1.3.5: Statistical Tests and Models

(In Person)

Session Objectives *(updated)*

1. Develop linear regression models and explore results.
2. Develop logistic regression models and explore results.
3. Perform t-tests and ANOVA and explore results.
4. Modeling with Complex Survey Weights

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0. Prework - Before You Begin

A. Install packages

If you do not have them already, install the following packages from CRAN (using the RStudio Menu "Tools/Install" Packages interface):

- `VIM` and `VIM` package website
- `gtsummary` and `gtsummary` website
- `easystats` and `easystats` website
- `car` and `car` BOOK website
- `effects`
- `olsrr` and `olsrr` website
- dplyr and `dplyr` website
- `ROCR` and `ROCR` website
- `effectsize` and `effectsize` website

B. Open/create an RStudio project for this lesson

Let's start with the `myfirstRproject` RStudio project you created in Module 1.3.2 - part 1. If you have not yet created this `myfirstRproject` RStudio project, go ahead and create a new RStudio Project for this lesson. *Feel free to name your project whatever you want, it does not need to be named* `myfirstRproject`*.*

1. Develop linear regression models and explore results.

Linear Regression Modeling

As we saw briefly in Module 1.3.4 - section 2 on missing data in regression models, linear regression can be accomplished using the built-in `lm()` function.

`lm()` stands for linear models. You can use this function for building both regression and ANOVA (analysis of variance) type models. `aov()` is another option for ANOVA as well.

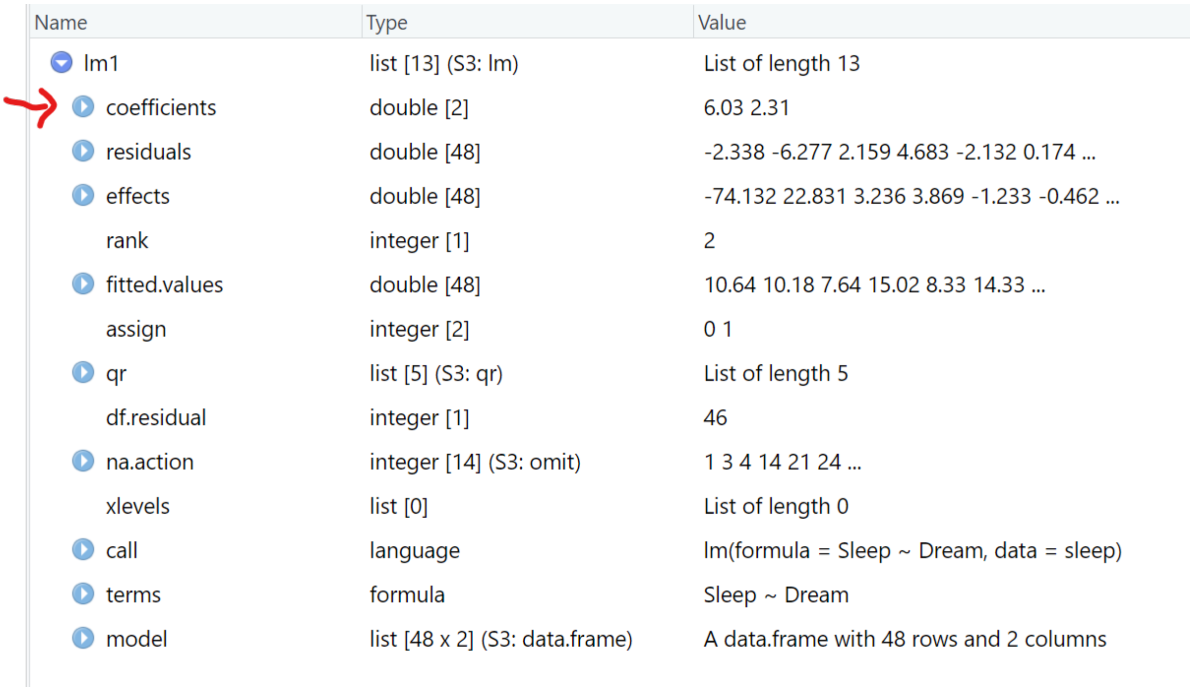
Let's take a closer look at the little linear model we ran for the `sleep` dataset from the `VIM` package. We will run the regression model again and save the output to an object called `lm1`. Look at default output.

Using the `lm()` function and exploring output

```r
# load VIM Package to get sleep dataset
library(VIM)

# run model for predicting "Sleep" from "Dream"
# save the output in lm1
lm1 <- lm(Sleep ~ Dream, data = sleep)

# look at default output
lm1
```

```

Call:
lm(formula = Sleep ~ Dream, data = sleep)

Coefficients:
(Intercept)        Dream
      6.027        2.305
```

Let's take a moment to take a look at the `lm1` object in the Global Environment. Notice that only the intercept and slope terms are printed in the default output, but the `lm1` object is actually a list of 13 elements only one of which are the "coefficients" from the model.



Name	Type	Value
lm1	list [13] (S3: lm)	List of length 13
coefficients	double [2]	6.03 2.31
residuals	double [48]	-2.338 -6.277 2.159 4.683 -2.132 0.174 ...
effects	double [48]	-74.132 22.831 3.236 3.869 -1.233 -0.462 ...
rank	integer [1]	2
fitted.values	double [48]	10.64 10.18 7.64 15.02 8.33 14.33 ...
assign	integer [2]	0 1
qr	list [5] (S3: qr)	List of length 5
df.residual	integer [1]	46
na.action	integer [14] (S3: omit)	1 3 4 14 21 24 ...
xlevels	list [0]	List of length 0
call	language	lm(formula = Sleep ~ Dream, data = sleep)
terms	formula	Sleep ~ Dream
model	list [48 x 2] (S3: data.frame)	A data.frame with 48 rows and 2 columns

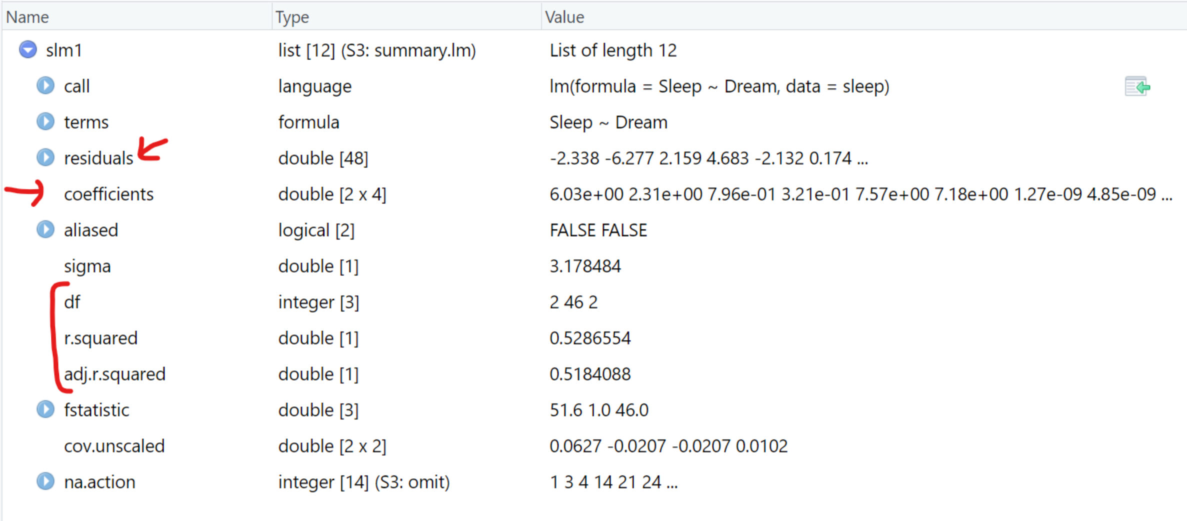
Next, to get more detailed output we need to run `summary(lm1)` which technically runs `summary.lm()` which is a special summary function specific for `lm` class type objects.

So, let's save the `summary(lm1)` output and also take a look at that object `slm1`.

```
# save the summary of lm1
slm1 <- summary(lm1)

# look at default output
slm1
```

```

Call:
lm(formula = Sleep ~ Dream, data = sleep)

Residuals:
    Min      1Q  Median      3Q     Max 
-6.2765 -2.0384 -0.1096  2.1599  9.2624 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)   6.0273     0.7960   7.572 1.27e-09 ***
Dream         2.3051     0.3209   7.183 4.85e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.178 on 46 degrees of freedom
  (14 observations deleted due to missingness)
Multiple R-squared:  0.5287,	Adjusted R-squared:  0.5184 
F-statistic: 51.59 on 1 and 46 DF,  p-value: 4.849e-09
```

But here is what is in the `slm1` object in the Global Environment - also a list with 12 elements. We get the `coefficients` again, but we get even more info - including the `df` (degrees of freedom), `r.squared` and `adj.r.squared`.



Name	Type	Value
slm1	list [12] (S3: summary.lm)	List of length 12
call	language	lm(formula = Sleep ~ Dream, data = sleep)
terms	formula	Sleep ~ Dream
residuals	double [48]	-2.338 -6.277 2.159 4.683 -2.132 0.174 ...
coefficients	double [2 x 4]	6.03e+00 2.31e+00 7.96e-01 3.21e-01 7.57e+00 7.18e+00 1.27e-09 4.85e-09 ...
aliased	logical [2]	FALSE FALSE
sigma	double [1]	3.178484
df	integer [3]	2 46 2
r.squared	double [1]	0.5286554
adj.r.squared	double [1]	0.5184088
fstatistic	double [3]	51.6 1.0 46.0
cov.unscaled	double [2 x 2]	0.0627 -0.0207 -0.0207 0.0102
na.action	integer [14] (S3: omit)	1 3 4 14 21 24 ...

Nicer formatted regression table using `gtsummary::tbl_regression`

We can get a nicer output using the `gtsummary::tbl_regression()` table.

```r
library(gtsummary)
tbl_regression(lm1)
```

Table 1

Characteristic	**Beta**	**95% CI**[1]	**p-value**
Dream	2.3	1.7, 3.0	<0.001

[1] CI = Confidence Interval

More output options for regression using `easystats`

Another suite of R packages that can be helpful to explore is the `easystats` package suite. In this example we will look at:

- `model_parameters()` from the `parameters` package that is part of `easystats` package suite; and
- `report()` from the `report` package that is also part of the `easystats` package suite.

