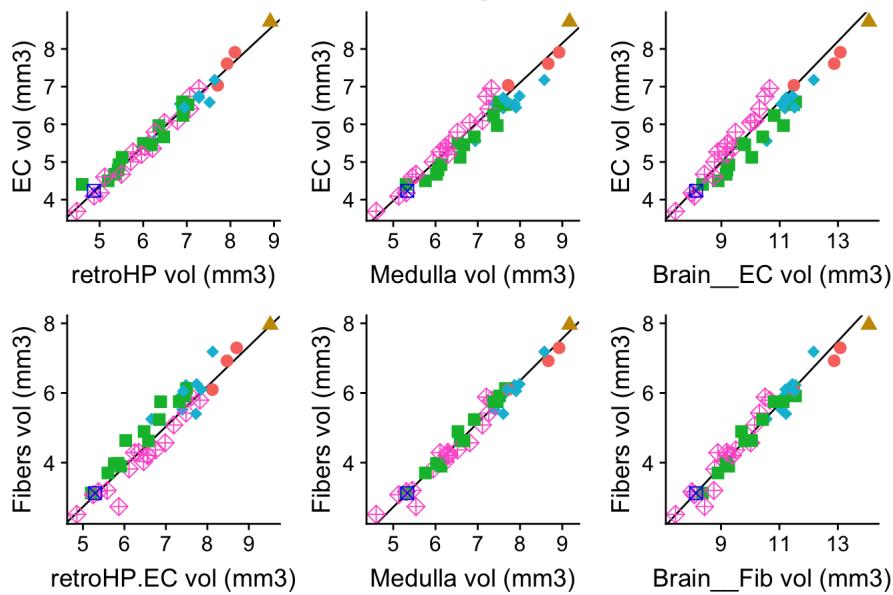


EC & Fibers multiplots

Hide

```
grid.arrange(EC.HP_res$xy_plot, EC.Med_res$xy_plot, EC.Brain_res$xy_plot,
            fibers.HP_res$xy_plot, fibers.Med_res$xy_plot, fibers.brain_res$xy_plot,
            ncol=3, top=textGrob("EC & Fiber Regressions", gp=gpar(fontsize=18)))
```

EC & Fiber Regressions

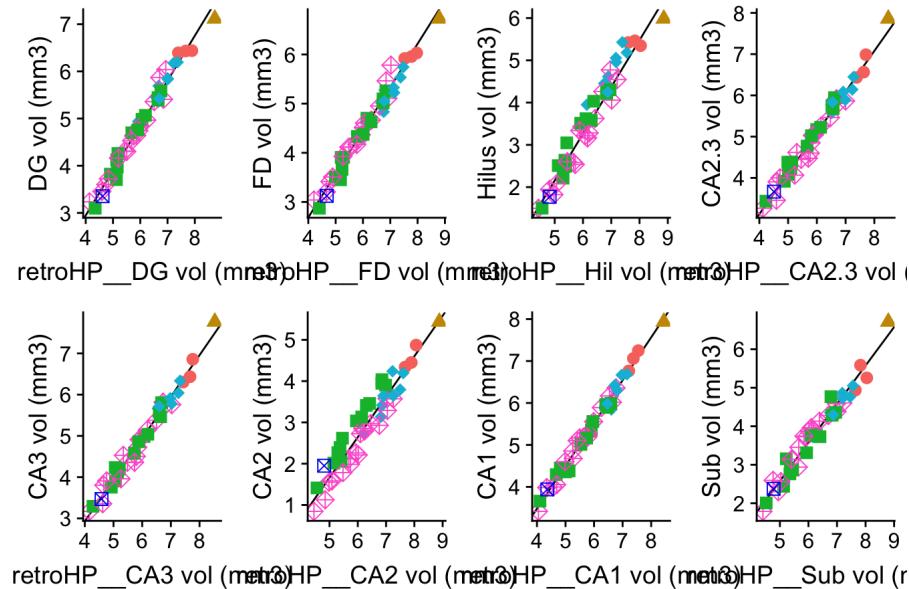


retroHP subfield multiplots

[Hide](#)

```
grid.arrange(DG.HP_res$xy_plot, FD.HP_res$xy_plot,
            Hilus.HP_res$xy_plot, CA2.3.HP_res$xy_plot,
            CA3.HP_res$xy_plot, CA2.HP_res$xy_plot,
            CA1.HP_res$xy_plot, Sub.HP_res$xy_plot,
            ncol=4, top=textGrob("retroHP Subfield Regressions", gp=gpar(fontsize=18)))
```

retroHP Subfield Regressions



Subfield Proportions

Plot the volumetric proportions of each subregion of the hippocampal complex.

Subfield Proportions

Residual Proportions

[Hide](#)

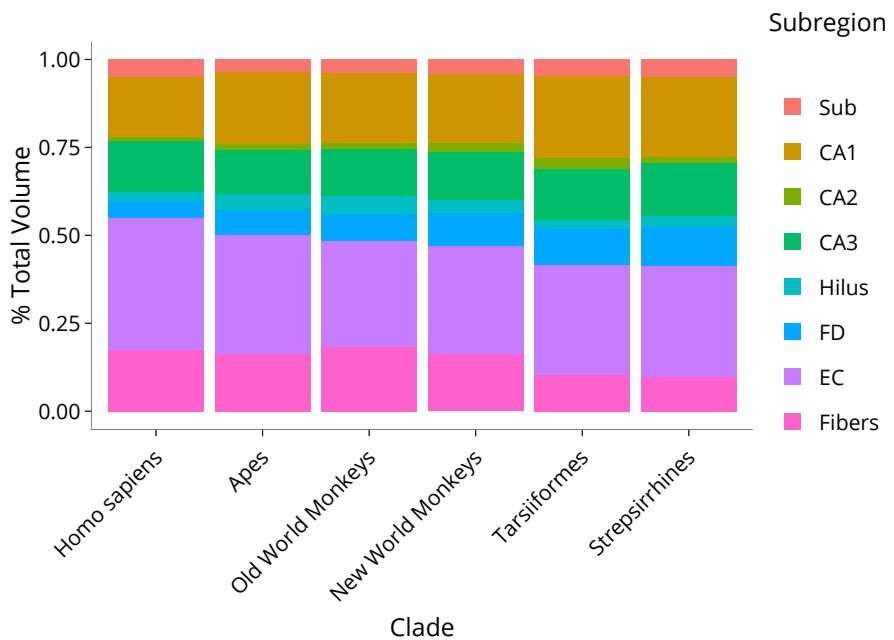
```

subregion_proportions <- function(HP_data, subregions){
  subfield_props <- HP_data %>%
    subset(select=c("Clade", subregions)) %>%
    mutate(HP_complex = rowSums( .[subregions])) %>%
    mutate_at(vars(-Clade), funs(./ HP_complex*100)) %>%
    group_by(Clade) %>%
    summarise_at(vars(-Clade), funs(mean(., na.rm=TRUE))) %>%
    subset(select=-HP_complex) %>%
    melt(id.vars = c("Clade"), variable.name = "Subregion", value.name = "% Total Volume") %>% arrange(Clade)
  subfield_props

  bp <- ggplot(subfield_props, aes(x=Clade, y = `% Total Volume`, fill = Subregion)) +
    geom_bar(position = "fill", stat="identity") + labs(x="Clade", y="% Total Volume") +
    theme(axis.text.x = element_text(angle = 45, hjust = 1))
  bp %>% ggplotly()
}

# Absolute
subregion_proportions(HP$data, c("Sub", "CA1", "CA2", "CA3", "Hilus", "FD", "EC", "Fibers"))

```



Summary stats

PGLS: Neuroanatomy regression stats

[Hide](#)

```

#pgls_function.out <- Sub.HP_res
extract_neuro <- function(pgls_function.out){
  # Get comparison name
  var_name <- paste(pgls_function.out$response_var,"res",sep="_")
  pgls_summary <- pgls_function.out$pgls_summary
  # Get model p.value
  f <- pgls_summary$fstatistic
  model.p <- round( pf(f[1],f[2],f[3],lower.tail=F) ,3)
  # Get other measures
  Multiple.R2 <- round(pgls_summary$r.squared,3)
  Adj.R2 <- round(pgls_summary$adj.r.squared[1],3)
  F.stat <- round(pgls_summary$fstatistic[1],3)
  Lambda <- round(pgls_summary$param[2],3)

  output <- list(Multiple.R2=Multiple.R2, Adj.R2=Adj.R2, F.stat=F.stat, Lambda=Lambda,
                 model.pval=model.p)
  return(output)
}

neuro.summ <- rbind(
  data.frame(Residual="retroHP.med_res", extract_neuro(HP.Med_res)),
  data.frame(Residual="EC.HP_res", extract_neuro(EC.HP_res)),
  data.frame(Residual="Fiber.HP_res", extract_neuro(fibers.HP_res)),
  data.frame(Residual="DG.HP_res", extract_neuro(DG.HP_res)),
  data.frame(Residual="FD.HP_res", extract_neuro(FD.HP_res)),
  data.frame(Residual="Hilus.HP_res", extract_neuro(Hilus.HP_res)),
  data.frame(Residual="CA2.3.HP_res", extract_neuro(CA2.3.HP_res)),
  data.frame(Residual="CA3.HP_res", extract_neuro(CA3.HP_res)),
  data.frame(Residual="CA2.HP_res", extract_neuro(CA2.HP_res)),
  data.frame(Residual="CA1.HP_res", extract_neuro(CA1.HP_res)),
  data.frame(Residual="Sub.HP_res", extract_neuro(Sub.HP_res))
)
# Bonferonni correction for multiple tests
alpha <- round(0.06/11, 4)
paste("Alpha = ", alpha)

```

```
## [1] "Alpha = 0.0055"
```

[Hide](#)

```

neuro.summ$Sig <- ifelse(neuro.summ$model.pval<0.05 & neuro.summ$model.pval>0.01, "*",
                           ifelse(neuro.summ$model.pval<0.01 & neuro.summ$model.pval>alpha, "**",
                                  ifelse(neuro.summ$model.pval<alpha, "***", "")))
row.names(neuro.summ)<-NULL
colnames(neuro.summ) <- c("Residual Name", "Multiple R2", "Adj. R2", "F stat.", "λ", "Model p-value", "Sig.")

createDT <- function(dt, caption, save=F, scrollY=700){
  if (save!=F){
    dir.create("./Tables", showWarnings=F)
    write.csv(dt, file=file.path("Tables", paste(save, "csv", sep=".") ), quote = F, row.names = F)
  }
  datatable( dt, caption=caption,
            extensions = 'Buttons', escape = F,
            options = list( dom = 'Bfrtip',
                            buttons = c('copy', 'csv', 'excel', 'pdf', 'print'),
                            scrollY = scrollY
            )
  )
}

createDT(neuro.summ, caption="Neuroanatomical PGLS Regressions Summary", save="neuro.results")

```

[Copy](#) [CSV](#) [Excel](#) [PDF](#) [Print](#)

Search:

Neuroanatomical PGLS Regressions Summary

	Residual Name	Multiple R ²	Adj. R ²	F stat.	λ	Model p-value	Sig.
1	retroHP.med_res	0.913	0.911	440.059	0.577		0 ***
2	EC.HP_res	0.974	0.974	1603.734	0		0 ***

3	Fiber.HP_res	0.897	0.894	364.37	0.562	0	***
4	DG.HP_res	0.978	0.978	1872.208	0	0	***
5	FD.HP_res	0.97	0.97	1378.024	0.25	0	***
6	Hilus.HP_res	0.919	0.917	478.632	0.576	0	***
7	CA2.3.HP_res	0.968	0.967	1266.379	0.335	0	***
8	CA3.HP_res	0.979	0.978	1919.583	0	0	***
9	CA2.HP_res	0.922	0.92	495.19	0.703	0	***
10	CA1.HP_res	0.987	0.987	3164.053	0	0	***

