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Data on sleeping habits in mammals is scant. In a study conducted by Allison and Cicchetti (1976), they surveyed the literature on the sleeping habits and physiological characteristics (e.g., body weight, brain weight, gestation, etc.) of the 1% of mammal species whose behaviours were studied and published. After conducting factor analysis, they found that sleeping habits in mammals were related to the size of the animal and their predation risk. In particular, they found that species in danger of predation will sleep less whilst bigger animals who are in less danger of predation sleep more.

Table 1

*Codebook: Description of Variables Used by Original research (Allison & Cicchetti, 1976)*

| Variable Label | Variable Name | Variable type | Variable values |
| --- | --- | --- | --- |
| Brain weight | brain_wt | continuous | In g 0.14 - 5712 |
| Body weight | body_wt | continuous | In kg 0.005-6654 |
| Dream Duration | dreaming | continuous | In hrs/day 0 - 6.6 |
| Predation risk index | predation | categorical | Scale 1-5: 1=least likely to be preyed upon; 5= most likely to be preyed upon. |
| Encephalisation quotient (Brain-body mass ratio) | EQ | continuous | Derived from weights by using Brain wt/body wt. |

| | |
|---|---|
| | Range 0-1 |

For this project, we used their data on the variables listed in Table 1 and derived a measure of relative cognitive complexity by dividing brain weight by body weight. All the variables in Table 1 were quantities mentioned in the literature except for the predation index. Allison and Cicchetti (1976) inferred the predation index from literature on the extent of predation for each species. They rated each species on a scale of 1 to 5; the definition of each level of predation index was not mentioned in their paper. Our derived variable, Encephalisation Quotient (EQ), is an established measure of cognitive complexity in mammals (Benson-Amram et al, 2016; Jerison, 1977; Williams, 2002). However, Deaner et al., (2007) present evidence contradictory to the established measure. We used the simplest form of EQ which is a brain to body mass ratio.

**Dreaming as an Adaptation to Predation by Intelligent Mammals**

Two major hypotheses are behind our data exploration. First is that dreaming functions as an adaptation to consolidate memories of predation as well as simulation of predation threats (Revonsuo, 2000; Revonsuo & Valli, 2000). This states that the relationship between dreaming length and predation risk is bound to increase. The next major hypothesis is that dreaming requires cognitive abilities, particularly object representation (Foulkes, 1993). Hence, more cognitively complex species are expected to dream longer. Our group will explore the question: Do more cognitively complex species dream longer and is this relationship stronger and of greater effect the higher the predation risk is? Building on the relationship that Allison and

Ciccetti (1976) found between size, predation risk, and sleeping habits, we attempted to explore the relationships of cognitive complexity with dreaming by using the brain to body mass ratio (a derived variable from brain weight and body weight) as an external measure of cognition to operationalise cognitive complexity. We then compared it to the length of time a species spends dreaming whilst controlling for their ecological niche (i.e. role in the environment) by using the predation risk score.

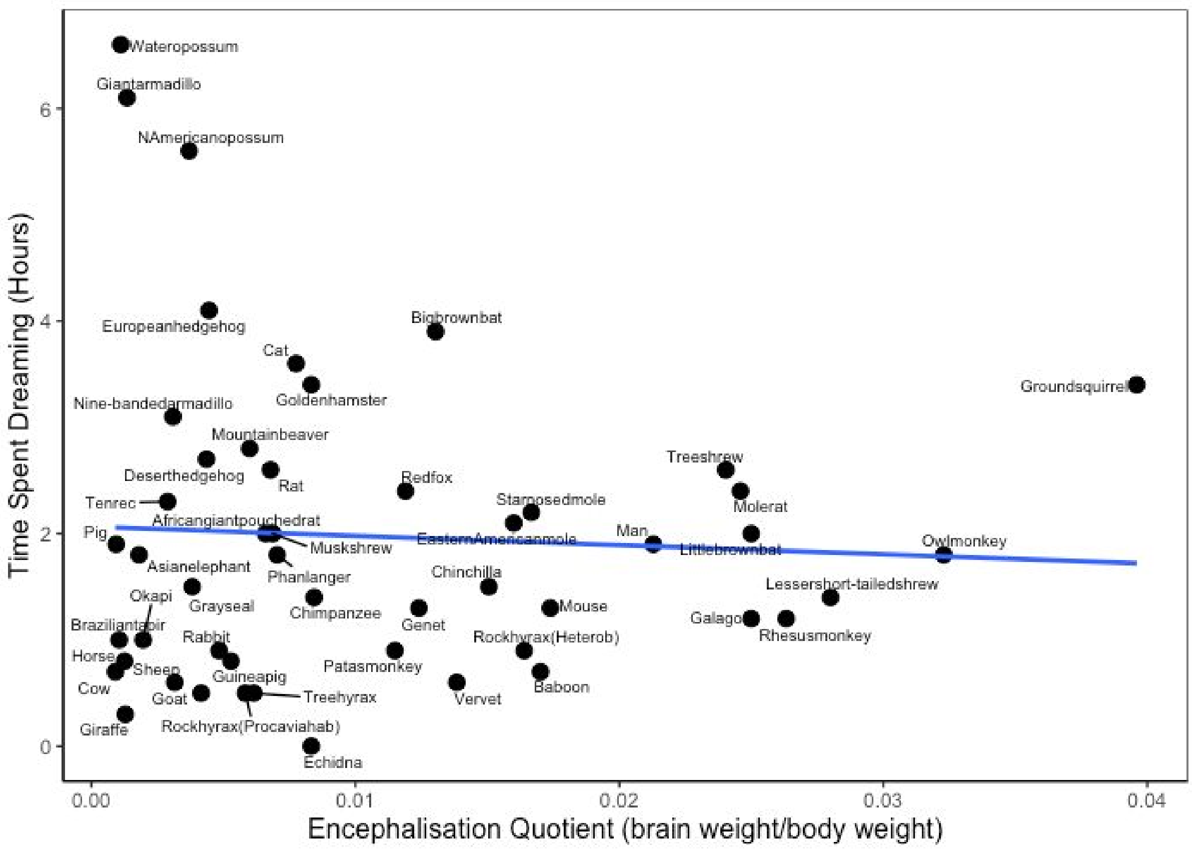



*Figure 1.* This graph shows the relationship between Encephalisation Quotient (Brain-Body mass ratio) and the number of hours spent dreaming for each species of mammals.

The first goal was to see if there is an overall relationship between the amount of time spent dreaming and EQ (brain-body mass ratio). We did this to see if simply EQ is driving the relationship. Figure 1 shows no correlation between the two variables. If dreaming does function as an adaptation to predation, then breaking the analysis down by predation level might clarify the relationship between EQ and dreaming. Nonetheless, it is interesting to note that small species like ground squirrels are deemed more 'cognitively complex' than humans on this scale of EQ.