Better formatted output table:

```r
library(easystats)
model_parameters(lm1)
```

```
Parameter   | Coefficient |   SE |       95% CI | t(46) |      p
-----------------------------------------------------------------
(Intercept) |        6.03 | 0.80 | [4.43, 7.63] |  7.57 | < .001
Dream       |        2.31 | 0.32 | [1.66, 2.95] |  7.18 | < .001
```

A nice summary with suggested interpretation verbiage:

```r
report(lm1)
```

```
We fitted a linear model (estimated using OLS) to predict Sleep with Dream
(formula: Sleep ~ Dream). The model explains a statistically significant and
substantial proportion of variance (R2 = 0.53, F(1, 46) = 51.59, p < .001,
adj.
R2 = 0.52). The model's intercept, corresponding to Dream = 0, is at 6.03
(95%
CI [4.43, 7.63], t(46) = 7.57, p < .001). Within this model:

  - The effect of Dream is statistically significant and positive (beta =
  2.31,
95% CI [1.66, 2.95], t(46) = 7.18, p < .001; Std. beta = 0.73, 95% CI [0.52,
0.93])

Standardized parameters were obtained by fitting the model on a standardized
version of the dataset. 95% Confidence Intervals (CIs) and p-values were
computed using a Wald t-distribution approximation.
```

Other options within `tidyverse` packages

In the `broom` package there are some additional functions that are helpful for exploring the model fit metrics and more.

```
library(broom)
tidy(lm1)
```

```
# A tibble: 2 x 5
  term        estimate std.error statistic       p.value
  <chr>          <dbl>     <dbl>     <dbl>         <dbl>
1 (Intercept)     6.03     0.796      7.57 0.00000000127
2 Dream           2.31     0.321      7.18 0.00000000485
```

```
glance(lm1)
```

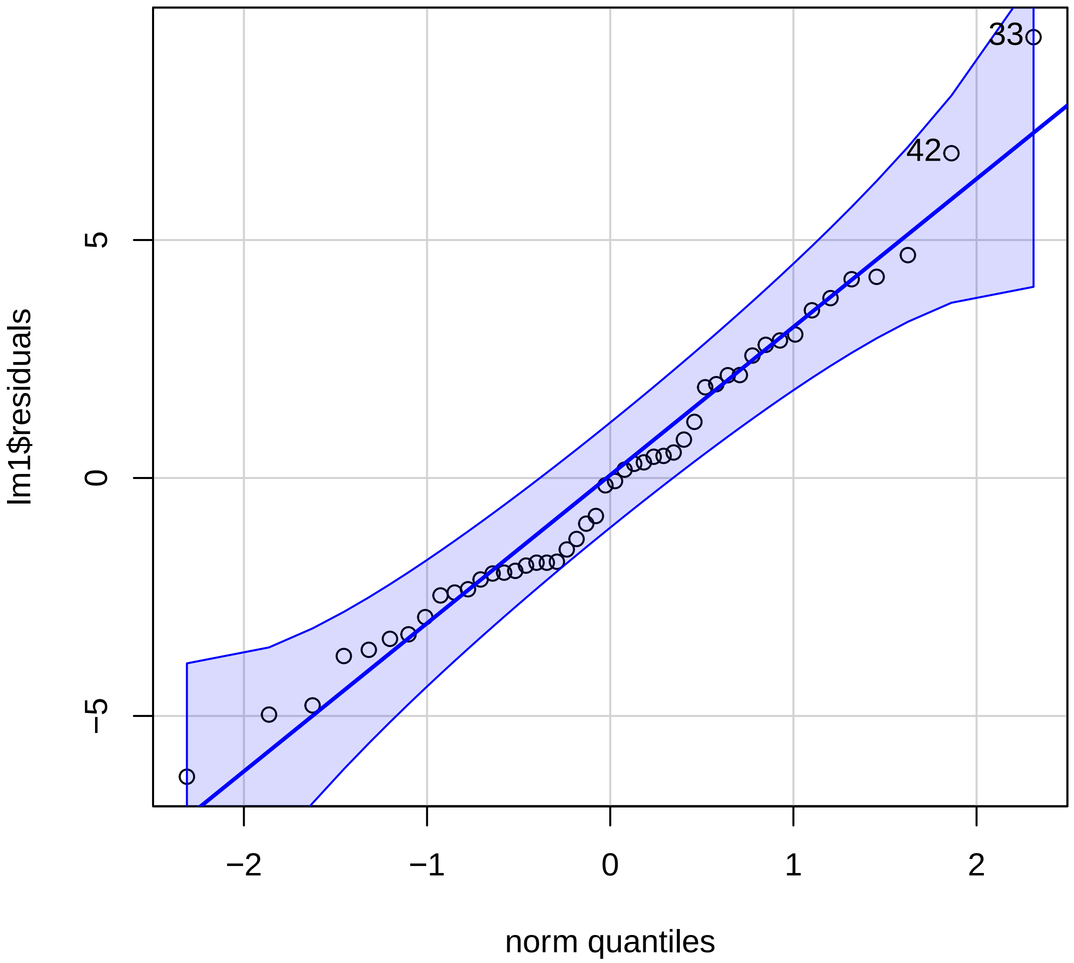
```
# A tibble: 1 x 12
  r.squared adj.r.squared sigma statistic       p.value    df logLik   AIC
  BIC
      <dbl>         <dbl> <dbl>     <dbl>         <dbl> <dbl>  <dbl> <dbl>
      <dbl>
1     0.529         0.518  3.18      51.6 0.00000000485     1  -123.  251.
257.
# i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

"Companion for Applied Regression" - the `car` and `effects` packages

John Fox has written an excellent set of books on applied regression that has an R companion book along with the `car` and `effects` packages with lots of helpful functions for doing regression modeling and analysis. Learn more at Applied Regression Book and R Companion for Applied Regression Book.

Get the normal probability plot of the model residuals.

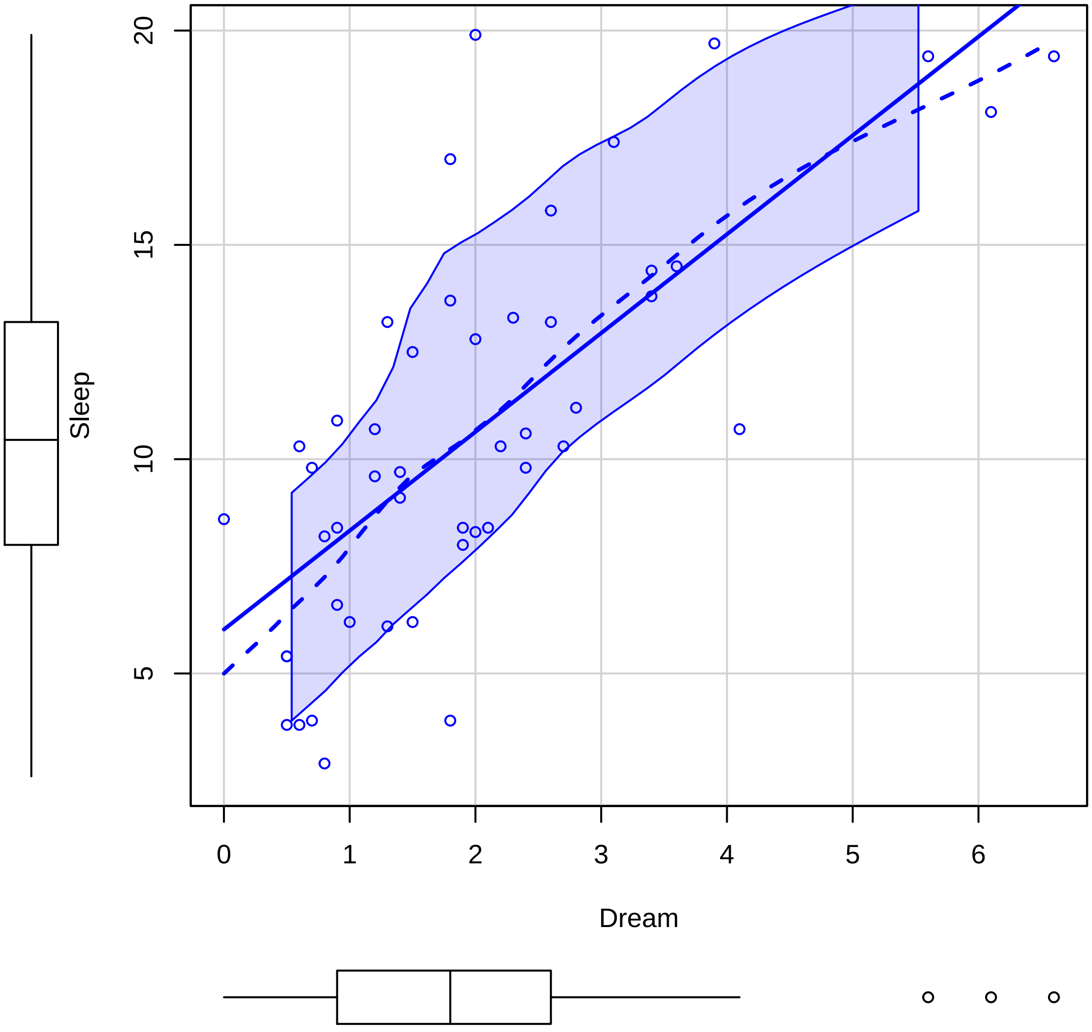
```r
library(car)

# get normal probability plot of the
# regression model residuals
car::qqPlot(lm1$residuals)
```



```
33 42
24 32
```

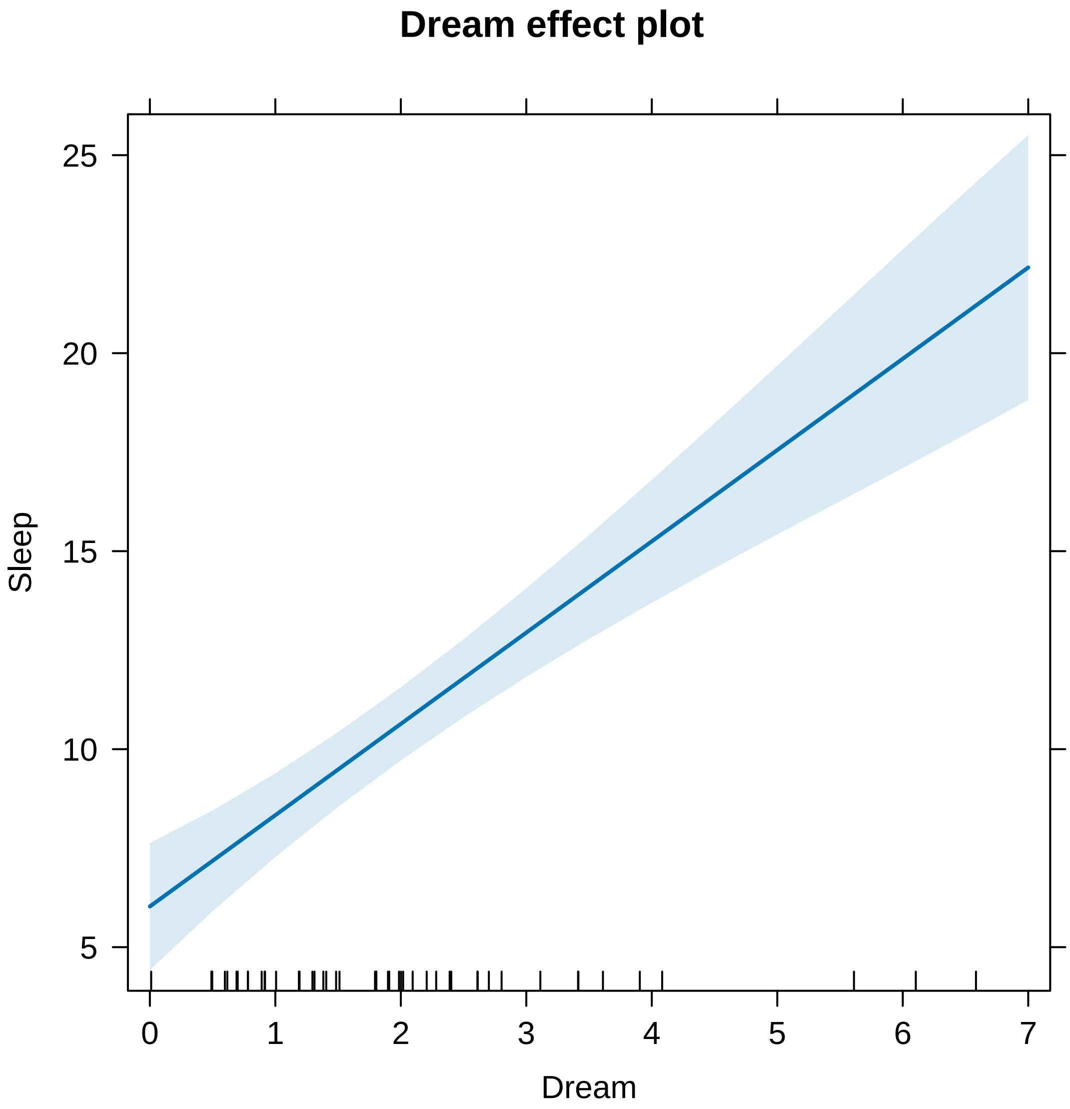
Overlay a best fit line on the scatterplot of the original data for the model - include 95% confidence intervals for the best fit line.

