Growth & Development in Primates

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Descriptive Statistics

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.2.3
```

```
## Warning: package 'ggplot2' was built under R version 4.2.3
```

```
## Warning: package 'tibble' was built under R version 4.2.3
```

```
## Warning: package 'tidyr' was built under R version 4.2.3
```

```
## Warning: package 'readr' was built under R version 4.2.3
```

```
## Warning: package 'purrr' was built under R version 4.2.3
```

```
## Warning: package 'dplyr' was built under R version 4.2.3
```

```
## Warning: package 'stringr' was built under R version 4.2.3
```

```
## Warning: package 'forcats' was built under R version 4.2.3
```

```
## Warning: package 'lubridate' was built under R version 4.2.3
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.1     v readr     2.1.4
## v forcats   1.0.0     v stringr   1.5.0
## v ggplot2   3.4.2     v tibble    3.2.1
## v lubridate 1.9.2     v tidyr     1.3.0
## v purrr     1.0.1
## -- Conflicts ------------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(ggplot2)
library(Hmisc)
```

```
## Warning: package 'Hmisc' was built under R version 4.2.3
```

```
##
## Attaching package: 'Hmisc'
##
## The following objects are masked from 'package:dplyr':
##
##     src, summarize
##
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
library(dplyr)
library(forcats)

# Load data
df_tissue <- read.csv("C:/Users/ktuos/Downloads/df_wide_tissue.csv")

df_ID <- read.csv("C:/Users/ktuos/OneDrive/Desktop/Tissue_ID.csv")

# Merge data

df  <- merge(df_ID, df_tissue, by = 'ID')
```

Examine structure of df

```
# Check df structure

str(df)
```

```
## 'data.frame':    82 obs. of  43 variables:
##  $ ID          : chr  "101" "11" "13" "14" ...
##  $ GENUS       : chr  "chlorocebus" "chlorocebus" "chlorocebus" "chlorocebus" ...
##  $ SEX         : chr  "M" "F" "M" "F" ...
##  $ AGE         : chr  "M3" "M1" "M3" "M3" ...
##  $ LENGTH..mm. : num  129.7 89.2 126.5 120.7 113 ...
##  $ Pixel_C.Ar  : int  1224744 641657 1301092 985308 1158326 1121248 1804662 647860 1020257 508195
##  $ Pixel_ECCC  : int  0 0 45373 52255 14168 6598 122073 0 14852 0 ...
##  $ Pixel_ELAM  : int  218250 659 18281 376 29392 1384 124163 17696 10188 1944 ...
##  $ Pixel_EPF   : int  0 0 0 0 0 0 0 962 3671 0 ...
##  $ Pixel_EPF.LAM : int  3508 2447 14364 10107 2592 7387 86510 21818 20274 9314 ...
##  $ Pixel_FLC   : int  0 0 0 0 0 0 0 0 0 3397 ...
##  $ Pixel_FLC.LZPO: int  3512 5546 0 3721 1846 0 0 69567 907 158362 ...
##  $ Pixel_HAV   : int  101630 38259 167289 73937 47126 63140 404409 81756 83675 12447 ...
##  $ Pixel_INT   : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
##  $ Pixel_LAM    : int  854922 497230 981041 775986 969959 1003419 984309 358844 793927 227744 ...
##  $ Pixel_PF     : int  0 2351 4295 0 0 0 2222 1017 1195 0 ...
##  $ Pixel_PF.LAM : int  7020 39483 23079 10729 4843 0 3175 30232 40593 59609 ...
##  $ Pixel_SF     : int  35902 55682 47370 58197 88400 39320 77801 65968 50975 35378 ...
##  $ Pixel_WOV    : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ C.Ar_C.Ar    : int  100 100 100 100 100 100 100 100 100 100 ...
##  $ C.Ar_ECCC    : num  0 0 3.49 5.3 1.22 ...
##  $ C.Ar_ELAM    : num  17.8201 0.1027 1.4051 0.0382 2.5375 ...
##  $ C.Ar_EPF     : num  0 0 0 0 0 ...
##  $ C.Ar_EPF.LAM : num  0.286 0.381 1.104 1.026 0.224 ...
##  $ C.Ar_FLC     : num  0 0 0 0 0 ...
##  $ C.Ar_FLC.LZPO : num  0.287 0.864 0 0.378 0.159 ...
##  $ C.Ar_HAV     : num  8.3 5.96 12.86 7.5 4.07 ...
##  $ C.Ar_INT     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ C.Ar_LAM     : num  69.8 77.5 75.4 78.8 83.7 ...
##  $ C.Ar_PF      : num  0 0.366 0.33 0 0 ...
##  $ C.Ar_PF.LAM  : num  0.573 6.153 1.774 1.089 0.418 ...
##  $ C.Ar_SF      : num  2.93 8.68 3.64 5.91 7.63 ...
##  $ C.Ar_WOV     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ P.Ar_FLC     : num  0 0 0 0 0 ...
##  $ P.Ar_FLC.LZPO : num  0.406 1.018 0 0.471 0.189 ...
##  $ P.Ar_LAM     : num  98.8 91.3 97.3 98.2 99.3 ...
##  $ P.Ar_PF      : num  0 0.432 0.426 0 0 ...
##  $ P.Ar_PF.LAM  : num  0.811 7.25 2.289 1.357 0.496 ...
##  $ P.Ar_WOV     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ E.Ar_ECCC    : num  0 0 58.2 83.3 30.7 ...
##  $ E.Ar_ELAM    : num  98.418 21.217 23.432 0.599 63.685 ...
##  $ E.Ar_EPF     : num  0 0 0 0 0 ...
##  $ E.Ar_EPF.LAM : num  1.58 78.78 18.41 16.11 5.62 ...
```

```r
# Convert GENUS, SEX, and AGE into factors

df$GENUS <- factor(df$GENUS, level = c("chlorocebus", "hylobates", "pan", "gorilla"))

df$SEX <- as.factor(df$SEX)
df$AGE <- factor(df$AGE, levels = c("DECID", "M1", "M2", "M3", "EPIPH"))

# Drop pixel count variables and Percent.C.Ar

df2 <- df[,-5:-20]

str(df2)
```

```
## 'data.frame':    82 obs. of  27 variables:
##  $ ID           : chr  "101" "11" "13" "14" ...
##  $ GENUS        : Factor w/ 4 levels "chlorocebus",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ SEX          : Factor w/ 3 levels "F","M","U": 2 1 2 1 1 1 2 1 1 2 ...
##  $ AGE          : Factor w/ 5 levels "DECID","M1","M2",..: 4 2 4 4 4 5 5 2 5 1 ...
##  $ C.Ar_ECCC    : num  0 0 3.49 5.3 1.22 ...
##  $ C.Ar_ELAM    : num  17.8201 0.1027 1.4051 0.0382 2.5375 ...
##  $ C.Ar_EPF     : num  0 0 0 0 0 ...
##  $ C.Ar_EPF.LAM : num  0.286 0.381 1.104 1.026 0.224 ...
##  $ C.Ar_FLC     : num  0 0 0 0 0 ...
##  $ C.Ar_FLC.LZPO: num  0.287 0.864 0 0.378 0.159 ...
```

3

```
##  $ C.Ar_HAV     : num  8.3 5.96 12.86 7.5 4.07 ...
##  $ C.Ar_INT     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ C.Ar_LAM     : num  69.8 77.5 75.4 78.8 83.7 ...
##  $ C.Ar_PF      : num  0 0.366 0.33 0 0 ...
##  $ C.Ar_PF.LAM  : num  0.573 6.153 1.774 1.089 0.418 ...
##  $ C.Ar_SF      : num  2.93 8.68 3.64 5.91 7.63 ...
##  $ C.Ar_WOV     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ P.Ar_FLC     : num  0 0 0 0 0 ...
##  $ P.Ar_FLC.LZPO: num  0.406 1.018 0 0.471 0.189 ...
##  $ P.Ar_LAM     : num  98.8 91.3 97.3 98.2 99.3 ...
##  $ P.Ar_PF      : num  0 0.432 0.426 0 0 ...
##  $ P.Ar_PF.LAM  : num  0.811 7.25 2.289 1.357 0.496 ...
##  $ P.Ar_WOV     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ E.Ar_ECCC    : num  0 0 58.2 83.3 30.7 ...
##  $ E.Ar_ELAM    : num  98.418 21.217 23.432 0.599 63.685 ...
##  $ E.Ar_EPF     : num  0 0 0 0 0 ...
##  $ E.Ar_EPF.LAM : num  1.58 78.78 18.41 16.11 5.62 ...
```

Check df structure again