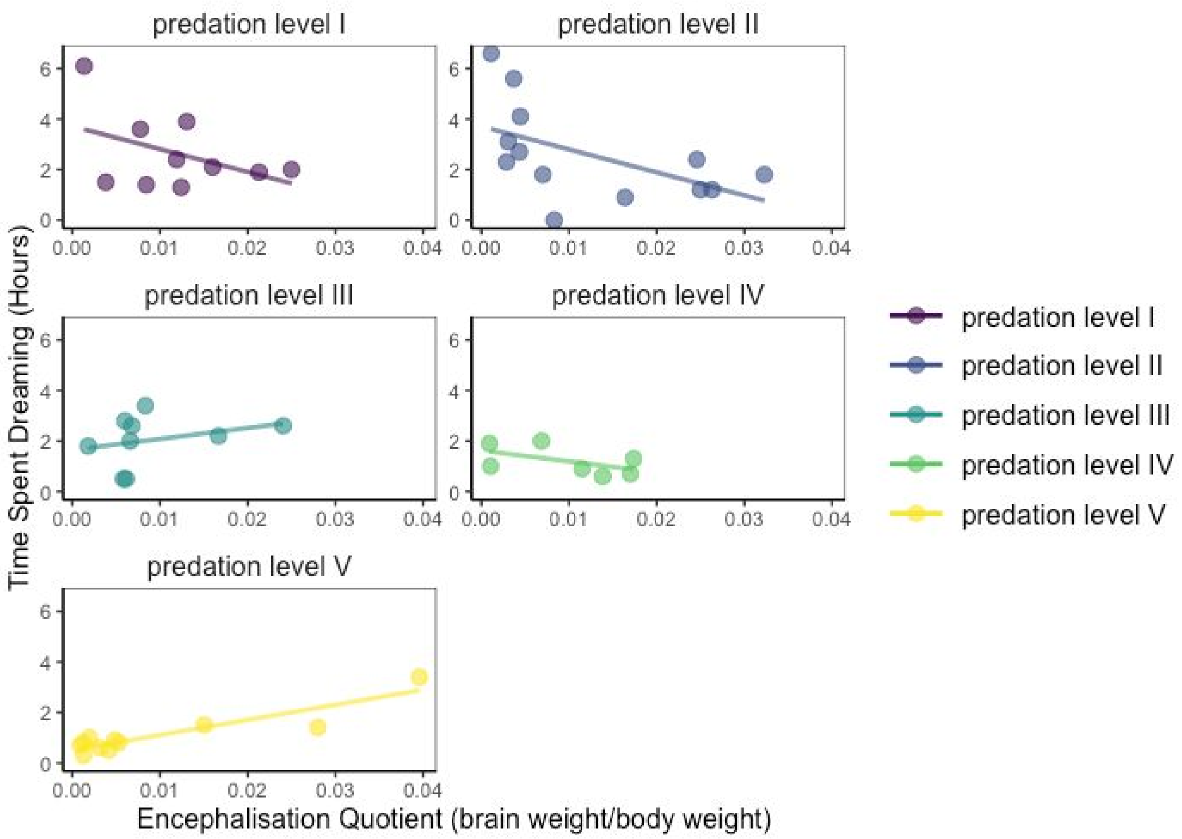


*Figure 2.* This graph shows the relationship between Encephalisation Quotient (Brain-Body mass ratio) and the number of hours spent dreaming by each species of Mammals when broken down into the 5 levels of predation risk.

At first glance, the data seem to agree with the prediction of the dreaming as an adaptation to predation hypothesis (Figure 2). EQ and dreaming length have stronger correlation as the predation risk level increases. Unsurprisingly, there is an inconsistency in direction of the correlation between these predation levels as shown in the general relationship plot (Figure 1). However, the inconsistency should be on gradually varying levels of steepness of the line towards a more positive relationship if the prediction of our hypothesis were supported. Instead, as seen on Figure 2, predation level 3 had a positive relationship but level 4 went back to a negative relationship. Furthermore, figure 2 shows that at level 5 it appears that the relationship is being strongly driven by an outlier with a high EQ (ground squirrel: see Figure 1 for species name of outlier). Nonetheless, this relationship is as expected by our hypothesis.

Overall our visualisations show that the function of dreaming as an adaptation to predation by intelligent individuals is still debatable. Whilst at level 5 the positive correlation predicted is seen, the other levels were fairly inconsistent with their directions. It is possible that with statistical tests, the rest of the levels would show no relationships and that level 5 is the only one with a statistically significant relationship with a meaningful effect. If this were the case then the data provide support for the hypothesis. This will require further investigation as to why this relationship only appears at predation level 5. Nonetheless, that step has to be done and what is apparent is that the data has inconsistencies with the predicted relationship, particularly in terms of direction.

## Limitations

Conclusions of our visualisations are limited by two critical issues: validity of EQ and a small, almost unrepresentative sample due to missing data. The validity of EQ as a measure of cognitive complexity has its limitations, however, it is widely used and is considered a valid measure of relative cognitive complexity. As we are comparing cognitive complexity across multiple species, EQ is considered the best measure of cognitive complexity in this scenario (Finlay, 2009). Nonetheless, Figure 1 shows that due to EQ being a ratio, small species can blow out the ratio (e.g. the ground squirrel seemingly becoming more cognitively complex than a human).

Considering that there are a total of 12 missing values in the dreaming variable, we decided to remove the missing data from Figures 1 and 2. We preferred to have a smaller sample size with a more accurate graph rather than calculating a mean as a substitute and possibly distorting the graph and data. As seen in Appendix A, a majority of the missing data came from species which do not have dreaming data. Two missing data had no sleeping data at all. Further breaking down the data we found that on level 1, 25 % of the data were missing. At level 2, ~ 28 % were missing. At level 3, ~21  % were missing. At level 5, ~13 % were missing. None of the data were missing at level 4. Considering the small sample size compared to the overall species of mammals (only 1 % of species represented by Allison and Ciccetti, 1976). This strongly undermines the generalisability and internal validity of our visualisation. As seen in Figure 2, the presence of outliers plus the reduced sample size may be driving relationships one way which undermines the internal validity (e.g. Predation level 5). Furthermore because of the small sample, we ran the risk of only applying our study to popular and easily accessible species. Ideally, studying more species will remedy this issue. Nonetheless, we decided to impute the overall mean sleeping time of all mammals into the missing data. This is because as shown in Appendix B, at levels 1 and 3 the missing data may have slightly smaller EQ than the actual data.

To see if there would be any differences compared to the graph with the missing data removed, in a separate graph we added mean impute values. Appendix C shows that filling in the missing data with a calculated mean results in presumably no major impact on the graph and the relationships remain fairly similar to Figure 2. Particularly, for levels 3 and 1, the slope changed very slightly towards the mean of the dreaming length. This is not surprising as we added more values to the plot and we used the mean. Nonetheless, because Appendix C shows similar relationships to Figure 2, our conclusion stayed the same. The next step is to study more mammals.

References:


Allison, T., & Cicchetti, D. V. (1976). Sleep in mammals: ecological and constitutional correlates. *Science*, *194*(4266), 732-734.

Benson-Amram, S., Dantzer, B., Stricker, G., Swanson, E. M., & Holekamp, K. E. (2016). Brain size predicts problem-solving ability in mammalian carnivores. *Proceedings of the National Academy of Sciences, 113*(9), 2532-2537.

Deaner, R. O., Isler, K., Burkart, J., & Van Schaik, C. (2007). Overall brain size, and not encephalization quotient, best predicts cognitive ability across non-human primates. *Brain, behavior and evolution, 70*(2), 115-124.