```
# scatterplot of fitted model
# using the car package, add the smooth option
car::scatterplot(Sleep ~ Dream, data = sleep,
                 smooth=TRUE)
```



Get an “effects” plot - for this model you only get one plot showing the slope of the line between `Dream` and `Sleep`:

```
library(effects)
plot(allEffects(lm1))
```



One more - the `olsrr` package

The `olsrr` package provides a helpful set of tolls for working with OLS (ordinary least squares) regression models. *Unfortunately, this set of package functions do NOT work with* `glm` *(generalized linear models) like logistic regression.*

Get detailed regression output including the standardized regression coefficients which are effect sizes, where std.beta = 0.1 is "small", 0.3 is "moderate" and 0.5 is "large".

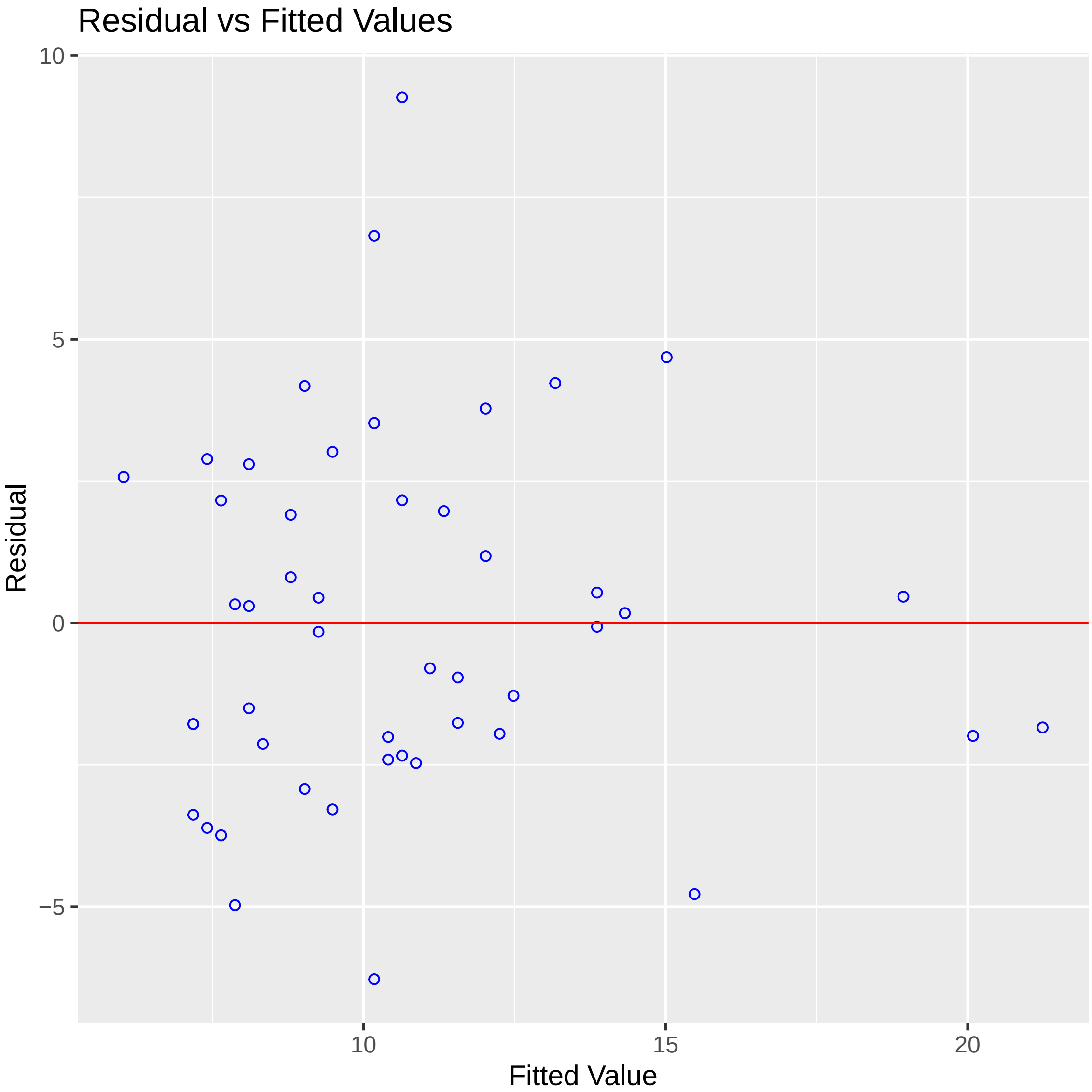
```r
# load olsrr package
library(olsrr)

# get detailed regression output
# including standardized coefficients
ols_regress(lm1)
```

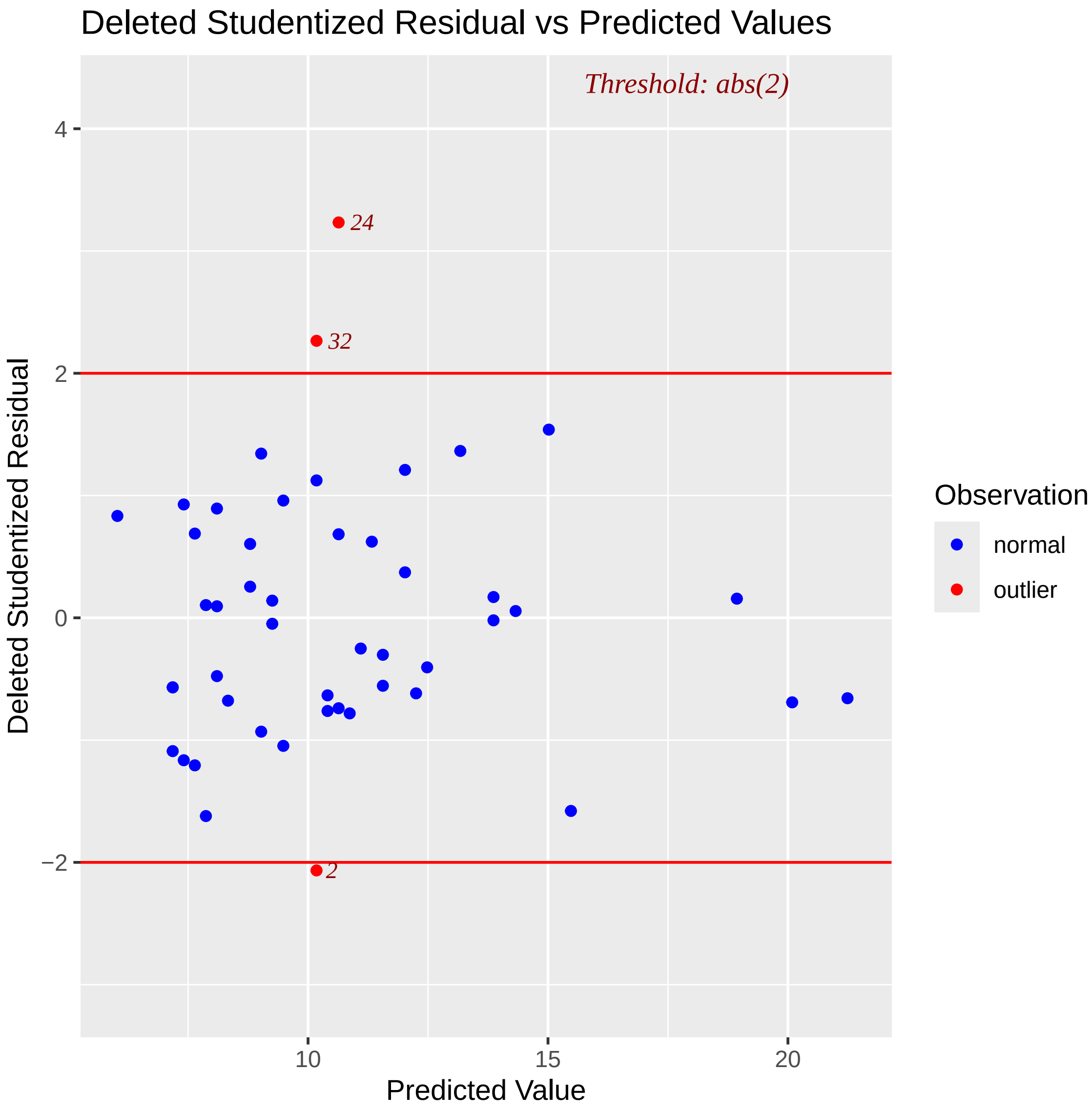
```
                         Model Summary
---------------------------------------------------------------
R                        0.727       RMSE                3.112
R-Squared                0.529       MSE                 9.682
Adj. R-Squared           0.518       Coef. Var          29.705
Pred R-Squared           0.494       AIC               251.190
MAE                      2.507       SBC               256.804
---------------------------------------------------------------
 RMSE: Root Mean Square Error
 MSE: Mean Square Error
 MAE: Mean Absolute Error
 AIC: Akaike Information Criteria
 SBC: Schwarz Bayesian Criteria

                               ANOVA
-------------------------------------------------------------------
               Sum of
              Squares        DF    Mean Square       F         Sig.
-------------------------------------------------------------------
Regression    521.233         1        521.233    51.593     0.0000
Residual      464.727        46         10.103
Total         985.960        47
-------------------------------------------------------------------