```
# Check df structure
```

```
str(df2)
```

```
## 'data.frame':    82 obs. of  27 variables:
##  $ ID           : chr  "101" "11" "13" "14" ...
##  $ GENUS        : Factor w/ 4 levels "chlorocebus",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ SEX          : Factor w/ 3 levels "F","M","U": 2 1 2 1 1 1 2 1 1 2 ...
##  $ AGE          : Factor w/ 5 levels "DECID","M1","M2",..: 4 2 4 4 4 5 5 2 5 1 ...
##  $ C.Ar_ECCC    : num  0 0 3.49 5.3 1.22 ...
##  $ C.Ar_ELAM    : num  17.8201 0.1027 1.4051 0.0382 2.5375 ...
##  $ C.Ar_EPF     : num  0 0 0 0 0 ...
##  $ C.Ar_EPF.LAM : num  0.286 0.381 1.104 1.026 0.224 ...
##  $ C.Ar_FLC     : num  0 0 0 0 0 ...
##  $ C.Ar_FLC.LZPO: num  0.287 0.864 0 0.378 0.159 ...
##  $ C.Ar_HAV     : num  8.3 5.96 12.86 7.5 4.07 ...
##  $ C.Ar_INT     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ C.Ar_LAM     : num  69.8 77.5 75.4 78.8 83.7 ...
##  $ C.Ar_PF      : num  0 0.366 0.33 0 0 ...
##  $ C.Ar_PF.LAM  : num  0.573 6.153 1.774 1.089 0.418 ...
##  $ C.Ar_SF      : num  2.93 8.68 3.64 5.91 7.63 ...
##  $ C.Ar_WOV     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ P.Ar_FLC     : num  0 0 0 0 0 ...
##  $ P.Ar_FLC.LZPO: num  0.406 1.018 0 0.471 0.189 ...
##  $ P.Ar_LAM     : num  98.8 91.3 97.3 98.2 99.3 ...
##  $ P.Ar_PF      : num  0 0.432 0.426 0 0 ...
##  $ P.Ar_PF.LAM  : num  0.811 7.25 2.289 1.357 0.496 ...
##  $ P.Ar_WOV     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ E.Ar_ECCC    : num  0 0 58.2 83.3 30.7 ...
##  $ E.Ar_ELAM    : num  98.418 21.217 23.432 0.599 63.685 ...
##  $ E.Ar_EPF     : num  0 0 0 0 0 ...
##  $ E.Ar_EPF.LAM : num  1.58 78.78 18.41 16.11 5.62 ...
```

Descriptive statistics by GENUS

```
by(df2, df$GENUS, summary)
```

```
## df$GENUS: chlorocebus
##       ID                  GENUS     SEX        AGE        C.Ar_ECCC
##  Length:30          chlorocebus:30   F:14   DECID:5    Min.   :0.0000
##  Class :character   hylobates  : 0   M:16   M1   :5    1st Qu.:0.0000
##  Mode  :character   pan        : 0   U: 0   M2   :6    Median :0.9229
##                     gorilla    : 0          M3   :8    Mean   :2.1989
##                                             EPIPH:6    3rd Qu.:3.4689
##                                                        Max.   :9.3229
##
##    C.Ar_ELAM          C.Ar_EPF         C.Ar_EPF.LAM        C.Ar_FLC
##  Min.   : 0.0000   Min.   :0.00000   Min.   :0.0000   Min.   : 0.000
##  1st Qu.: 0.1306   1st Qu.:0.00000   1st Qu.:0.3102   1st Qu.: 0.000
##  Median : 0.8814   Median :0.00000   Median :1.0163   Median : 0.000
##  Mean   : 1.9713   Mean   :0.07825   Mean   :1.5850   Mean   : 1.294
##  3rd Qu.: 2.0742   3rd Qu.:0.08574   3rd Qu.:1.9715   3rd Qu.: 0.000
##  Max.   :17.8201   Max.   :0.74543   Max.   :7.2874   Max.   :20.362
##
##  C.Ar_FLC.LZPO         C.Ar_HAV          C.Ar_INT    C.Ar_LAM
##  Min.   : 0.00000   Min.   : 0.000   Min.   :0    Min.   : 0.00
##  1st Qu.: 0.02222   1st Qu.: 4.041   1st Qu.:0    1st Qu.:60.19
##  Median : 0.55944   Median : 8.250   Median :0    Median :71.99
##  Mean   : 7.98325   Mean   : 7.671   Mean   :0    Mean   :65.02
##  3rd Qu.: 2.27902   3rd Qu.:10.259   3rd Qu.:0    3rd Qu.:80.47
##  Max.   :61.90831   Max.   :22.409   Max.   :0    Max.   :90.11
##
##     C.Ar_PF         C.Ar_PF.LAM         C.Ar_SF          C.Ar_WOV
##  Min.   : 0.0000   Min.   : 0.0000   Min.   : 2.931   Min.   :0
##  1st Qu.: 0.0000   1st Qu.: 0.1927   1st Qu.: 4.563   1st Qu.:0
##  Median : 0.0000   Median : 1.4314   Median : 6.778   Median :0
##  Mean   : 0.6443   Mean   : 4.2660   Mean   : 7.285   Mean   :0
##  3rd Qu.: 0.3269   3rd Qu.: 6.6660   3rd Qu.: 9.774   3rd Qu.:0
##  Max.   :10.5376   Max.   :28.4687   Max.   :14.373   Max.   :0
##
##     P.Ar_FLC        P.Ar_FLC.LZPO        P.Ar_LAM          P.Ar_PF
##  Min.   : 0.000   Min.   : 0.0000   Min.   :  0.00   Min.   : 0.0000
##  1st Qu.: 0.000   1st Qu.: 0.0271   1st Qu.: 83.45   1st Qu.: 0.0000
##  Median : 0.000   Median : 0.6468   Median : 97.38   Median : 0.0000
##  Mean   : 1.445   Mean   : 9.3202   Mean   : 83.35   Mean   : 0.7579
##  3rd Qu.: 0.000   3rd Qu.: 3.0287   3rd Qu.: 99.30   3rd Qu.: 0.4153
##  Max.   :22.912   Max.   :74.8187   Max.   :100.00   Max.   :11.8576
##
##   P.Ar_PF.LAM         P.Ar_WOV    E.Ar_ECCC          E.Ar_ELAM
##  Min.   : 0.0000   Min.   :0    Min.   : 0.00   Min.   : 0.00
##  1st Qu.: 0.2805   1st Qu.:0    1st Qu.: 0.00   1st Qu.:10.33
##  Median : 1.8230   Median :0    Median :37.44   Median :21.84
##  Mean   : 5.1230   Mean   :0    Mean   :31.61   Mean   :30.21
##  3rd Qu.: 8.0095   3rd Qu.:0    3rd Qu.:50.83   3rd Qu.:40.65
##  Max.   :32.0348   Max.   :0    Max.   :83.29   Max.   :99.43
```