Finlay, B. (2009) Brain Evolution: Developmental Constraints and Relative Developmental Growth. *Encyclopedia of Neuroscience,* 337-345.

Foulkes, D. (1993). Dreaming and REM sleep. *Journal of Sleep Research, 2*(4), 199-202.

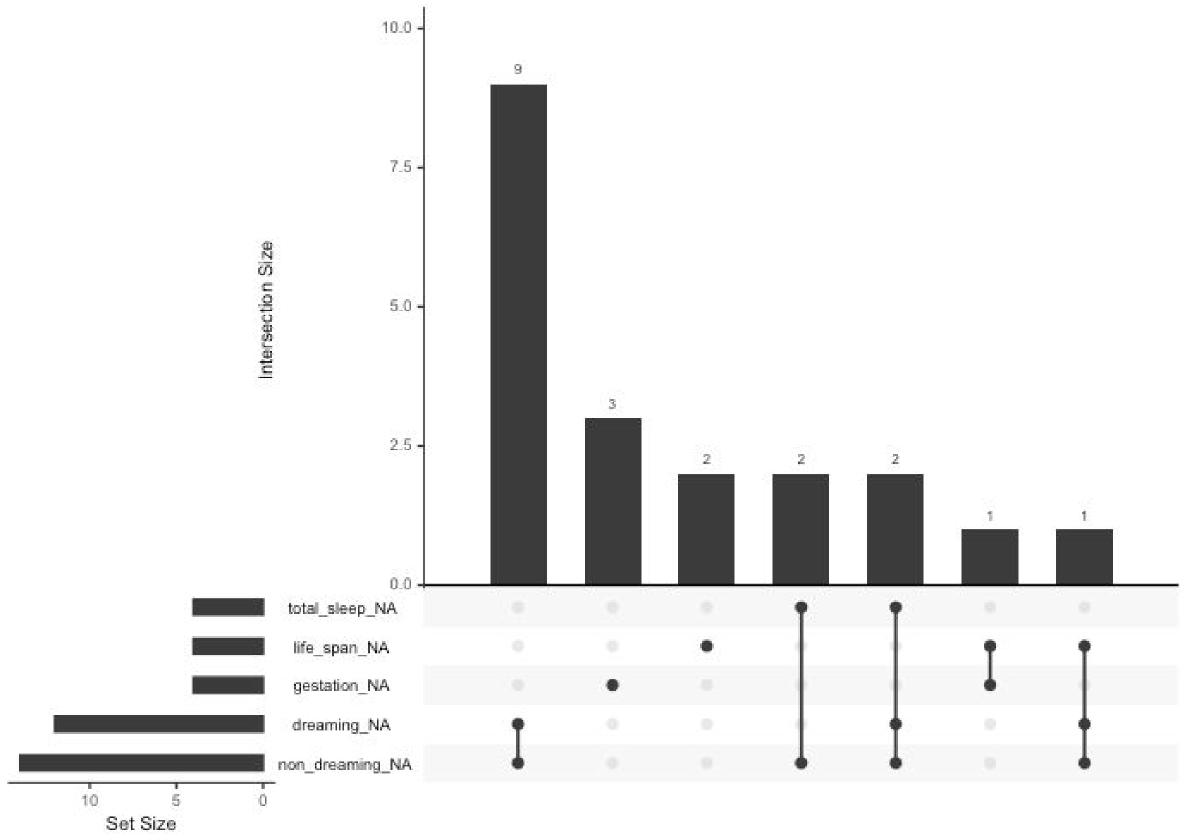
Jerison, H. J. (1977). The theory of encephalization. *Annals of the New York Academy of Sciences*, 299, 146-160.

Revonsuo, A. (2000). The reinterpretation of dreams: An evolutionary hypothesis of the function of dreaming. *Behavioral and Brain Sciences, 23*(6), 877-901.

Revonsuo, A., & Valli, K. (2000). Dreaming and consciousness: Testing the threat simulation theory of the function of dreaming. *Psyche: An Interdisciplinary Journal of Research on Consciousness*.

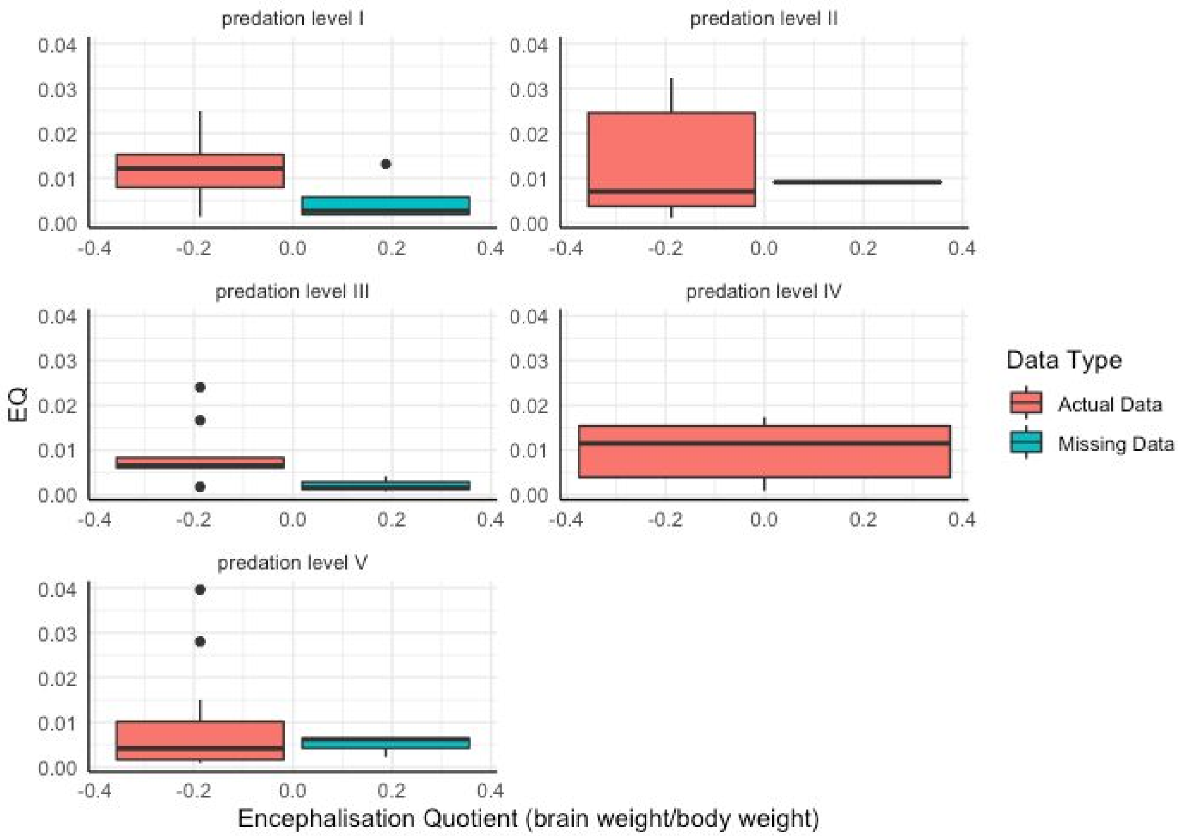
Williams, M. F. (2002). Primate encephalization and intelligence. *Medical hypotheses, 58*(4), 284-290.

