

# Problem set, group 3

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```
# keep this chunk in all your RMarkdown scripts
```

```
knitr::opts_chunk$set(echo = TRUE)
```

```
knitr::opts_chunk$set(tidy.opts = list(width.cutoff = 60), tidy = TRUE)
```

```
# List required packages
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
## v dplyr      1.1.4      v readr      2.1.5
```

```
## v forcats    1.0.0      v stringr    1.5.1
```

```
## v ggplot2    3.5.1      v tibble     3.2.1
```

```
## v lubridate  1.9.3      v tidyr      1.3.1
```

```
## v purrr      1.0.2
```

```
## -- 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(openxlsx)
```

```
library(ppcor)
```

```
## Loading required package: MASS
```

```
##
```

```
## Attaching package: 'MASS'
```

```
##
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##      select
```

```
library(table1)
```

```
##
```

```
## Attaching package: 'table1'
```

```
##
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      units, units<-
```

```
library(lmtest)
```

```
## Loading required package: zoo
##
## Attaching package: 'zoo'
##
## The following objects are masked from 'package:base':
##
##      as.Date, as.Date.numeric
```

```
library(janitor)
```

```
##
## Attaching package: 'janitor'
##
## The following objects are masked from 'package:stats':
##
##      chisq.test, fisher.test
```

```
library(dplyr)
```

```
# Initial data loading
mammals_sleep <- read.xlsx("mammals_sleep.xlsx")

# Cleaning column names
colnames(mammals_sleep) <- sub(pattern = "\\.(.*?)\\", replacement = "",
  colnames(mammals_sleep))
colnames(mammals_sleep) <- sub(pattern = "\\((.*?)\\", replacement = "",
  colnames(mammals_sleep))
mammals_sleep <- clean_names(mammals_sleep)

# Update cells with missing data to NA
mammals_sleep[mammals_sleep == -999] <- NA

# Rename columns
mammals_sleep <- mammals_sleep %>%
  rename(SWS = slow_wave_sleep, PS = paradoxical_sleep)

# Calculate proportion of dreaming sleep - for analysis 1
mammals_sleep$dream_sleep_ratio <- (mammals_sleep$PS/mammals_sleep$total_sleep) *
  100

# Add predator_status column - for analysis 2
mammals_sleep <- mammals_sleep %>%
  mutate(predator_status = ifelse(sleep_exposure_index <= 2,
    "Low Exposure", "High Exposure"))

# Transform type into factor - for analysis 3
mammals_sleep <- mammals_sleep %>%
  mutate(predation_index = as.factor(predation_index))

# Add weight_group column - for analysis 4
```

```

mammals_sleep <- mammals_sleep %>%
  mutate(weight_group = cut(body_weight, breaks = c(0, 0.9,
    9, 99, 1999, Inf), labels = c("lightest", "light", "midweight",
    "heavy", "heaviest")))

## Analysis 1

# Filter data to only include needed columns
filtered_mammals_a1 <- mammals_sleep[, c("brain_weight_body_weight_percent",
  "dream_sleep_ratio")]

# Remove rows with invalid or missing values
filtered_mammals_a1 <- na.omit(filtered_mammals_a1)

# Summary Statistics
table1(data = filtered_mammals_a1, ~brain_weight_body_weight_percent +
  dream_sleep_ratio, topclass = "Rtable1-zebra", rowlabelhead = "Variables")

```

Variables	Overall
	(N=48)
<b>brain_weight_body_weight_percent</b>	
Mean (SD)	1.11 (0.944)
Median [Min, Max]	0.740 [0.0910, 3.96]
<b>dream_sleep_ratio</b>	
Mean (SD)	18.6 (8.95)
Median [Min, Max]	17.6 [0, 46.2]

```

# Perform linear regression
model <- lm(dream_sleep_ratio ~ brain_weight_body_weight_percent,
  data = filtered_mammals_a1)

# Summary of the model
summary(model)

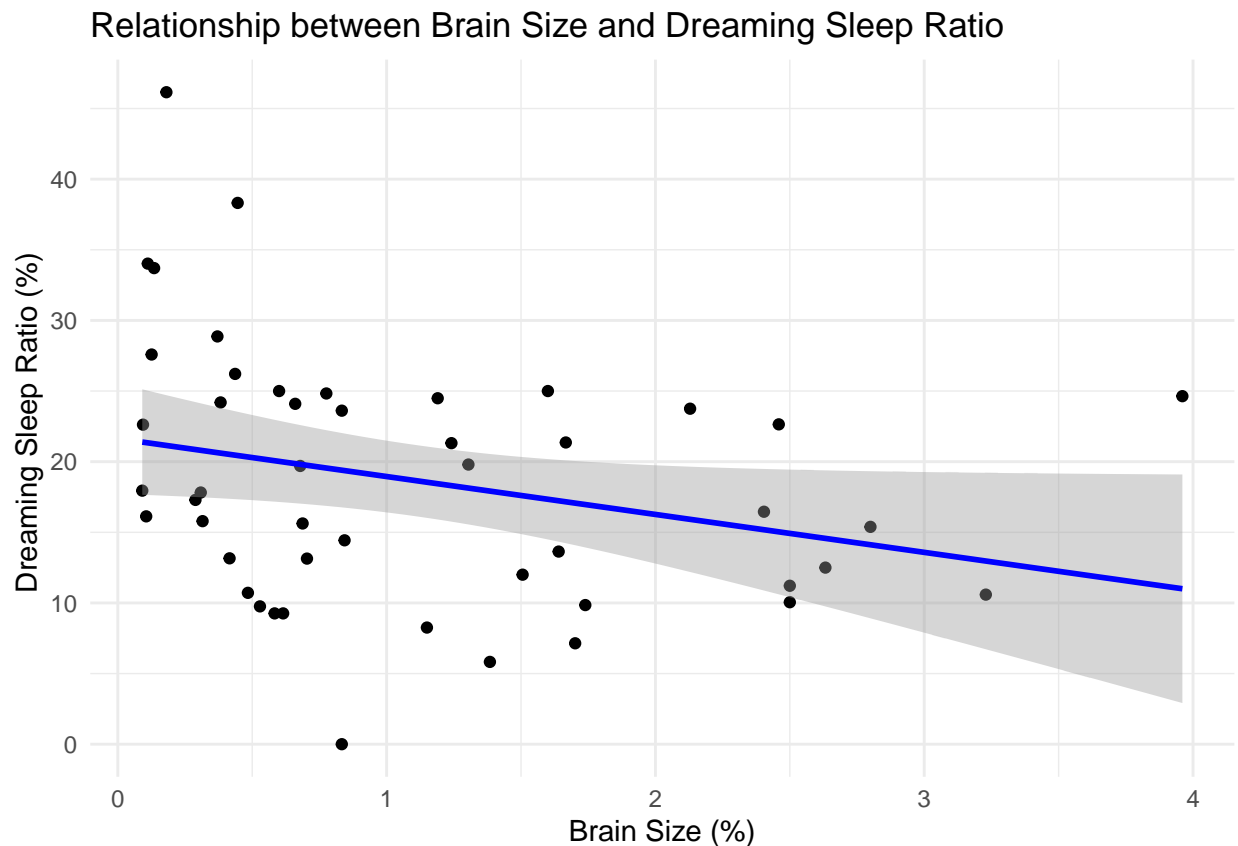
##
## Call:
## lm(formula = dream_sleep_ratio ~ brain_weight_body_weight_percent,
##     data = filtered_mammals_a1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.396  -5.312  -1.091   5.396  25.007
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      21.632      1.947  11.109 1.29e-14 ***
## brain_weight_body_weight_percent  -2.684      1.341  -2.002  0.0513 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.679 on 46 degrees of freedom

```

```
## Multiple R-squared:  0.08011,    Adjusted R-squared:  0.06012
## F-statistic: 4.006 on 1 and 46 DF,  p-value: 0.05125
```

```
# Plot the relationship
ggplot(filtered_mammals_a1, aes(x = brain_weight_body_weight_percent,
  y = dream_sleep_ratio)) + geom_point() + geom_smooth(method = "lm",
  color = "blue") + labs(title = "Relationship between Brain Size and Dreaming Sleep Ratio",
  x = "Brain Size (%)", y = "Dreaming Sleep Ratio (%) ") +
  theme_minimal()
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```