```
##                                 NA's   :2         NA's   :2
##     E.Ar_EPF        E.Ar_EPF.LAM
##  Min.   :  0.000   Min.   : 0.00
##  1st Qu.:  0.000   1st Qu.:16.57
##  Median :  0.000   Median :28.41
##  Mean   :  5.361   Mean   :32.82
##  3rd Qu.:  2.414   3rd Qu.:48.18
##  Max.   :100.000   Max.   :94.02
##  NA's   :2         NA's   :2
## --------------------------------------------------------------
## df$GENUS: hylobates
##      ID               GENUS       SEX       AGE       C.Ar_ECCC
##  Length:27         chlorocebus: 0   F:12   DECID:4   Min.   :0.00000
##  Class :character  hylobates  :27   M:15   M1   :3   1st Qu.:0.00000
##  Mode  :character  pan        : 0   U: 0   M2   :5   Median :0.03014
##                    gorilla    : 0          M3   :9   Mean   :0.28498
##                                            EPIPH:6   3rd Qu.:0.18219
##                                                      Max.   :3.85941
##     C.Ar_ELAM         C.Ar_EPF        C.Ar_EPF.LAM        C.Ar_FLC
##  Min.   : 0.04173  Min.   :0.000   Min.   : 0.00000   Min.   :0.00000
##  1st Qu.: 2.29681  1st Qu.:0.000   1st Qu.: 0.02175   1st Qu.:0.00000
##  Median : 3.20296  Median :0.000   Median : 0.26242   Median :0.00000
##  Mean   : 4.27919  Mean   :0.109   Mean   : 1.41175   Mean   :0.07192
##  3rd Qu.: 5.22262  3rd Qu.:0.000   3rd Qu.: 1.08646   3rd Qu.:0.00000
##  Max.   :21.33671  Max.   :1.255   Max.   :10.36260   Max.   :1.63126
##  C.Ar_FLC.LZPO     C.Ar_HAV        C.Ar_INT           C.Ar_LAM
##  Min.   :0.0000  Min.   :25.49   Min.   :0.000000   Min.   : 5.619
##  1st Qu.:0.0000  1st Qu.:33.25   1st Qu.:0.005712   1st Qu.:29.676
##  Median :0.3425  Median :37.39   Median :0.034601   Median :47.169
##  Mean   :1.2994  Mean   :38.59   Mean   :0.082563   Mean   :42.454
##  3rd Qu.:1.0135  3rd Qu.:45.15   3rd Qu.:0.056785   3rd Qu.:57.189
##  Max.   :8.7175  Max.   :56.97   Max.   :0.662440   Max.   :67.912
##     C.Ar_PF          C.Ar_PF.LAM        C.Ar_SF          C.Ar_WOV
##  Min.   : 0.0000  Min.   : 0.2055   Min.   :0.685   Min.   :0
##  1st Qu.: 0.0000  1st Qu.: 1.0661   1st Qu.:1.672   1st Qu.:0
##  Median : 0.0000  Median : 2.9025   Median :2.338   Median :0
##  Mean   : 1.6441  Mean   : 7.0403   Mean   :2.732   Mean   :0
##  3rd Qu.: 0.2213  3rd Qu.:14.0816   3rd Qu.:2.823   3rd Qu.:0
##  Max.   :18.1982  Max.   :20.0758   Max.   :6.872   Max.   :0
##     P.Ar_FLC        P.Ar_FLC.LZPO      P.Ar_LAM          P.Ar_PF
##  Min.   :0.0000   Min.   : 0.0000   Min.   :13.94   Min.   : 0.0000
##  1st Qu.:0.0000   1st Qu.: 0.0000   1st Qu.:63.16   1st Qu.: 0.0000
##  Median :0.0000   Median : 0.5455   Median :94.20   Median : 0.0000
##  Mean   :0.1239   Mean   : 2.9208   Mean   :77.10   Mean   : 3.9784
##  3rd Qu.:0.0000   3rd Qu.: 2.1714   3rd Qu.:97.59   3rd Qu.: 0.4385
##  Max.   :2.4007   Max.   :21.6320   Max.   :99.58   Max.   :35.7555
##   P.Ar_PF.LAM       P.Ar_WOV    E.Ar_ECCC         E.Ar_ELAM
##  Min.   : 0.3632  Min.   :0   Min.   : 0.000   Min.   : 18.17
##  1st Qu.: 2.0073  1st Qu.:0   1st Qu.: 0.000   1st Qu.: 73.52
##  Median : 5.6051  Median :0   Median : 1.018   Median : 90.66
##  Mean   :15.8728  Mean   :0   Mean   : 3.368   Mean   : 80.19
##  3rd Qu.:29.4622  3rd Qu.:0   3rd Qu.: 2.342   3rd Qu.: 98.04
##  Max.   :61.1103  Max.   :0   Max.   :34.859   Max.   :100.00
##     E.Ar_EPF        E.Ar_EPF.LAM
```

```
##  Min.   : 0.0000   Min.    : 0.0000
##  1st Qu.: 0.0000   1st Qu.: 0.6114
##  Median : 0.0000   Median : 9.3399
##  Mean   : 0.7741   Mean   :15.6712
##  3rd Qu.: 0.0000   3rd Qu.:25.8017
##  Max.   :12.3389   Max.   :54.5535
## ------------------------------------------------------------
## df$GENUS: pan
##      ID                  GENUS      SEX      AGE      C.Ar_ECCC
##  Length:12        chlorocebus: 0   F:4   DECID:2   Min.   :0.0000
##  Class :character hylobates  : 0   M:2   M1   :1   1st Qu.:0.0000
##  Mode  :character pan        :12   U:6   M2   :4   Median :0.2410
##                   gorilla    : 0         M3   :3   Mean   :0.5348
##                                          EPIPH:2   3rd Qu.:0.7035
##                                                    Max.   :2.7815
##    C.Ar_ELAM          C.Ar_EPF         C.Ar_EPF.LAM        C.Ar_FLC
##  Min.   :0.0000   Min.   :0.00000   Min.   :0.09269   Min.   :0.0000
##  1st Qu.:0.3089   1st Qu.:0.00000   1st Qu.:0.24950   1st Qu.:0.0000
##  Median :0.6119   Median :0.01428   Median :1.01113   Median :0.0000
##  Mean   :1.1372   Mean   :0.44646   Mean   :1.38940   Mean   :0.1754
##  3rd Qu.:1.6864   3rd Qu.:0.17748   3rd Qu.:1.90048   3rd Qu.:0.0000
##  Max.   :4.3057   Max.   :4.07886   Max.   :4.29542   Max.   :1.6045
##  C.Ar_FLC.LZPO       C.Ar_HAV         C.Ar_INT          C.Ar_LAM
##  Min.   : 0.06919   Min.   :37.72   Min.   :0.00000   Min.   : 1.49
##  1st Qu.: 4.10445   1st Qu.:45.93   1st Qu.:0.04434   1st Qu.:19.35
##  Median : 6.51659   Median :53.52   Median :0.13739   Median :28.31
##  Mean   : 8.83554   Mean   :54.02   Mean   :0.14255   Mean   :27.66
##  3rd Qu.:14.42910   3rd Qu.:58.16   3rd Qu.:0.21339   3rd Qu.:36.66
##  Max.   :19.31842   Max.   :78.13   Max.   :0.31959   Max.   :54.04
##    C.Ar_PF          C.Ar_PF.LAM        C.Ar_SF           C.Ar_WOV
##  Min.   :0.0000   Min.   : 0.0000   Min.   :0.2136   Min.   :0
##  1st Qu.:0.0000   1st Qu.: 0.1628   1st Qu.:1.2635   1st Qu.:0
##  Median :0.0000   Median : 0.2225   Median :2.0921   Median :0
##  Mean   :0.8791   Mean   : 2.4496   Mean   :2.3271   Mean   :0
##  3rd Qu.:0.0000   3rd Qu.: 1.5175   3rd Qu.:2.9897   3rd Qu.:0
##  Max.   :8.8210   Max.   :17.9447   Max.   :5.6981   Max.   :0
##    P.Ar_FLC        P.Ar_FLC.LZPO       P.Ar_LAM          P.Ar_PF
##  Min.   :0.0000   Min.   : 0.2737   Min.   : 3.924   Min.   : 0.000
##  1st Qu.:0.0000   1st Qu.: 7.4961   1st Qu.:54.844   1st Qu.: 0.000
##  Median :0.0000   Median :19.3470   Median :79.154   Median : 0.000
##  Mean   :0.5624   Mean   :21.1635   Mean   :68.743   Mean   : 2.765
##  3rd Qu.:0.0000   3rd Qu.:31.3091   3rd Qu.:92.199   3rd Qu.: 0.000
##  Max.   :5.2078   Max.   :50.4456   Max.   :98.404   Max.   :28.631
##   P.Ar_PF.LAM        P.Ar_WOV    E.Ar_ECCC         E.Ar_ELAM
##  Min.   : 0.0000   Min.   :0   Min.   : 0.000   Min.   : 0.00
##  1st Qu.: 0.3882   1st Qu.:0   1st Qu.: 0.000   1st Qu.:25.94
##  Median : 0.8104   Median :0   Median : 9.253   Median :44.63
##  Mean   : 6.7657   Mean   :0   Mean   :15.434   Mean   :41.81
##  3rd Qu.: 3.7800   3rd Qu.:0   3rd Qu.:24.397   3rd Qu.:58.13
##  Max.   :47.2618   Max.   :0   Max.   :45.662   Max.   :86.07
##    E.Ar_EPF        E.Ar_EPF.LAM
##  Min.   : 0.000   Min.   : 9.432
##  1st Qu.: 0.000   1st Qu.:22.016
##  Median : 2.369   Median :34.173
```