## Appendix A



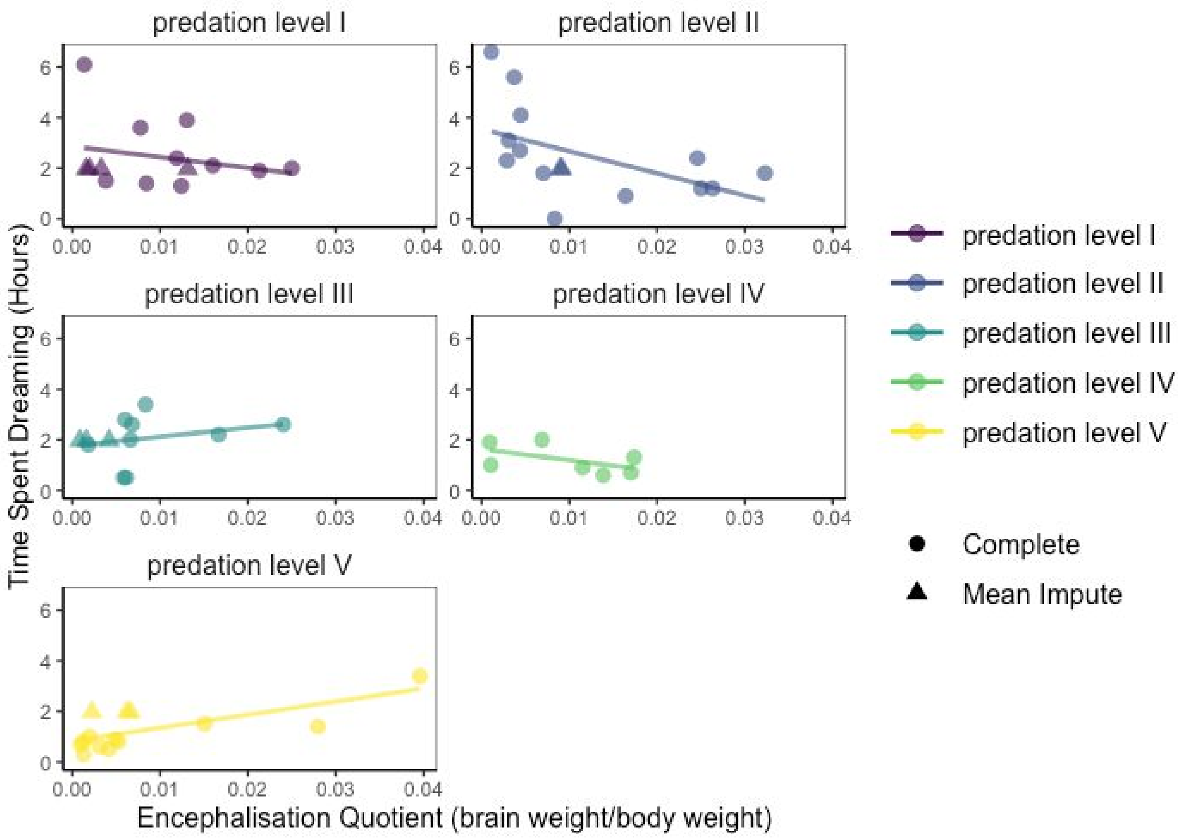

*Appendix A*. This figure shows which variables are the sources for missing data and whether they're related to other variables.

## Appendix B




*Appendix B.* Comparing missing data from actual data to see if they are from different distributions along the EQ axis.

## Appendix C




*Appendix C.* This graph shows the relationship between Encephalisation Quotient (Brain-Body mass ratio) and the number of hours spent dreaming by each species of mammals when broken down into the 5 levels of predation risk. Missing sleep data were imputed using the mean sleep data for all mammals.

# Data Visualisation Code- Dreaming, Predation, and Cognitive Complexity

Ezekiel Gading

03/11/2020

The data are from Allison's and Ciccetti's (1976) study on mammals. [Download as a CSV file](#)

The following code was used to produce the figures and numerical descriptives used in the paper:

```
###required packages
require(tidyverse)

## Loading required package: tidyverse

## ── Attaching packages ──────────────────────────────────────────────────
tidyverse 1.3.0 ──

## ✓ ggplot2 3.3.2     ✓ purrr   0.3.4
## ✓ tibble  3.0.4     ✓ dplyr   1.0.2
## ✓ tidyr   1.1.2     ✓ stringr 1.4.0
## ✓ readr   1.4.0     ✓ forcats 0.5.0

## ── Conflicts ───────────────────────────────────────────────────────────
tidyverse_conflicts() ──
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

require(here)#for reading files

## Loading required package: here

## here() starts at /Users/ezekielfrancogading/Desktop/Psyc3031A

require(psych)#descriptives

## Loading required package: psych

##
## Attaching package: 'psych'
```

```
## The following objects are masked from 'package:ggplot2':
##
##     %+%, alpha
```

```
require(naniar)#for missing variables
```

```
## Loading required package: naniar
```

```
require(jtools)#for theme APA theme
```

```
## Loading required package: jtools
```

```
require(lemon)#to add axis ticks to all subplots
```

```
## Loading required package: lemon
```

```
##
## Attaching package: 'lemon'
```

```
## The following object is masked from 'package:purrr':
##
##     %||%
```

```
## The following objects are masked from 'package:ggplot2':
##
##     CoordCartesian, element_render
```

```
require(broom)#make tibbles for output of descriptives
```

```
## Loading required package: broom
```

```
require(ggrepel) #text labels for species name
```

```
## Loading required package: ggrepel
```

```
mammal.sleep <- read_csv(here('Data','Group work','mammals.csv'))#read data
frame into this variable, see supplementary data file for the shared csv file
on google drive.
```

```
##
## ── Column specification
────────────────────────────────────────────────────────────────────────────
──────────────────────────
```

```
## cols(
##   species = col_character(),
##   body_wt = col_double(),
##   brain_wt = col_double(),
```

```
##   non_dreaming = col_double(),
##   dreaming = col_double(),
##   total_sleep = col_double(),
##   life_span = col_double(),
##   gestation = col_double(),
##   predation = col_double(),
##   exposure = col_double(),
##   danger = col_double()
## )

mammal.sleep <- mammal.sleep %>% mutate(EQ=(brain_wt/1000)/body_wt,#makes the derived encephalisation quotient by converting brain weight from g to kg then dividign by body weight

predation=factor(predation,c('1','2','3','4','5')),#recodes predation risk and other categorical info to factors
                                        predation=fct_recode(predation,
'predation level I'='1','predation level II'='2','predation level III'='3','predation level IV'='4','predation level V'='5'),

exposure=factor(exposure,c('1','2','3','4','5')),

danger=factor(danger,c('1','2','3','4','5')),

sleep.missing=if_else(is.na(dreaming),'Missing Data','Actual Data')) #makes a new column marking which on the dreaming column have missing data. This was added after missing data exploration
#let's make descriptives to assess normality and other issues like missing data
summary(mammal.sleep)#for descriptives overall continuous  descriptives. Ignore variables with star

##    species             body_wt            brain_wt         non_dreaming
##  Length:62          Min.   :   0.005   Min.   :   0.14   Min.   : 2.100
##  Class :character   1st Qu.:   0.600   1st Qu.:   4.25   1st Qu.: 6.250
##  Mode  :character   Median :   3.342   Median :  17.25   Median : 8.350
##                     Mean   : 198.790   Mean   : 283.13   Mean   : 8.673
##                     3rd Qu.:  48.202   3rd Qu.: 166.00   3rd Qu.:11.000
##                     Max.   :6654.000   Max.   :5712.00   Max.   :17.900
##                                                          NA's   :14
##     dreaming      total_sleep      life_span         gestation
##  Min.   :0.000   Min.   : 2.60   Min.   :  2.000   Min.   : 12.00
##  1st Qu.:0.900   1st Qu.: 8.05   1st Qu.:  6.625   1st Qu.: 35.75
##  Median :1.800   Median :10.45   Median : 15.100   Median : 79.00
```

```
##  Mean   :1.972   Mean   :10.53   Mean   : 19.878   Mean   :142.35
##  3rd Qu.:2.550   3rd Qu.:13.20   3rd Qu.: 27.750   3rd Qu.:207.50
##  Max.   :6.600   Max.   :19.90   Max.   :100.000   Max.   :645.00
##  NA's   :12      NA's   :4       NA's   :4         NA's   :4
##                 predation  exposure danger       EQ
##  predation level I  :14   1:27     1:19   Min.   :0.0008584
##  predation level II :15   2:13     2:14   1st Qu.:0.0031026
##  predation level III:12   3: 4     3:10   Median :0.0066109
##  predation level IV : 7   4: 5     4:10   Mean   :0.0096242
##  predation level V  :14   5:13     5: 9   3rd Qu.:0.0136684
##                                           Max.   :0.0396040
##
##  sleep.missing
##  Length:62
##  Class :character
##  Mode  :character
##
##
##
##
```

```
describe(mammal.sleep) #for categorical overall descriptives. Look at 
predation in particular
```