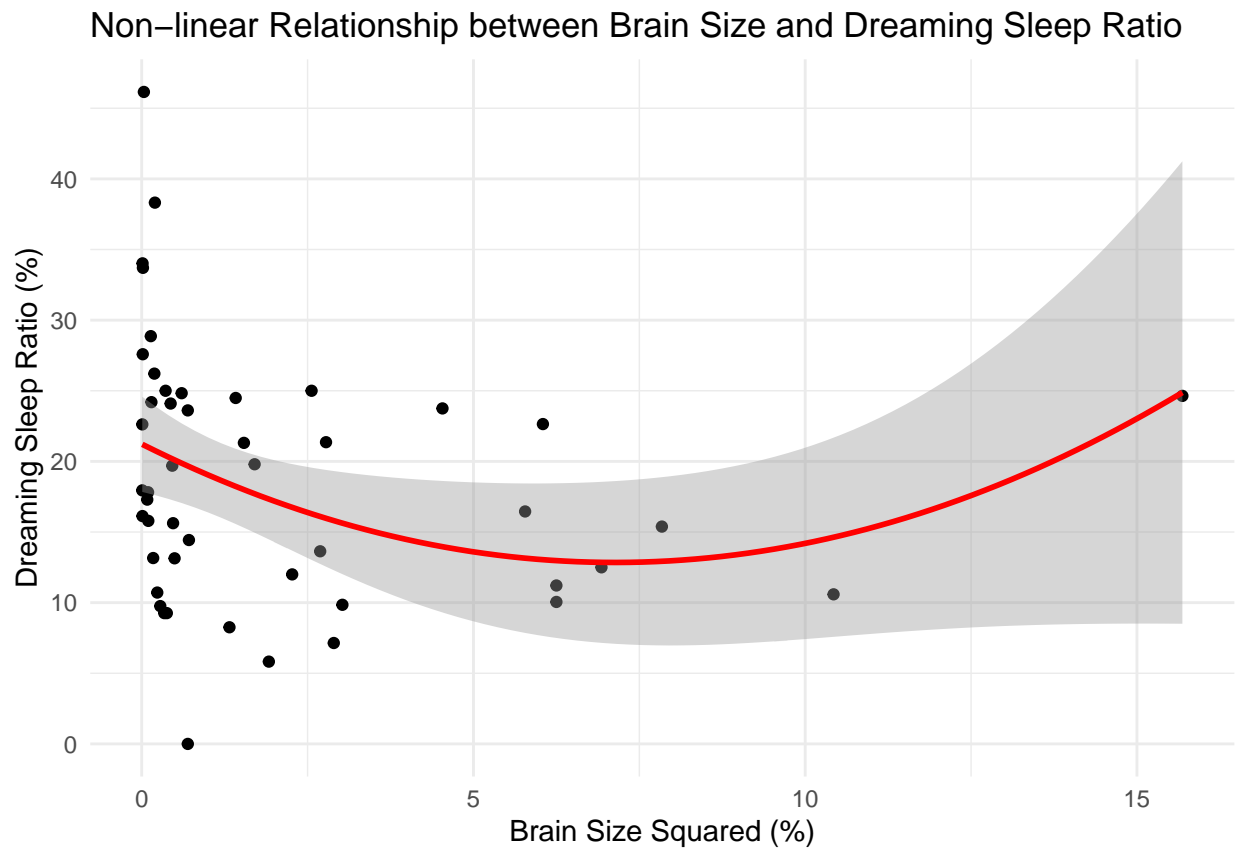
```
# Non-linear
filtered_non_linear <- filtered_mammals_a1 %>%
  mutate(brain_size_sq = brain_weight_body_weight_percent^2)

nonlinear_model <- lm(dream_sleep_ratio ~ brain_weight_body_weight_percent +
  brain_size_sq, data = filtered_non_linear)
summary(nonlinear_model)
```

```
##
## Call:
## lm(formula = dream_sleep_ratio ~ brain_weight_body_weight_percent +
##     brain_size_sq, data = filtered_non_linear)
```

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.869  -6.626  -1.092   5.782  22.314
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      25.936      2.557   10.143 3.33e-13 ***
## brain_weight_body_weight_percent -12.129      4.078   -2.974  0.00471 **
## brain_size_sq       2.939      1.205    2.438  0.01877 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.247 on 45 degrees of freedom
## Multiple R-squared:  0.1875, Adjusted R-squared:  0.1514
## F-statistic: 5.191 on 2 and 45 DF,  p-value: 0.009364
```

```
# Plot quadratic relationship
ggplot(filtered_non_linear, aes(x = brain_size_sq, y = dream_sleep_ratio)) +
  geom_point() + geom_smooth(method = "lm", formula = y ~ x +
    I(x^2), color = "red") + labs(title = "Non-linear Relationship between Brain Size and Dreaming Sleep",
    x = "Brain Size Squared (%)", y = "Dreaming Sleep Ratio (%)") +
  theme_minimal()
```



## ## Analysis 2

```
grouped_data_a2 <- mammals_sleep %>%
  dplyr::select(brain_weight_body_weight_percent, PS, total_sleep,
    predator_status) %>%
  filter(!is.na(brain_weight_body_weight_percent) & !is.na(PS) &
    !is.na(total_sleep) & !is.na(predator_status)) %>%
  mutate(dream_sleep_ratio = (PS/total_sleep) * 100)
```

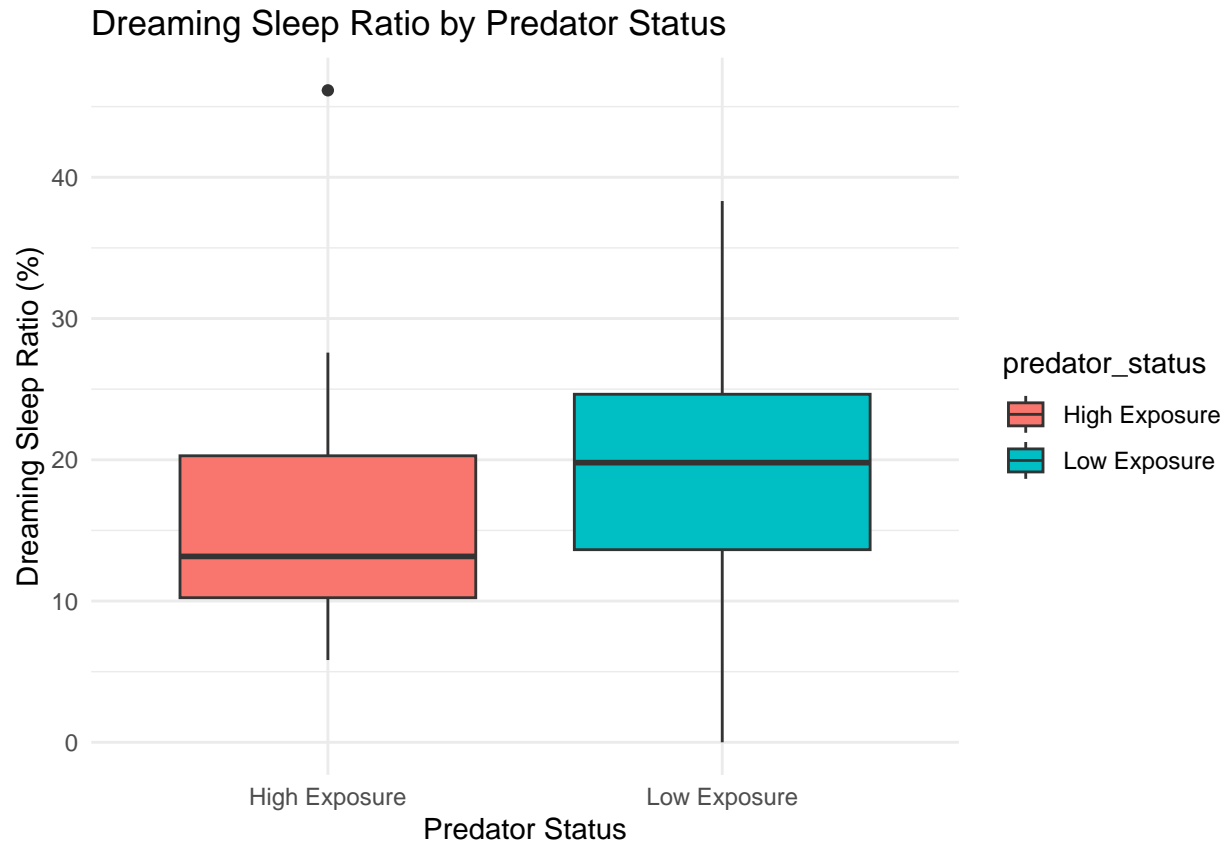
### # summary stats

```
table1(data = grouped_data_a2, ~brain_weight_body_weight_percent +
  dream_sleep_ratio | predator_status, topclass = "Rtable1-zebra",
  rowlabelhead = "Variables")
```

Variables	High Exposure	Low Exposure	Overall
	(N=15)	(N=33)	(N=48)
<b>brain_weight_body_weight_percent</b>			
Mean (SD)	0.740 (0.762)	1.28 (0.980)	1.11 (0.944)
Median [Min, Max]	0.416 [0.0910, 2.63]	0.833 [0.111, 3.96]	0.740 [0.0910, 3.96]
<b>dream_sleep_ratio</b>			
Mean (SD)	16.7 (10.3)	19.6 (8.26)	18.6 (8.95)
Median [Min, Max]	13.2 [5.83, 46.2]	19.8 [0, 38.3]	17.6 [0, 46.2]

### # Boxplot of predator status vs. dreaming sleep ratio

```
ggplot(grouped_data_a2, aes(x = predator_status, y = dream_sleep_ratio,
  fill = predator_status)) + geom_boxplot() + labs(title = "Dreaming Sleep Ratio by Predator Status",
  x = "Predator Status", y = "Dreaming Sleep Ratio (%)") +
  theme_minimal()
```



```
# Test group differences (e.g., t-test)
t_test_predator_status <- t.test(dream_sleep_ratio ~ predator_status,
  data = grouped_data_a2)
t_test_predator_status
```

```
##
## Welch Two Sample t-test
##
## data: dream_sleep_ratio by predator_status
## t = -0.95773, df = 22.467, p-value = 0.3484
## alternative hypothesis: true difference in means between group High Exposure and group Low Exposure is not equal to 0
## 95 percent confidence interval:
## -9.185580 3.377063
## sample estimates:
## mean in group High Exposure mean in group Low Exposure
## 16.65154 19.55580
```

#### ## Analysis 3

```
# Reformat data to longer pivot with selected columns
select_predation_pivot <- mammals_sleep %>%
  dplyr::select(species, predation_index, SWS, PS, total_sleep) %>%
  pivot_longer(cols = c(SWS, PS, total_sleep), names_to = "sleep_pattern",
    values_to = "sleep_time")
```