```
##  Mean   : 7.520   Mean   :35.236
##  3rd Qu.: 6.898   3rd Qu.:44.919
##  Max.   :47.568   Max.    :84.677
## --------------------------------------------------------------
## df$GENUS: gorilla
##       ID                  GENUS      SEX      AGE        C.Ar_ECCC
##  Length:13        chlorocebus: 0    F:6    DECID:6   Min.   :0.0000
##  Class :character hylobates  : 0    M:7    M1   :5   1st Qu.:0.1979
##  Mode  :character pan        : 0    U:0    M2   :1   Median :1.2400
##                   gorilla    :13           M3   :0   Mean   :1.9015
##                                            EPIPH:1   3rd Qu.:2.4669
##                                                      Max.   :6.8015
##
##    C.Ar_ELAM         C.Ar_EPF          C.Ar_EPF.LAM       C.Ar_FLC
##  Min.   :0.0000   Min.   :0.00000   Min.   :0.000   Min.   : 0.0000
##  1st Qu.:0.7901   1st Qu.:0.03459   1st Qu.:2.254   1st Qu.: 0.5275
##  Median :2.0309   Median :0.27231   Median :2.663   Median : 1.0732
##  Mean   :1.8282   Mean   :0.46061   Mean   :3.348   Mean   :12.0096
##  3rd Qu.:2.7046   3rd Qu.:0.45965   3rd Qu.:4.051   3rd Qu.: 6.4893
##  Max.   :3.5638   Max.   :2.62287   Max.   :9.259   Max.   :80.0351
##
##  C.Ar_FLC.LZPO      C.Ar_HAV          C.Ar_INT          C.Ar_LAM
##  Min.   : 0.000   Min.   : 0.7467   Min.   :0.0000   Min.   : 0.000
##  1st Qu.: 6.682   1st Qu.:39.1317   1st Qu.:0.2266   1st Qu.: 0.000
##  Median :10.627   Median :56.2680   Median :0.4778   Median : 1.188
##  Mean   :11.305   Mean   :46.9643   Mean   :0.6712   Mean   : 3.803
##  3rd Qu.:13.299   3rd Qu.:60.0234   3rd Qu.:0.6725   3rd Qu.: 4.623
##  Max.   :26.648   Max.   :78.3484   Max.   :3.0295   Max.   :17.065
##
##     C.Ar_PF         C.Ar_PF.LAM        C.Ar_SF          C.Ar_WOV
##  Min.   : 0.2468  Min.   : 0.0000   Min.   :0.0000   Min.   : 0.0000
##  1st Qu.: 0.8057  1st Qu.: 0.4068   1st Qu.:0.0000   1st Qu.: 0.0000
##  Median : 3.5209  Median : 4.4674   Median :0.3002   Median : 0.0000
##  Mean   : 6.2115  Mean   : 4.4650   Mean   :1.0127   Mean   : 6.0194
##  3rd Qu.: 9.9755  3rd Qu.: 6.0300   3rd Qu.:1.7760   3rd Qu.: 0.4158
##  Max.   :17.5020  Max.   :13.7611   Max.   :3.6414   Max.   :55.5706
##
##     P.Ar_FLC        P.Ar_FLC.LZPO     P.Ar_LAM         P.Ar_PF
##  Min.   : 0.000   Min.   : 0.00    Min.   : 0.000   Min.   : 0.5243
##  1st Qu.: 1.364   1st Qu.:12.75    1st Qu.: 0.000   1st Qu.: 2.4332
##  Median : 3.319   Median :21.40    Median : 4.012   Median :10.8885
##  Mean   :16.700   Mean   :28.28    Mean   :15.173   Mean   :18.1784
##  3rd Qu.:20.462   3rd Qu.:41.13    3rd Qu.:13.961   3rd Qu.:24.5860
##  Max.   :86.606   Max.   :65.74    Max.   :85.332   Max.   :54.5269
##
##   P.Ar_PF.LAM        P.Ar_WOV         E.Ar_ECCC         E.Ar_ELAM
##  Min.   : 0.0000   Min.   : 0.000   Min.   : 2.769   Min.   : 0.000
##  1st Qu.: 0.8191   1st Qu.: 0.000   1st Qu.:11.962   1st Qu.: 9.168
##  Median :15.0803   Median : 0.000   Median :22.879   Median :29.283
##  Mean   :13.5572   Mean   : 8.113   Mean   :21.033   Mean   :27.676
##  3rd Qu.:22.0082   3rd Qu.: 1.311   3rd Qu.:29.031   3rd Qu.:33.761
##  Max.   :35.5724   Max.   :55.989   Max.   :45.512   Max.   :83.301
##                                     NA's   :1        NA's   :1
##     E.Ar_EPF          E.Ar_EPF.LAM
```

```
##  Min.   : 0.000   Min.   : 6.557
##  1st Qu.: 1.843   1st Qu.:38.654
##  Median : 4.654   Median :45.770
##  Mean   : 5.345   Mean   :45.946
##  3rd Qu.: 7.111   3rd Qu.:53.302
##  Max.   :13.935   Max.   :85.330
##  NA's   :1        NA's   :1
```

Descriptive statistics by GENUS and AGE

```r
# List of variables you want to summarize
vars_to_summarize <- colnames(df2[, sapply(df2, is.numeric)])

# Summarize by Genus and AGE
df_summary <- df2 %>%
  group_by(GENUS, AGE) %>%
  summarise_at(
    .vars = vars_to_summarize,
    .funs = list(mean = ~mean(., na.rm = TRUE),
                 sd = ~sd(., na.rm = TRUE),
                 min = ~min(., na.rm = TRUE),
                 max = ~max(., na.rm = TRUE),
                 count = ~sum(!is.na(.)))
  )

df_summary
```

```
## # A tibble: 19 x 117
## # Groups:   GENUS [4]
##    GENUS    AGE   C.Ar_~1 C.Ar_~2 C.Ar_~3 C.Ar_~4 C.Ar_~5 C.Ar_~6 C.Ar_~7 C.Ar_~8
##    <fct>    <fct>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
##  1 chloro~ DECID  0.134   0.257  5.22e-2    1.12    7.47    40.9    1.76  0
##  2 chloro~ M1     0       0.806  1.79e-1    1.45    0.293   5.34    6.20  0
##  3 chloro~ M2     3.21    0.663  1.23e-1    1.51    0       0.933   6.82  0
##  4 chloro~ M3     2.94    3.98   1.17e-2    1.42    0       0.196   9.98  0
##  5 chloro~ EPIPH  3.76    3.01   6.00e-2    2.38    0       0.150   11.6  0
##  6 hyloba~ DECID  1.17    8.82   5.93e-1    6.37    0.0776  2.45    42.4  0.248
##  7 hyloba~ M1     0.659   8.39   1.90e-1    2.27    0       6.28    40.6  0.207
##  8 hyloba~ M2     0.132   1.73   0          0.562   0.326   0.974   34.7  0.0226
##  9 hyloba~ M3     0.0298  3.50   0          0.183   0       0.166   37.4  0.0338
## 10 hyloba~ EPIPH  0.0216  2.49   1.10e-5    0.227   0       0.0106  40.2  0.0332
## 11 pan     DECID  0.513   0.00285 2.43e+0   3.88    0.802   12.3    56.7  0.103
## 12 pan     M1     0       1.90   1.77e-1    1.60    0       19.3    41.3  0.119
## 13 pan     M2     1.04    1.85   7.29e-2    1.57    0.125   12.2    51.5  0.182
## 14 pan     M3     0.319   0.374  8.88e-3    0.207   0       2.94    59.4  0.133
## 15 pan     EPIPH  0.135   1.60   5.86e-3    0.205   0       2.23    54.6  0.130
## 16 gorilla DECID  2.37    1.31   6.40e-1    3.68    24.5    13.9    30.9  0.382
## 17 gorilla M1     1.93    2.12   3.61e-1    3.58    1.75    12.4    57.4  1.07
## 18 gorilla M2     0.602   2.03   1.38e-1    3.32    0.259   1.82    60.0  0.673
## 19 gorilla EPIPH  0.198   3.28   2.01e-1    0.258   0       0       78.3  0.404
## # ... with 107 more variables: C.Ar_LAM_mean <dbl>, C.Ar_PF_mean <dbl>,
```

9

```
## #   C.Ar_PF.LAM_mean <dbl>, C.Ar_SF_mean <dbl>, C.Ar_WOV_mean <dbl>,
## #   P.Ar_FLC_mean <dbl>, P.Ar_FLC.LZPO_mean <dbl>, P.Ar_LAM_mean <dbl>,
## #   P.Ar_PF_mean <dbl>, P.Ar_PF.LAM_mean <dbl>, P.Ar_WOV_mean <dbl>,
## #   E.Ar_ECCC_mean <dbl>, E.Ar_ELAM_mean <dbl>, E.Ar_EPF_mean <dbl>,
## #   E.Ar_EPF.LAM_mean <dbl>, C.Ar_ECCC_sd <dbl>, C.Ar_ELAM_sd <dbl>,
## #   C.Ar_EPF_sd <dbl>, C.Ar_EPF.LAM_sd <dbl>, C.Ar_FLC_sd <dbl>, ...
```

Descriptive statistics by GENUS, AGE, and SEX