                                Parameter Estimates
-------------------------------------------------------------------------------------
      model      Beta     Std. Error     Std. Beta       t        Sig       lower
      upper
```

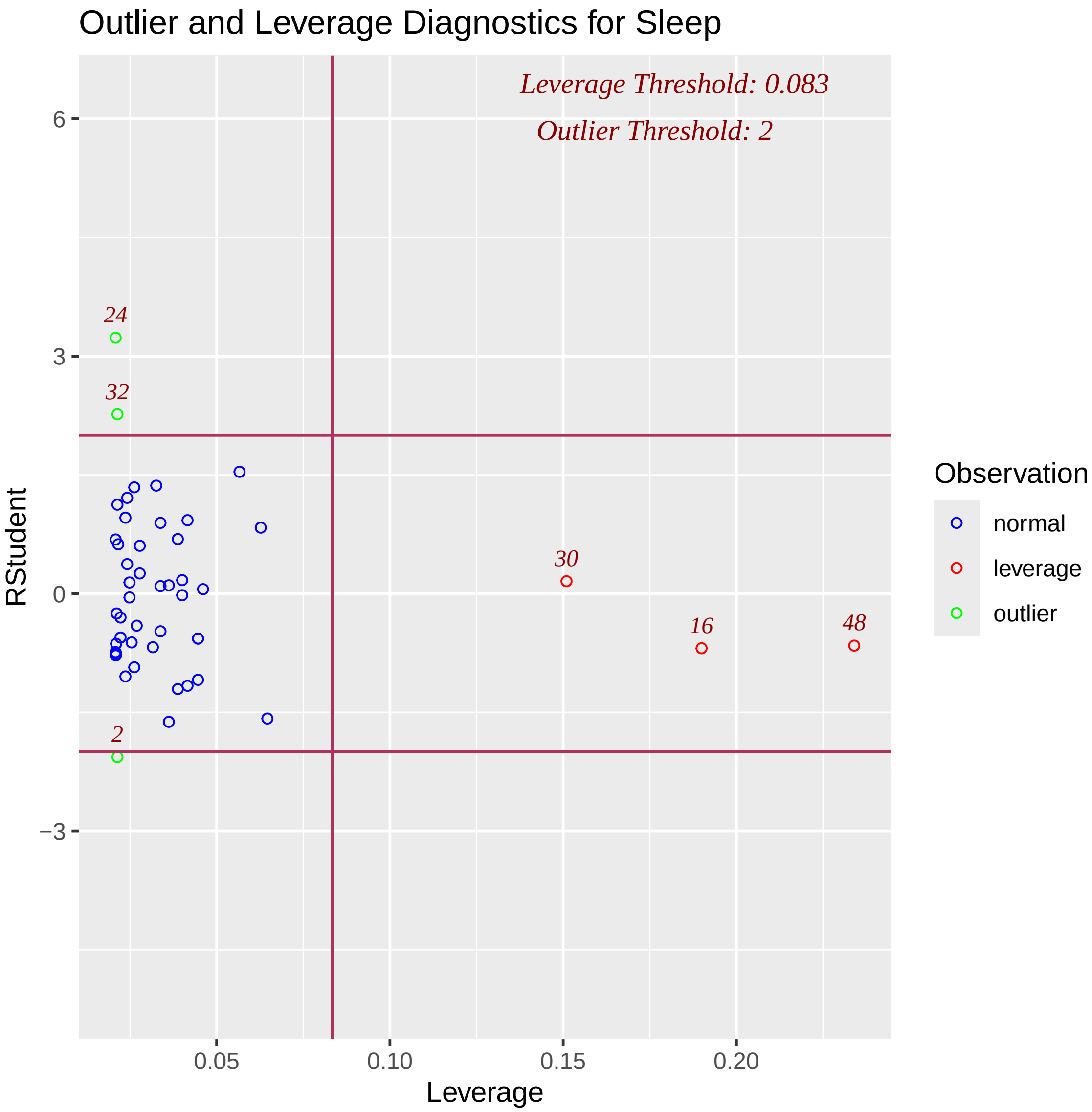
```
------------------------------------------------------------------------------------
(Intercept)    6.027         0.796                 7.572    0.000    4.425
7.630
      Dream    2.305         0.321        0.727    7.183    0.000    1.659
      2.951
------------------------------------------------------------------------------------
```

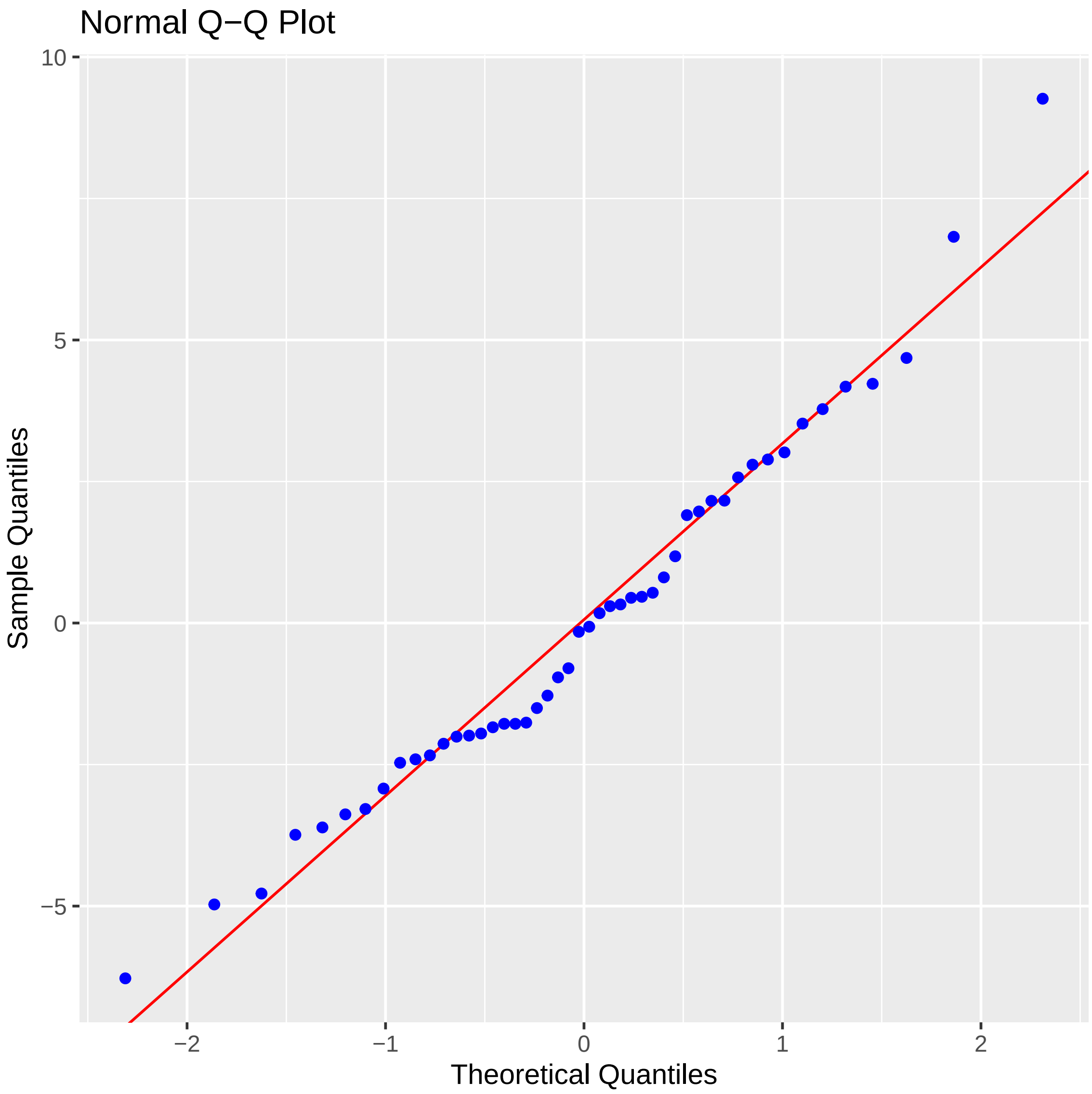
Get diagnostic plots.

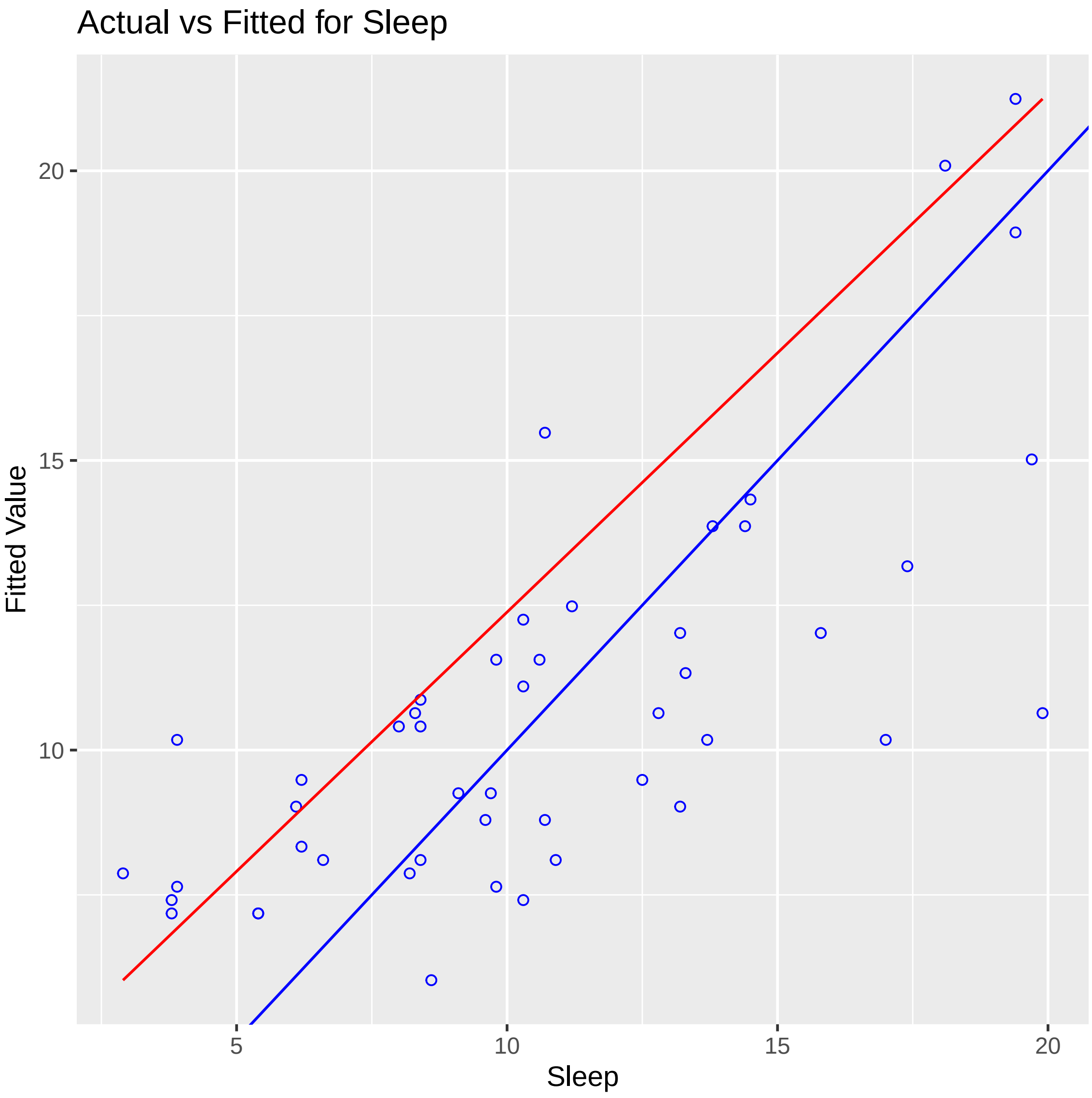
```
# diagnostic plots
# check for new output windows
ols_plot_diagnostics(lm1)
```

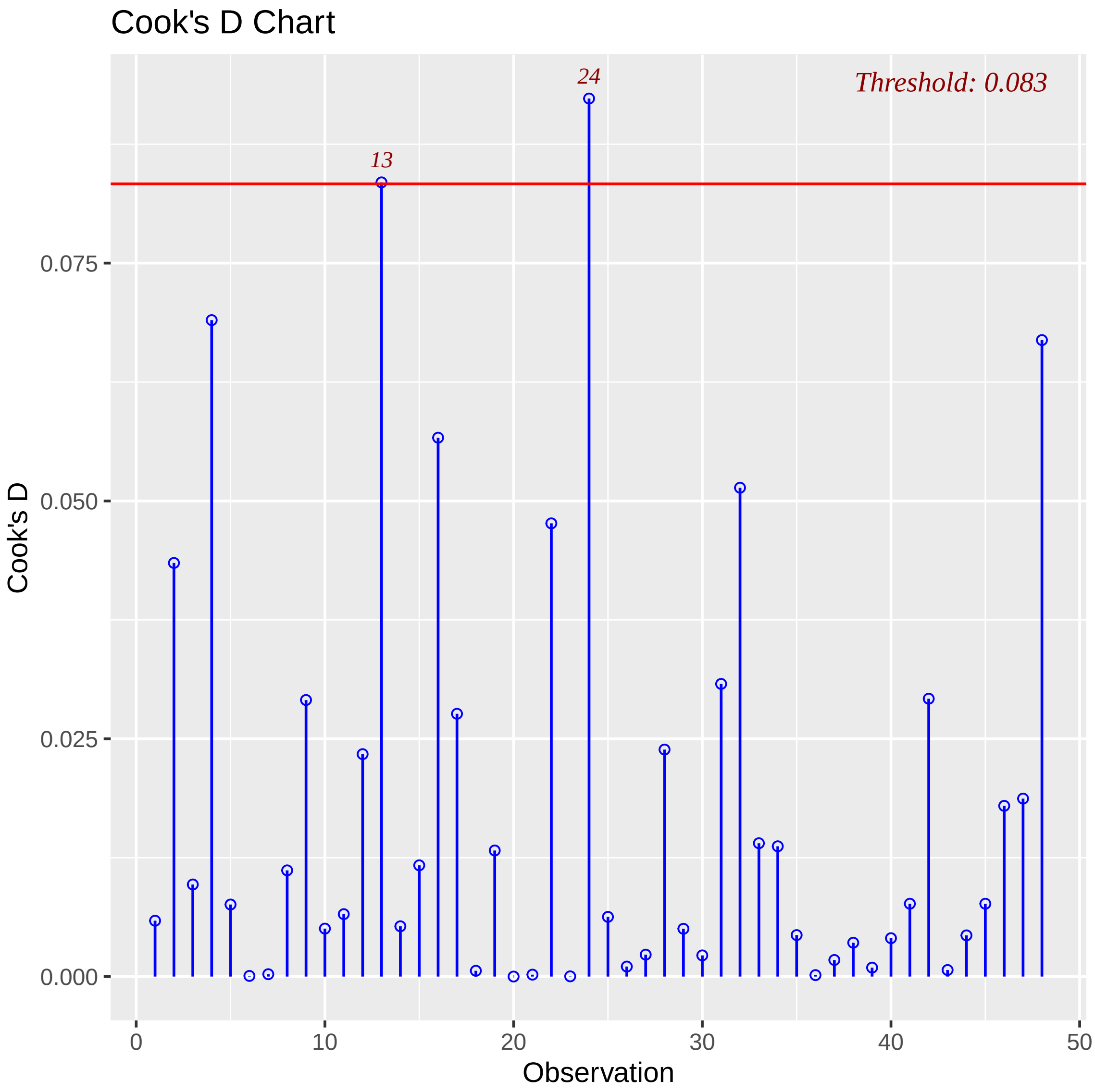


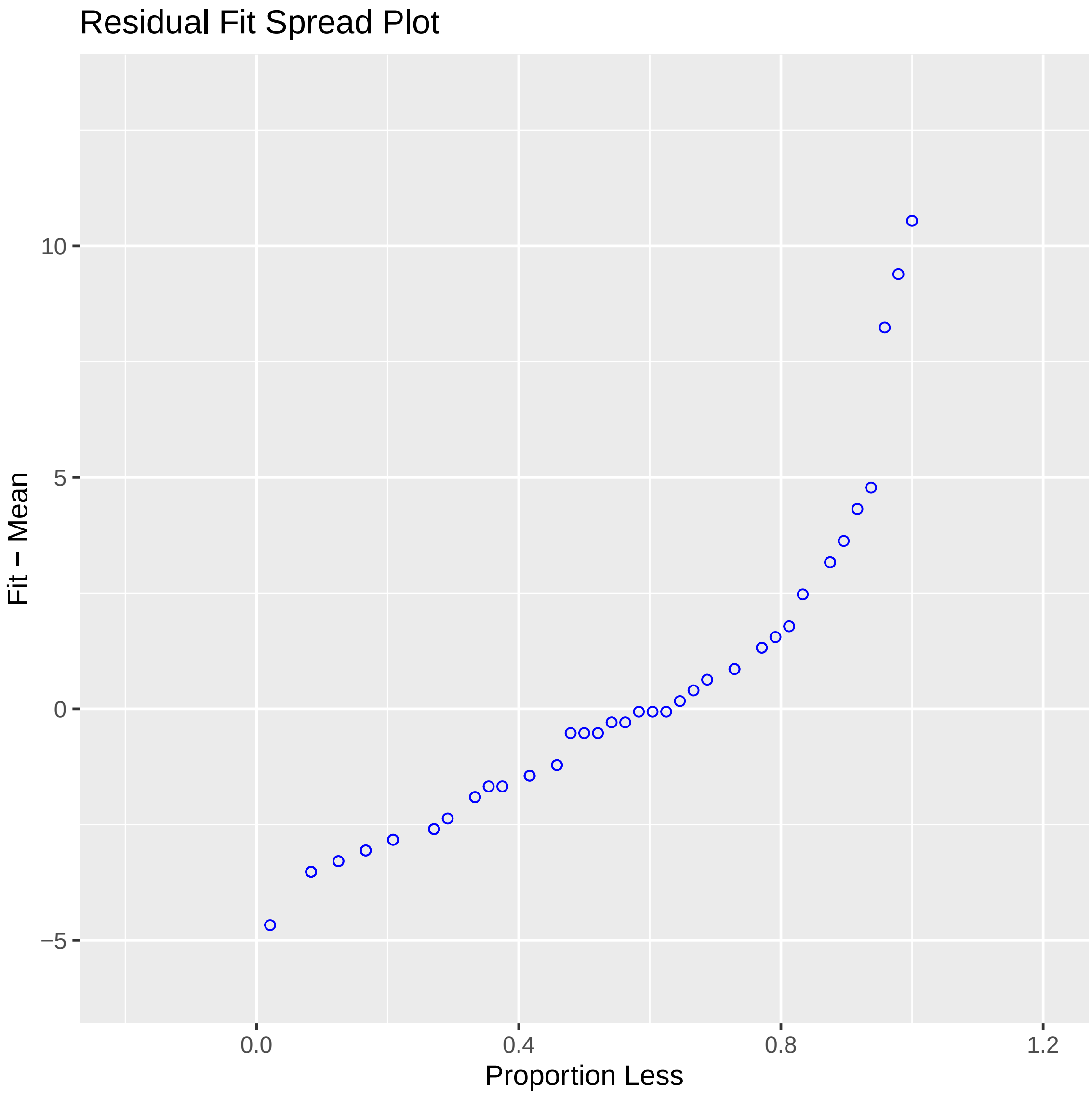

Deleted Studentized Residual vs Predicted Values
Threshold: abs(2)
24
32
2
4
2
0
−2
10
15
20