```

# Summary of central tendency, variables, confidence
# intervals
summary_total_sleep <- mammals_sleep %>%
  drop_na(total_sleep) %>%
  group_by(predation_index) %>%
  summarise(mean_sleep = mean(total_sleep), sd = sd(total_sleep),
            median = median(total_sleep), number = n(), low_CI = mean(total_sleep) -
              1.96 * sd(total_sleep)/sqrt(n()), high_CI = mean(total_sleep) +
              1.96 * sd(total_sleep)/sqrt(n()))

table1(data = mammals_sleep, ~total_sleep | predation_index,
       topclass = "Rtable1-zebra", rowlabelhead = "Variables")

```

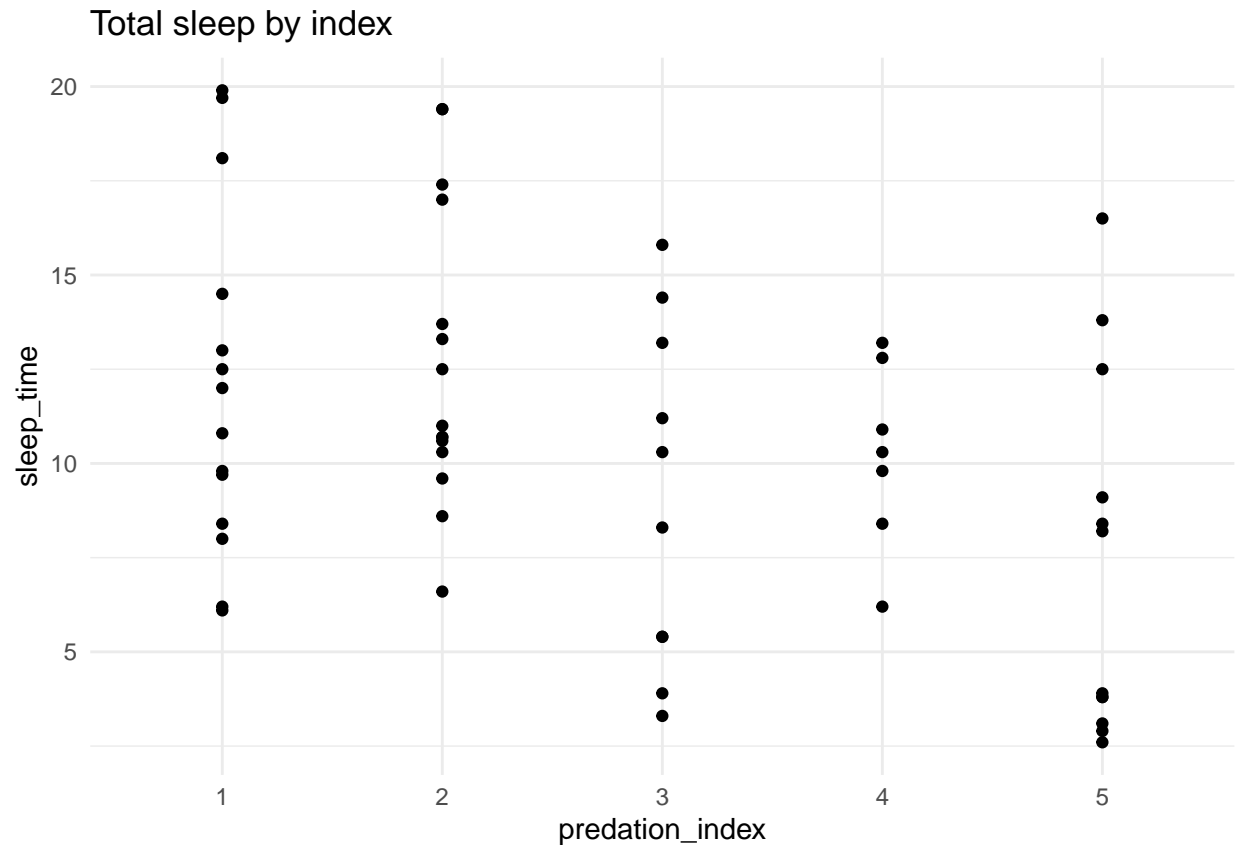
Variables	1	2	3	4	5	Overall
	(N=14)	(N=15)	(N=12)	(N=7)	(N=14)	(N=62)
<b>total_sleep</b>						
Mean (SD)	12.1 (4.60)	12.7 (3.93)	9.12 (4.53)	10.2 (2.44)	7.38 (4.81)	10.5 (4.53)
Median [Min, Max]	11.4 [6.10, 19.9]	11.0 [6.60, 19.4]	9.30 [3.30, 15.8]	10.3 [6.20, 13.2]	6.05 [2.60, 16.5]	10.5 [2.60, 19.9]
Missing	0 (0%)	0 (0%)	2 (16.7%)	0 (0%)	2 (14.3%)	4 (6.5%)

```

# Scatter plot of sleep time and index
select_predation_pivot %>%
  drop_na(sleep_time) %>%
  group_by(predation_index) %>%
  filter(sleep_pattern == "total_sleep") %>%
  ggplot(aes(x = predation_index, y = sleep_time)) + geom_point() +
  labs(title = "Total sleep by index") + theme_minimal()

```

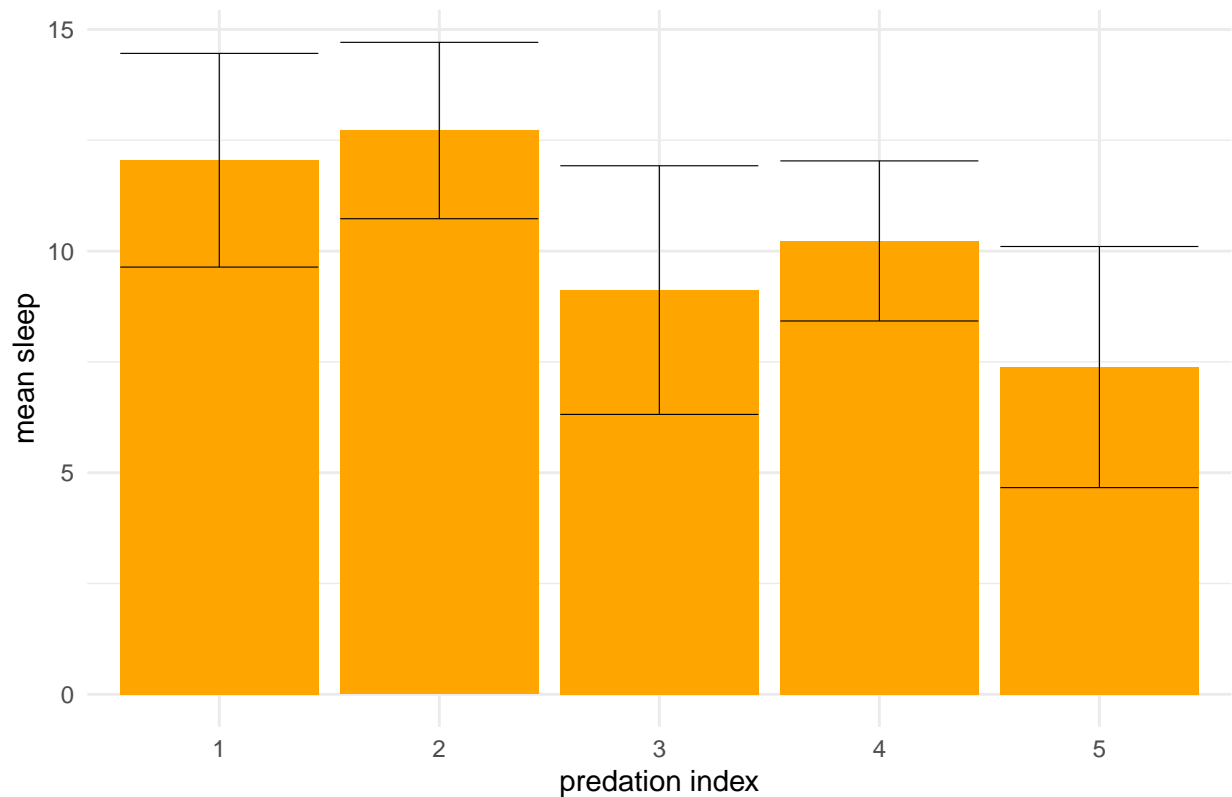




```
# Bar graph of average sleep duration by predation index
summary_total_sleep %>%
  ggplot(aes(x = predation_index, y = mean_sleep)) + geom_bar(stat = "identity",
    fill = "orange") + geom_errorbar(aes(ymin = low_CI, ymax = high_CI),
    size = 0.2) + labs(title = "Bar graph of average total sleep in hours/day",
    x = "predation index", y = "mean sleep") + theme(plot.title = element_text(size = 10),
    plot.caption = element_text(size = 10)) + theme_minimal()
```

```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use 'linewidth' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

Bar graph of average total sleep in hours/day



```
# Boxplot of sleep duration for each predation index
mammals_sleep %>%
  drop_na(total_sleep) %>%
  ggplot(aes(x = factor(predation_index), y = total_sleep)) +
  geom_boxplot(, color = "orange", fill = "pink") + labs(title = "Boxplot of total sleep time by predation index",
  x = "predation index", y = "total sleep", caption = "Figure 2: Boxplot of total sleep time in hours
  of mammals for each predation levels") +
  theme(plot.title = element_text(size = 10), plot.caption = element_text(size = 10,
    hjust = 0.5)) + theme_minimal()
```