```r
# Summarize by Genus, AGE, and SEX
df_summary2 <- df2 %>%
  group_by(GENUS, AGE, SEX) %>%
  summarise_at(
    .vars = vars_to_summarize,
    .funs = list(mean = ~mean(., na.rm = TRUE),
                 sd = ~sd(., na.rm = TRUE),
                 min = ~min(., na.rm = TRUE),
                 max = ~max(., na.rm = TRUE),
                 count = ~sum(!is.na(.)))
  )

df_summary2
```

```
## # A tibble: 36 x 118
## # Groups:   GENUS, AGE [19]
##    GENUS     AGE    SEX   C.Ar_~1 C.Ar_~2 C.Ar_~3 C.Ar_~4 C.Ar_~5 C.Ar_~6 C.Ar_~7
##    <fct>     <fct>  <fct>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
##  1 chloroce~ DECID  F       0       0.214 0         3.36    0.350 20.4      2.21
##  2 chloroce~ DECID  M       0.167   0.267 0.0652    0.557   9.25  46.1      1.65
##  3 chloroce~ M1     F       0       0.776 0.223     1.46    0      4.03     7.48
##  4 chloroce~ M1     M       0       0.928 0         1.39    1.47  10.6      1.07
##  5 chloroce~ M2     F       5.52    1.32  0.120     3.16    0      1.22     9.44
##  6 chloroce~ M2     M       2.05    0.335 0.125     0.681   0      0.788    5.50
##  7 chloroce~ M3     F       4.08    2.34  0         2.13    0      0.134    6.62
##  8 chloroce~ M3     M       1.80    5.61  0.0233    0.713   0      0.257   13.3
##  9 chloroce~ EPIPH  F       2.31    1.00  0.120     1.48    0      0.0296   8.84
## 10 chloroce~ EPIPH  M       5.21    5.01  0         3.28    0      0.270   14.3
## # ... with 26 more rows, 108 more variables: C.Ar_INT_mean <dbl>,
## #   C.Ar_LAM_mean <dbl>, C.Ar_PF_mean <dbl>, C.Ar_PF.LAM_mean <dbl>,
## #   C.Ar_SF_mean <dbl>, C.Ar_WOV_mean <dbl>, P.Ar_FLC_mean <dbl>,
## #   P.Ar_FLC.LZPO_mean <dbl>, P.Ar_LAM_mean <dbl>, P.Ar_PF_mean <dbl>,
## #   P.Ar_PF.LAM_mean <dbl>, P.Ar_WOV_mean <dbl>, E.Ar_ECCC_mean <dbl>,
## #   E.Ar_ELAM_mean <dbl>, E.Ar_EPF_mean <dbl>, E.Ar_EPF.LAM_mean <dbl>,
## #   C.Ar_ECCC_sd <dbl>, C.Ar_ELAM_sd <dbl>, C.Ar_EPF_sd <dbl>, ...
```

Contingency table

```r
# GENUS
table(df2$GENUS)
```

```
## 
## chlorocebus   hylobates         pan     gorilla
##          30          27          12          13
```

```r
# GENUS & AGE
table(df2$GENUS, df2$AGE)
```

```
## 
##              DECID M1 M2 M3 EPIPH
##   chlorocebus     5  5  6  8     6
##   hylobates       4  3  5  9     6
##   pan             2  1  4  3     2
##   gorilla         6  5  1  0     1
```

```r
# GENUS & SEX
table(df2$GENUS, df2$SEX)
```

```
## 
##                F  M  U
##   chlorocebus 14 16  0
##   hylobates   12 15  0
##   pan          4  2  6
##   gorilla      6  7  0
```

```r
# GENUS, AGE, & SEX
table(df2$GENUS, df2$AGE, df2$SEX)
```

```
## , ,  = F
## 
## 
##              DECID M1 M2 M3 EPIPH
##   chlorocebus     1  4  2  4     3
##   hylobates       2  2  1  4     3
##   pan             1  0  1  2     0
##   gorilla         4  2  0  0     0
## 
## , ,  = M
## 
## 
##              DECID M1 M2 M3 EPIPH
##   chlorocebus     4  1  4  4     3
##   hylobates       2  1  4  5     3
##   pan             0  0  1  0     1
##   gorilla         2  3  1  0     1
## 
## , ,  = U
## 
```

```
##
##            DECID M1 M2 M3 EPIPH
##   chlorocebus     0  0  0  0     0
##   hylobates       0  0  0  0     0
##   pan             1  1  2  1     1
##   gorilla         0  0  0  0     0
```

Sub setting data by cortical area

```r
# Sub-cortical area dfs

# Percent tissue type of cortical area df
df_c.ar <- df2[,-18:-27]

# Long format
df_c <- df_c.ar %>%
  gather(key = "Tissue", value = "Amount", -ID, -GENUS, -AGE, -SEX)

# Add two new columns with biological knowledge (cortex location and deposition speed)

# Cortex location

df_c$Category <- sapply(df_c$Tissue, function(tissue) {
  if (tissue %in% c("C.Ar_ECCC", "C.Ar_ELAM", "C.Ar_EPF", "C.Ar_EPF.LAM")) {
    return("Endosteal")
  } else if (tissue %in% c("C.Ar_SF", "C.Ar_HAV", "C.Ar_INT")) {
    return("Cortex")
  } else {
    return("Periosteal")
  }
})

# Deposition speed

df_c$Speed <- sapply(df_c$Tissue, function(tissue) {
  if (tissue %in% c("C.Ar_SF", "C.Ar_HAV", "C.Ar_INT", "C.Ar_ECCC")) {
    return("Neutral")
  } else if (tissue %in% c("C.Ar_ELAM", "C.Ar_LAM")) {
    return("Slow")
  } else if (tissue %in% c("C.Ar_WOV", "C.Ar_FLC")) {
    return("Fast")
  } else {
    return("Moderate")
  }
})

# Rename tissue names
df_c$Tissue <- recode(df_c$Tissue,
                      `C.Ar_WOV` = "WOV",
                      `C.Ar_FLC` = "FLC",
                      `C.Ar_FLC.LZPO` = "FLC-LZPO",
```

```r
                        `C.Ar_PF` = "PF",
                        `C.Ar_PF.LAM` = "PF-LAM",
                        `C.Ar_LAM` = "LAM",
                        `C.Ar_ECCC` = "CCC",
                        `C.Ar_EPF` = "EPF",
                        `C.Ar_EPF.LAM` = "EPF-LAM",
                        `C.Ar_ELAM` = "ELAM",
                        `C.Ar_INT` = "INT",
                        `C.Ar_SF` = "SF",
                        `C.Ar_HAV` = "HAV",
                        )


# Reordering tissue types by category and speed

# Ensure the columns are factors
df_c$Tissue <- factor(df_c$Tissue, levels = c("WOV", "FLC", "FLC-LZPO", "PF",
                     "PF-LAM", "LAM", "EPF", "EPF-LAM", "ELAM", "CCC", "SF", "INT", "HAV"))



# Percent periosteal tissue type

df_p.ar <- df2[, c(1:4, 18:23)]

# Long format
df_p <- df_p.ar %>%
  gather(key = "Tissue", value = "Amount", -ID, -GENUS, -AGE, -SEX)

# Add one new column with biological knowledge (deposition speed)

# Deposition speed

df_p$Speed <- sapply(df_p$Tissue, function(tissue) {
  if (tissue %in% c("P.Ar_WOV", "P.Ar_FLC")) {
    return("Fast")
  } else if (tissue %in% c("P.Ar_LAM")) {
    return("Slow")
  } else {
    return("Moderate")
  }
})


# Rename tissue names
df_p$Tissue <- recode(df_p$Tissue,
                     `P.Ar_WOV` = "WOV",
                     `P.Ar_FLC` = "FLC",
                     `P.Ar_FLC.LZPO` = "FLC-LZPO",
                     `P.Ar_PF` = "PF",
                     `P.Ar_PF.LAM` = "PF-LAM",
                     `P.Ar_LAM` = "LAM"
                     )
```

```r
# Reordering tissue types by category and speed

# Ensure the columns are factors
df_p$Tissue <- factor(df_p$Tissue, levels = c("WOV", "FLC", "FLC-LZPO", "PF",
                            "PF-LAM", "LAM"))


# Percent endosteal tissue type

df_e.ar <- df2[,-5:-23 ]

# Long format
df_e <- df_e.ar %>%
  gather(key = "Tissue", value = "Amount", -ID, -GENUS, -AGE, -SEX)

# Add one new column with biological knowledge (deposition speed)

# Deposition speed

df_e$Speed <- sapply(df_e$Tissue, function(tissue) {
  if (tissue %in% c("E.Ar_LAM")) {
    return("Slow")
  } else if (tissue %in% c("E.Ar_ECCC")) {
    return("Neutral")
  } else {
    return("Moderate")
  }
})