Showing 1 to 10 of 11 entries

Previous 1 2 Next

PGLS: HP-eco stats

[Hide](#)

```
#pgls_function.out <- Sub.HP_res
extract_eco <- function(pgls_function.out){
  # Get comparison name
  var_name <- paste(pgls_function.out$response_var,"res",sep="_")
  run_eco.out <- run_eco(pgls_function.out)
  pgls_eco_summary <- run_eco.out$pgls_eco_summary
  # Get model p.value
  f <- pgls_eco_summary$fstatistic
  model.p <- round( pf(f[1],f[2],f[3],lower.tail=F) ,3)
  # Get other measures
  Multiple.R2 <- round(pgls_eco_summary$r.squared,3)
  Adj.R2 <- round(pgls_eco_summary$adj.r.squared[1],3)
  F.stat <- round(pgls_eco_summary$fstatistic[1],3)
  Lambda <- round(pgls_eco_summary$param[2],3)

  output <- list(Multiple.R2=Multiple.R2, Adj.R2=Adj.R2, F.stat=F.stat, Lambda=Lambda,
                  model.pval=model.p)
  return(output)
}

eco.summ <- rbind(
  data.frame(Residual="retroHP.med_res", extract_eco(HP.Med_res)),
  data.frame(Residual="EC.HP_res", extract_eco(EC.HP_res)),
  data.frame(Residual="Fiber.HP_res", extract_eco(fibers.HP_res)),
  data.frame(Residual="DG.HP_res", extract_eco(DG.HP_res)),
  data.frame(Residual="FD.HP_res", extract_eco(FD.HP_res)),
  data.frame(Residual="Hilus.HP_res", extract_eco(Hilus.HP_res)),
  data.frame(Residual="CA2.3.HP_res", extract_eco(CA2.3.HP_res)),
  data.frame(Residual="CA3.HP_res", extract_eco(CA3.HP_res)),
  data.frame(Residual="CA2.HP_res", extract_eco(CA2.HP_res)),
  data.frame(Residual="CA1.HP_res", extract_eco(CA1.HP_res)),
  data.frame(Residual="Sub.HP_res", extract_eco(Sub.HP_res))
)
# Bonferroni correction for multiple tests
alpha <- round(0.05/11, 4)
paste("Alpha = ", alpha)
```

```

## [1] "Alpha = 0.0045"

eco.summ$Sig <- ifelse(eco.summ$model.pval<0.05 & eco.summ$model.pval>0.01, "*",
                      ifelse(eco.summ$model.pval<0.01 & eco.summ$model.pval>alpha, "**",
                      ifelse(eco.summ$model.pval<alpha, "***", ""))
row.names(eco.summ)<-NULL
colnames(eco.summ) <- c("Residual Name", "Multiple R2", "Adj. R2", "F stat.", "λ", "Model p-value", "Sig.")
createDT(eco.summ, caption="Ecological PGLS Regressions Summary", save = "eco.results")

```

[Hide](#)

[Copy](#)

[CSV](#)

[Excel](#)

[PDF](#)

[Print](#)

Search:

Ecological PGLS Regressions Summary

	Residual Name	Multiple R ²	Adj. R ²	F stat.	λ	Model p-value	Sig.
1	retroHP.med_res	0.238	0.13	2.192	0.908		0.077
2	EC.HP_res	0.188	0.072	1.617	0		0.181
3	Fiber.HP_res	0.191	0.075	1.65	0.487		0.173
4	DG.HP_res	0.228	0.117	2.063	0		0.094
5	FD.HP_res	0.261	0.155	2.47	0.4		0.051
6	Hilus.HP_res	0.375	0.285	4.193	0	0.004	***
7	CA2.3.HP_res	0.198	0.083	1.726	0.664		0.154
8	CA3.HP_res	0.185	0.069	1.59	0.695		0.189
9	CA2.HP_res	0.093	-0.036	0.72	0.88		0.613
10	CA1.HP_res	0.38	0.291	4.29	0.789	0.004	***

Showing 1 to 10 of 11 entries

Previous

1

2

Next

Multidimensional plots

Set up interactive 3D plots & PCA data

[Hide](#)

```

# Select which vars to put in PCA
## All residuals
all.vars <- c("retroHP_res", "EC_res", "Fibers_res", "DG_res", "FD_res", "Hilus_res", "CA2.3_res", "CA3_res", "CA2_res", "CA1_res", "Sub_res")
## Simplified
vars <- c("EC_res", "Fibers_res", "FD_res", "Hilus_res", "CA3_res", "CA2_res", "CA1_res", "Sub_res")
Clade <- factor(HP$data$Clade, c("Homo sapiens", "Apes", "Old World Monkeys", "New World Monkeys", "Tarsiiformes", "Strepsirrhines"), ordered=T)
plot.alldata <- dplyr::select(HP$data, one_of(all.vars)) %>% na.omit()
plot.data <- dplyr::select(HP$data, one_of(vars)) %>% na.omit()

```

Non-phylogenetic PCA

[Hide](#)

```

PCA <- prcomp(plot.data, scale=TRUE, center=TRUE)
pander::pander(PCA$rotation[,1:4]) # Show PC1-4

```

	PC1	PC2	PC3	PC4
EC_res	-0.2766	-0.4391	0.1012	0.6389
Fibers_res	-0.4483	0.002024	-0.4163	0.04329
FD_res	-0.05577	0.4477	0.5404	0.1329
Hilus_res	0.005114	0.5717	-0.4629	0.05015
CA3_res	-0.4739	-0.1786	0.2891	-0.1639
CA2_res	-0.4072	-0.1464	-0.3702	-0.2326
CA1_res	0.4678	-0.2191	-0.2991	0.4474
Sub_res	0.332	-0.4225	0.0002254	-0.5373

[Hide](#)

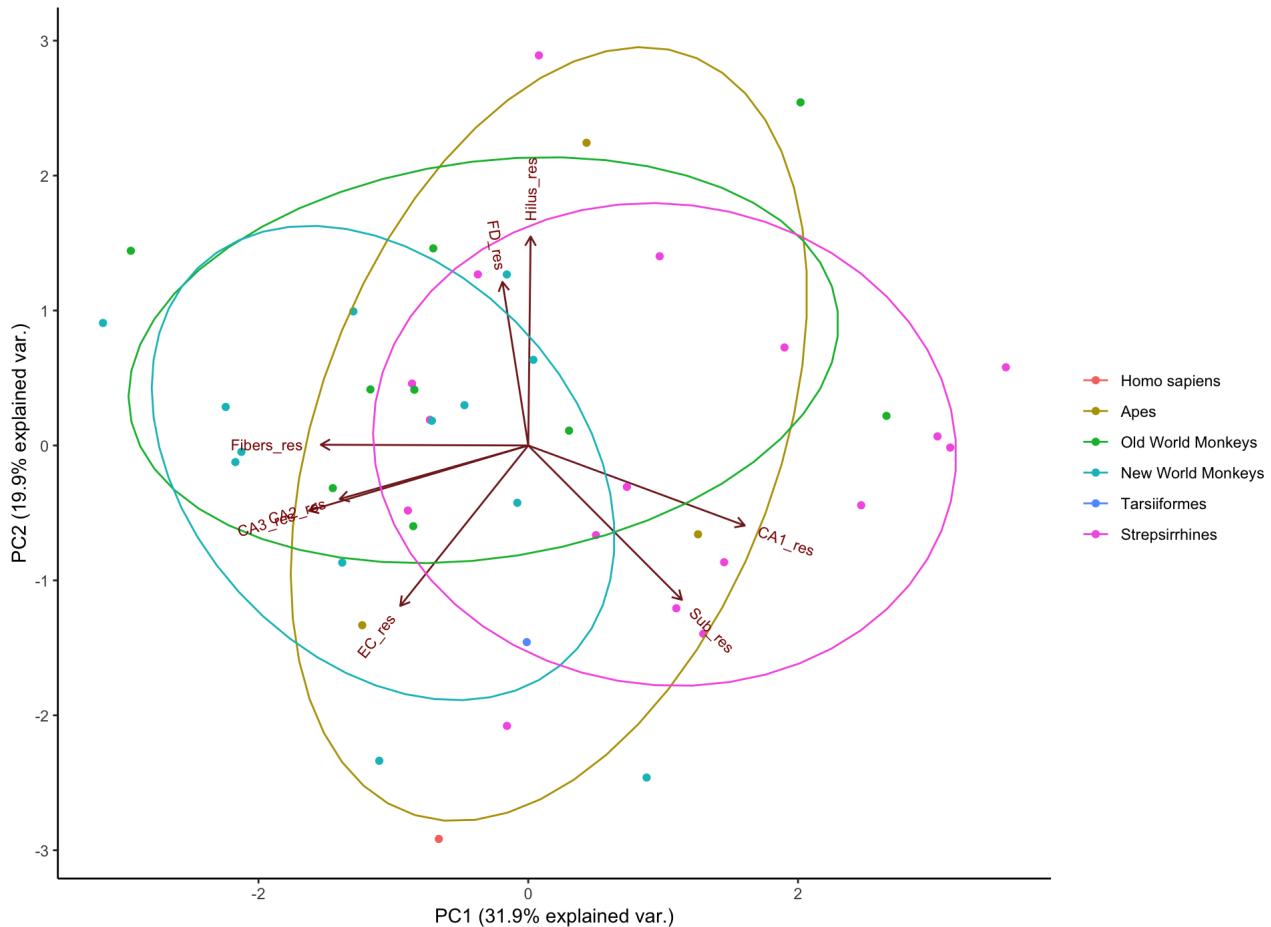
```

summPCA <- summary(PCA)

# Simple biplot
##biplot(PCA)
# Fancy biplot

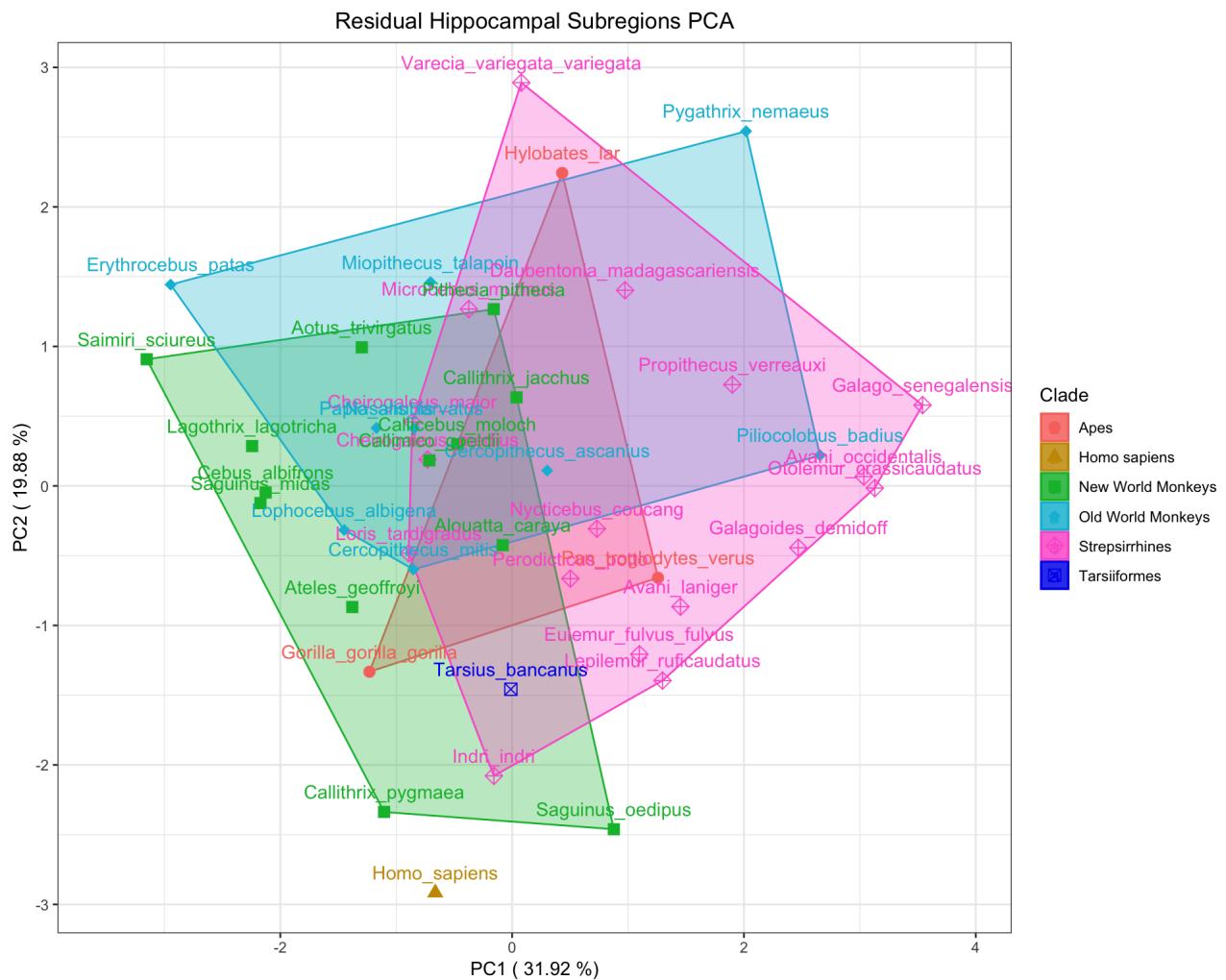
ggbiplot(PCA, obs.scale=1, var.scale=1, groups=Clade, ellipse=T, circle=F, alpha=1) +
  scale_color_discrete(name = '') + theme_classic()