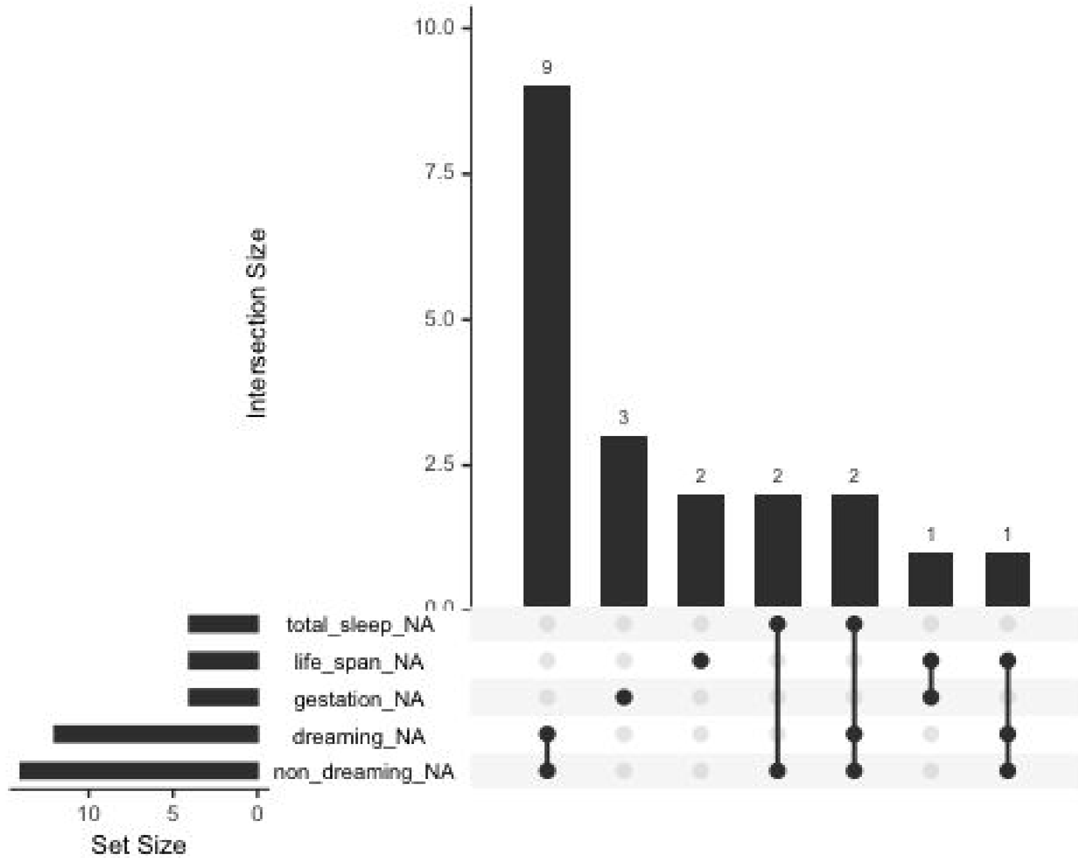
```
##                 vars  n   mean     sd median trimmed   mad   min     max 
range
## species*           1 62  31.50  18.04  31.50   31.50 22.98  1.00   62.00 
61.00
## body_wt            2 62 198.79 899.16   3.34   27.18  4.80  0.00 6654.00 
6654.00
## brain_wt           3 62 283.13 930.28  17.25   81.84 25.03  0.14 5712.00 
5711.86
## non_dreaming       4 48   8.67   3.67   8.35    8.56  3.85  2.10   17.90 
15.80
## dreaming           5 50   1.97   1.44   1.80    1.76  1.26  0.00    6.60 
6.60
## total_sleep        6 58  10.53   4.61  10.45   10.39  4.08  2.60   19.90 
17.30
## life_span          7 58  19.88  18.21  15.10   17.18 14.23  2.00  100.00 
98.00
## gestation          8 58 142.35 146.81  79.00  118.28 85.62 12.00  645.00 
633.00
## predation*         9 62   2.87   1.48   3.00    2.84  1.48  1.00    5.00 
4.00
```

```
## exposure*        10 62   2.42   1.60   2.00    2.28  1.48  1.00    5.00
4.00
## danger*          11 62   2.61   1.44   2.00    2.52  1.48  1.00    5.00
4.00
## EQ               12 62   0.01   0.01   0.01    0.01  0.01  0.00    0.04
0.04
## sleep.missing*   13 62   1.19   0.40   1.00    1.12  0.00  1.00    2.00
1.00
##                skew kurtosis     se
## species*       0.00    -1.26   2.29
## body_wt        6.25    40.60 114.19
## brain_wt       4.83    23.24 118.15
## non_dreaming   0.28    -0.44   0.53
## dreaming       1.37     1.78   0.20
## total_sleep    0.19    -0.65   0.60
## life_span      1.91     5.00   2.39
## gestation      1.60     2.32  19.28
## predation*     0.22    -1.37   0.19
## exposure*      0.65    -1.25   0.20
## danger*        0.36    -1.28   0.18
## EQ             1.28     1.04   0.00
## sleep.missing* 1.51     0.30   0.05

#see breakdown descriptives
#grouped descriptive
#choose relevant variables first
mammal.sleep.relevant.cont <-mammal.sleep %>% #chooses relevant continuous
variables to the study (body wt, brain wt, dreaming )
  select (EQ,dreaming,predation) #makes a data frame of relevant variables

mammal.sleep.relevant.cat <-mammal.sleep %>% #chooses relevant categorical
variables to the study (body wt, brain wt, dreaming )
  select (species,predation) #makes a data frame of relevant variables
#grouped descriptives for continuous variables
describeBy(mammal.sleep.relevant.cont,mammal.sleep.relevant.cat$predation)#
grouped descriptives  for continuous variables. Grouped by predation risk
level

##
##  Descriptive statistics by group
## group: predation level I
##            vars  n mean   sd median trimmed  mad min  max range skew
kurtosis
## EQ             1 14 0.01 0.01   0.01    0.01 0.01 0.0 0.03  0.02 0.46
```

```
-0.99
## dreaming      2 10 2.62 1.51   2.05    2.35 0.89 1.3 6.10  4.80 1.14
0.06
## predation*    3 14 1.00 0.00   1.00    1.00 0.00 1.0 1.00  0.00  NaN
NaN
##              se
## EQ         0.00
## dreaming   0.48
## predation* 0.00
## ---------------------------------------------------------------
## group: predation level II
##            vars  n mean   sd median trimmed  mad min  max range skew
kurtosis
## EQ            1 15 0.01 0.01   0.01    0.01 0.01   0 0.03  0.03 0.72
-1.15
## dreaming      2 13 2.59 1.88   2.30    2.46 1.63   0 6.60  6.60 0.77
-0.50
## predation*    3 15 2.00 0.00   2.00    2.00 0.00   2 2.00  0.00  NaN
NaN
##              se
## EQ         0.00
## dreaming   0.52
## predation* 0.00
## ---------------------------------------------------------------
## group: predation level III
##            vars  n mean   sd median trimmed  mad min  max range  skew
kurtosis
## EQ            1 12 0.01 0.01   0.01    0.01 0.00 0.0 0.02  0.02  1.32
0.72
## dreaming      2  9 2.04 0.99   2.20    2.04 0.59 0.5 3.40  2.90 -0.47
-1.25
## predation*    3 12 3.00 0.00   3.00    3.00 0.00 3.0 3.00  0.00   NaN
NaN
##              se
## EQ         0.00
## dreaming   0.33
## predation* 0.00
## ---------------------------------------------------------------
## group: predation level IV
##            vars n mean   sd median trimmed  mad min  max range  skew
kurtosis
## EQ            1 7 0.01 0.01   0.01    0.01 0.01 0.0 0.02  0.02 -0.21
-1.89
## dreaming      2 7 1.20 0.56   1.00    1.20 0.44 0.6 2.00  1.40  0.39
```