# Rename tissue names
df_e$Tissue <- recode(df_e$Tissue,
                      `E.Ar_ECCC` = "CCC",
                      `E.Ar_EPF` = "EPF",
                      `E.Ar_EPF.LAM` = "EPF-LAM",
                      `E.Ar_ELAM` = "ELAM"
                      )

# Reordering tissue types by speed

# Ensure the columns are factors
df_e$Tissue <- factor(df_e$Tissue, levels = c("EPF", "EPF-LAM", "ELAM", "CCC"))
```

Color palettes for plots

```r
# Tissue type color palette - all tissue
color_palette <- c("darkgreen", "forestgreen", "mediumseagreen", "seagreen3", "aquamarine3", "aquamarin

# Tissue type color palette - periosteal tissue
color_palette1 <- c("darkgreen", "forestgreen", "mediumseagreen", "seagreen3", "aquamarine3", "aquamari
```

```r
# Tissue type color palette - endosteal tissue
color_palette2 <- c("indianred4", "indianred", "indianred2", "darkgoldenrod1")
```

```r
# Bar plot
ggplot(df_c, aes(GENUS, Amount, fill = Tissue), stat="identity", position = "dodge") +
  stat_summary(fun.y = mean, geom = "bar", position = "dodge") +
  stat_summary(fun.data = mean_cl_normal, geom = "errorbar", position = position_dodge(width = .96), wic
  theme_bw() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylim(0, 80) +
  scale_fill_manual(values= color_palette)
```

```
## Warning: The 'fun.y' argument of 'stat_summary()' is deprecated as of ggplot2 3.3.0.
## i Please use the 'fun' argument instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

```
## Warning: Removed 10 rows containing non-finite values ('stat_summary()').
## Removed 10 rows containing non-finite values ('stat_summary()').
```
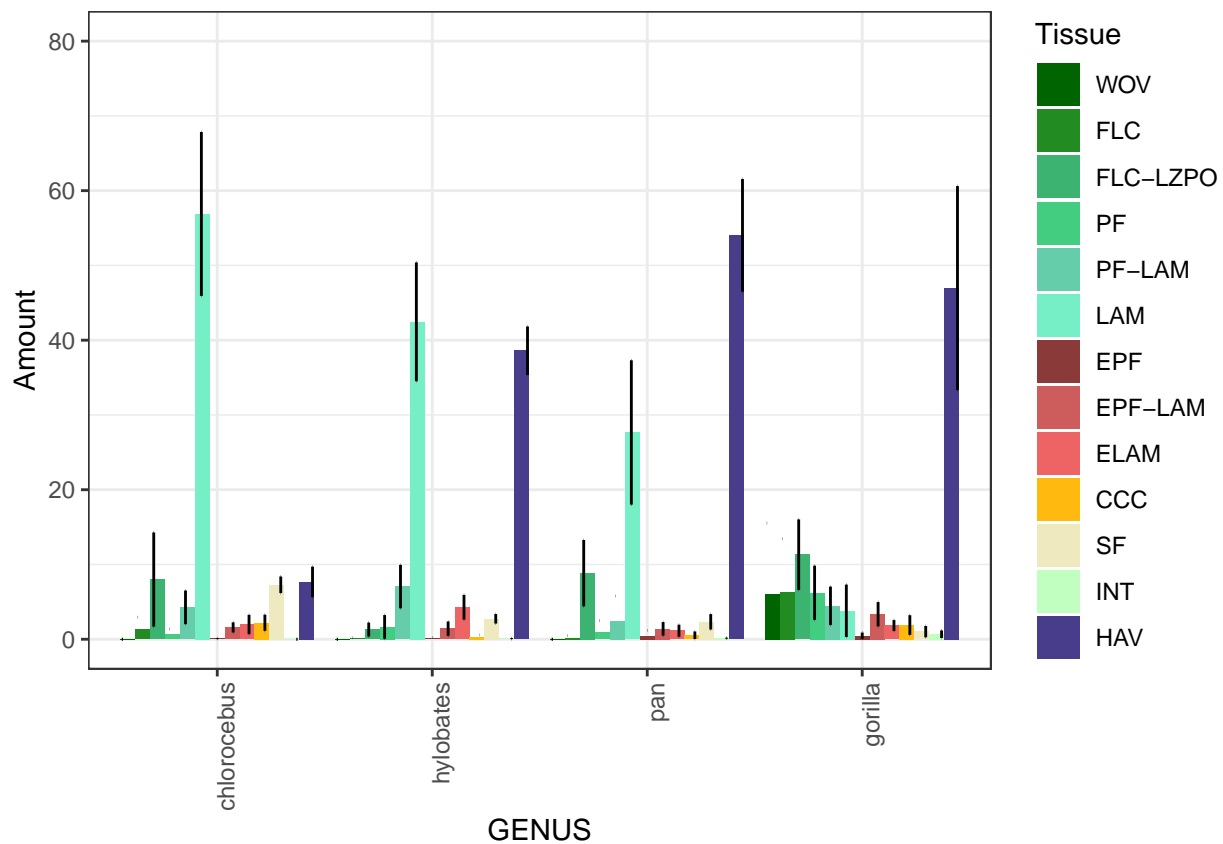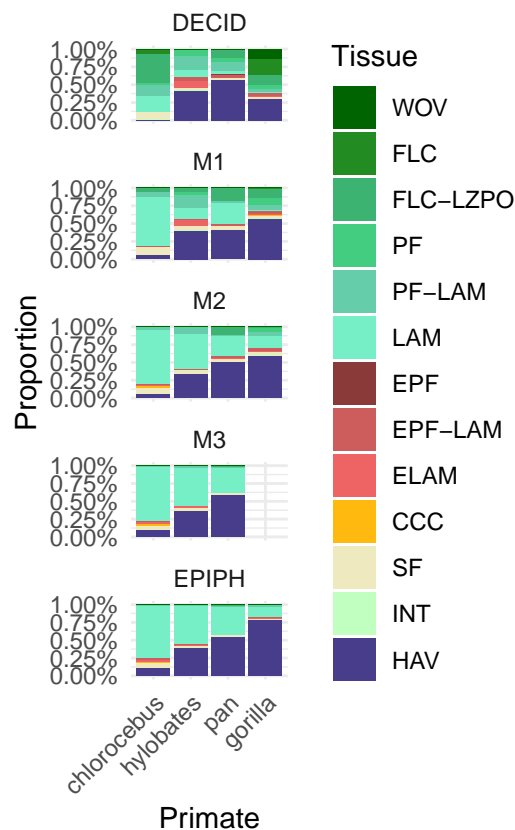


```r
# The Amounts are based on means for each primate
```