```



Hide

```
# Polygonal PCA
## Prep PCA data
grouped.omit <- na.omit(all)
Species <- rownames(HP$data)
levels(Species) <- Species
DFforPlot <- data.frame(PC1=PCA$x[,1], PC2=PCA$x[,2], Species=Species)
DFforPlot["Clade"] <- HP$data$Clade
Ape <- subset(DFforPlot, Clade=="Apes")
NWM <- subset(DFforPlot, Clade=="New World Monkeys")
OWM <- subset(DFforPlot, Clade=="Old World Monkeys")
Stp <- subset(DFforPlot, Clade=="Strepsirrhines")
Trs <- subset(DFforPlot, Clade=="Tarsiiformes")
## Plot PCA
ggplot(data=DFforPlot, aes(x=PC1, y=PC2, color=Clade, fill=Clade, shape=Clade, label=Species)) +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5)) +
  geom_polygon(aes(x=PC1, y=PC2), alpha=.3, data=Ape[chull(Ape$PC1, Ape$PC2),]) +
  geom_polygon(aes(x=PC1, y=PC2), alpha=.3, data=NWM[chull(NWM$PC1, NWM$PC2),]) +
  geom_polygon(aes(x=PC1, y=PC2), alpha=.3, data=OWM[chull(OWM$PC1, OWM$PC2),]) +
  geom_polygon(aes(x=PC1, y=PC2), alpha=.3, data=Stp[chull(Stp$PC1, Stp$PC2),]) +
  geom_polygon(aes(x=PC1, y=PC2), alpha=.3, data=Trs[chull(Trs$PC1, Trs$PC2),]) +
  geom_point(size=3) + labs(title = "Residual Hippocampal Subregions PCA", x = paste("PC1", "(", round(summPCA$importance[2,1]*100, 2), "%)", y = paste("PC2", "(", round(summPCA$importance[2,2]*100, 2), "%)")) +
  geom_text(aes(label=Species), vjust=-1, hjust=.5) +
  scale_x_continuous(expand = c(.1, .1)) + scale_shape_manual(values=shapes) + scale_color_manual(values=colors) + scale_fill_manual(values = colors)
```



3D PCA

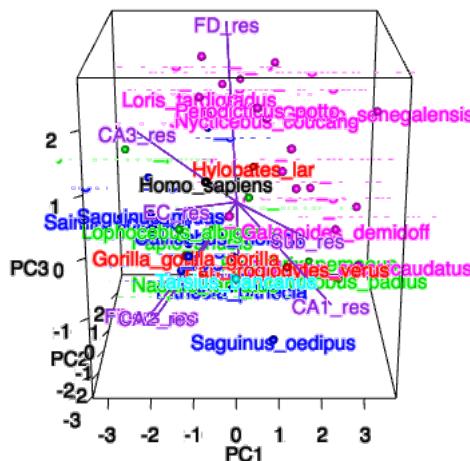
Hide

```

plot3d(PCA$x[,1:3], col=as.numeric(as.factor(Clade)), size=1, type='s', main="3D PCA: Residual Hippocampal Subregions")
# Add 3D vectors
text3d(PCA$x[,1:3], texts=rownames(PCA$x), col=as.numeric(as.factor(Clade))) # points
text3d(PCA$rotation[,1:3]*5, texts=rownames(PCA$rotation), col="purple3") # vectors
coords <- NULL
for (i in 1:nrow(PCA$rotation)) {
  coords <- rbind(coords, rbind(c(0,0,0),PCA$rotation[i,1:3]))
}
lines3d(coords*5, col="purple3", lwd=2)
#legend3d("topright", legend=unique(Clade), col=as.numeric(unique(Clade)))

```

3D PCA: Residual Hippocampal Subregions



Phylogenetic PCA

NOTE: By including DG_res and CA2.3_res, you're inflating the contribution of those regions (which, as it so happens, are extremely divergent in humans). So adding combinations of these measures multiple times overinflates how unique humans are.

[Hide](#)

```
phy.PCA <- phyl.pca(HP$phy, plot.data, method="lambda")
pander::pander(phy.PCA$L[,1:4]) # Show PC1-4
```

	PC1	PC2	PC3	PC4
EC_res	-0.3342	0.4201	-0.3168	0.1267
Fibers_res	-0.4089	-0.006708	0.02873	-0.5205
FD_res	-0.2924	-0.5867	0.3084	0.367
Hilus_res	0.3159	-0.8103	0.2186	-0.2173
CA3_res	-0.896	0.2314	-0.1422	0.1376
CA2_res	-0.4666	0.2318	0.1652	-0.7517
CA1_res	0.8051	0.1888	-0.5326	-0.1439
Sub_res	0.4387	0.7011	0.5472	0.06834

[Hide](#)

```
phy.PCA$lambda # Show lambda
```

```
## [1] 0.4992058
```

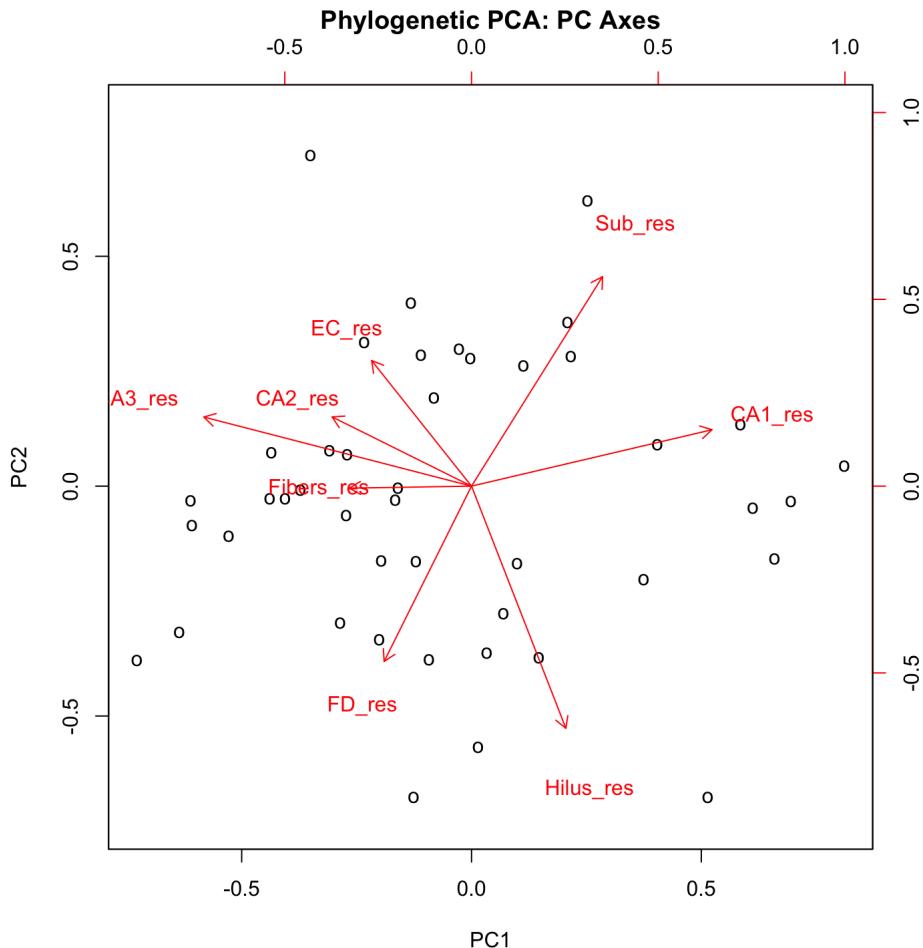
[Hide](#)

```
# Select which vars to put in PCA
summPCA <- summary(phy.PCA)
```

```
## Importance of components:
##                 PC1       PC2       PC3       PC4
## Standard deviation 0.04926423 0.04254499 0.03056124 0.02850324
## Proportion of Variance 0.33223914 0.24779020 0.12785840 0.11121818
## Cumulative Proportion 0.33223914 0.58002934 0.70788774 0.81910592
##                 PC5       PC6       PC7       PC8
## Standard deviation 0.02351801 0.02094232 0.01783295 0.003422999
## Proportion of Variance 0.07571611 0.06003948 0.04353449 0.001603987
## Cumulative Proportion 0.89482204 0.95486152 0.99839601 1.000000000
```

[Hide](#)

```
# Simple biplot
biplot(phy.PCA$S, phy.PCA$L, xlabs=rep("o", nrow(phy.PCA$S)), main = "Phylogenetic PCA: PC Axes")
```

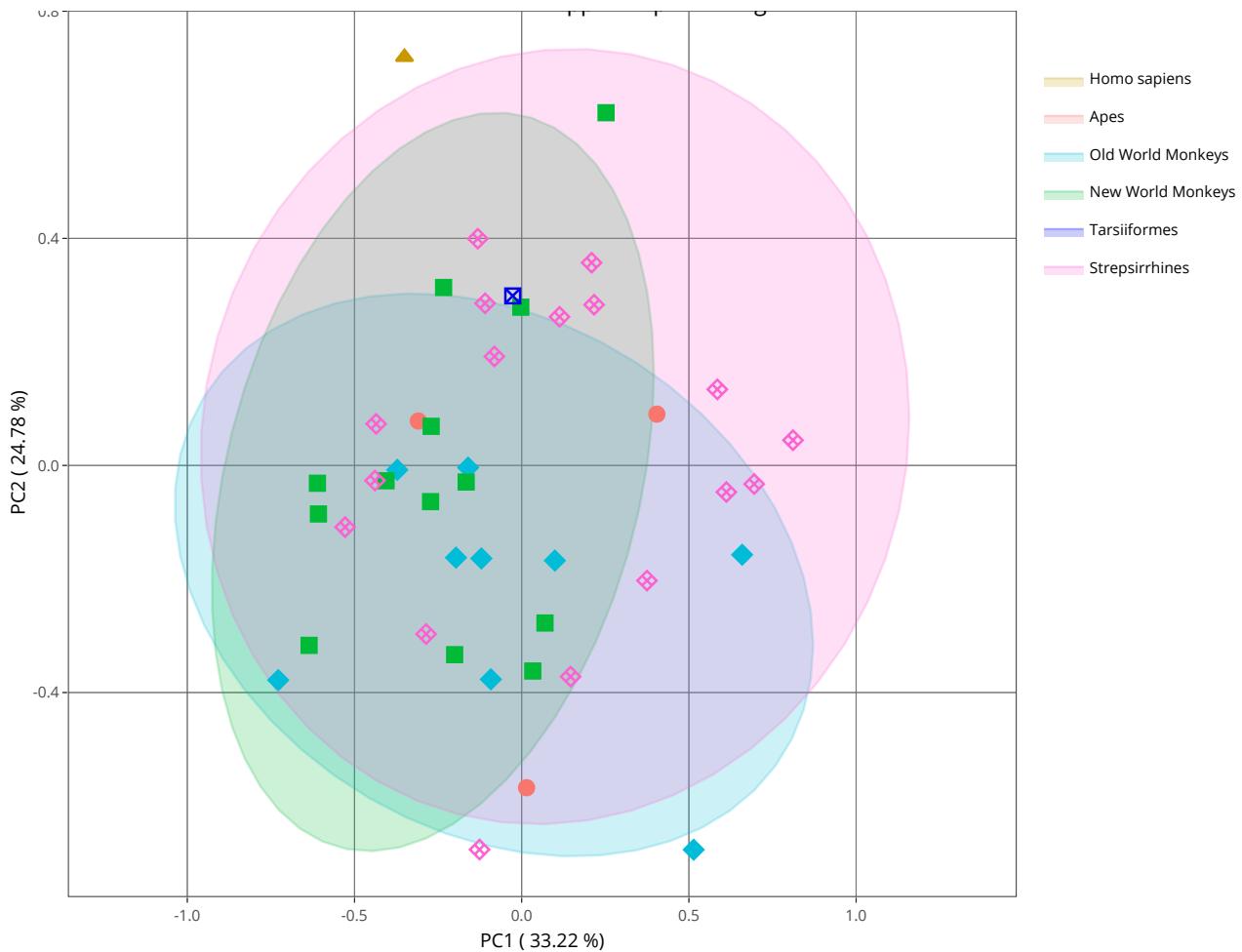


(ggbioplot doesn't recognize phyl.pca format)

```
# Polygonal PCA
## Get Propotion of Variance for each PC
POV <- diag(phy.PCA$Eval)/sum(phy.PCA$Eval)*100
## PC1 vs. PC2
grouped_omit <- na.omit(all)
Species <- rownames(HP$data)
levels(Species) <- Species
DFforPlot <- data.frame(PC1=phy.PCA$S[,1], PC2=phy.PCA$S[,2], Species=Species)
DFforPlot["Clade"] <- HP$data$Clade
  Ape <- subset(DFforPlot, Clade=="Apes")
  NWM <- subset(DFforPlot, Clade=="New World Monkeys")
  OWM <- subset(DFforPlot, Clade=="Old World Monkeys")
  Stp <- subset(DFforPlot, Clade=="Strepsirrhines")
  Trs <- subset(DFforPlot, Clade=="Tarsiiformes")
## Plot PCA
PC12 <- ggplot(data=DFforPlot, aes(x=PC1, y=PC2, color=Clade, fill=Clade, shape=Clade, label=Species)) +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5)) +
  stat_ellipse(geom="polygon", level=0.95, alpha=0.2) +
  geom_point(size=3) + labs(title = "Phylogenetic PCA: \nResidual Hippocampal Subregions", x = paste("PC1", "(", round(POV[1], 2), "%)"), y = paste("PC2", "(", round(POV[2], 2), "%)")) +
  scale_x_continuous(expand = c(.1, .1)) +
  scale_shape_manual(values=shapes) + scale_color_manual(values=colors) + scale_fill_manual(values = colors) +
  geom_text_repel(aes(label=Species), box.padding=unit(0.35, "lines"),
                 point.padding = unit(0.1, "lines"))
PC12 %>% ggplotly()
```