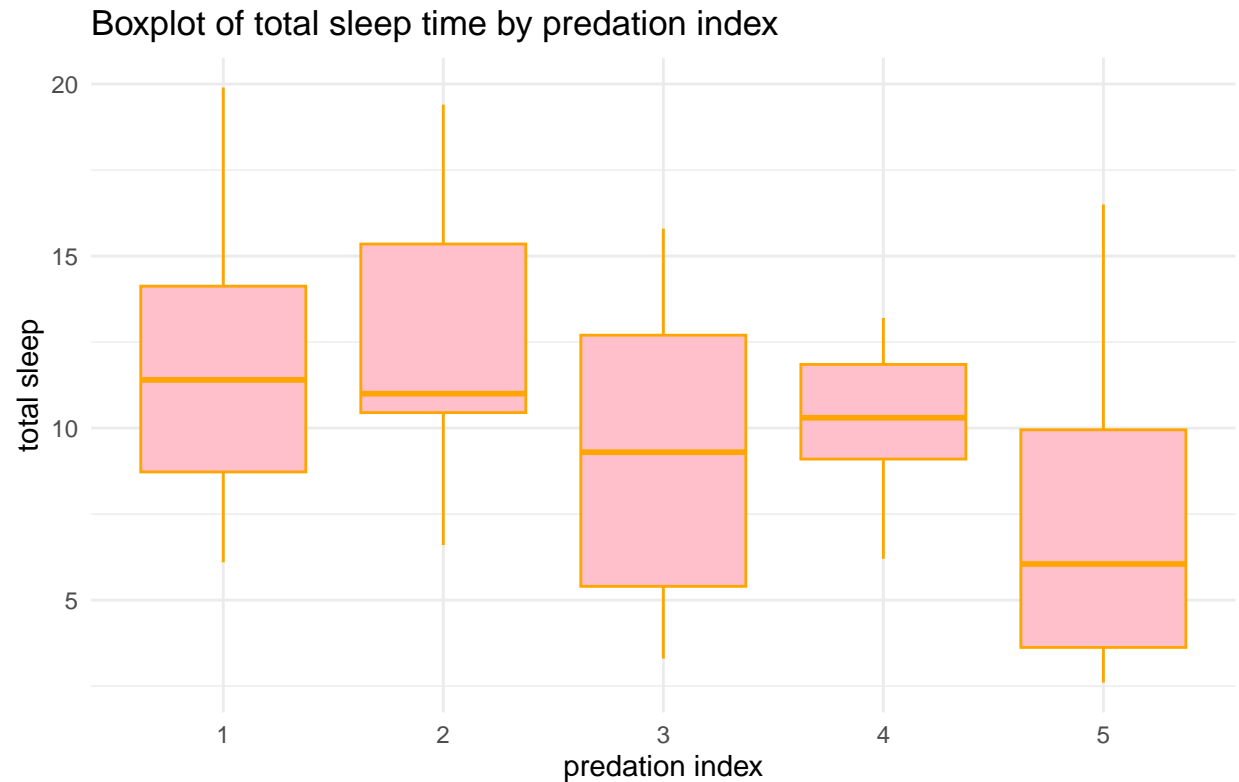


Figure 2: Boxplot of total sleep time in hours per day of mammals for each predation levels

```
# Linear regression between index level and total sleep
lm_totalsleep <- mammals_sleep %>%
  drop_na(total_sleep) %>%
  lm(total_sleep ~ predation_index, data = .)
summary(lm_totalsleep)
```

```
##
## Call:
## lm(formula = total_sleep ~ predation_index, data = .)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.1200 -3.5833 -0.3243  2.5411  9.1167
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    12.050     1.141   10.561 1.21e-14 ***
## predation_index2    0.670     1.587    0.422  0.67451
## predation_index3   -2.930     1.768   -1.658  0.10332
## predation_index4   -1.821     1.976   -0.922  0.36090
## predation_index5   -4.667     1.680   -2.779  0.00754 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.269 on 53 degrees of freedom
## Multiple R-squared:  0.2014, Adjusted R-squared:  0.1411
```

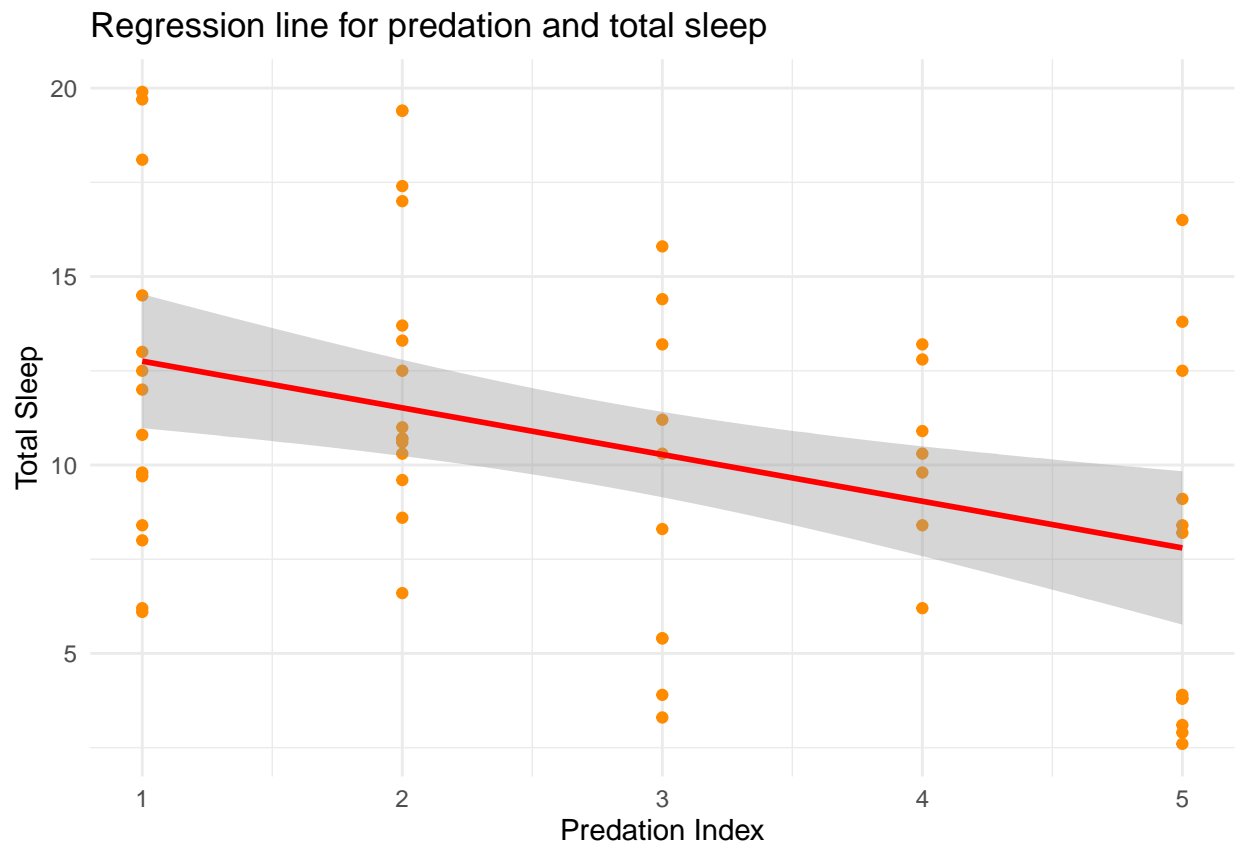
```
## F-statistic: 3.341 on 4 and 53 DF, p-value: 0.01636
```

```
# Linear regression graph with confidence interval  
ggplot(mammals_sleep, aes(x = as.numeric(predation_index), y = total_sleep)) +  
  geom_point(color = "dark orange") + theme_minimal() + geom_smooth(method = "lm",  
    se = TRUE, color = "red") + labs(title = "Regression line for predation and total sleep",  
    x = "Predation Index", y = "Total Sleep") + theme(plot.title = element_text(size = 9)) +  
  theme_minimal()
```