Deleted Studentized Residual
Predicted Value
Observation
normal
outlier

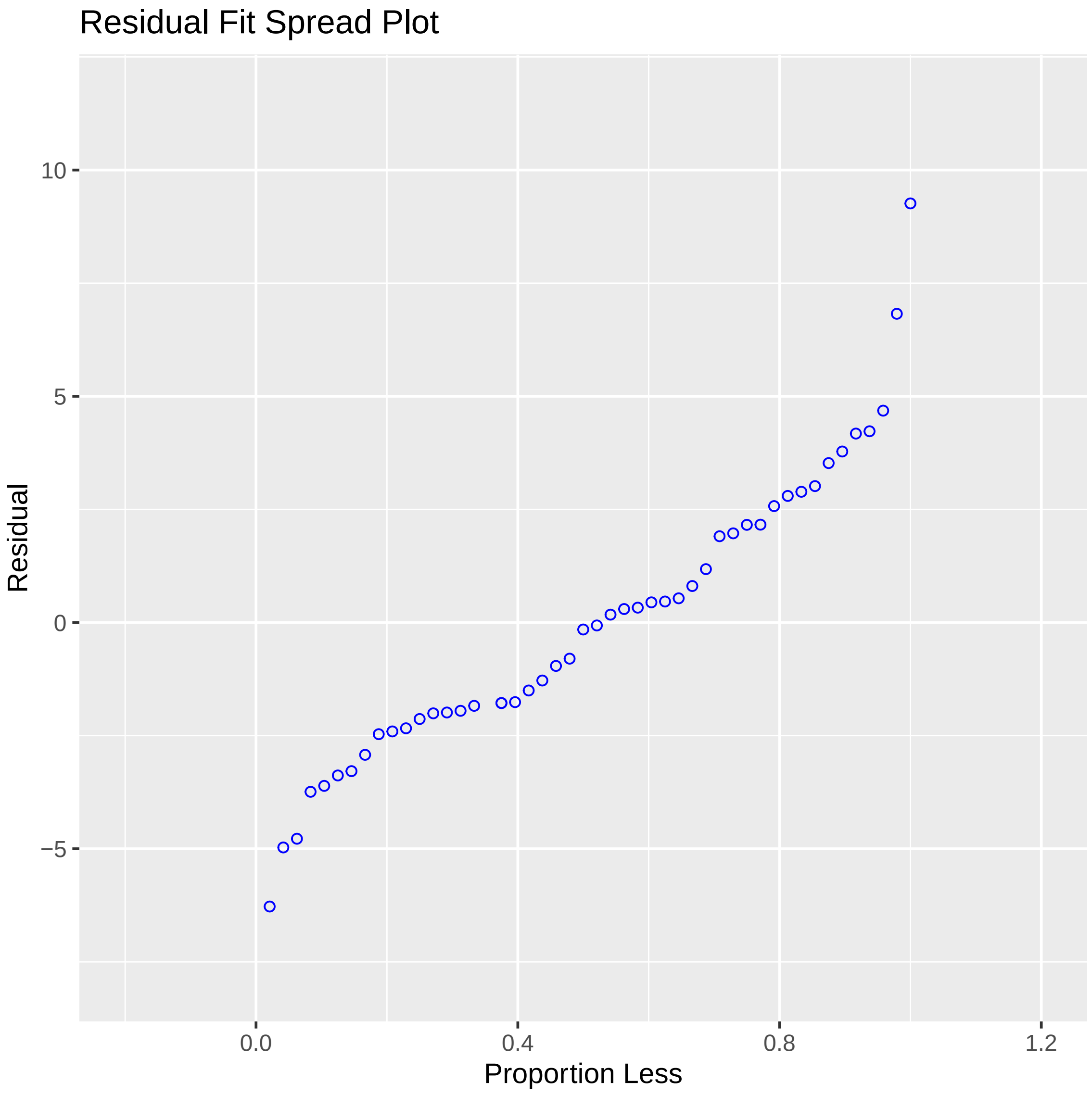

Outlier and Leverage Diagnostics for Sleep
Leverage Threshold: 0.083
Outlier Threshold: 2
24
32
30
16
48
2
6
3
0
−3
RStudent
0.05
0.10
0.15
0.20
Leverage
Observation
normal
leverage
outlier

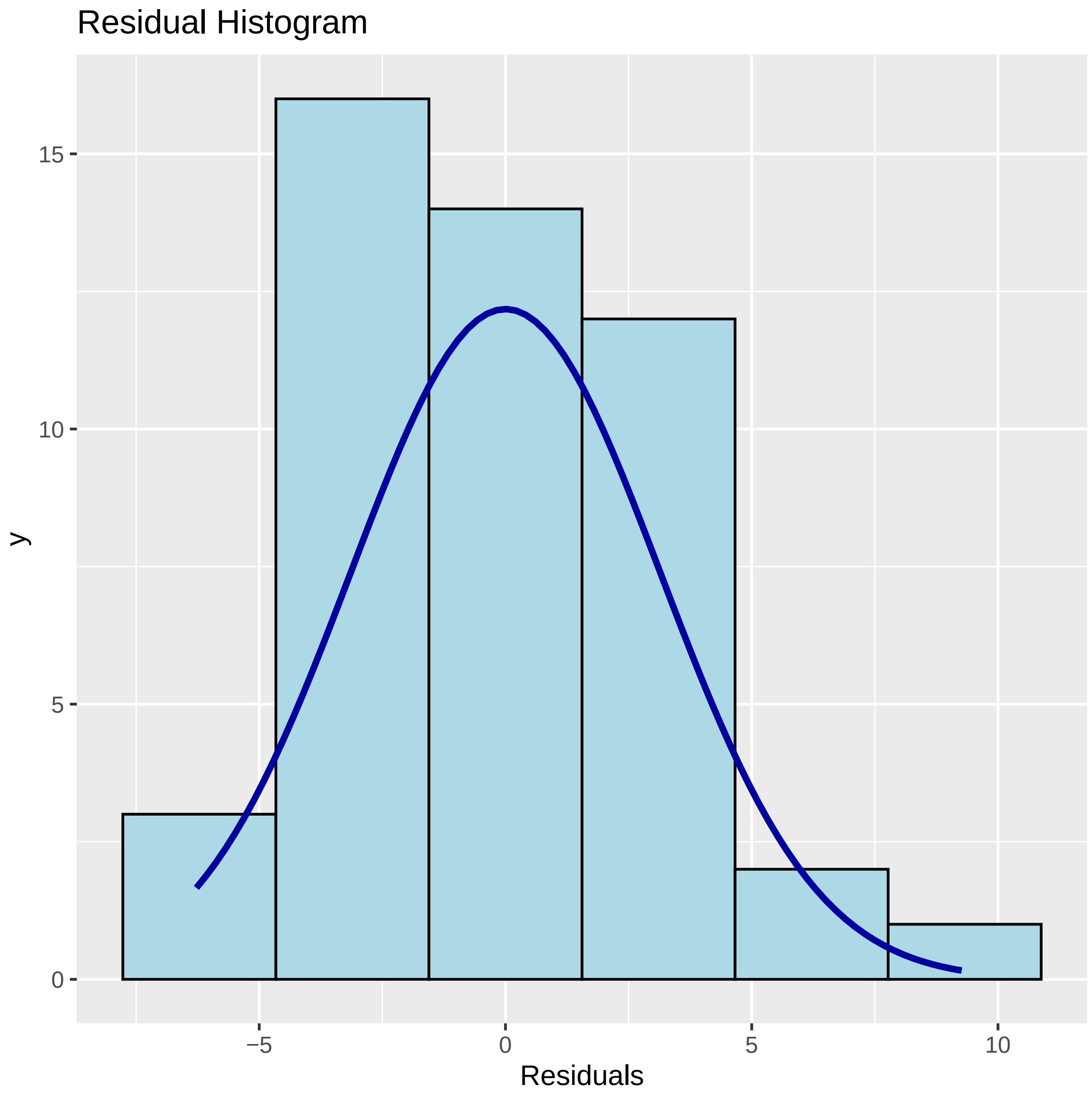

Normal Q−Q Plot
10
5
0
−5
Sample Quantiles
−2
−1
0
1
2
Theoretical Quantiles

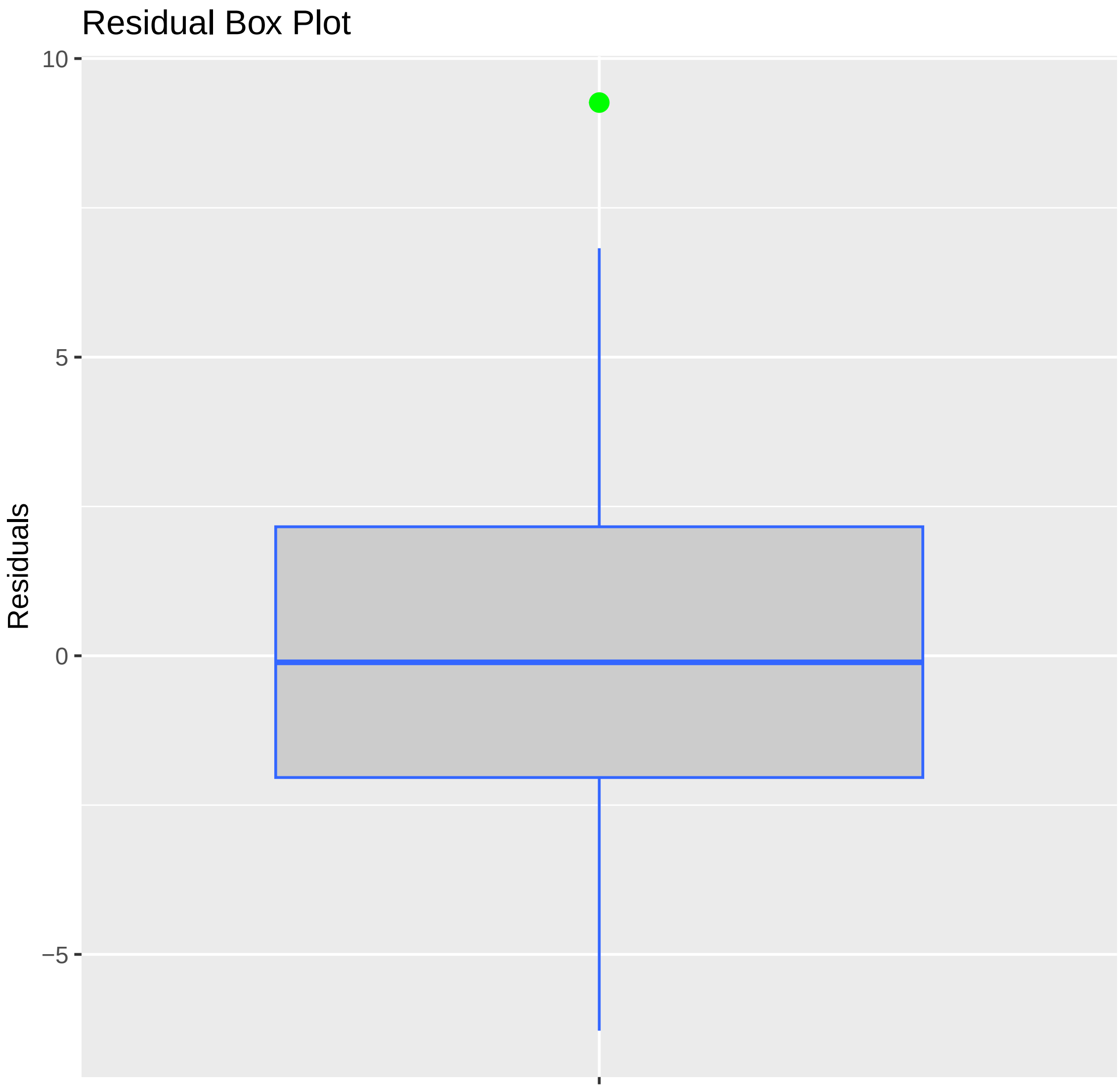

Actual vs Fitted for Sleep
Fitted Value
20
15
10
5
10
15
20
Sleep

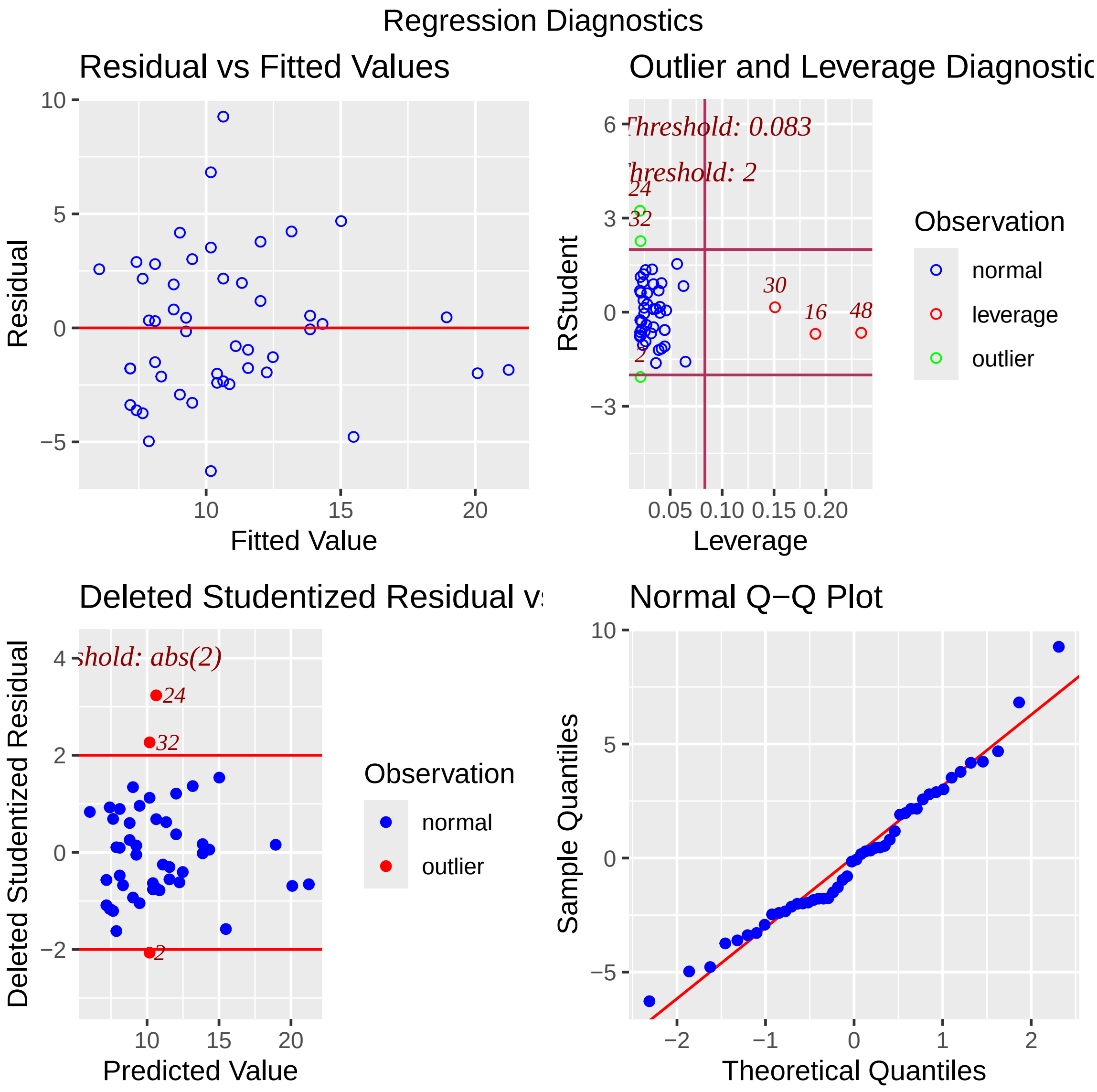

Cook's D Chart
Threshold: 0.083
13
24
Cook's D
0.000
0.025
0.050
0.075
0
10
20
30
40
50
Observation

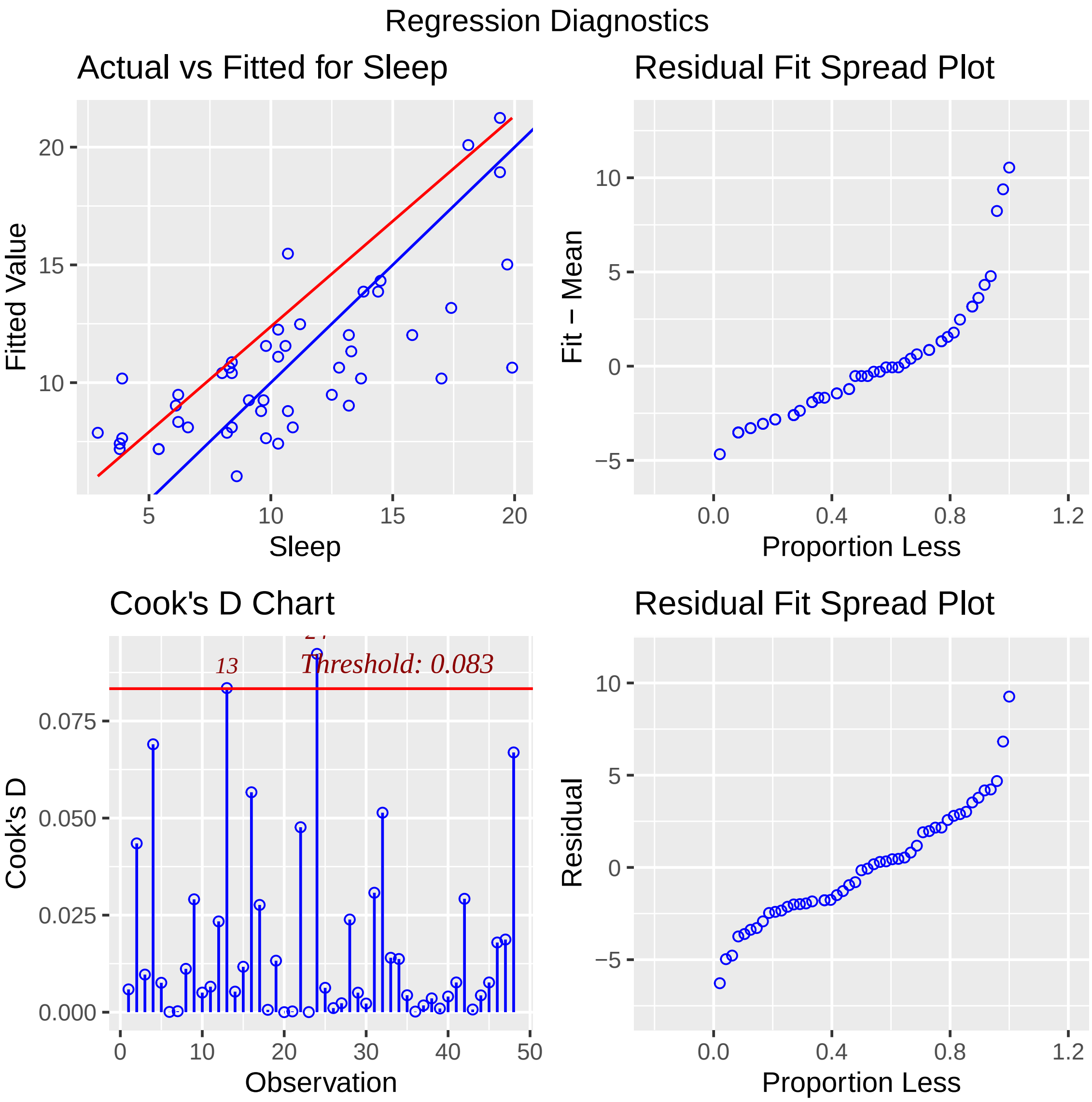

Residual Fit Spread Plot
Fit – Mean
10
5
0
−5
0.0
0.4
0.8
1.2
Proportion Less

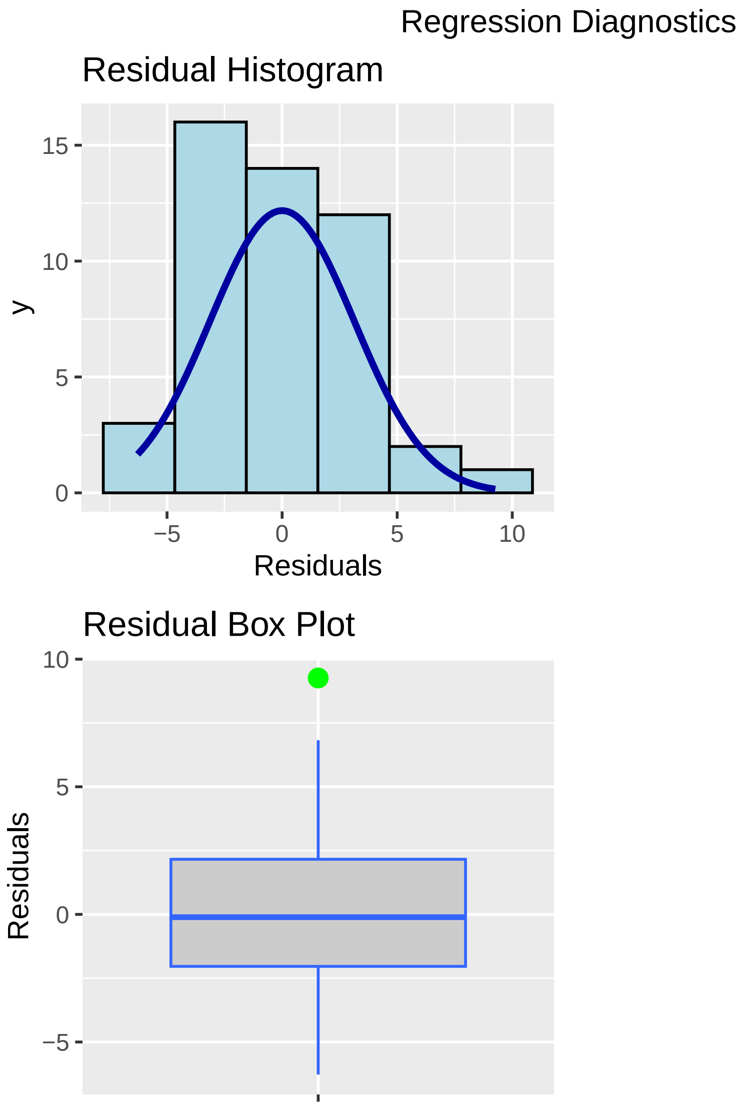

Residual Fit Spread Plot
Residual
10
5
0
−5
0.0
0.4
0.8
1.2
Proportion Less


Residual Histogram
y
15
10
5
0
−5
0
5
10
Residuals


Residual Box Plot