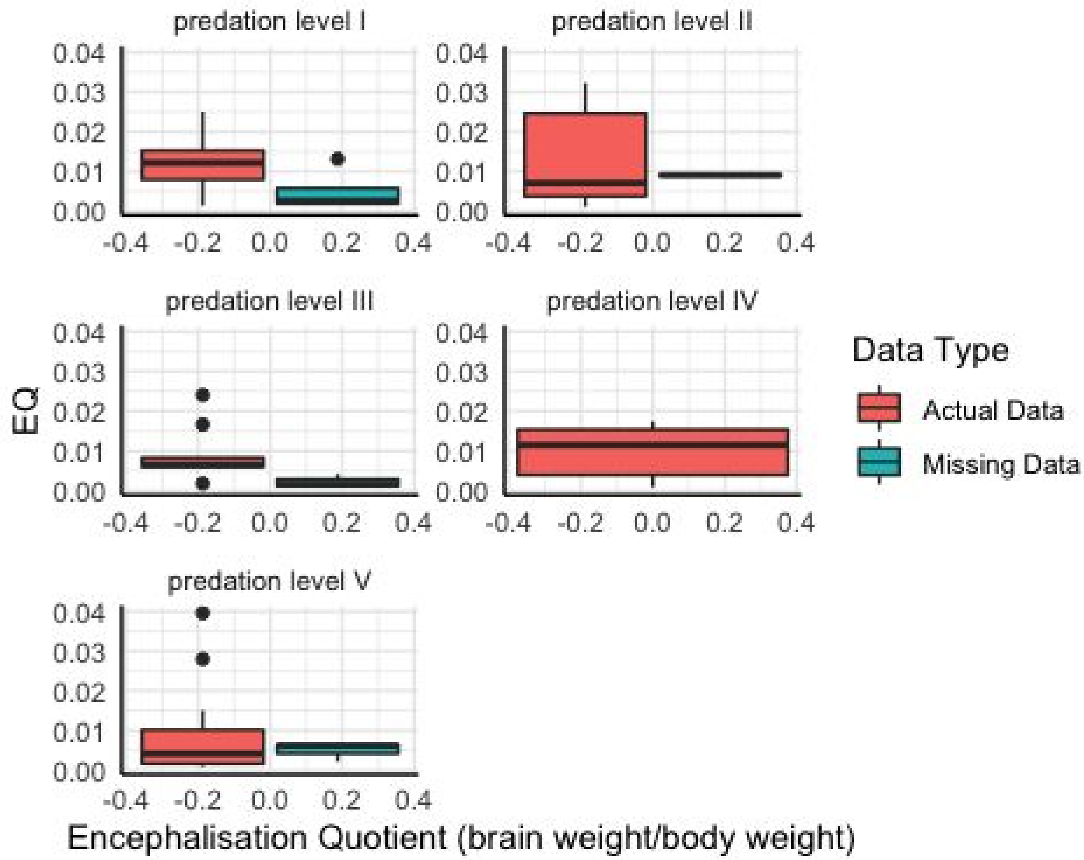
```
-1.76
## predation*    3 7 4.00 0.00   4.00    4.00 0.00 4.0 4.00  0.00   NaN
NaN
##              se
## EQ         0.00
## dreaming   0.21
## predation* 0.00
## ------------------------------------------------------------
## group: predation level V
##            vars  n mean   sd median trimmed mad min  max range skew
kurtosis
## EQ            1 14 0.01 0.01    0.0    0.01 0.0 0.0 0.04  0.04 1.66
1.44
## dreaming      2 11 1.08 0.85    0.8    0.91 0.3 0.3 3.40  3.10 1.75
2.21
## predation*    3 14 5.00 0.00    5.0    5.00 0.0 5.0 5.00  0.00  NaN
NaN
##              se
## EQ         0.00
## dreaming   0.26
## predation* 0.00

#descriptives for categorical
mammal.sleep.relevant.cat %>% #takes relevant categorical variables
  summary() #and makes a summary output for all the counts

##    species                           predation
##  Length:62          predation level I  :14
##  Class :character   predation level II :15
##  Mode  :character   predation level III:12
##                     predation level IV : 7
##                     predation level V  :14

#some missing data here because when plot codes were ran warnings appeared so
let's explore missing data
#missing data exploration
missing_data_summary <- mammal.sleep %>%
  select(predation,dreaming) %>% #selects necessary variables
  group_by(predation) %>% #groups per predation level
  miss_var_summary()

View(missing_data_summary)#opens a new tab with missing variables

# find out the Missing data... where do they come from?
```

```
#get the plot for missing data per variable
gg_miss_upset(mammal.sleep) #shows which variables have missing data and
where missing data were connected
```