Phylogenetic PCA:
Residual Hippocampal Subregions

Clade

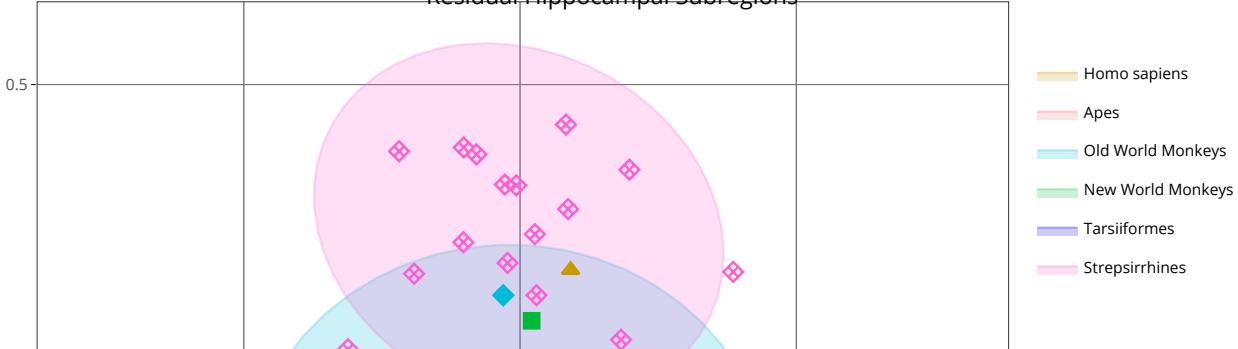


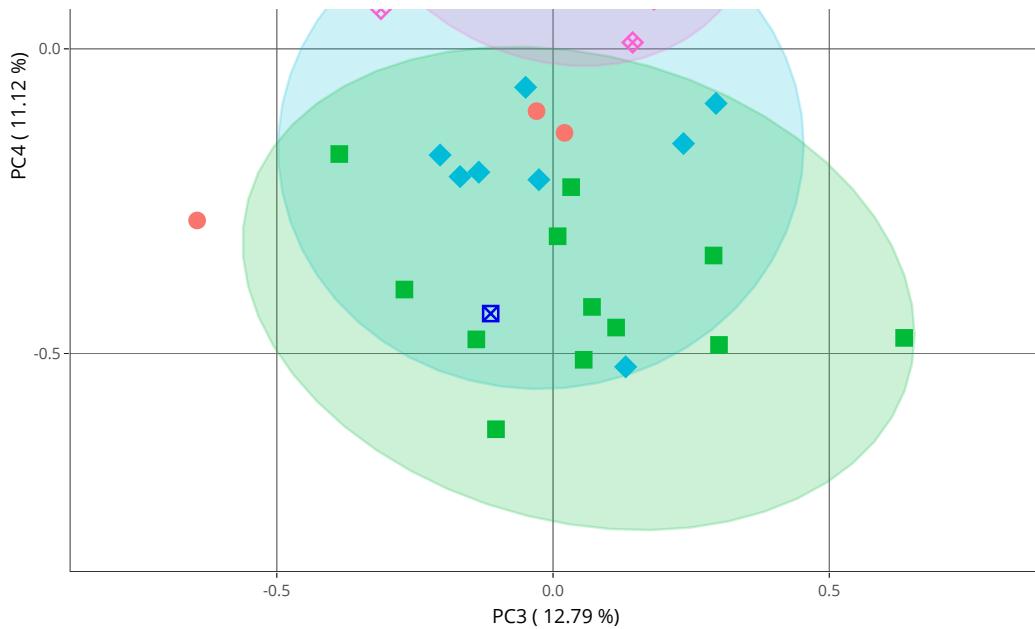
Hide

```
## PC3 vs. PC4
DFforPlot <- data.frame(PC3=phy.PCA$S[,3], PC4=phy.PCA$S[,4], Species=Species)
DFforPlot["Clade"] <- HP$data$Clade
Ape <- subset(DFforPlot, Clade=="Apes")
NWM <- subset(DFforPlot, Clade=="New World Monkeys")
OWM <- subset(DFforPlot, Clade=="Old World Monkeys")
Stp <- subset(DFforPlot, Clade=="Strepsirrhines")
Trs <- subset(DFforPlot, Clade=="Tarsiiformes")
## Plot PCA
PC34 <- ggplot(data=DFforPlot, aes(x=PC3, y=PC4, color=Clade, fill=Clade, shape=Clade, label=Species)) +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5)) +
  stat_ellipse(geom="polygon", level=0.95, alpha=0.2) +
  geom_point(size=3) + labs(title = "Phylogenetic PCA: \nResidual Hippocampal Subregions", x = paste("PC3", "(", round(POV[3], 2), "%)"), y = paste("PC4", "(", round(POV[4], 2), "%)")) +
  scale_x_continuous(expand = c(.1, .1)) +
  scale_shape_manual(values=shapes) + scale_color_manual(values=colors) +   scale_fill_manual(values = colors) +
  geom_text_repel(aes(label=Species), box.padding=unit(0.35, "lines"),
                  point.padding = unit(0.1, "lines"))
PC34 %>% ggplotly()
```

Phylogenetic PCA:
Residual Hippocampal Subregions

Clade



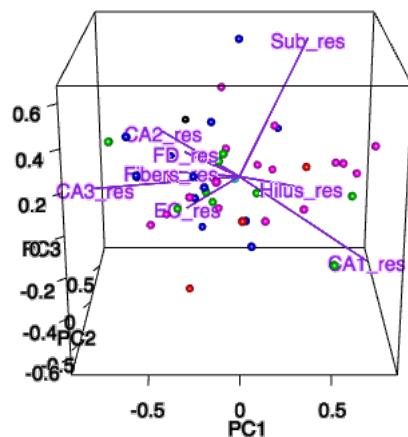


3D Phylogenetic PCA

[Hide](#)

```
plot3d(phy.PCA$S[,1:3], col=as.numeric(as.factor(Clade)), size=1, type='s', main="Phylogenetic 3D PCA: Residual Hippo campal Subregions")
# Add 3D vectors
#text3d(phy.PCA$S[,1:3], texts=rownames(phy.PCA$S), col=as.numeric(as.factor(Clade))) #points
text3d(phy.PCA$L[,1:3], texts=rownames(phy.PCA$L), col="purple3") # vectors
coords <- NULL
for (i in 1:nrow(phy.PCA$L)) {
  coords <- rbind(coords, rbind(c(0,0,0),phy.PCA$L[i,1:3]))
}
lines3d(coords, col="purple3", lwd=2)
#legend3d("topright", legend=unique(Clade), col=c("blue","turquoise","green","black","red","magenta"))
```

Phylogenetic 3D PCA: Residual Hippocampal Subregions



Hierarchical Clustering + Heatmap

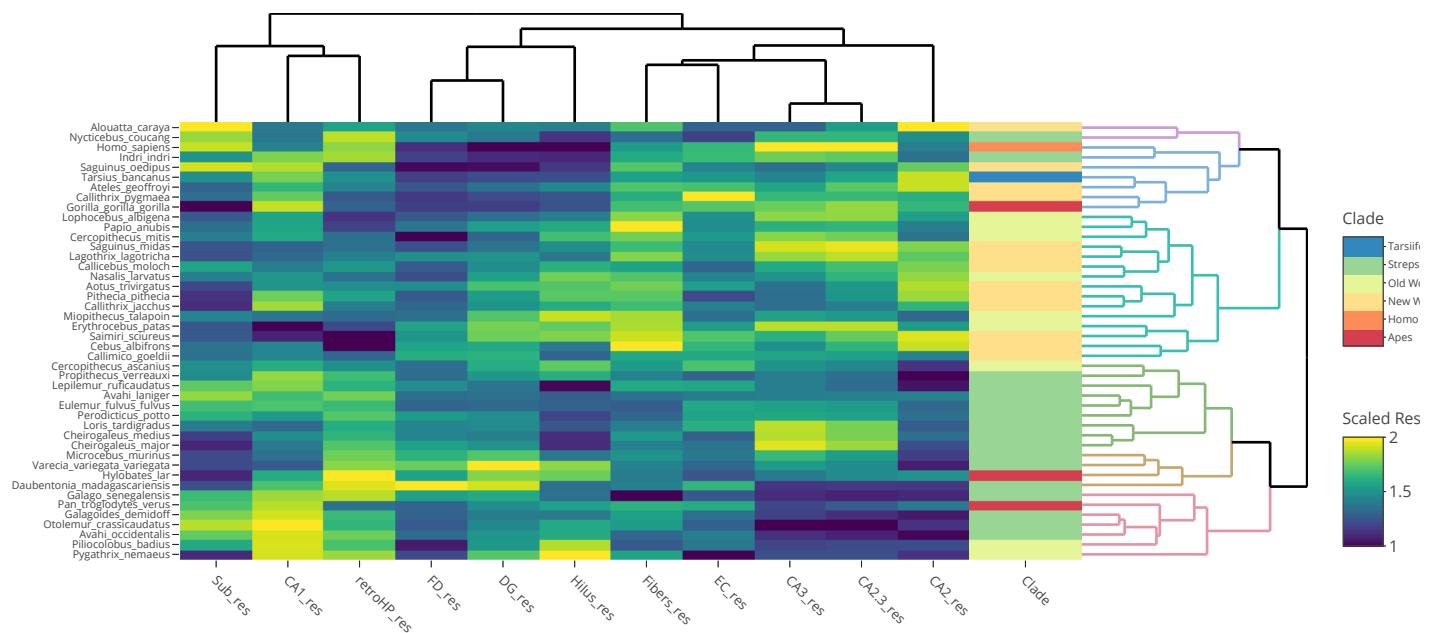
Heatmaply Phylo.heatmap

[Hide](#)

```

Spectral <- grDevices::colorRampPalette(RColorBrewer::brewer.pal( length(orderedClades), "Spectral"))
heatmaply(plot.alldata, k_row = length(orderedClades), plot_method= "plotly", fontsize_row = 8,
  row_side_colors = list(Clafe=Clade), row_side_palette = Spectral,
  colorbar_xpos = 1.02, key.title="Scaled Residuals") %>%
  colorbar( len = 0.3, tickfont = list(size = 8), titlefont = list(size = 12), which = 2)

```



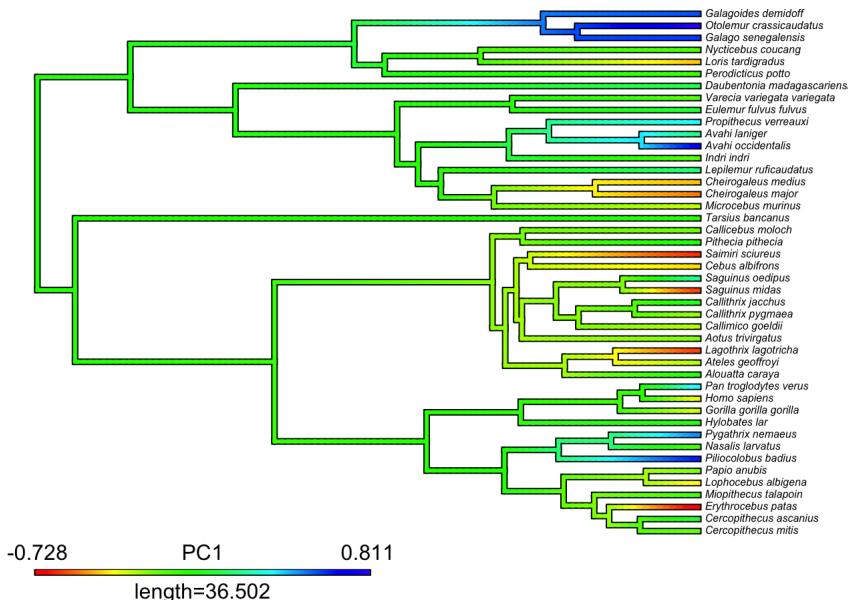
Principal Components: Trees

PC1 ContMap

```

phy.PC1 <- phy.PCA$[,1]
res_phylo_plot <- contMap(HP$phy, phy.PC1, type="phylogram", plot=FALSE)
plot(res_phylo_plot, leg.txt="PC1", lwd=3, fsize=c(0.5, 1))