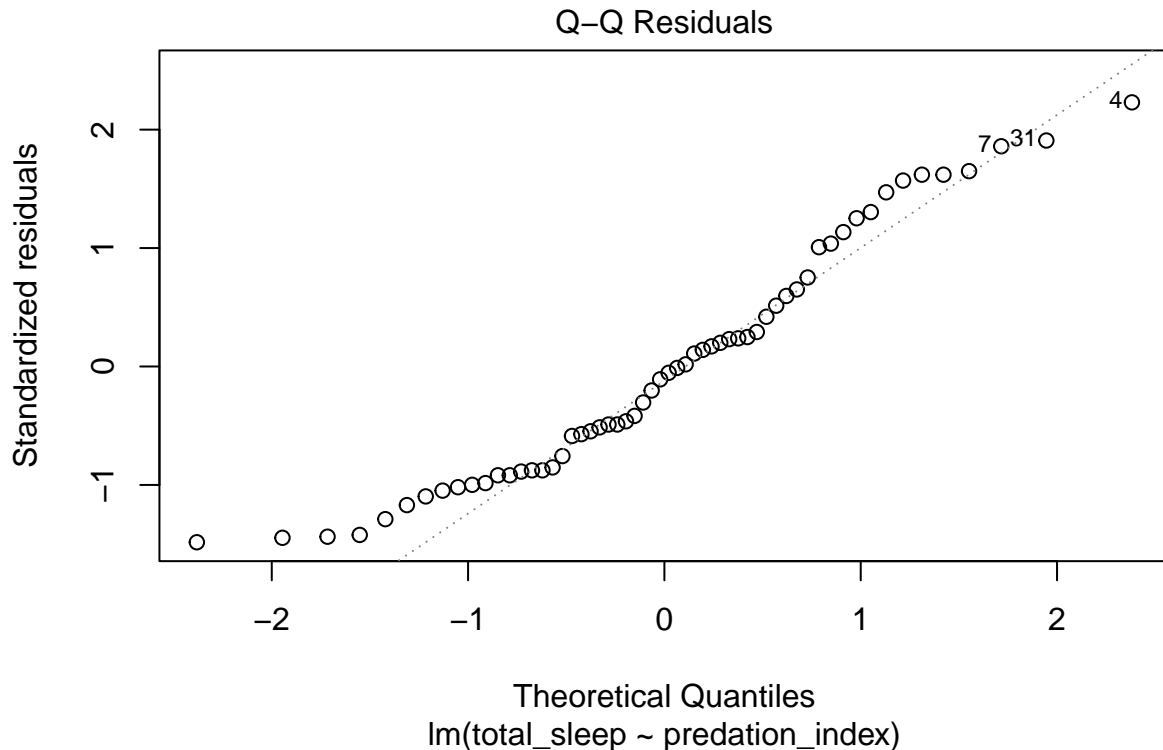
```
## 'geom_smooth()' using formula = 'y ~ x'
```

```
## Warning: Removed 4 rows containing non-finite outside the scale range  
## ('stat_smooth()').
```

```
## Warning: Removed 4 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



```
# Check assumptions for residuals normal distribution  
plot(lm_totalsleep, which = 2)
```



```
# Confidence interval for slope
confint(lm_totalsleep)
```

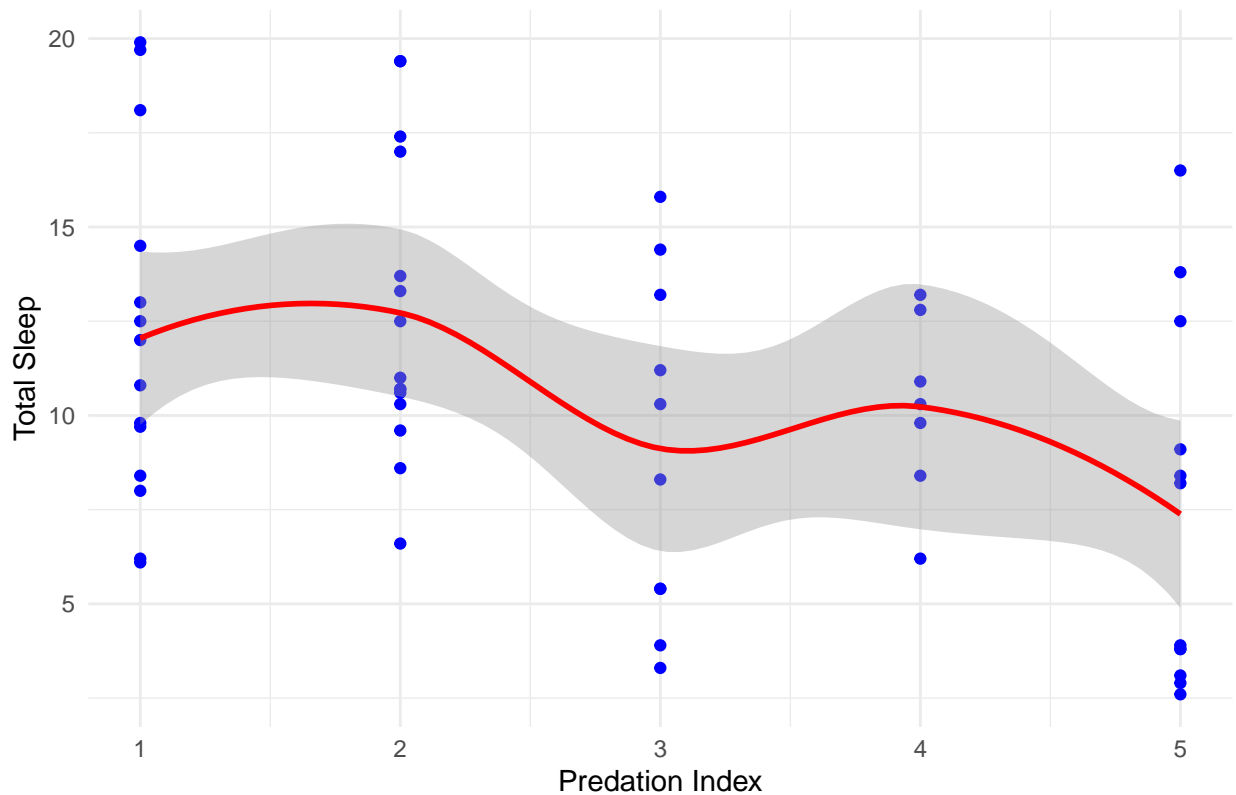
```
##              2.5 %      97.5 %
## (Intercept)  9.761384 14.3386157
## predation_index2 -2.512191  3.8521910
## predation_index3 -6.475508  0.6155082
## predation_index4 -5.785427  2.1425701
## predation_index5 -8.035418 -1.2979156
```

```
# Assess linearity with LOESS
ggplot(mammals_sleep, aes(x = as.numeric(predation_index), y = total_sleep)) +
  geom_point(color = "blue") + geom_smooth(method = "loess",
  se = TRUE, color = "red") + labs(title = "LOESS for predation index and total sleep",
  x = "Predation Index", y = "Total Sleep") + theme(plot.title = element_text(size = 9)) +
  theme_minimal()
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```

```
## Warning: Removed 4 rows containing non-finite outside the scale range ('stat_smooth()').
## Removed 4 rows containing missing values or values outside the scale range
## ('geom_point()').
```

## LOESS for predation index and total sleep



```
# independence of residuals, Durbin-Watson test
dwtest(lm_totalsleep)
```

```
##
## Durbin-Watson test
##
## data:  lm_totalsleep
## DW = 1.9047, p-value = 0.3321
## alternative hypothesis: true autocorrelation is greater than 0
```

### ## Analysis 4

```
# Summary table for mean graphs
summary_table_weight <- mammals_sleep %>%
  group_by(weight_group) %>%
  summarize(total = n(), mean_gest = mean(gestation_time, na.rm = TRUE),
            sd_gest = sd(gestation_time, na.rm = TRUE), se_gest = sd_gest/sqrt(n()),
            CI_low_gest = mean_gest - 1.96 * se_gest, CI_high_gest = mean_gest +
              1.96 * se_gest, mean_sleep = mean(total_sleep, na.rm = TRUE),
            sd_sleep = sd(total_sleep, na.rm = TRUE), se_sleep = sd_sleep/sqrt(n()),
            CI_low_sleep = mean_sleep - 1.96 * se_sleep, CI_high_sleep = mean_sleep +
              1.96 * se_sleep)
summary_table_weight
```

```
## # A tibble: 5 x 12
```

```
## weight_group total mean_gest sd_gest se_gest CI_low_gest CI_high_gest
## <fct> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 lightest 19 61.0 56.4 12.9 35.7 86.4
## 2 light 21 78.4 68.2 14.9 49.2 108.
## 3 midweight 11 170. 84.4 25.5 120. 220.
## 4 heavy 9 298. 123. 40.9 218. 378.
## 5 heaviest 2 634. 14.8 10.5 614. 655.
## # i 5 more variables: mean_sleep <dbl>, sd_sleep <dbl>, se_sleep <dbl>,
## # CI_low_sleep <dbl>, CI_high_sleep <dbl>
```

```
# Descriptive statistics table
```

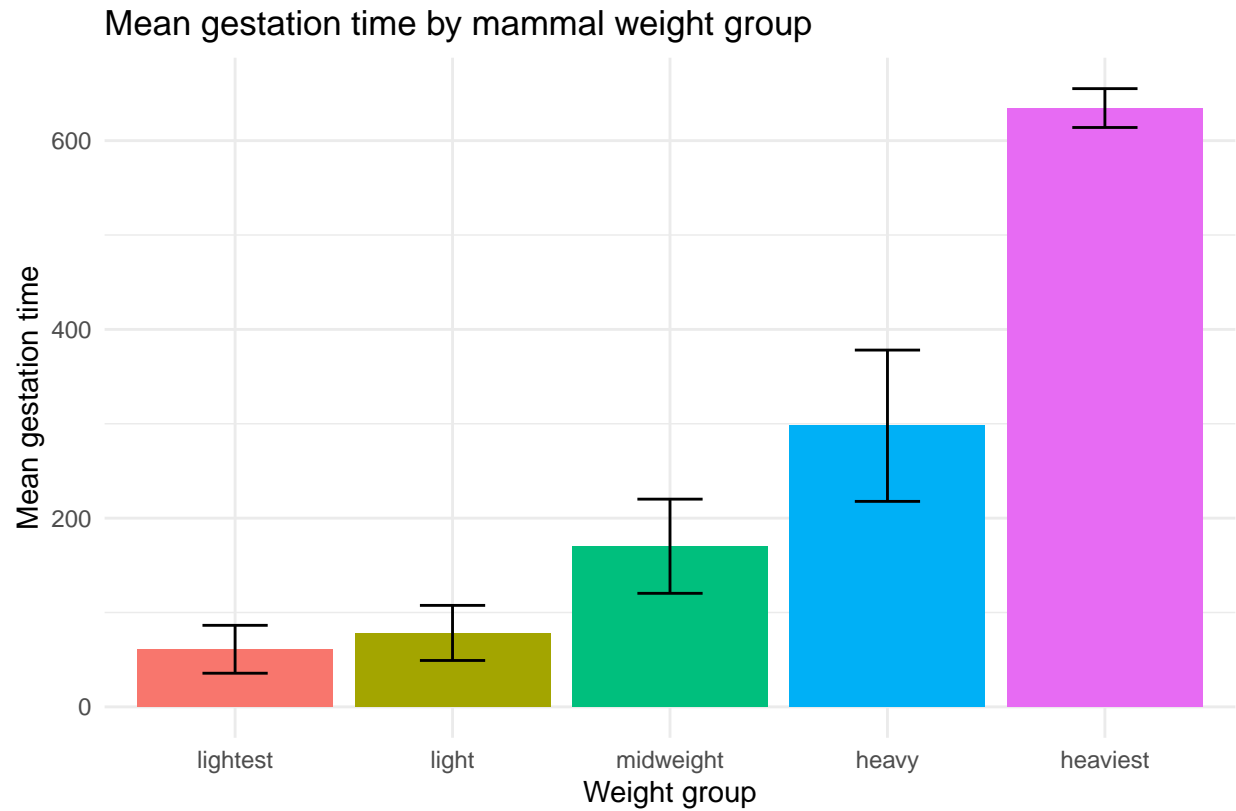
```
table1(data = mammals_sleep, ~gestation_time + body_weight +
  total_sleep | weight_group, topclass = "Rtable1-zebra", rowlabelhead = "Variables")
```