Residuals
10
5
0
−5


Regression Diagnostics
Residual vs Fitted Values
Residual
Fitted Value
10
5
0
−5
10
15
20
Outlier and Leverage Diagnostic
RStudent
Leverage
Threshold: 0.083
Threshold: 2
24
32
30
16
48
2
6
3
0
−3
0.05
0.10
0.15
0.20
Observation
normal
leverage
outlier
Deleted Studentized Residual v
Deleted Studentized Residual
Predicted Value
Threshold: abs(2)
24
32
2
4
2
0
−2
10
15
20
Observation
normal
outlier
Normal Q−Q Plot
Sample Quantiles
Theoretical Quantiles
10
5
0
−5
−2
−1
0
1
2


Regression Diagnostics
Actual vs Fitted for Sleep
Fitted Value
20
15
10
5
10
15
20
Sleep
Residual Fit Spread Plot
Fit − Mean
10
5
0
−5
0.0
0.4
0.8
1.2
Proportion Less
Cook's D Chart
13
Threshold: 0.083
Cook's D
0.075
0.050
0.025
0.000
0
10
20
30
40
50
Observation
Residual Fit Spread Plot
Residual
10
5
0
−5
0.0
0.4
0.8
1.2
Proportion Less


Regression Diagnostics
Residual Histogram
15
10
5
0
y
−5
0
5
10
Residuals
Residual Box Plot
10
5
0
−5
Residuals

Get a normality test for the residuals.