Plot composition of tissues relative to each other GENUS only consideration

```
# Calculate the composition of tissues relative to each other
df_c_proportions <- df_c %>%
  group_by(GENUS) %>%
  mutate(Proportion = Amount / sum(Amount, na.rm = TRUE))

# The data represents the relative composition of tissues in terms of their contribution to the entire

# Plot composition of tissues relative to each other
ggplot(df_c_proportions, aes(x = GENUS, y = Proportion, fill = Tissue)) +
  geom_bar(stat = "identity", position = "stack", width = 0.90) +
  scale_y_continuous(labels = scales::percent_format(scale = 1)) +
  labs(y = "Proportion", x = "Primate") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1), aspect.ratio = 5/10) +
  scale_fill_manual(values= color_palette)
```
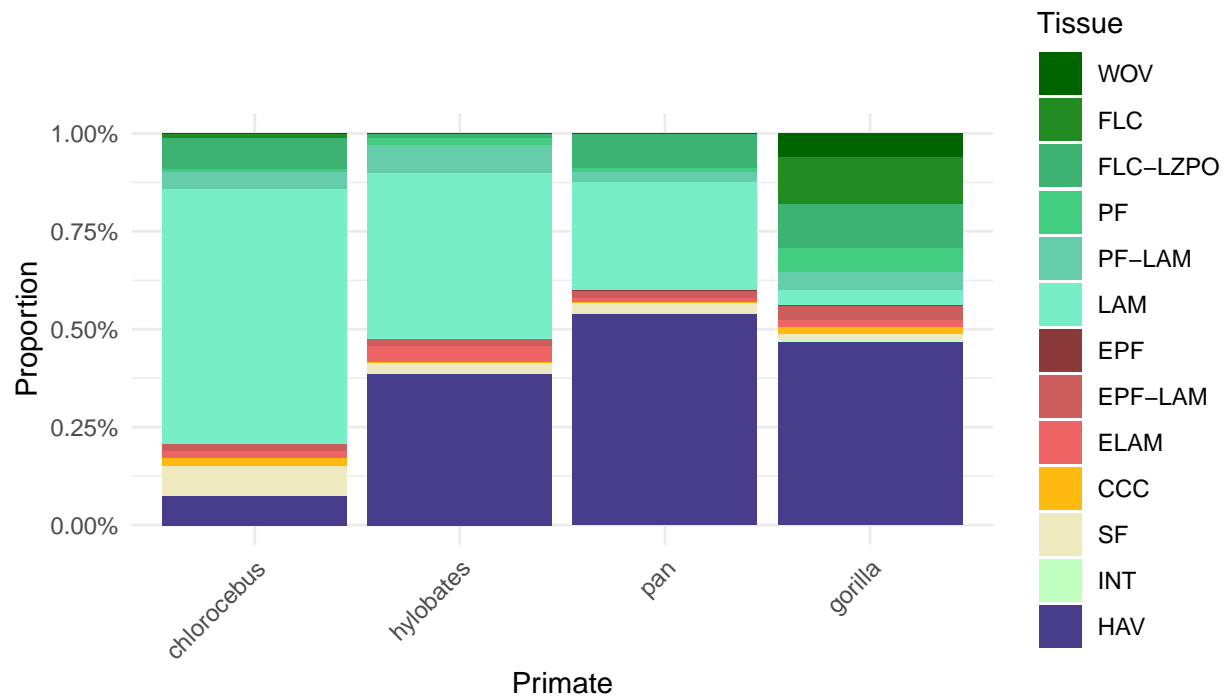
All cortical bone tissue types bar plot

```
# Bar plot
ggplot(df_c, aes(GENUS, Amount, fill = Tissue), stat="identity", position = "dodge") +
  stat_summary(fun.y = mean, geom = "bar", position = "dodge") +
  facet_wrap(~ AGE) +
  stat_summary(fun.data = mean_cl_normal, geom = "errorbar", position = position_dodge(width = .96), wi
  theme_bw() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylim(0, 80) +
  scale_fill_manual(values= color_palette)
```

```
## Warning: Removed 10 rows containing non-finite values ('stat_summary()').
## Removed 10 rows containing non-finite values ('stat_summary()').
```
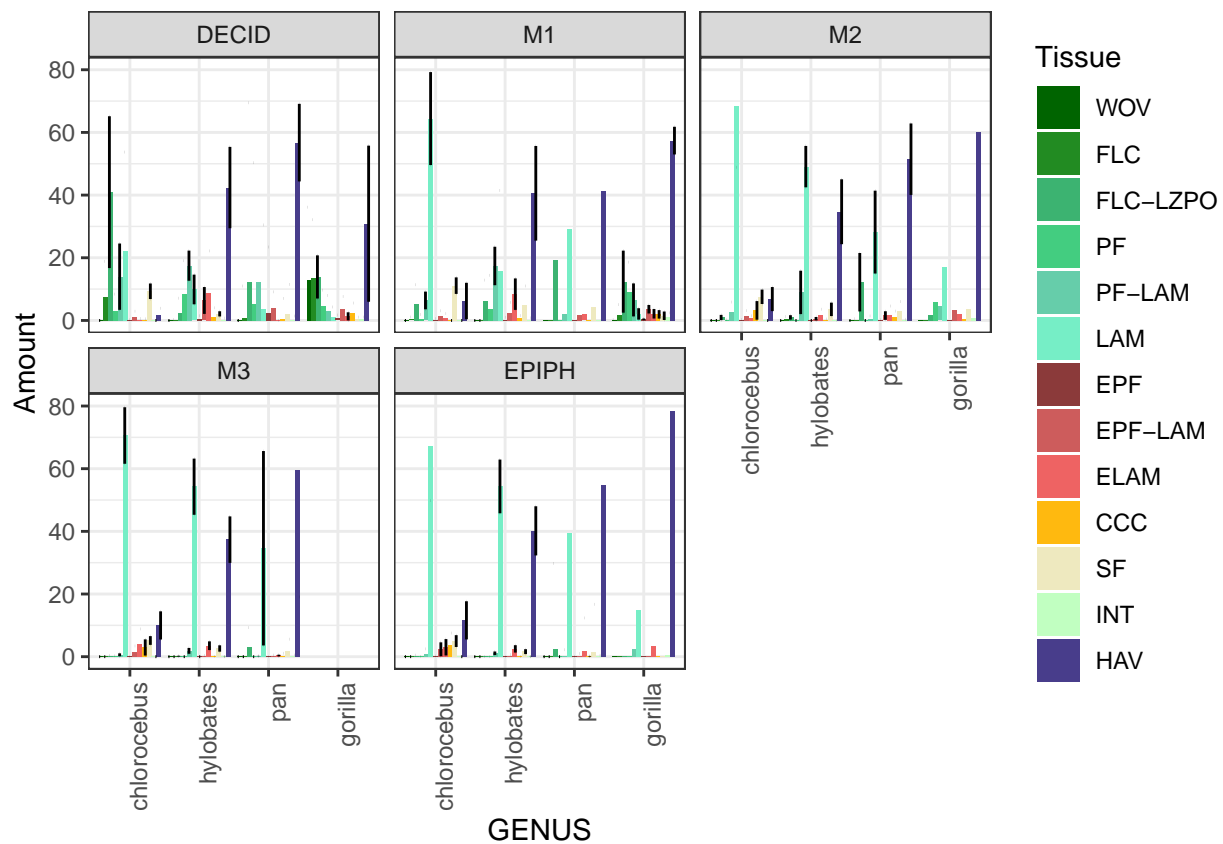

Plot composition of tissues relative to each other

```
# Calculate the composition of tissues relative to each other
df_c_proportions <- df_c %>%
  group_by(GENUS, AGE) %>%
  mutate(Proportion = Amount / sum(Amount, na.rm = TRUE))
```

```
# The data represents the relative composition of tissues in terms of their contribution to the entire

# Plot composition of tissues relative to each other
ggplot(df_c_proportions, aes(x = GENUS, y = Proportion, fill = Tissue)) +
  geom_bar(stat = "identity", position = "stack", width = 0.90) +
  scale_y_continuous(labels = scales::percent_format(scale = 1)) +
  labs(y = "Proportion", x = "Primate") +
  facet_wrap(~ AGE, ncol = 1) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1), aspect.ratio = 5/10) +
  scale_fill_manual(values= color_palette)
```