Variables	lightest	light	midweight	heavy	heaviest
	(N=19)	(N=21)	(N=11)	(N=9)	(N=2)
<b>gestation_time</b>					
Mean (SD)	61.0 (56.4)	78.4 (68.2)	170 (84.4)	298 (123)	635 (14.8)
Median [Min, Max]	42.0 [16.0, 225]	56.0 [12.0, 225]	161 [33.0, 310]	336 [100, 440]	635 [624, 645]
Missing	2 (10.5%)	1 (4.8%)	1 (9.1%)	0 (0%)	0 (0%)
<b>body_weight</b>					
Mean (SD)	0.266 (0.292)	2.80 (1.50)	40.8 (24.3)	290 (167)	4600 (2900)
Median [Min, Max]	0.120 [0.00500, 0.900]	3.00 [0.920, 6.80]	36.3 [10.0, 85.0]	207 [100, 529]	4600 [2550, 6650]
<b>total_sleep</b>					
Mean (SD)	12.8 (3.55)	11.4 (4.30)	8.59 (4.78)	6.76 (3.73)	3.60 (0.424)
Median [Min, Max]	12.8 [6.60, 19.9]	10.7 [5.40, 19.4]	8.85 [2.60, 18.1]	6.20 [2.90, 12.0]	3.60 [3.30, 3.90]
Missing	0 (0%)	1 (4.8%)	1 (9.1%)	2 (22.2%)	0 (0%)

```
# Bar chart showing mean gestation time by weight group
```

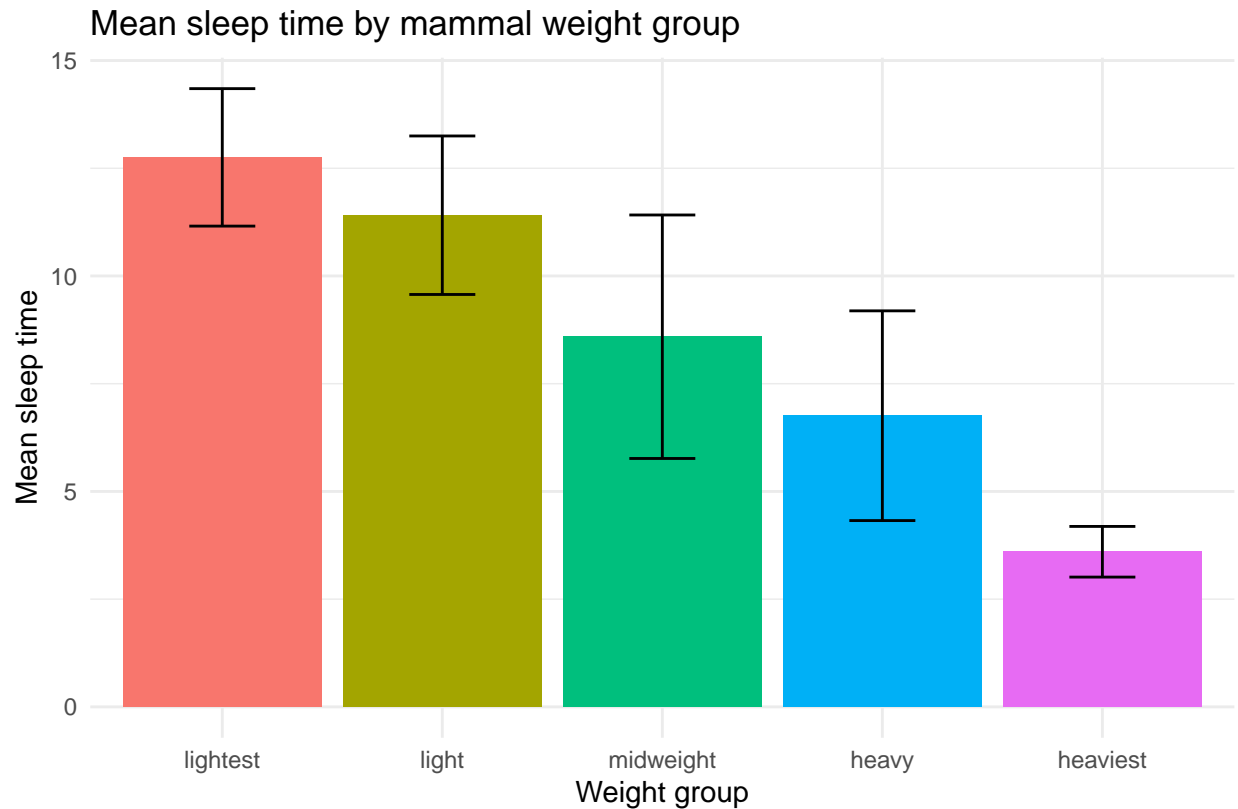
```
summary_table_weight %>%
```

```
ggplot(aes(x = weight_group, y = mean_gest, fill = weight_group)) +
  geom_col(show.legend = FALSE) + geom_errorbar(aes(ymin = CI_low_gest,
  ymax = CI_high_gest), width = 0.3, color = "black") + labs(title = "Mean gestation time by mammal w
  x = "Weight group", y = "Mean gestation time", caption = "Bar graph demonstrating that gestation ti
  theme_minimal()
```



```
# Bar chart showing mean sleep time by weight group
summary_table_weight %>%
  ggplot(aes(x = weight_group, y = mean_sleep, fill = weight_group)) +
  geom_col(show.legend = FALSE) + geom_errorbar(aes(ymin = CI_low_sleep,
  ymax = CI_high_sleep), width = 0.3, color = "black") + labs(title = "Mean sleep time by mammal weight",
  x = "Weight group", y = "Mean sleep time", caption = "Bar graph demonstrating that sleep time decreases as mammal weight increases")
  theme_minimal()
```





```
# Line graph correlation between sleep time and gestation
# time
na.omit(mammals_sleep) %>%
  ggplot(aes(x = total_sleep, y = gestation_time)) + geom_point() +
  geom_smooth(aes(color = "linear"), se = FALSE, method = "lm",
    show.legend = FALSE) + geom_smooth(aes(color = "loess"),
    se = FALSE, span = 0.9, show.legend = FALSE) + labs(title = "Comparing total sleep time to gestation
x = "Total sleep time (hr/day)", y = "Gestation time (days)",
caption = "Figure 8.1: Scatter plot demonstrating relationship between sleep time and gestation time",
theme_minimal()
```

```
## 'geom_smooth()' using formula = 'y ~ x'
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
```