```



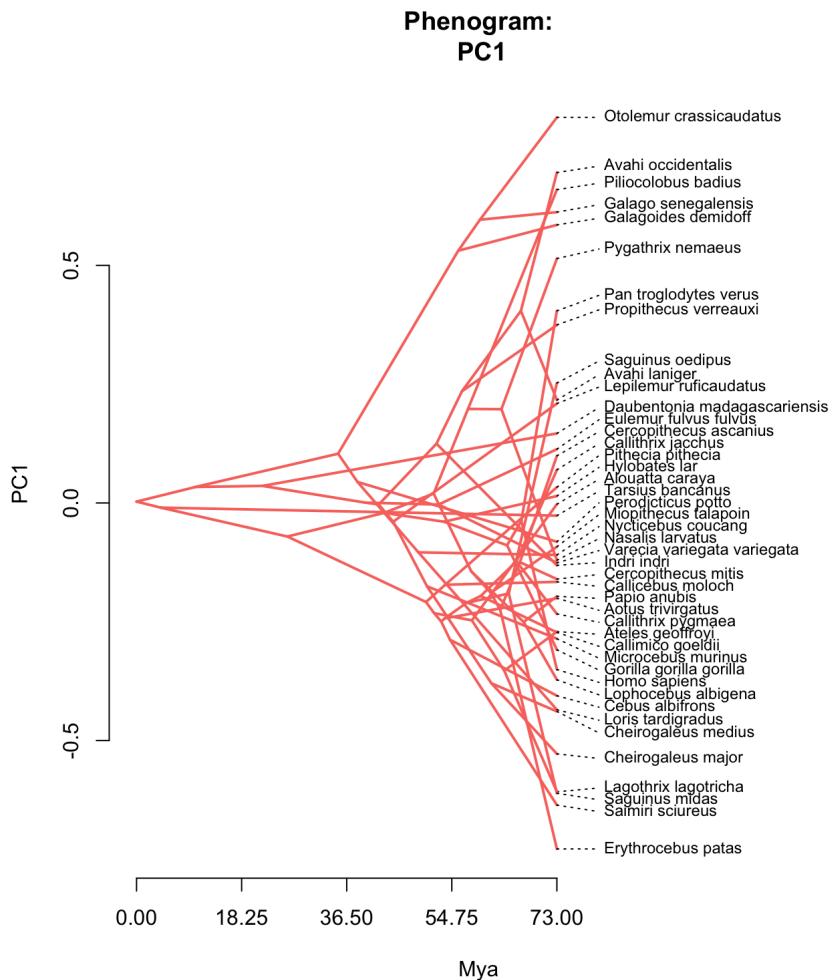
PC1 Phenogram

```

phenogram(HP$phy, x=phy.PC1, spread.labels=T, fsize=.75, colors=colz, axes=c(time, phy.PC1), main="Phenogram:\n n PC1",
xlab="Mya", ylab="PC1") #spread.cost = c(1, 0),

```

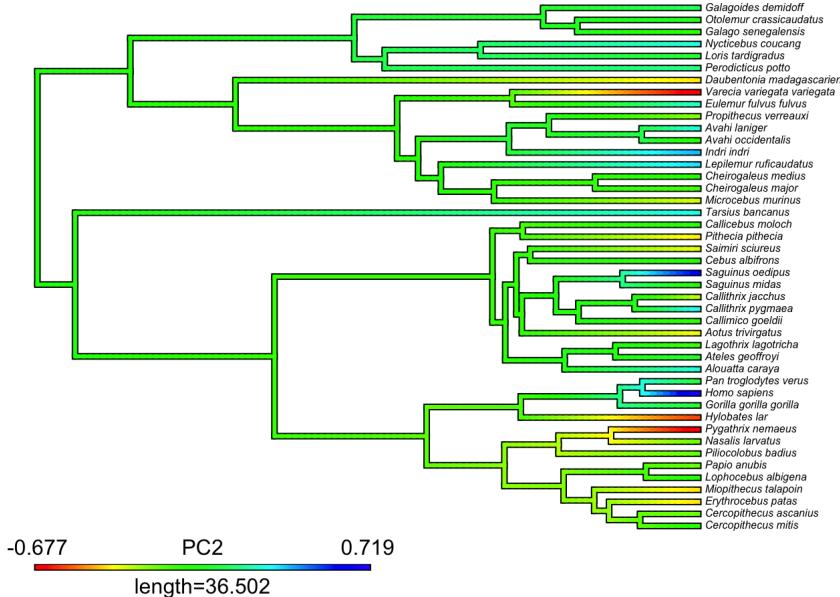
```
## Optimizing the positions of the tip labels...
```



PC2 ContMap

[Hide](#)

```
phy.PC2 <- phy.PCA[,2]
res_phylo_plot <- contMap(HP$phy, phy.PC2, type="phylogram", plot=FALSE)
plot(res_phylo_plot, leg.txt="PC2", lwd=3, fsize=c(0.5, 1))
```



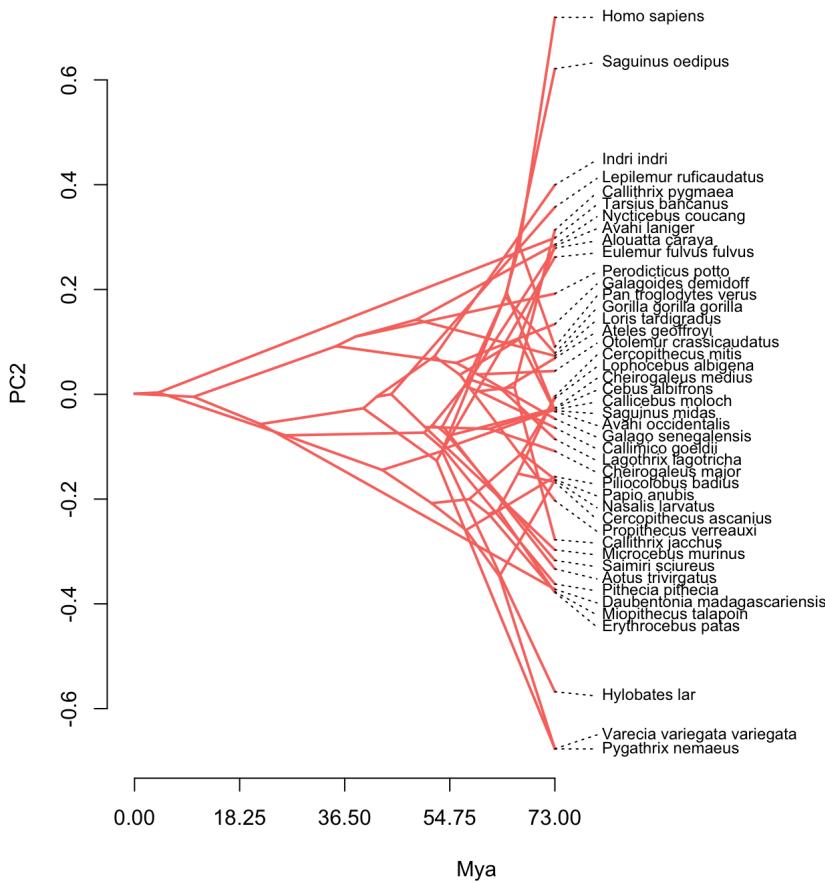
PC2 Phenogram

Hide

```
phenogram(HP$phy, x=phy.PC2, spread.labels=T, fsize=.75, colors=colz, axes=c(time, phy.PC2), main="Phenogram:\n PC2",
xlab="Mya", ylab="PC2") #spread.cost = c(1, 0),
```

```
## Optimizing the positions of the tip labels...
```

**Phenogram:
PC2**

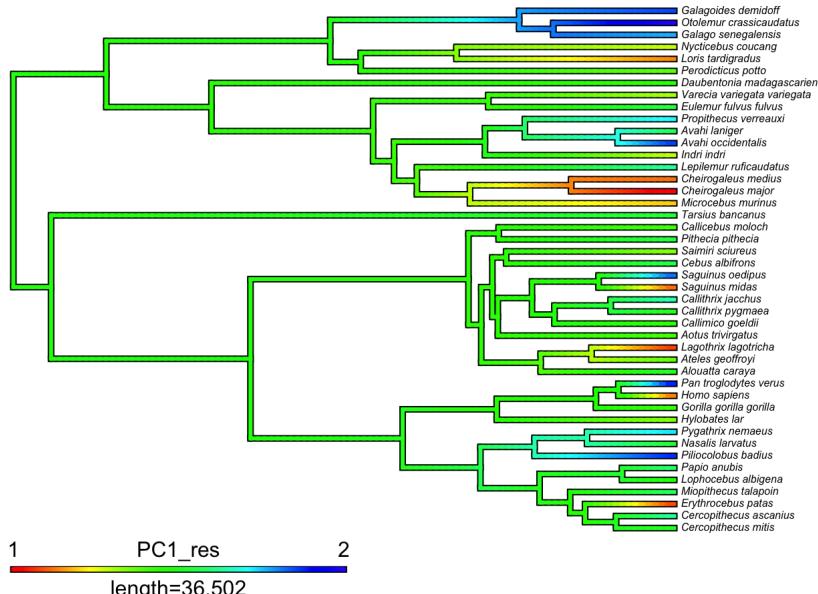


Principal Components: Scaling

PC1 vs. retroHP_res

Hide

```
#Hyp: The hippocampus becomes increasingly reorganized as residual retroHP becomes larger.  
HP$data$PC1 <- scales::rescale(phy.PC1,c(1,2))  
#PC1.HP_res <- pgls_function(HP, "PC1", "retroHP") # No relationship  
#PC1.Brain <- pgls_function(HP, "PC1", "BrainVol") # No relationship  
PC1.HPres_res <- pgls_function(HP, "PC1", "retroHP_res")  
  
##  
## Call:  
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),  
##     data = comp_data, lambda = "ML")  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -0.046301 -0.012976  0.000066  0.007543  0.025552  
##  
## Branch length transformations:  
##  
## kappa [Fix] : 1.000  
## lambda [ ML] : 0.000  
##    lower bound : 0.000, p = 1  
##    upper bound : 1.000, p = 8.6975e-06  
##  95.0% CI : (NA, 0.623)  
## delta [Fix] : 1.000  
##  
## Coefficients:  
##                               Estimate Std. Error t value  
## (Intercept)                 0.145203  0.062044  2.3403  
## log(eval(parse(text = predictor_var))) 0.483763  0.135102  3.5807  
##                                         Pr(>|t|)  
## (Intercept)                   0.0240930 *  
## log(eval(parse(text = predictor_var))) 0.0008821 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.01772 on 42 degrees of freedom  
## Multiple R-squared: 0.2339, Adjusted R-squared: 0.2156  
## F-statistic: 12.82 on 1 and 42 DF,  p-value: 0.0008821
```



```

## [1] "Top 5 Positive Residuals: PC1_res"
##           species      res
## 1 Otolemur_crassicaudatus 0.3043376
## 2 Pan_troglodytes_verus 0.2533469
## 3 Piliocolobus_badius 0.2377245
## 4 Avahi_occidentalis 0.2307420
## 5 Galagooides_demidoff 0.2215353
## [1] "====="
## [1] "Top 5 Negative Residuals: PC1_res"
##           species      res
## 1 Cheirogaleus_major -0.2878240
## 2 Lagothrix_lagotricha -0.2460136
## 3 Erythrocebus_patas -0.2408588
## 4 Saguinus_midas -0.2244946
## 5 Homo_sapiens -0.2183799

```

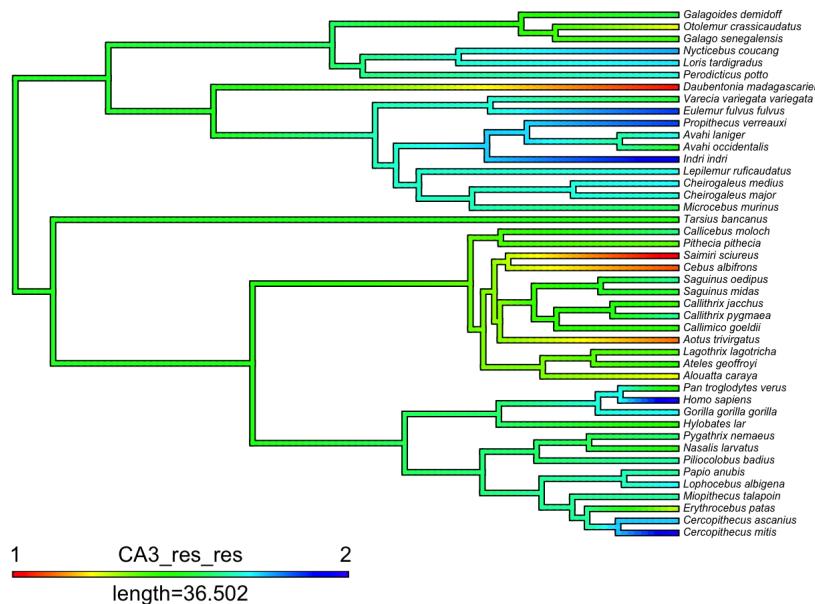
[Hide](#)

```
CA3.PC1_res <- pgls_function(HP, "CA3_res", "PC1") # Strong relationship, duh.
```

```

##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -0.021785 -0.005385  0.003205  0.006585  0.030170
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.494
##   lower bound : 0.000, p = 0.025655
##   upper bound : 1.000, p = 0.0022414
##   95.0% CI   : (0.035, 0.906)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                 0.733110  0.040293 18.195
## log(eval(parse(text = predictor_var))) -0.909407  0.072158 -12.603
##                               Pr(>|t|)
## (Intercept)                 < 2.2e-16 ***
## log(eval(parse(text = predictor_var))) 8.882e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01051 on 42 degrees of freedom
## Multiple R-squared: 0.7909, Adjusted R-squared: 0.7859
## F-statistic: 158.8 on 1 and 42 DF,  p-value: 7.323e-16