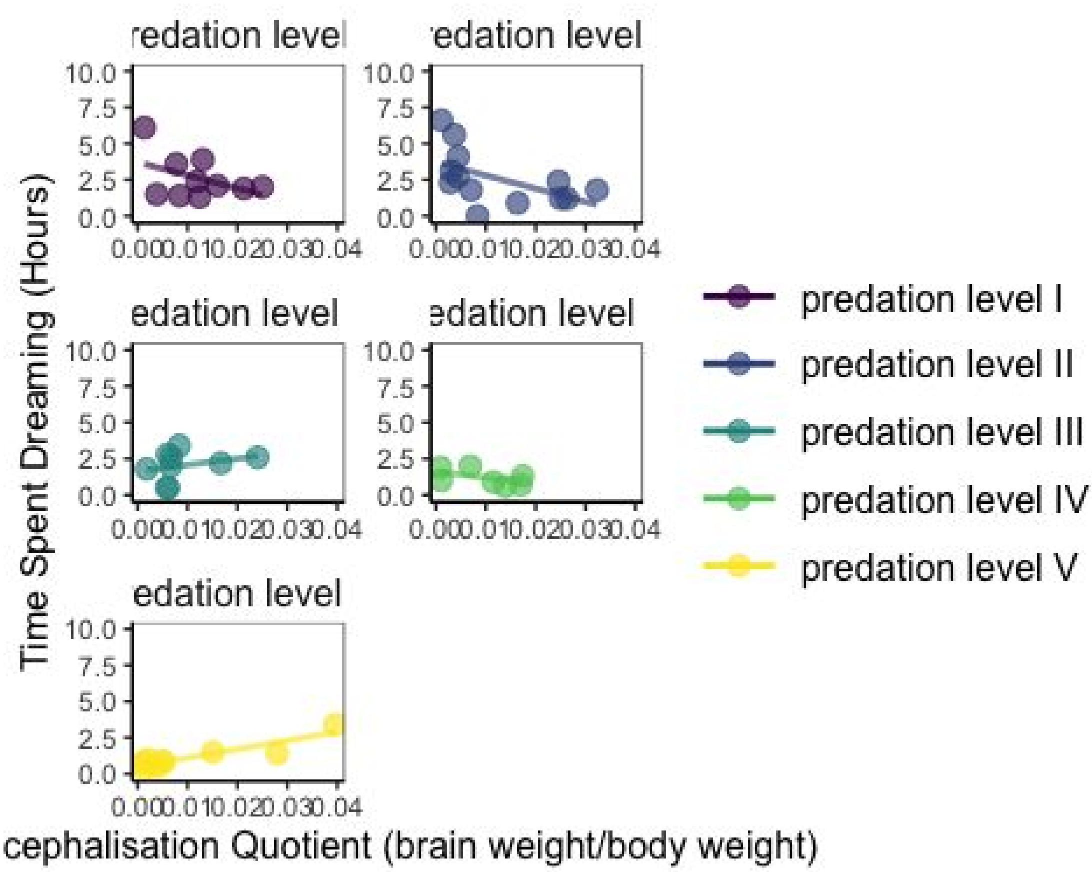

```
#EXPLORING MISSING DATA graphical: are the missing sleep data distributed
evenly across EQ?
#broken down to predation level
ggplot(mammal.sleep) +
  aes(y=EQ,fill=sleep.missing) +
  geom_boxplot()+ #makes boxplots for distributions of missing data and
actual data
  theme_minimal()+ #removes grey theme
  theme(axis.line=element_line()) +#adds axis lines
  labs(fill ='Data Type')+ #renames legend
  xlab('Encephalisation Quotient (brain weight/body weight)')+ # adds x axis
label
  facet_rep_wrap(vars(predation), nrow = 3,ncol=2,repeat.tick.labels =
```

```
'all')#makes the plot  panelled per predation level. connected with lemon
package, also makes sure that all subplots have axes ticks
```