## Comparing total sleep time to gestation time in mammals

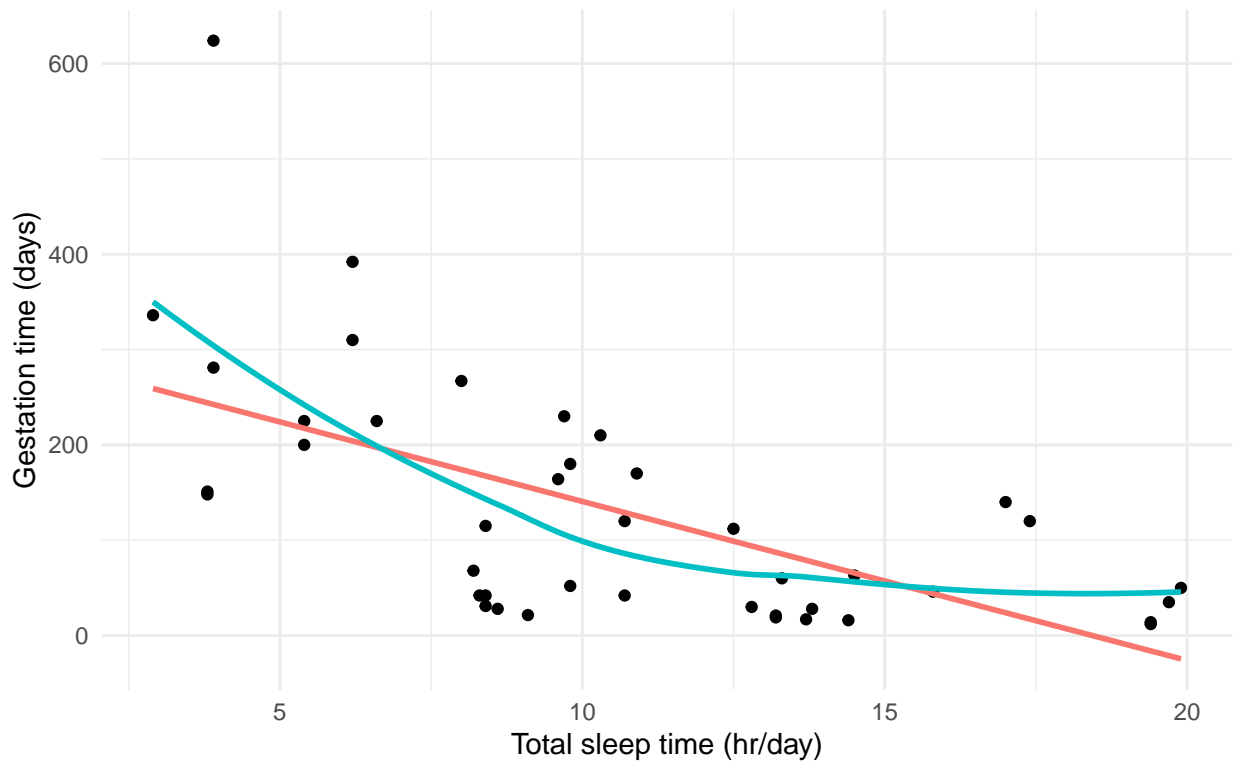


Figure 8.1: Scatter plot demonstrating relationship between sleep time and gestation time

```
# Line graph correlation between sleep time and body weight
na.omit(mammals_sleep) %>%
  ggplot(aes(x = total_sleep, y = body_weight)) + geom_point() +
  geom_smooth(aes(color = "linear"), se = FALSE, method = "lm",
    show.legend = FALSE) + geom_smooth(aes(color = "loess"),
    se = FALSE, span = 0.9, show.legend = FALSE) + labs(title = "Comparing total sleep time to body weight",
    x = "Total sleep time (hr/day)", y = "Body weight (kg)",
    caption = "Figure 8.2: Scatter plot demonstrating relationship between sleep time and body weight")
  theme_minimal()
```

```
## 'geom_smooth()' using formula = 'y ~ x'
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
```

## Comparing total sleep time to body weight in mammals

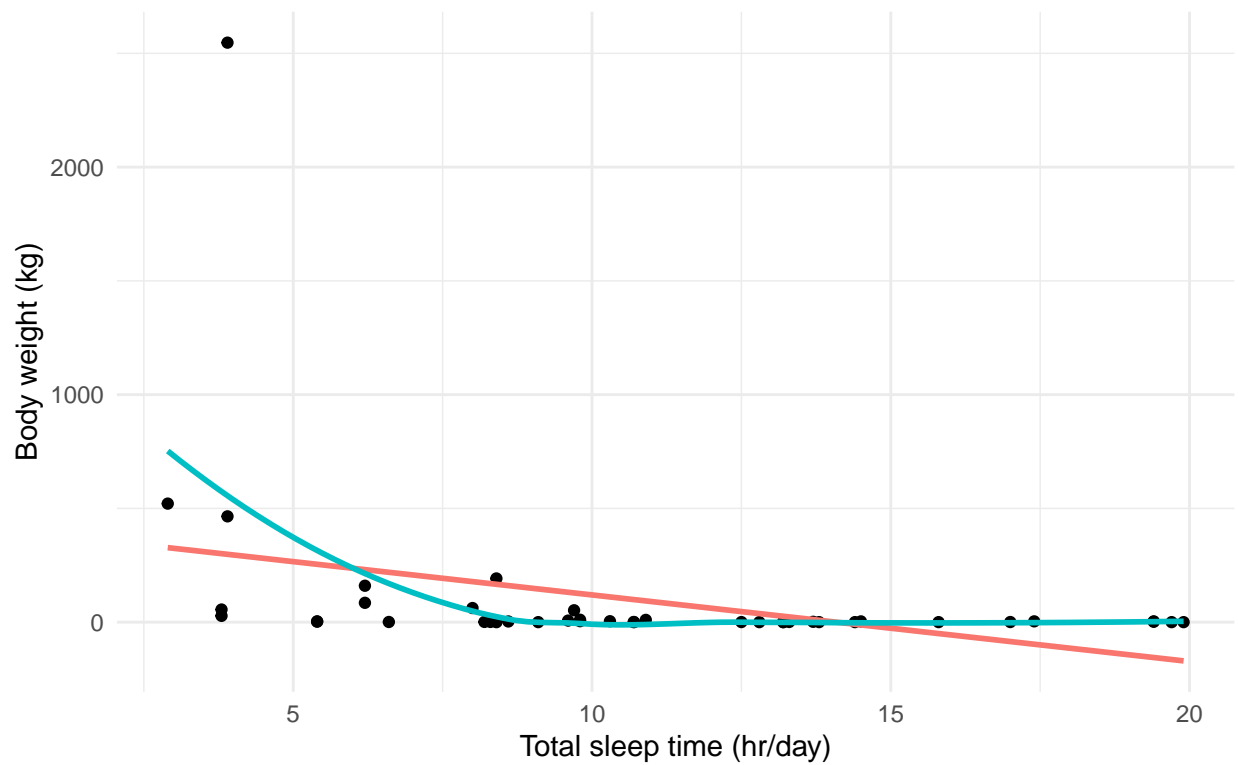


Figure 8.2: Scatter plot demonstrating relationship between sleep time and body weight

```
# Testing for normality qq plot of gestation time data
ggplot(na.omit(mammals_sleep), aes(sample = gestation_time)) +
  stat_qq(show.legend = FALSE) + geom_abline(aes(intercept = mean(x = gestation_time),
  slope = sd(x = gestation_time))) + labs(title = "QQ plot of gestation time data",
  caption = "Figure 7.1") + theme_minimal()
```

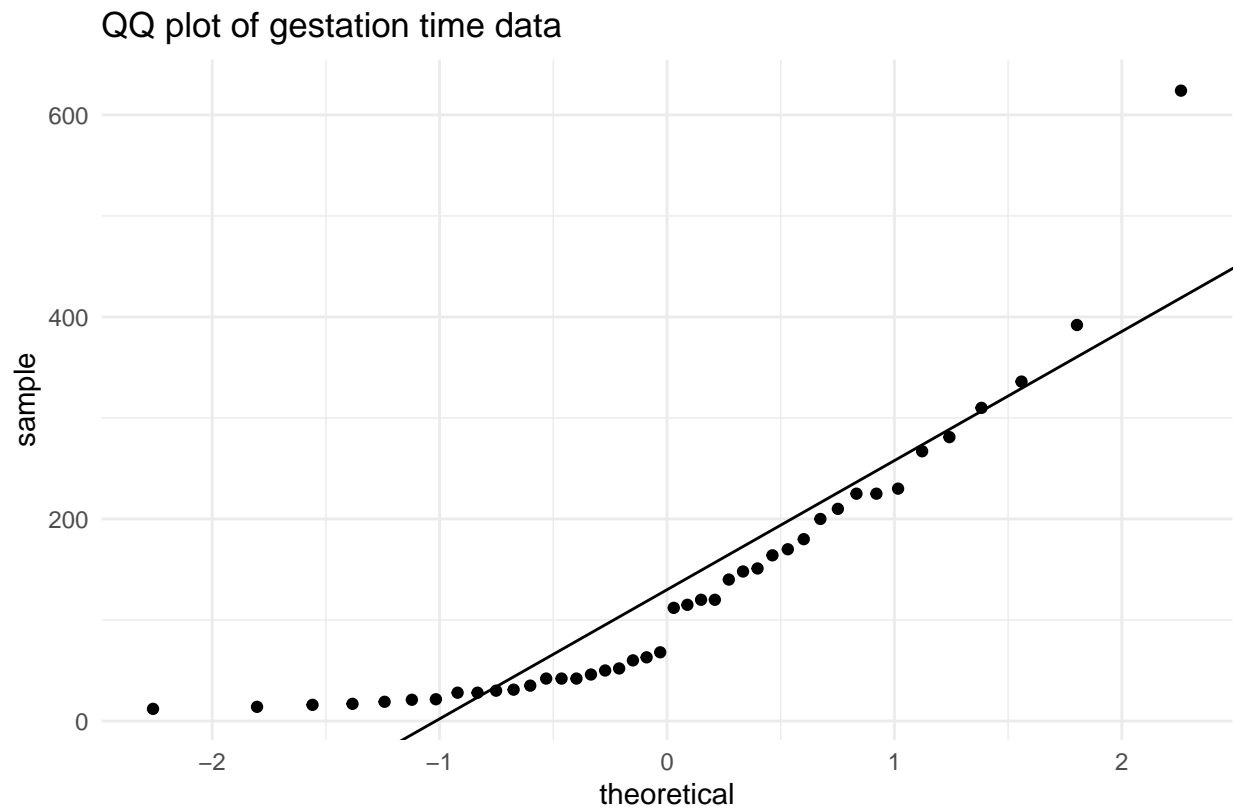


Figure 7.1

```
# qq plot of body weight data
ggplot(na.omit(mammals_sleep), aes(sample = body_weight)) + stat_qq(show.legend = FALSE) +
  geom_abline(aes(intercept = mean(x = gestation_time), slope = sd(x = gestation_time))) +
  labs(title = "QQ plot of body weight data", caption = "Figure 7.2") +
  theme_minimal()
```