```



```
## [1] "Top 5 Positive Residuals: CA3_res_res"
##           species      res
## 1      Homo_sapiens 0.1595291
## 2     Cercopithecus_mitis 0.1530054
## 3      Indri_indri 0.1400509
## 4     Eulemur_fulvus_fulvus 0.1141412
## 5 Propithecus_verreauxi 0.1120924
## [1] "=====
## [1] "Top 5 Negative Residuals: CA3_res_res"
##           species      res
## 1     Saimiri_sciureus -0.1923016
## 2 Daubentonia_madagascariensis -0.1785349
## 3      Cebus_albifrons -0.1587581
## 4      Aotus_trivirgatus -0.1477182
## 5      Alouatta_caraya -0.1052251
```

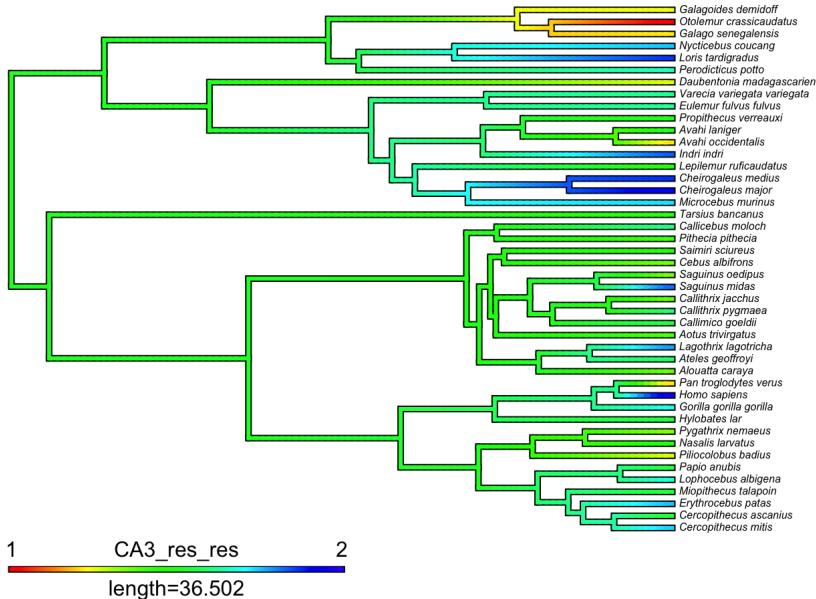
Hide

```
#Hyp: Since PC1 is largely driven by CA2.3_res, and PC1 correlates with retroHP_res, is there a relationship between
retroHP_res and CA3_res?
CA3.HPres_res <- pgls_function(HP, "CA3_res", "retroHP_res") #Result: Approaching sig.
```

```

## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.027754 -0.008338  0.000178  0.013720  0.048362
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 2.0392e-05
## 95.0% CI : (NA, 0.757)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                0.539202  0.067931  7.9375
## log(eval(parse(text = predictor_var))) -0.287866  0.147920 -1.9461
##                               Pr(>|t|)
## (Intercept)                6.843e-10 ***
## log(eval(parse(text = predictor_var))) 0.05835 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0194 on 42 degrees of freedom
## Multiple R-squared: 0.08272, Adjusted R-squared: 0.06088
## F-statistic: 3.787 on 1 and 42 DF,  p-value: 0.05835

```



```

## [1] "Top 5 Positive Residuals: CA3_res_res"
##           species      res
## 1     Homo_sapiens 0.3280246
## 2 Cheirogaleus_major 0.2892187
## 3 Cheirogaleus_medi 0.2425722
## 4 Loris_tardigradus 0.2403541
## 5 Indri_indri 0.2155975
## [1] "=====
## [1] "Top 5 Negative Residuals: CA3_res_res"
##           species      res
## 1 Otolemur_crassicaudatus -0.3942419
## 2 Pan_troglodytes_verus -0.2527245
## 3 Avahi_occidentalis -0.2428427
## 4 Galago_senegalensis -0.2351995
## 5 Galagooides_demidoff -0.2144560

```

Hide

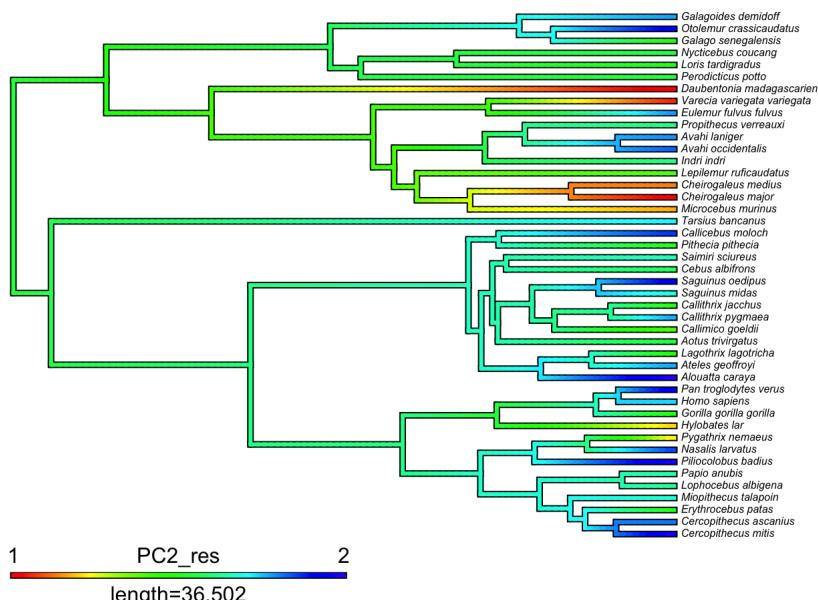
```
#Result: Significant positive relationship! But somewhat weak R2
```

PC2 vs. retroHP_res

[Hide](#)

```
#Hyp: The hippocampus becomes increasingly reorganized as residual retroHP becomes larger.
HP$data$PC2 <- scales::rescale(phy.PC2,c(1,2))
#PC2.HPres_res <- pgls_function(HP, "PC2", "retroHP") # No relationship
#PC2.HPres_res <- pgls_function(HP, "PC2", "BrainVol") # No relationship
#PC2.HPres_res <- pgls_function(HP, "PC2", "retroHP_res") # No relationship
PC2.HPres_res <- pgls_function(HP, "PC2", "Hilus_res") # Strong correlation, duh.

##
## Call:
## pgls(formula = log(eval(parse(text = response_var))) ~ log(eval(parse(text = predictor_var))),
##       data = comp_data, lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max 
## -0.0293898 -0.0063614  0.0006185  0.0084970  0.0236566
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.283
## lower bound : 0.000, p = 0.2961
## upper bound : 1.000, p = 0.0091761
## 95.0% CI : (NA, 0.924)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                0.631484   0.041324 15.2811
## log(eval(parse(text = predictor_var))) -0.731923   0.087700 -8.3457
##                                     Pr(>|t|)    
## (Intercept) < 2.2e-16 ***
## log(eval(parse(text = predictor_var))) 1.852e-10 ***
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01201 on 42 degrees of freedom
## Multiple R-squared: 0.6238, Adjusted R-squared: 0.6149
## F-statistic: 69.65 on 1 and 42 DF, p-value: 1.852e-10
```



```
## [1] "Top 5 Positive Residuals: PC2_res"
##           species      res
## 1     Alouatta_caraya 0.1544254
## 2   Cercopithecus_mitis 0.1495736
## 3   Piliocolobus_badius 0.1492647
## 4   Pan_troglodytes_verus 0.1372806
## 5   Saguinus_oedipus 0.1334370
## [1] "====="
## [1] "Top 5 Negative Residuals: PC2_res"
##           species      res
## 1 Daubentonia_madagascariensis -0.2089132
## 2     Cheirogaleus_major -0.2049607
## 3 Varecia_variegata_variegata -0.1895278
## 4     Cheirogaleus_medius -0.1597717
## 5   Microcebus_murinus -0.1471130
```

Hide

#Result: No relationship.

Principal Component: Eco

PC-eco functions

Hide

```

# Run eco PC
PCrun_eco <- function(comp_data, response_var){
  HP.noHomo <- subset(comp_data, subset=! Genus=="Homo")
  pgls_eco_raw <- pgls(data=HP.noHomo, formula=
    eval(parse(text=paste(response_var)))) ~
      DietBreadth + PopulationDensity_n_km2 +
      GroupSize_filled + Home_Range + Residual_HomeRange,
      lambda='ML')
  pgls_eco_summary <- summary(pgls_eco_raw)

  output <- list(pgls_eco_summary=pgls_eco_summary, pgls_eco_raw=pgls_eco_raw, response_var=response_var, comp_data=comp_data)
  return(output)
}

# Plot PC1-eco
PCeco_plots <- function(eco_var, run_eco.out, figLabel){

  pgls_eco_summary <- run_eco.out$pgls_eco_summary
  response_var <- run_eco.out$response_var
  data <- run_eco.out$comp_data$data
  brain <- data[,paste(run_eco.out$response_var)]
  eco_x <- data[,paste(eco_var)]
  slope <- as.numeric(pgls_eco_summary$coefficients[eco_var,1])
  p <- as.numeric(pgls_eco_summary$coefficients[eco_var,4])

  # Initialize plot
  eco_plot <- ggplot(data, aes(y=brain, x=eco_x, fill=Clade, color=Clade, shape=Clade)) +
    theme_classic() + ggtitle(figLabel)

  # Conditionally add regression line
  if (p<=0.05){
    eco_plot <- eco_plot +
      geom_smooth(na.rm=F, inherit.aes=F, method="lm", alpha = .15, data=data, aes(y=brain, x=eco_x))
  }
  # Conditionally add legend
  if (eco_var == "Residual_HomeRange"){
    eco_plot = eco_plot + theme(legend.position=c(1.75, 0.35), legend.background = element_rect(fill="whitesmoke"),
                                 plot.title = element_text(hjust= -.3))
  } else{
    eco_plot = eco_plot + theme( legend.position="none",
                                 plot.title = element_text(hjust= -.3))
  }
  # Add remaining features
  eco_plot <- eco_plot + geom_point(size=3, alpha=.7) +
    xlab(paste(eco_var,sep="")) + ylab(paste(response_var,"res",sep="_")) +
    scale_shape_manual(values=shapes) + scale_color_manual(values=colors) + scale_fill_manual(values=colors)

  #geom_abline(slope=SLOPE, intercept=INTERCEPT)
  #assign(paste("eco_plot",paste(response_var,"res",sep="_"), "vs",eco_var,sep=".") ,eco_plot)
  return(eco_plot) # %>% ggplotly()
}

# MAKE MORE FLEXIBLE (dependent on which model variables actually used)
PCall_eco_plots <- function(comp_data, response_var){
  eco=PCrun_eco(comp_data, response_var)
  e1 <- PCeco_plots(eco_var = "DietBreadth", run_eco.out=eco, figLabel="A")
  e4 <- PCeco_plots(eco_var = "PopulationDensity_n_km2", run_eco.out=eco, figLabel="B")
  e11 <- PCeco_plots(eco_var = "GroupSize_filled", run_eco.out=eco, figLabel="C")
  e12 <- PCeco_plots(eco_var = "Home_Range", run_eco.out=eco, figLabel="D")
  e13 <- PCeco_plots(eco_var = "Residual_HomeRange", run_eco.out=eco, figLabel="E")

  # mod_vars <- list(eco_vars=c("DietBreadth","PopulationDensity_n_km2","GroupSize_filled", "Home_Range", "Residual_HomeRange"))

  gridExtra::grid.arrange(e1,e4,e11,e12,e13, ncol=3, top=paste("Ecological Plots:",response_var ) )
  # subplot(e1,e4,e11,e12,e13, nrows = 2, share=F, shareX=F, titleX = T, titleY=T)
}