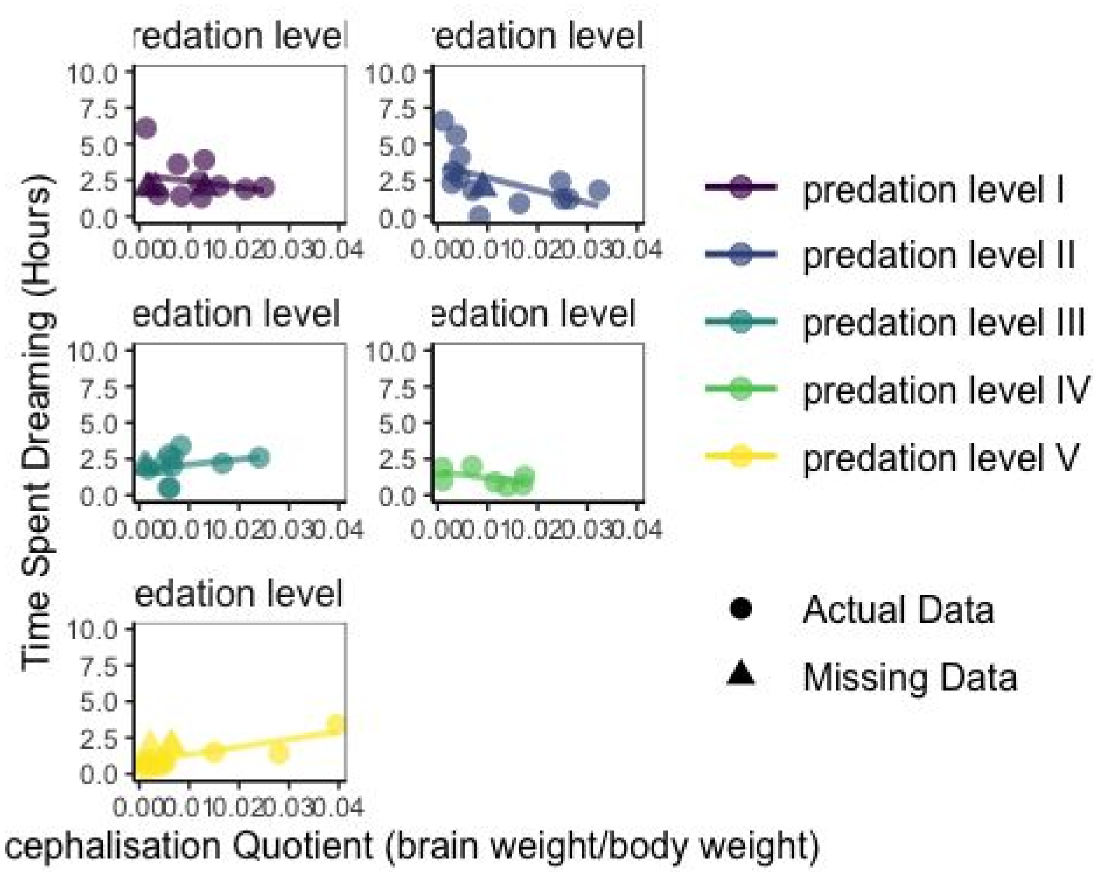



```
#a quarter of each level is missing data so might worth exploring for
limitations
#data frame with imputed mean for missing data run this before running the
plots and after deciding
#whether it's worth imputing data
mean.impute.mammal.sleep <- mammal.sleep %>%
  mutate(dreaming= replace(dreaming, #replace dreaming data with average
dreaming rate for all species
                   is.na(dreaming),
                   mean(dreaming, na.rm = TRUE)))

#panelled correlation plots without missing data
#ggplot 2 removes missing data automatically so no filtering is required
ggplot(mammal.sleep,aes(x = EQ, y = dreaming,colour= predation)) + #colours
```

```
them by predation level
  ylim(0,10)+ #adds zero to y axis
  geom_point(size = 3) +
  geom_smooth(method=lm,formula=y~x,se=F)+ #for linear regression line
  scale_color_ordinal(alpha = 0.65) + #applies colour pallete and makes
points semi transparent to see overlap
  xlab('Encephalisation Quotient (brain weight/body weight)')+# adds x axis
label
  ylab('Time Spent Dreaming (Hours)')+
  theme_apa()+ #removes grey theme
  theme(axis.line=element_line()) + #adds lines
  facet_rep_wrap(vars(predation), nrow = 3,ncol=2,repeat.tick.labels =
'all')# panels and axis labels

## Warning: Removed 12 rows containing non-finite values (stat_smooth).

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

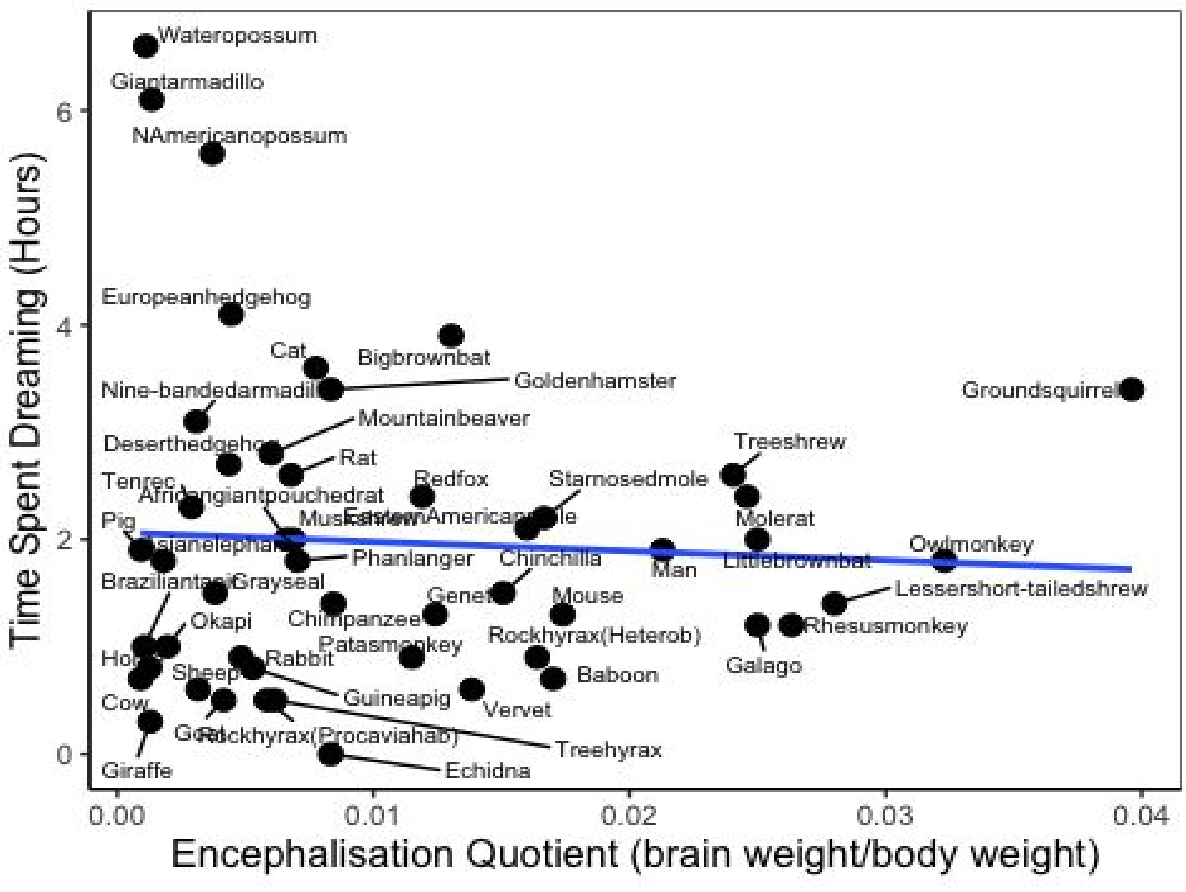


```
#imputed missing data plot
ggplot(mean.impute.mammal.sleep,aes(x = EQ, y = dreaming,group=predation,
,colour=predation, shape=sleep.missing)) + # marks the imputed missing data
with a different shape
  geom_point(size = 3) +
  geom_smooth(method=lm,formula=y~x,se=F)+ #for linear regression line
  scale_color_ordinal(alpha=0.65) + #applies colour pallete
  ylim(0,10)+
  xlab('Encephalisation Quotient (brain weight/body weight)')+# adds x axis
label
  ylab('Time Spent Dreaming (Hours)')+
  theme_apa()+ #removes grey theme
  theme(axis.line=element_line(),) + #adds lines
  facet_rep_wrap(vars(predation), nrow = 3,ncol=2,repeat.tick.labels =
'all')# panels and axis labels
```



```
#one whole graph for all
 ggplot(mammal.sleep,aes(x = EQ,y = dreaming,label=species)) +
  geom_point(size = 3) +
  geom_smooth(method=lm,formula=y~x,se=F)+ #for linear regression line
  geom_text_repel(size=2.5)+# labels data points per species.will be shown as
part of limitation of EQ as a measure
  xlab('Encephalisation Quotient (brain weight/body weight)')+# adds x axis
label
  ylab('Time Spent Dreaming (Hours)')+
  theme_apa()+ #removes grey theme
  theme(axis.line=element_line()) #adds lines
```

```
## Warning: Removed 12 rows containing non-finite values (stat_smooth).

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

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



Member Contributions:

Ezekiel Gading (214629042)- chose the data set, hypothesis, and style of visualisation; wrote and compiled all of the code including comments, explored the data for inaccuracies/ limitations (e.g. missing data etc.,) interpreted the graphs and descriptives in the write up as well as the in depth explanation of the question, goals and results as well as limitations. Provided all but 1 of the references listed, reported to team members the results of analyses and code. Formatted the write up including figure captions, order of plots, and appendices

Kimberly Nguyen (216597162) - Part of the write-up

Shaya Samet (216848731) - Conducted literature search on the validity of encephalization quotient as a measure of cognitive complexity, provided APA citation and reference. Read through and verified R code. Contributed to write-up.