```
# normality tests for residuals
ols_test_normality(lm1)
```

```
-----------------------------------------------
       Test             Statistic       pvalue
-----------------------------------------------
Shapiro-Wilk              0.9736         0.3468
Kolmogorov-Smirnov        0.108          0.6307
Cramer-von Mises          3.1824         0.0000
Anderson-Darling          0.4289         0.2980
-----------------------------------------------
```

2. Develop logistic regression models and explore results.

Similar to what we did above, we can use `glm()` instead of `lm()` to perform a logistic regression. `glm()` is the generalized linear modeling function in base R. The "generalized" part of this is due to this function handling different "families" of output distributions. The "gaussian" family is the default for continuous variables with a normal distribution (the assumption for OLS). The family for logistic regression is the "binomial" since we are predicting the probability of someone being in group 1 or group 2 for the 2 possible outcomes in a logistic regression. And there are more families that can be fit including "poisson" which works for count-based variables (like number of children, miscarriages, etc).

This function can actually do a simple linear regression by leaving the default setting for `family = "gaussian"`. Learn more by running `help(glm, package = "stats")`.

Let's keep working with the `sleep` dataset, but first let's split the `Dream` variable into values <= 2 and those > 2. *Note: The median for `Dream` was 1.8, so this should split data approximately 50/50.*

This time we will treat "`Dream` > 2" as the positive (or target) outcome for our logistic regression model. And then we will see how "`Dream` > 2" is predicted by amount of `Sleep` and `Danger` scores.

Simple `glm()` output

```r
# create outcome variable
sleep$dream_gt2 <- as.numeric(sleep$Dream > 2)

# fit the logistic regression model
glm1 <- glm(dream_gt2 ~ Sleep + Danger,
            data = sleep,
            family = "binomial")

# look at basic output
glm1
```

```
Call:  glm(formula = dream_gt2 ~ Sleep + Danger, family = "binomial",
    data = sleep)

Coefficients:
(Intercept)        Sleep       Danger
    -1.5953       0.2677      -0.8381
```

```
Degrees of Freedom: 47 Total (i.e. Null);  45 Residual
  (14 observations deleted due to missingness)
Null Deviance:      63.51
Residual Deviance: 41.79    AIC: 47.79
```

⚠ WARNING: Exponentiate Raw Coefficients

The default output from `glm()` only provides for the RAW logistic regression coefficients. To get the odds ratios, we must first exponentiate these coefficients.

Get the odds ratios by exponentiating the coefficients.