```

Run PC-eco

Hide

```

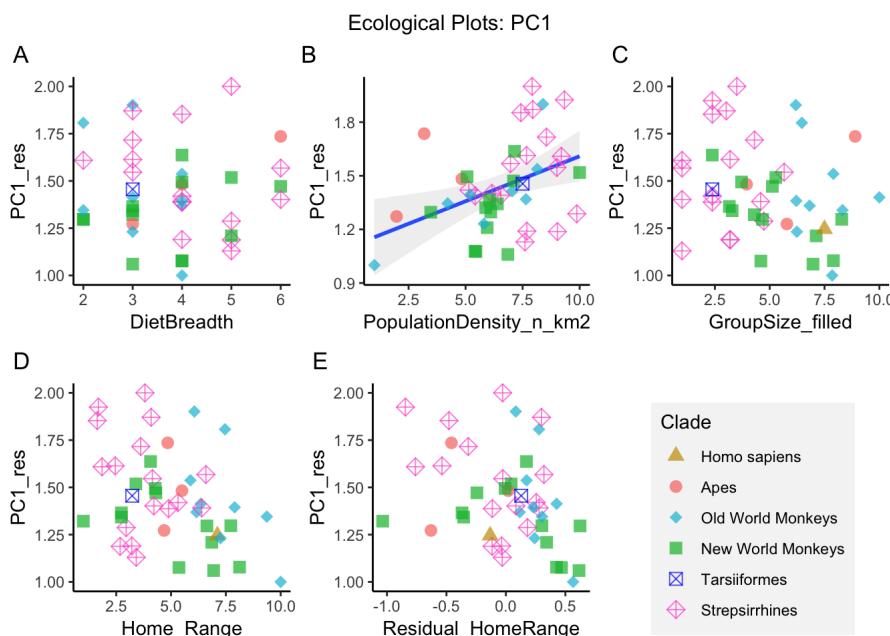
## PC1 (models + plots)
PC1_eco.out <- PCrun_eco(HP, "PC1"); PC1_eco.out$pgls_eco_summary

##
## Call:
## pgls(formula = eval(parse(text = paste(response_var)))) ~ DietBreadth +
##   PopulationDensity_n_km2 + GroupSize_filled + Home_Range +
##   Residual_HomeRange, data = HP.noHomo, lambda = "ML")
##
## Residuals:
##      Min        1Q    Median        3Q       Max 
## -0.053448 -0.022765 -0.002138  0.011144  0.069918 
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.742
## lower bound : 0.000, p = 0.016433
## upper bound : 1.000, p = 0.033772
## 95.0% CI   : (0.148, 0.989)
## delta [Fix] : 1.000
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 0.9526226 0.3232423 2.9471 0.005676 ** 
## DietBreadth  0.0061024 0.0269044 0.2268 0.821884  
## PopulationDensity_n_km2 0.0622104 0.0228364 2.7242 0.009991 ** 
## GroupSize_filled -0.0081957 0.0208938 -0.3923 0.697249  
## Home_Range   0.0235301 0.0413797 0.5686 0.573231  
## Residual_HomeRange -0.2242149 0.1590190 -1.4100 0.167368 
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03078 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.3138, Adjusted R-squared: 0.2157 
## F-statistic: 3.201 on 5 and 35 DF,  p-value: 0.01751

```

Hide

```
PCall_eco_plots(HP, "PC1")
```



Hide

```

## PC2
PC2_eco <- PCrun_eco(HP, "PC2"); PC2_eco$pgls_eco_summary

```

```

## Call:
## pgls(formula = eval(parse(text = paste(response_var)))) ~ DietBreadth +
##   PopulationDensity_n_km2 + GroupSize_filled + Home_Range +
##   Residual_HomeRange, data = HP.noHomo, lambda = "ML")
##
## Residuals:
##      Min       1Q    Median       3Q      Max 
## -0.072543 -0.014605 -0.004042  0.006167  0.047582
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
##   lower bound : 0.000, p = 1
##   upper bound : 1.000, p = 0.001975
## 95.0% CI : (NA, 0.370)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)           1.6830716  0.2763604  6.0901 5.875e-07 ***
## DietBreadth          -0.0133485  0.0273196 -0.4886   0.6282    
## PopulationDensity_n_km2 -0.0054613  0.0203782 -0.2680   0.7903    
## GroupSize_filled        -0.0145846  0.0175890 -0.8292   0.4126    
## Home_Range            -0.0129972  0.0351789 -0.3695   0.7140    
## Residual_HomeRange     -0.1348578  0.1417524 -0.9514   0.3479    
## ---                
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02204 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.2159, Adjusted R-squared: 0.1039
## F-statistic: 1.928 on 5 and 35 DF, p-value: 0.1145

```

Hide

```

## PC3
HP$data$PC3 <- scales::rescale(phy.PCA[,3],c(1,2))
PC3_eco <- PCrun_eco(HP, "PC3"); PC3_eco$pgls_eco_summary

```

```

## Call:
## pgls(formula = eval(parse(text = paste(response_var)))) ~ DietBreadth +
##   PopulationDensity_n_km2 + GroupSize_filled + Home_Range +
##   Residual_HomeRange, data = HP.noHomo, lambda = "ML")
##
## Residuals:
##      Min       1Q    Median       3Q      Max 
## -0.033493 -0.015185 -0.003380  0.008582  0.052928
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
##   lower bound : 0.000, p = 1
##   upper bound : 1.000, p = 0.0007902
## 95.0% CI : (NA, 0.367)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)           1.40583111  0.24946456  5.6354 2.336e-06 ***
## DietBreadth          0.03381417  0.02466077  1.3712   0.1790    
## PopulationDensity_n_km2 -0.00071629  0.01839493 -0.0389   0.9692    
## GroupSize_filled        0.00521311  0.01587719  0.3283   0.7446    
## Home_Range            -0.01085088  0.03175527 -0.3417   0.7346    
## Residual_HomeRange     0.17654536  0.12795678  1.3797   0.1764    
## ---                
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01989 on 35 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.1552, Adjusted R-squared: 0.03454
## F-statistic: 1.286 on 5 and 35 DF, p-value: 0.2919

```

[Hide](#)

```
## PC4
HP$data$PC4 <- scales::rescale(phy.PCA[,4],c(1,2))
PC4_eco <- PCrun_eco(HP, "PC4"); PC4_eco$pgls_eco_summary

##
## Call:
## pgls(formula = eval(parse(text = paste(response_var)))) ~ DietBreadth +
##   PopulationDensity_n_km2 + GroupSize_filled + Home_Range +
##   Residual_HomeRange, data = HP.noHomo, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.049229 -0.017165  0.007111  0.029152  0.050760
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.815
## lower bound : 0.000, p = 4.8048e-07
## upper bound : 1.000, p = 0.074294
## 95.0% CI : (0.463, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)           1.8702472  0.3217949  5.8119 1.366e-06 ***
## DietBreadth          -0.0235148  0.0261256 -0.9001   0.3742    
## PopulationDensity_n_km2 -0.0106191  0.0223858 -0.4744   0.6382    
## GroupSize_filled       -0.0011542  0.0205401 -0.0562   0.9555    
## Home_Range            -0.0289135  0.0411179 -0.7032   0.4866    
## Residual_HomeRange     0.1652155  0.1568180  1.0535   0.2993    
## ---                
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03191 on 35 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared: 0.05182, Adjusted R-squared: -0.08363
## F-statistic: 0.3826 on 5 and 35 DF,  p-value: 0.8573
```

Inter-subregional Correlations

[Hide](#)

```

# Potential issue: According to the SURFACE publication, "...as the method assumes that traits have independent rates
of adaptation (a) and diffusion (r2), traits with strong evolutionary correlations should be avoided."
# Composite traits like CA2.3_res and DG_rest are obviously colinear. But other seemingly less related traits (e.g. C
A3_res vs. CA1_res; r = -0.65) are also highly correlated, in some cases even more so than composite measures and their
components! (e.g. DG_res vs. Hilus_res; r = 0.64).

# From another perspective, inter-subregional correlations might reveal interesting relationships about how some subregions
tend to evolve together.

# Set up variables
cor.vars <- c("BrainVol", "BrainVol_res", "retroHP", "retroHP_res", "EC_res", "Fibers_res", "DG_res", "FD_res", "Hilus_res",
"CA2.3_res", "CA3_res", "CA2_res", "CA1_res", "Sub_res")
cor.data <- dplyr::select(HP$data, one_of(cor.vars)) %>% na.omit()

# Non-phylogenetic cors
cor <- Hmisc::rcorr(as.matrix(cor.data), type="pearson")
cor.matrix <- cor$r
cor.p <- cor$P
#cor.test(plot.data$CA3_res, plot.data$CA1_res)

# Phylogenetic cors
## For some reason can't add PCs this...

cor.phylo <- corphylo(X=cor.data, phy=HP$phy)
cor.phylo.matrix <- cor.phylo$cor.matrix
colnames(cor.phylo.matrix) <- colnames(cor.data)
row.names(cor.phylo.matrix) <- colnames(cor.data)
cor.phylo.matrix

# Mantel test: See if non-phylo and phylo corr matrices are sig different
mantel.test(cor.matrix, cor.phylo.matrix, graph=T, nperm = 10000)

# Plot corr matrices
# Non-phylo
#corrplot(cor.matrix, method="circle", order="hclust", addrect=3, tl.col="black", p.mat=cor.p, insig="blank", sig.level=0.05)
corrplot.mixed(cor.matrix, order="original", addrect=3, tl.col="black", p.mat=cor.p,
insig="blank", sig.level=0.05, upper="square", lower="number", tl.pos="lt", diag="u", tl.srt=45)

# Phylo
# Need to get p-val matrix for phylocor, how?...
#corrplot(cor.phylo.matrix, method="circle", order="hclust", addrect=3, tl.col="black")
corrplot.mixed(cor.phylo.matrix, order="original", addrect=3, tl.col="black",
upper="square", lower="number", tl.pos="lt", diag="u", tl.srt=45)

```

Selective Regime Analysis

|lou Function

- Is AICc the right model for convergence detection?
- Try HPeco analyses

[Hide](#)

```

# Parallelize to speed up
# nCores <- parallel::detectCores()
# ?llou:::plot.llou

#install_github("khabbazian/llou")
llou <- function(tree, dat, model="pBIC", abbrev_species=F, multi=F){

  # Shorten species names
  if (abbrev_species==T){
    abbrevSpecies <- function(spNames) {
      species <- lapply(strsplit(spNames, "_"), `[^`, 2)
      genusAbrv <- substr(spNames, 1, 1)
      abrvNames <- paste(paste(genusAbrv,".",sep=""), species, sep="_")
      return(abrvNames)
    }
    rownames(dat) <- abbrevSpecies(rownames(dat))
    tree$tip.label <- abbrevSpecies(tree$tip.label)
  }

  #Selective regime analysis
  ## Make species in tree and data the same order
  tree.dat <- adjust_data(tree, dat)
  Y <- tree.dat$Y
  # # Conduct main anaylsis
  # #### ***** Setting the nCores argument creates an error in the next step!
  # eModel <- estimate_shift_configuration(tree.dat$tree, tree.dat$Y)#
  # nCores = nCores
  # ## Compute the information criterion score for a given configuration
  # config_IC <- configuration_ic(tree.dat$tree, eModel$Y, eModel$shift.configuration,
  #                                 criterion=paste(model))
  #
  #
  ## building llou object out of the second best score
  # eModel2 = configuration_ic(eModel$tree, eModel$Y, eModel$profile$configurations[[2]],
  # fit.OU.model=TRUE, llou.options=eModel$llou.options)
  # eModel2_plot <- plot(eModel2, edge.width=3); eModel2_plot

  #Convergence
  ## first fit a model to find individual shifts (no convergence assumed):
  fit_ind <- estimate_shift_configuration(tree, Y, criterion="AICc", nCores=4)
  ## then detect which of these shifts are convergent:
  fit_conv <- estimate_convergent_regimes(fit_ind, criterion="AICc", nCores=4)

  # Plot
  #par(mar=c(2,2,2,2))
  if (multi==F){
    fitconv_plot <- llou:::plot.llou(model = fit_conv, edge.width=3)
  } else {
    fitconv_plot <- llou:::plot.llou(model = fit_conv, cex=1, edge.width=3,
                                      edge.ann.cex = 1.1, edge.shift.adj = 1.2, label.offset=0.02)
  }

  # edge.label.pos = 1, x.lim=c(15,1)
  fitconv_plot

  output <- list(tree.dat=tree.dat, #config_IC=config_IC,
                 # eModel2=eModel2, eModel2_plot=eModel2_plot,
                 fit_ind=fit_ind, fit_conv=fit_conv, fitconv_plot=fitconv_plot)
  return(output)
}

## Fix tree for llou
tree <- force.ultrametric(HP$phy)
is.ultrametric(tree)

## [1] TRUE

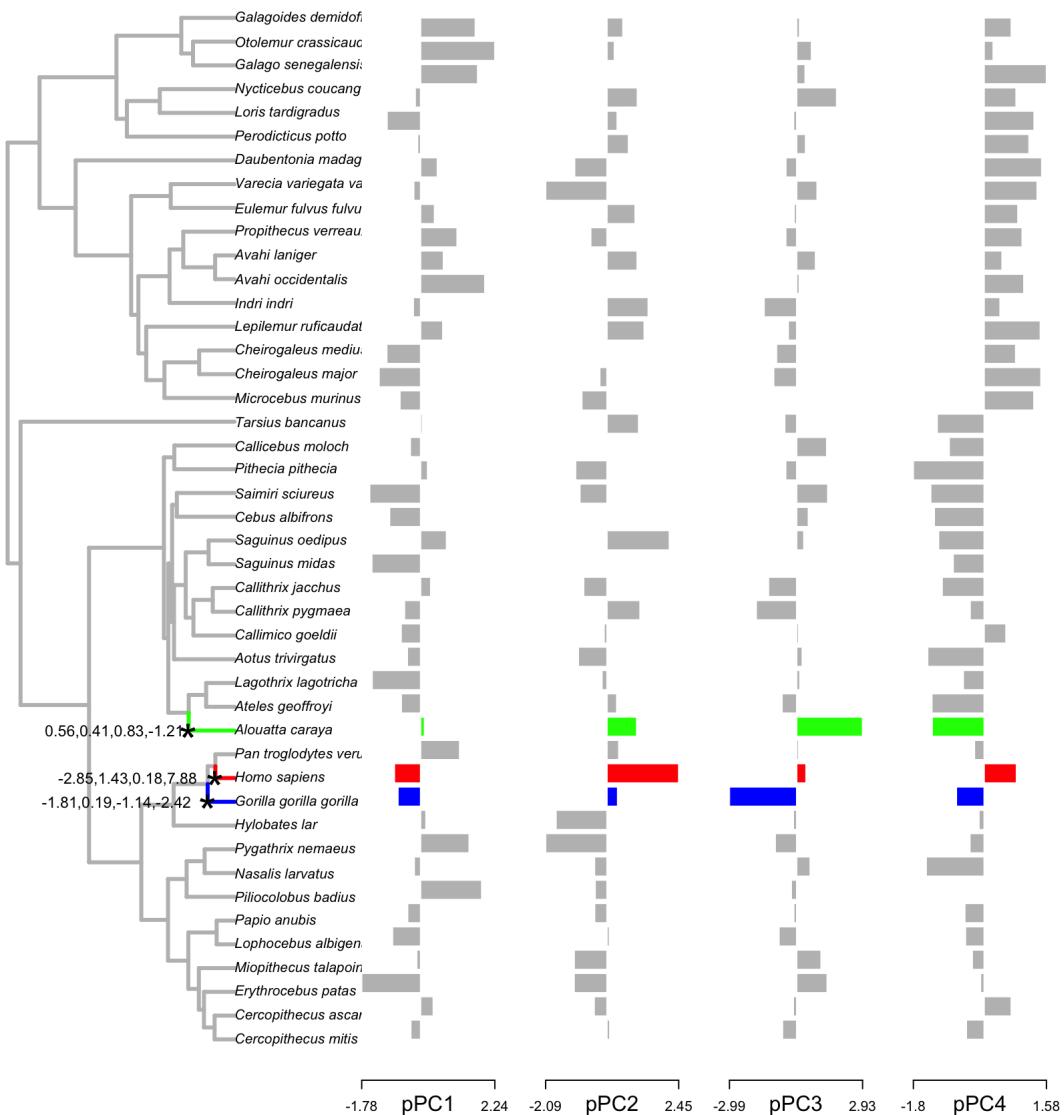
```