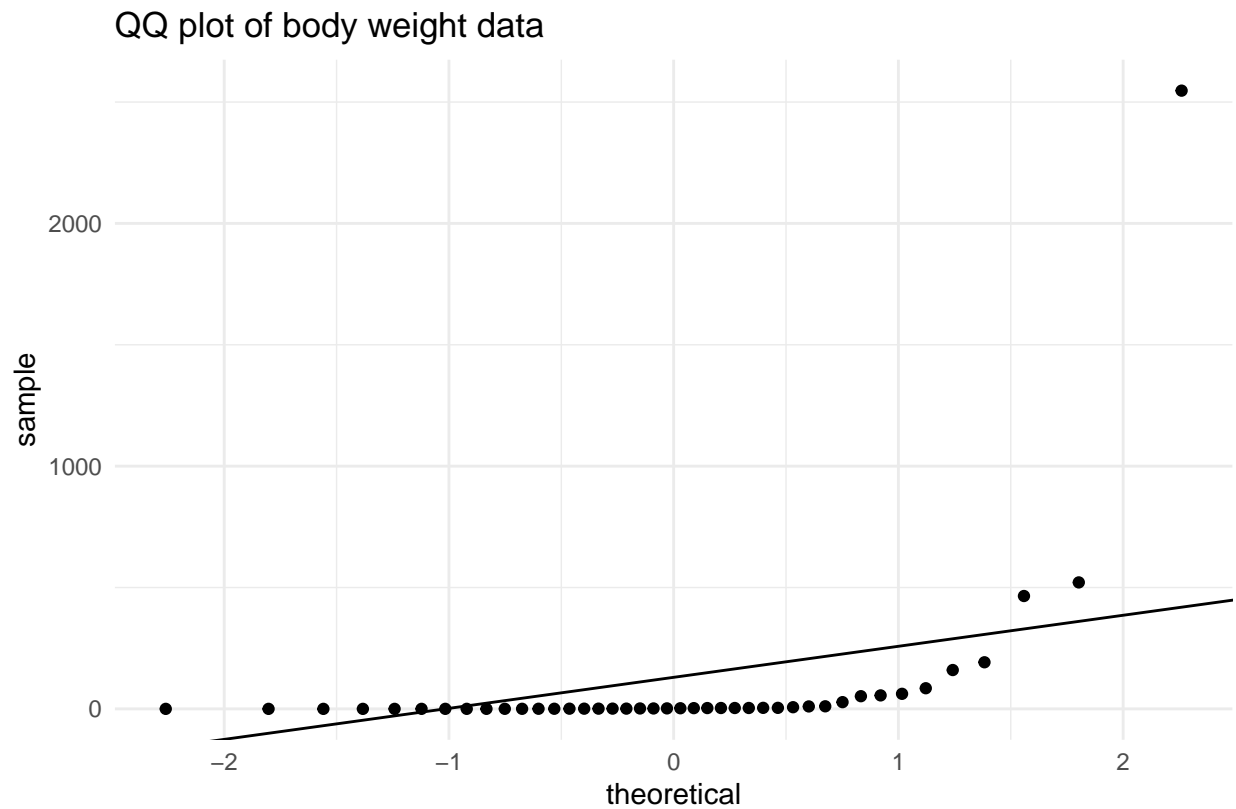


Figure 7.2

```
# qq plot of sleep time data
ggplot(na.omit(mammals_sleep), aes(sample = total_sleep)) + stat_qq(show.legend = FALSE) +
  geom_abline(aes(intercept = mean(x = total_sleep), slope = sd(x = total_sleep))) +
  labs(title = "QQ plot of sleep time data", caption = "Figure 7.3") +
  theme_minimal()
```

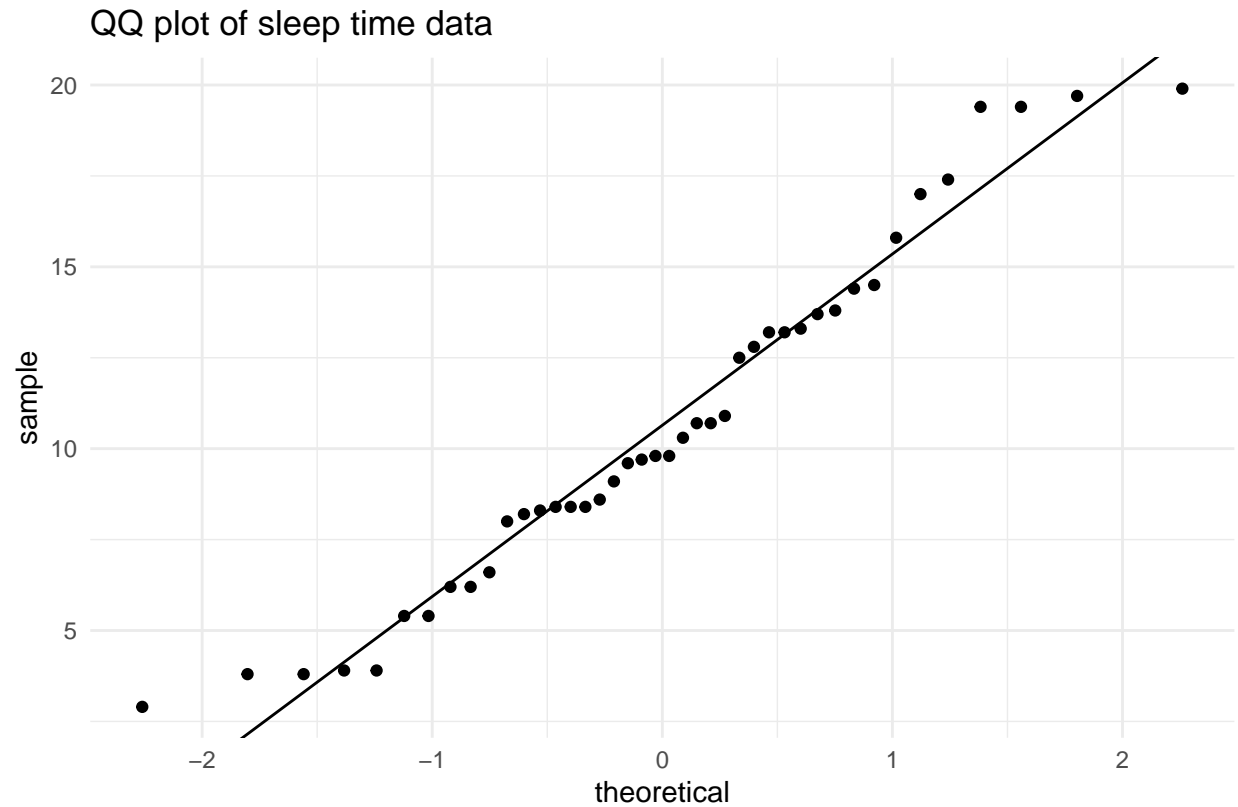


Figure 7.3

```
# Testing for homoscedasticity
bptest(formula = total_sleep ~ gestation_time, data = mammals_sleep) #result is not significant, so homoscedasticity is not rejected

##
## studentized Breusch-Pagan test
##
## data: total_sleep ~ gestation_time
## BP = 0.43886, df = 1, p-value = 0.5077

bptest(formula = total_sleep ~ body_weight, data = mammals_sleep) #result is not significant, so homoscedasticity is not rejected

##
## studentized Breusch-Pagan test
##
## data: total_sleep ~ body_weight
## BP = 0.22225, df = 1, p-value = 0.6373

# Spearman's correlation because gestation data is not normally distributed
cor.test(x = na.omit(mammals_sleep)$total_sleep, y = na.omit(mammals_sleep)$gestation_time,
         method = "spearman", exact = FALSE)

##
## Spearman's rank correlation rho
```

```
##
## data: na.omit(mammals_sleep)$total_sleep and na.omit(mammals_sleep)$gestation_time
## S = 20327, p-value = 3.638e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.6471232

# Spearman's correlation because body weight data is not
# normally distributed
cor.test(x = na.omit(mammals_sleep)$total_sleep, y = na.omit(mammals_sleep)$body_weight,
         method = "spearman", exact = FALSE)

##
## Spearman's rank correlation rho
##
## data: na.omit(mammals_sleep)$total_sleep and na.omit(mammals_sleep)$body_weight
## S = 19822, p-value = 2.092e-05
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.6062105

mammals_sub <- na.omit(mammals_sleep) %>%
  dplyr::select(body_weight, total_sleep, gestation_time)

# Partial correlation with Spearman
pcor(x = mammals_sub, method = "spearman")

## $estimate
##           body_weight total_sleep gestation_time
## body_weight    1.0000000  -0.2784975      0.5135019
## total_sleep   -0.2784975   1.0000000     -0.3903110
## gestation_time  0.5135019  -0.3903110      1.0000000
##
## $p.value
##           body_weight total_sleep gestation_time
## body_weight    0.000000000  0.07787088  0.000595627
## total_sleep    0.077870878  0.00000000  0.011639901
## gestation_time 0.000595627  0.01163990  0.000000000
##
## $statistic
##           body_weight total_sleep gestation_time
## body_weight    0.0000000  -1.810860  3.737165
## total_sleep   -1.810860   0.000000  -2.647482
## gestation_time  3.737165  -2.647482  0.000000
##
## $n
## [1] 42
##
## $gp
## [1] 1
##
```

```
## $method  
## [1] "spearman"
```