Periosteal tissue types bar plot

```
# Bar plot
ggplot(df_p, aes(GENUS, Amount, fill = Tissue), stat="identity", position = "dodge") +
  stat_summary(fun.y = mean, geom = "bar", position = "dodge") +
  facet_wrap(~ AGE) +
  stat_summary(fun.data = mean_cl_normal, geom = "errorbar", position = position_dodge(width = .96), wi
  theme_bw() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
```

```
  ylim(0, 80) +
  scale_fill_manual(values= color_palette1)
```
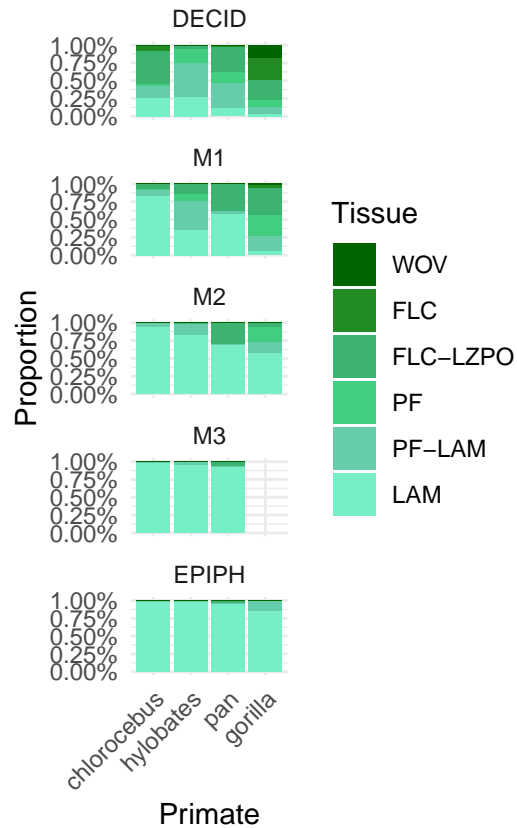
```
## Warning: Removed 49 rows containing non-finite values ('stat_summary()').
## Removed 49 rows containing non-finite values ('stat_summary()').
```
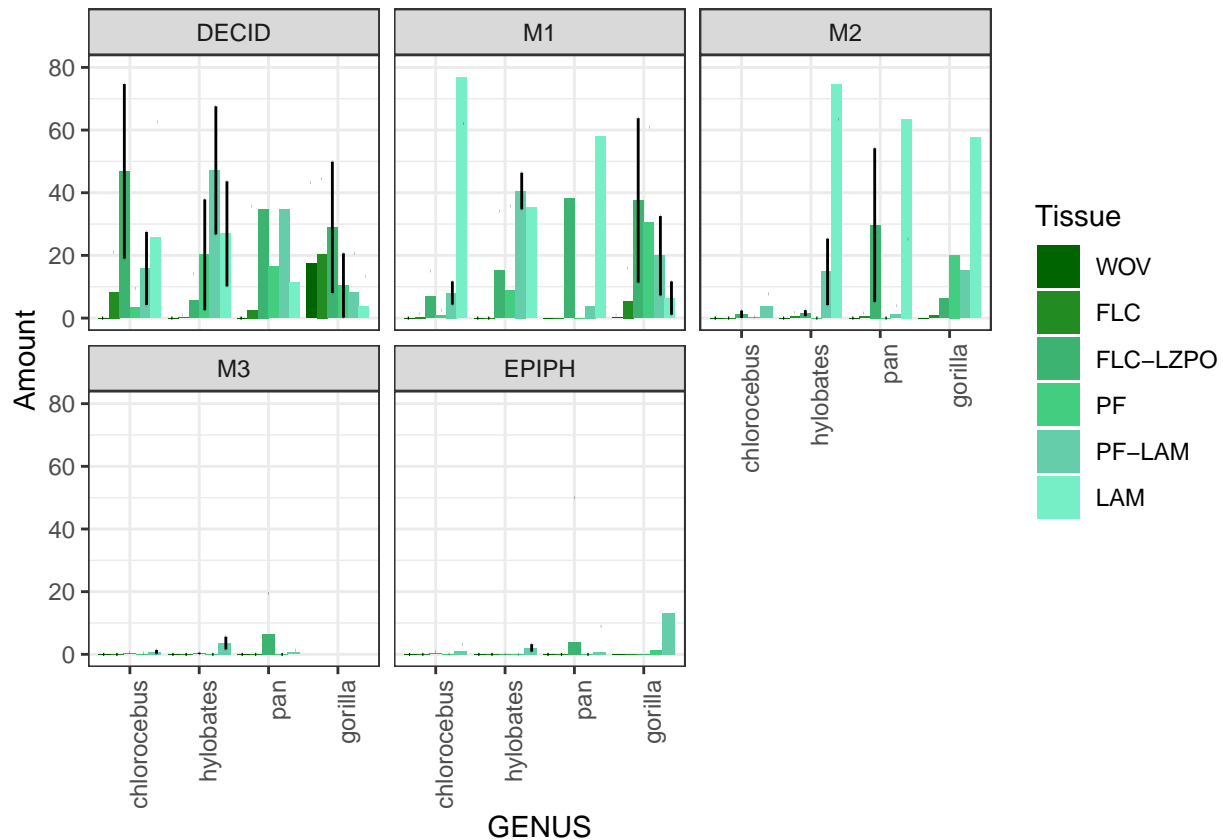

Plot composition of tissues relative to each other for periosteal area

```
# Calculate the composition of tissues relative to each other
df_p_proportions <- df_p %>%
  group_by(GENUS, AGE) %>%
  mutate(Proportion = Amount / sum(Amount, na.rm = TRUE))

# Plot composition of tissues relative to each other
ggplot(df_p_proportions, aes(x = GENUS, y = Proportion, fill = Tissue)) +
  geom_bar(stat = "identity", position = "stack", width = 0.90) +
  scale_y_continuous(labels = scales::percent_format(scale = 1)) +
  labs(y = "Proportion", x = "Primate") +
  facet_wrap(~ AGE, ncol = 1) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1), aspect.ratio = 5/10) +
  scale_fill_manual(values= color_palette1)
```

Endosteal bone tissue types bar plot

```r
# Bar plot
ggplot(df_e, aes(GENUS, Amount, fill = Tissue), stat="identity", position = "dodge") +
  stat_summary(fun.y = mean, geom = "bar", position = "dodge") +
  facet_wrap(~ AGE) +
  stat_summary(fun.data = mean_cl_normal, geom = "errorbar", position = position_dodge(width = .96), wid
  theme_bw() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylim(0, 80) +
  scale_fill_manual(values= color_palette2)
```

```
## Warning: Removed 37 rows containing non-finite values (`stat_summary()`).
## Removed 37 rows containing non-finite values (`stat_summary()`).
```
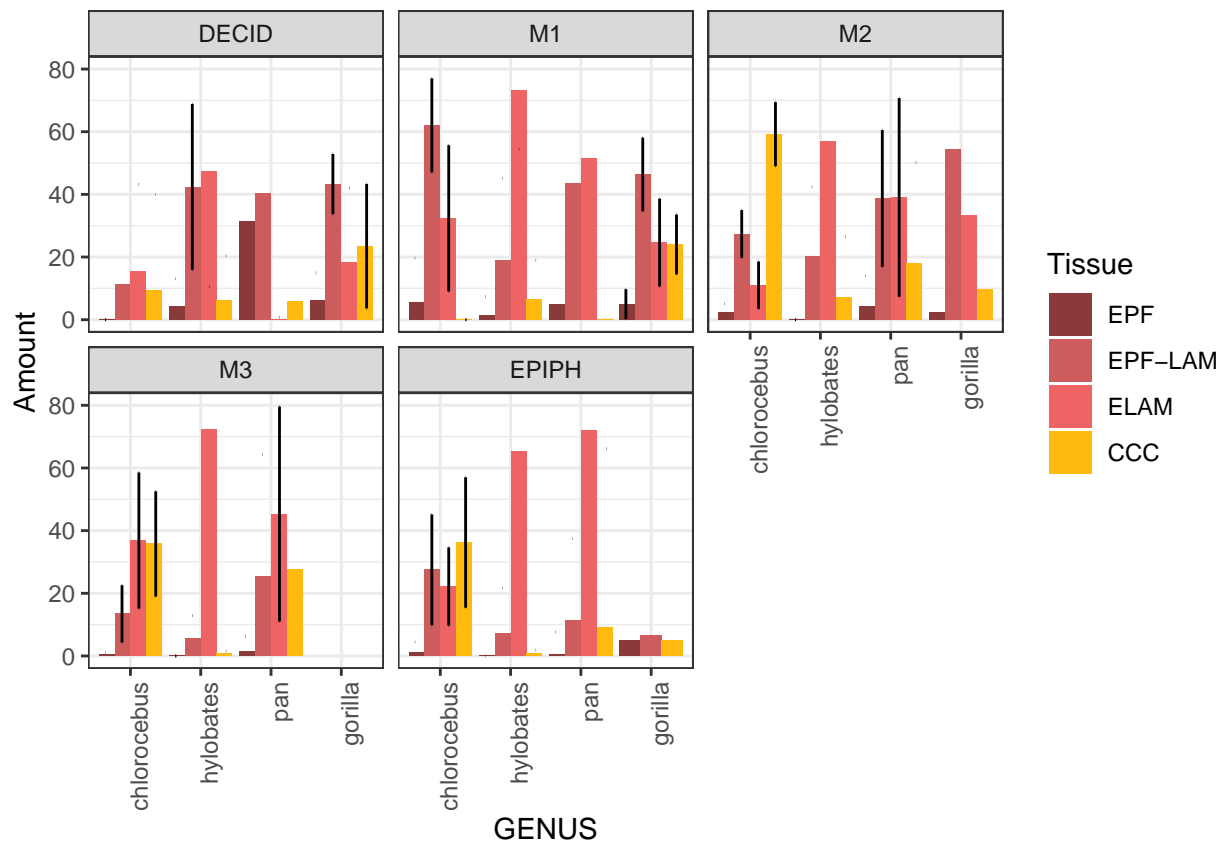
Plot composition of tissues relative to each other for the endosteal area

```
# Calculate the composition of tissues relative to each other
df_e_proportions <- df_e %>%
  group_by(GENUS, AGE) %>%
  mutate(Proportion = Amount / sum(Amount, na.rm = TRUE))

# Plot composition of tissues relative to each other
ggplot(df_e_proportions, aes(x = GENUS, y = Proportion, fill = Tissue)) +
  geom_bar(stat = "identity", position = "stack", width = 0.90) +
  scale_y_continuous(labels = scales::percent_format(scale = 1)) +
  labs(y = "Proportion", x = "Primate") +
  facet_wrap(~ AGE, ncol = 1) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1), aspect.ratio = 5/10) +
  scale_fill_manual(values= color_palette2)
```

```
## Warning: Removed 12 rows containing missing values (`position_stack()`).
```