llou: Multivariate Analyses

Hide

```
pcDF <- phy.PCA$[,1:4]
colnames(pcDF) <- paste("p",colnames(pcDF), sep="")
PCs1_4.pBIC <- l1ou(tree, dat=pcDF, model="pBIC", multi=T)
```

```
## the new tree is normalized: each tip at distance 1 from the root.
## Starting first LASSO (alpha=0) to find a list of candidate configurations.
## Starting second LASSO (alpha= 0.04 0.12 0.1 0.01 ) for another list of candidates.
```



Individual Subregions

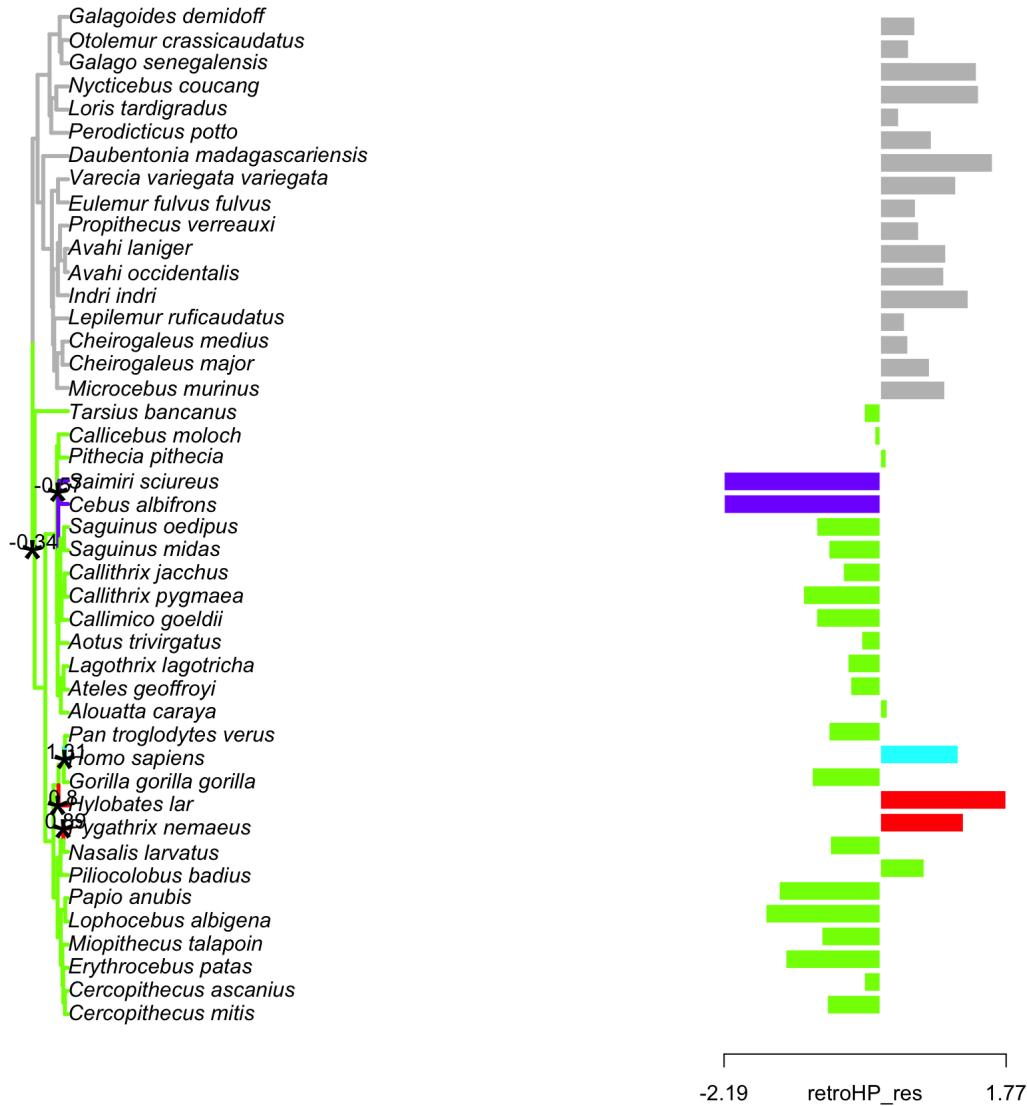
|l1ou: HPres |l1ou: EC_res |l1ou: Fibers_res |l1ou: DG/FD/Hilus_res |l1ou: CA2.3/2/3_res |l1ou: CA1_res |l1ou: Sub_res

|l1ou: Ecological Variables

Hide

```
#out.extra='style="margin: 200px"'
# fig.height=9, fig.width=9
HPres.pBIC <- l1ou(tree, dat=dplyr::select(plot.alldata,retroHP_res), model="pBIC")
```

```
## the new tree is normalized: each tip at distance 1 from the root.
## new Y: matrix of size 44 x 1
## Starting first LASSO (alpha=0) to find a list of candidate configurations.
## Starting second LASSO (alpha= 0.07 ) for another list of candidates.
```



Tests

Node ages

Hide

```
t <- tree
plot(t)

node.nums <- cbind(t$tip.label, t$node.label)
nodes <- round(heights(t)$start,2) #node.height()
names(nodes) <- nodes
tr <- makeNodeLabel(t, method = "user", nodeList = nodes)
plot(tr, show.node.label = T)

plot.phylo(t, show.node.label = F)
nodelabels(round(heights(t)$start,2))

plotTree.wBars(t)

# Export as nexus and then open in FigTree to get node ages
write.nexus(tree,file="primate_tree.nex")
```

Draw HC Network

[Hide](#)

```
species <- "Homo_sapiens"

n <- dplyr::select(HP$data, BrainVol_res, EC, FD, Hilus, CA3, CA2, CA1, Sub)
n$BrainVol_res <- scales::rescale(n$BrainVol_res, c(1, 150)) # Scale Brain_res
n$Species <- row.names(n)
n$Clade <- HP$data$Clade
n <- dplyr::filter(n, Species==paste(species)) # Select species
library(reshape2); library(dplyr)
melt.nodez <- melt(n, id.vars=c("Species", "Clade"), measure.vars=
  c("BrainVol_res", "EC", "FD", "Hilus", "CA3", "CA2", "CA1", "Sub"),
  variable.name="Region", value.name="Size") %>%
dplyr::select(Region, Size)

melt.nodez[2:8, "Size"] <- scales::rescale(melt.nodez[2:8, "Size"]) / sum(melt.nodez[2:8, "Size"]), c(1, 100))
nodes <- melt.nodez

links <- rbind(data.frame(from="BrainVol_res", to="EC"),
  data.frame(from="EC", to="BrainVol_res"),
  data.frame(from="EC", to="FD"),
  data.frame(from="FD", to="Hilus"),
  data.frame(from="Hilus", to="CA3"),
  data.frame(from="CA3", to="CA2"),
  data.frame(from="CA2", to="CA1"),
  data.frame(from="CA1", to="Sub"),
  data.frame(from="Sub", to="EC"))

library(igraph)
net <- graph_from_data_frame(d=links, vertices=nodes, directed=T)
net

E(net)      # The edges of the "net" object
V(net)$Size  # The vertices of the "net" object
E(net)$Width <- c(V(net)$Size[1], V(net)$Size)
library(RColorBrewer)
V(net)$colors <- rainbow(length(V(net)), alpha=.5) #brewer.pal(length(V(net)), "Paired")

rbPal <- colorRampPalette(c('grey', 'green'))
E(net)$colors <- rbPal(10)[as.numeric(cut(E(net)$Width, breaks = 9))]

plot(net, vertex.shape="circle", vertex.label.dist=2, vertex.size= V(net)$Size,
  vertex.color=V(net)$colors,
  edge.width=E(net)$Width/4, edge.arrow.size=E(net)$Width/100,
  edge.curved=0.3, edge.color=E(net)$colors,
  layout=layout_with_fr(net), main=paste("Hippocampal Complex Network:", species))
```

Interactive Plots

[Hide](#)

```
tkid <- tkplot(net) #tkid is the id of the tkplot that will open
l <- tkplot.getcoords(tkid) # grab the coordinates from tkplot
plot(net, edge.arrow.size=.4, vertex.shape="circle",
  # vertex.size= V(net)$Size, edge.width=V(net)$Size/5, edge.curved=.1,
  # vertex.color=V(net)$color, vertex.label.dist=2, layout=l)

library(visNetwork)
visNetwork(nodes, links, width="100%", height="400px", main=paste("Hippocampal Complex Network:", species))

nodes$shape <- "dot"
nodes$shadow <- TRUE # Nodes will drop shadow
nodes$title <- nodes$Region # Text on click
nodes$label <- nodes$Region # Node label
nodes$size <- nodes$Size # Node size
nodes$borderWidth <- 2 # Node border width

nodes$color.background <- c("slategrey", "tomato", "gold")[nodes$media.type]
nodes$color.border <- "black"
nodes$color.highlight.background <- "orange"
nodes$color.highlight.border <- "darkred"

visNetwork(nodes, links)
```

Save Results

Save the updated data in a new table

[Hide](#)

```
createDT(HP$data, caption = "Complete Data", save = "HP_eco_full_results", scrollY = F)
```

[Copy](#) [CSV](#) [Excel](#) [PDF](#) [Print](#)

Search:

Complete Data

	Species_David	Sub	CA1	CA2	CA3	Hilus	FD	Body_Size	HippocampusTotal
Cercopithecus_ascanius	Cercopithecus_ascanius	77.57	362.05	23.02	240.6	85.7	150.46	3400	1189
Cercopithecus_mitis	Cercopithecus_mitis	77.48	378.84	30.44	288.47	86.05	125.58	6300	1366.39
Erythrocebus_patas	Erythrocebus_patas	76.65	345.54	39.46	327.74	101.09	195.13	7800	1590.53
Miopithecus_talapoin	Miopithecus_talapoin	41.31	183.4	15.31	134.6	51.91	87.59	1200	704.87
Avahi_laniger	Avahi_laniger	48.13	178.89	15.29	112.49	24.93	78.82	1285	526.25
Avahi_occidentalis	Avahi_occidentalis	41.61	175.41	9.13	90.39	30.86	72.03	860	475.58
Cheirogaleus_major	Cheirogaleus_major	18.9	107.42	8.32	92.66	13.22	61.26	450	347.35
Cheirogaleus_medium	Cheirogaleus_medium	9.97	54.4	4.72	44.89	6.19	30.44	177	174.36
Daubentonia_madagascariensis	Daubentonia_madagascariensis	100.01	577.11	35.54	316.55	94.14	324.55	2800	1776.1
Eulemur_fulvus_fulvus	Eulemur_fulvus_fulvus	62.23	258.65	19.52	171.72	37.46	106.06	1400	752.1

Showing 1 to 10 of 44 entries

Previous

[1](#)

[2](#)

[3](#)

[4](#)

[5](#)

Next