```r
exp(coef(glm1))
```

```
(Intercept)       Sleep      Danger 
  0.2028428   1.3069544   0.4325214 
```

Get detailed `glm()` regression output.

```
sglm1 <- summary(glm1)
sglm1
```

```

Call:
glm(formula = dream_gt2 ~ Sleep + Danger, family = "binomial",
    data = sleep)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.5953     1.5922  -1.002   0.3164
Sleep         0.2677     0.1151   2.325   0.0201 *
Danger       -0.8381     0.3888  -2.156   0.0311 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 63.510  on 47  degrees of freedom
Residual deviance: 41.795  on 45  degrees of freedom
  (14 observations deleted due to missingness)
AIC: 47.795

Number of Fisher Scoring iterations: 5
```

Use gtsummary::tbl_regression()

Get a nicer table and set `exponentiate = TRUE`.

```
tbl_regression(glm1, exponentiate = TRUE)
```

Table 2

Characteristic	**OR**[1]	**95% CI**[1]	**p-value**
Sleep	1.31	1.07, 1.70	0.020
Danger	0.43	0.18, 0.87	0.031

[1] OR = Odds Ratio, CI = Confidence Interval

Interpret Odds Ratios as Effect Sizes

Interpreting odds ratios as effect sizes is a little tricky. However, this website on Computation of Effect Sizes is really helpful - see items 14 and 16. By playing with this simple conversion tool to convert between effect sizes, we can see that:

- large effect sizes d=0.8, r=0.5, odds ratio =~ 4.27-8.12
- moderate effect sizes d=0.5, r=0.3, odds ratio =~ 2.48-3.13
- small effect sizes d=0.2, r=0.1, odds ratio =~ 1.44

where Cohen's d is used for t-tests; r is used for correlations (and are the same for standardized regression coefficient "betas"); and odds ratios are from logistic regression.

AUC and ROC curve plot

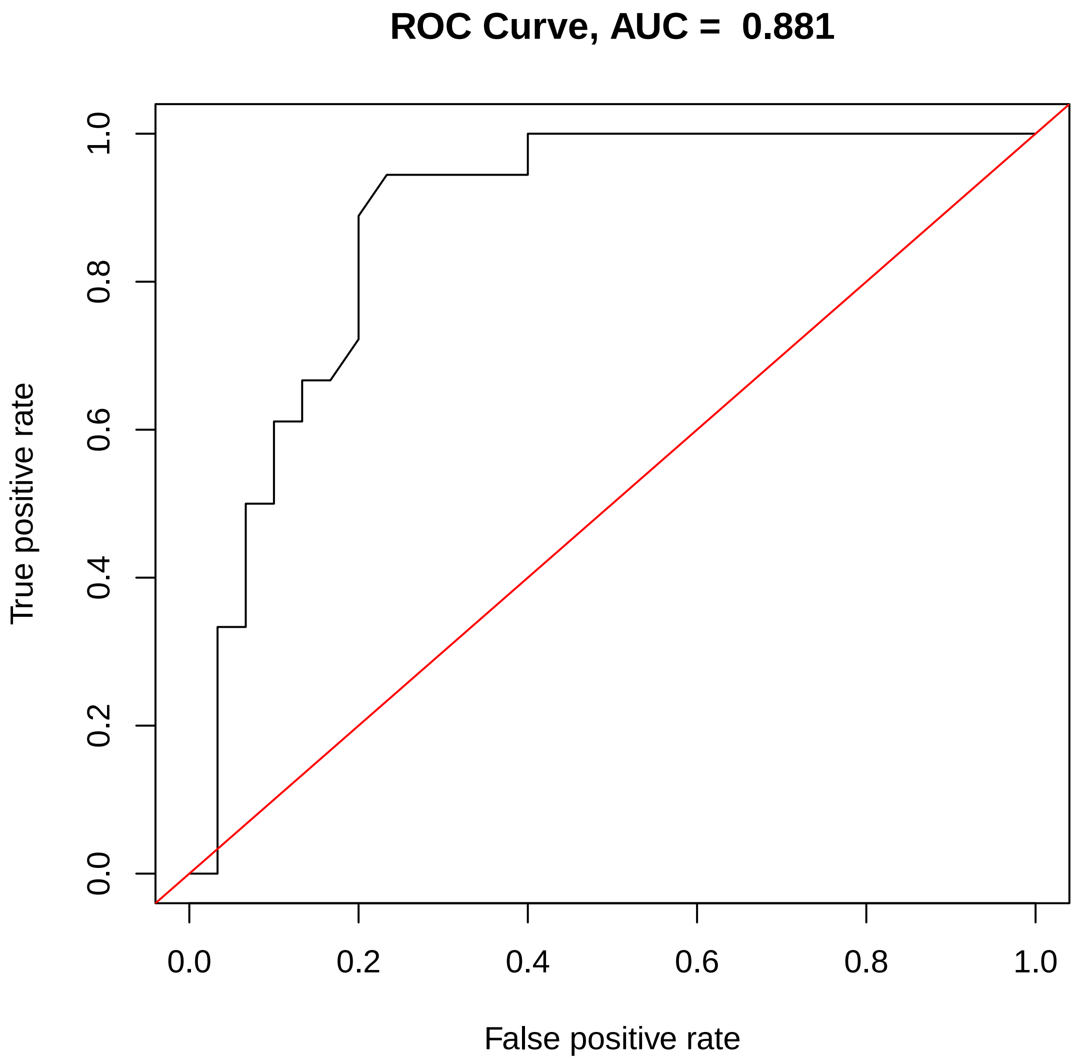
The area under the curve (AUC) or "C-statistic" is often reported instead of R2 for logistic regression models. The code below will compute the AUC for this model and make the receiver operating characteristic curve (ROC) plot.

Ideally you want AUC as close to 1 as possible:

- AUC > 0.9 is great
- AUC > 0.8 is good
- AUC > 0.7 is ok
- AUC < 0.7 is not very good
- AUC around 0.5 is no better than flipping a fair coin which is a useless model

As you can see below, the AUC for this model was 0.881 which is very good.

```r
# NOTE: We need only the COMPLETE data
# for the 3 variables we used in this model
library(dplyr)
s1 <- sleep %>%
  select(Sleep, Danger, dream_gt2) %>%
  filter(complete.cases(.))

# compute AUC and get ROC curve
library(ROCR)
p <- predict(glm1, newdata=s1,
             type="response")
pr <- prediction(p, as.numeric(s1$dream_gt2))
prf <- performance(pr, measure = "tpr", x.measure = "fpr")

# compute AUC, area under the curve
# also called the C-statistic
auc <- performance(pr, measure = "auc")
auc <- auc@y.values[[1]]

# also - add title to plot with AUC in title
plot(prf,
     main = paste("ROC Curve, AUC = ", round(auc, 3)))
abline(0, 1, col="red")
```


ROC Curve, AUC = 0.881
True positive rate
False positive rate
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0

3. Perform t-tests explore results.

T-tests

Given the split we did above looking at animals with `Dream` scores above and below 2, let's run a t-test for the `Sleep` variable.

```
# run t-test, save results
# default is an unequal variance "unpooled" t.test
tt1 <- t.test(Sleep ~ dream_gt2,
              data = sleep)
tt1
```

```

    Welch Two Sample t-test

data:  Sleep by dream_gt2
t = -4.5307, df = 38.191, p-value = 5.633e-05
alternative hypothesis: true difference in means between group 0 and group 1
is not equal to 0
95 percent confidence interval:
 -7.420174 -2.837604
sample estimates:
mean in group 0 mean in group 1
       8.776667       13.905556
```

```
# get the equal variance "pooled" t.test
tt2 <- t.test(Sleep ~ dream_gt2,
              data = sleep,
              var.equal = TRUE)
tt2
```

```

    Two Sample t-test

data:  Sleep by dream_gt2
t = -4.4417, df = 46, p-value = 5.566e-05
alternative hypothesis: true difference in means between group 0 and group 1
is not equal to 0
95 percent confidence interval:
 -7.453219 -2.804558
sample estimates:
```

```
mean in group 0 mean in group 1
       8.776667       13.905556
```

We can test the assumption of equal variance in a couple of ways. One simple way is to look at the standard deviations of each group and see if the ratio is larger than 2.

```r
sd0 <- sleep %>%
  filter(dream_gt2 == 0) %>%
  select(Sleep) %>%
  unlist() %>%
  sd(na.rm = TRUE)
sd1 <- sleep %>%
  filter(dream_gt2 == 1) %>%
  select(Sleep) %>%
  unlist() %>%
  sd(na.rm = TRUE)
sd0
```

```
[1] 3.980615
```

```r
sd1
```

```
[1] 3.682306
```

These standard deviations are similar, so a pooled t-test should be fine.

You can also run a formal test of equal variance, using `bartlett.test()`. However, this test and others like this are sensitive to small deviations from normality, so I often check the standard deviations and will run both the pooled and unpooled tests and see if I get the same conclusion either way.

As you can see, the p-value below is not significant, so we can not reject the null hypothesis assumption of equal variance - the pooled t-test is fine.

```r
bartlett.test(Sleep ~ dream_gt2,
              data = sleep)
```

```

	Bartlett test of homogeneity of variances

data:  Sleep by dream_gt2
Bartlett's K-squared = 0.12522, df = 1, p-value = 0.7234
```

Compute effect size for t-test

Use the `effectsize` package which is part of the `easystats` suite of packages.

The effect size computed is rather large, d=1.32.

```
library(effectsize)
options(es.use_symbols = TRUE)

cohens_d(Sleep ~ dream_gt2,
         data = sleep,
         na.action = na.omit)
```

```
Cohen's d |         95% CI
--------------------------
-1.32     | [-1.96, -0.67]

- Estimated using pooled SD.
```

Get a simple summary table

As you see below, the difference in Sleep scores between the 2 dream groups is approximately 13.9-8.8 = 5.1 and the approximate average SD =~ 3.9, so the ratio of the mean differences to "pooled" SD =~ 5.1/3.85 =~ 1.33 which is close to the Cohen's d we computed above.

I also added some custom statistical tests to the table.

```r
# create factor variable with labels
sleep$dream_gt2.f <- factor(
  sleep$dream_gt2,
  levels = c(0, 1),
  labels = c("Dream <= 2",
             "Dream > 2")
)

tbl_summary(
  sleep,
  by = dream_gt2.f,
  include = c(Sleep, Danger),
  type = all_continuous() ~ "continuous2",
  statistic = all_continuous() ~ c("{N_nonmiss}", "{mean} ({sd})")
) %>%
  add_p(test = list(Sleep ~ "t.test", Danger ~ "wilcox.test"),
        test.args = list(Sleep ~ list(var.equal = TRUE))
        )
```

Table 3

Characteristic	**Dream <= 2** N = 32[1]	**Dream > 2** N = 18[1]	**p-value**[2]
Sleep			<0.001
N Non-missing	30	18	
Mean (SD)	8.8 (4.0)	13.9 (3.7)	
Unknown	2	0	
Danger			<0.001
1	5 (16%)	9 (50%)	
2	6 (19%)	6 (33%)	
3	5 (16%)	3 (17%)	
4	9 (28%)	0 (0%)	
5	7 (22%)	0 (0%)	

[1] n (%)

[2] Two Sample t-test; Wilcoxon rank sum test

4. Modeling with Complex Survey Weights

See PRAMS Module

R Code For This Module

- `module_135.R`

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Other Helpful Resources

Other Helpful Resources