Project 0

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Introduction

Cortisol measurements spike after waking then decrease over time.

```r
#load data

cortdat <- read.csv("~/Downloads/Project0_Clean_v2.csv")


#load packages

library(naniar)

library(tidyr)

library(dplyr)
```

```
##

## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':

##

##     filter, lag
```

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

##

##     intersect, setdiff, setequal, union
```

```
library(olsrr)
```

```
##

## Attaching package: 'olsrr'

## The following object is masked from 'package:datasets':

##

##     rivers
```

```
#fill in reported wake time for all rows.

cortdat <- cortdat %>%

  mutate(Sleep.Diary.reported.wake.time =

  ↪   na_if(Sleep.Diary.reported.wake.time, "")) %>%

  fill(Sleep.Diary.reported.wake.time, .direction="down")


##Calcute time since waking

  #1. convert time variables to POSIXct so we can take differences


cortdat$timeBook <- as.POSIXct(cortdat$Booket..Clock.Time, format="%H:%M")

cortdat$timeMEM <- as.POSIXct(cortdat$MEMs..Clock.Time, format="%H:%M")
```

```r
cortdat$timeWake <- as.POSIXct(cortdat$Sleep.Diary.reported.wake.time,
↪   format="%H:%M")


  #2. minutes since waking up for MEM and Booklet
cortdat$minWakeMEM <- as.numeric(difftime(cortdat$timeMEM,cortdat$timeWake,
↪   units="mins"))
cortdat$minWakeBook <-
↪   as.numeric(difftime(cortdat$timeBook,cortdat$timeWake, units="mins"))


#Booklet time minus MEM time
cortdat$disc <- as.numeric(difftime(cortdat$timeBook,cortdat$timeMEM,
↪   units="mins"))


#replace "" and 9999 with NA
cortdat <- cortdat %>%
  mutate(Booket..Clock.Time = na_if(Booket..Clock.Time, "")) %>%
  mutate(MEMs..Clock.Time = na_if(MEMs..Clock.Time, ""))


#replace impossible cortisol and DHEA levels with missing to remove
↪   outliers.
is.na(cortdat$Cortisol..nmol.L.) <- cortdat$Cortisol..nmol.L. >= 80
is.na(cortdat$DHEA..nmol.L.) <- cortdat$DHEA..nmol.L. >= 5.205
```

```
#Q1: Use linear mixed effect regression to regress Booklet time since
↪   waking on MEM time since waking.
mod1 <- lmerTest::lmer(minWakeMEM ~ minWakeBook +
↪   (1|SubjectID),data=cortdat)
summary(mod1)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [

lmerModLmerTest]

Formula: minWakeMEM ~ minWakeBook + (1 | SubjectID)

Data: cortdat

##

REML criterion at convergence: 2786.5

##

Scaled residuals:

Min   1Q Median   3Q   Max

-4.3591 -0.2958 -0.1806 -0.0200 5.9957

##

Random effects:

Groups   Name   Variance Std.Dev.

SubjectID (Intercept)   44.84   6.696

Residual   985.03   31.385

Number of obs: 285, groups: SubjectID, 31

4

```
##
## Fixed effects:
##               Estimate Std. Error        df t value Pr(>|t|)
## (Intercept) 1.017e+01   2.878e+00 6.362e+01    3.534 0.000769 ***
## minWakeBook 9.910e-01   7.029e-03 2.627e+02 140.978  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## minWakeBook -0.628
```

```r
#Q2: Proportions of adherence


cortdat$idealSampleTime <- ifelse(cortdat$Collection.Sample == 1 |
↪   cortdat$Collection.Sample == 3, cortdat$minWakeBook,
↪   ifelse(cortdat$Collection.Sample==4, 600, 30) )


#1 if difference between booklet recorded time and ideal time is less than
↪   7.5 minutes
cortdat$adherence7.5 <-
↪   ifelse(abs(cortdat$minWakeBook-cortdat$idealSampleTime)<=7.5, 1,0)
cortdat$adherence15 <-
↪   ifelse(abs(cortdat$minWakeBook-cortdat$idealSampleTime)<=15, 1,0)
```

```r
#Filter only Collection Samples 2,4 (30m since wake, 600m since wake)

cortdatq2 <- cortdat[cortdat$Collection.Sample == 2 |
↪   cortdat$Collection.Sample == 4,]

x7.5 <- sum(!is.na(cortdatq2$adherence7.5))

x15  <- sum(!is.na(cortdatq2$adherence15))

y <- length(cortdatq2$SubjectID)

prop7.5 <- prop.test(x7.5,y)

prop15  <- prop.test(x15,y)
```
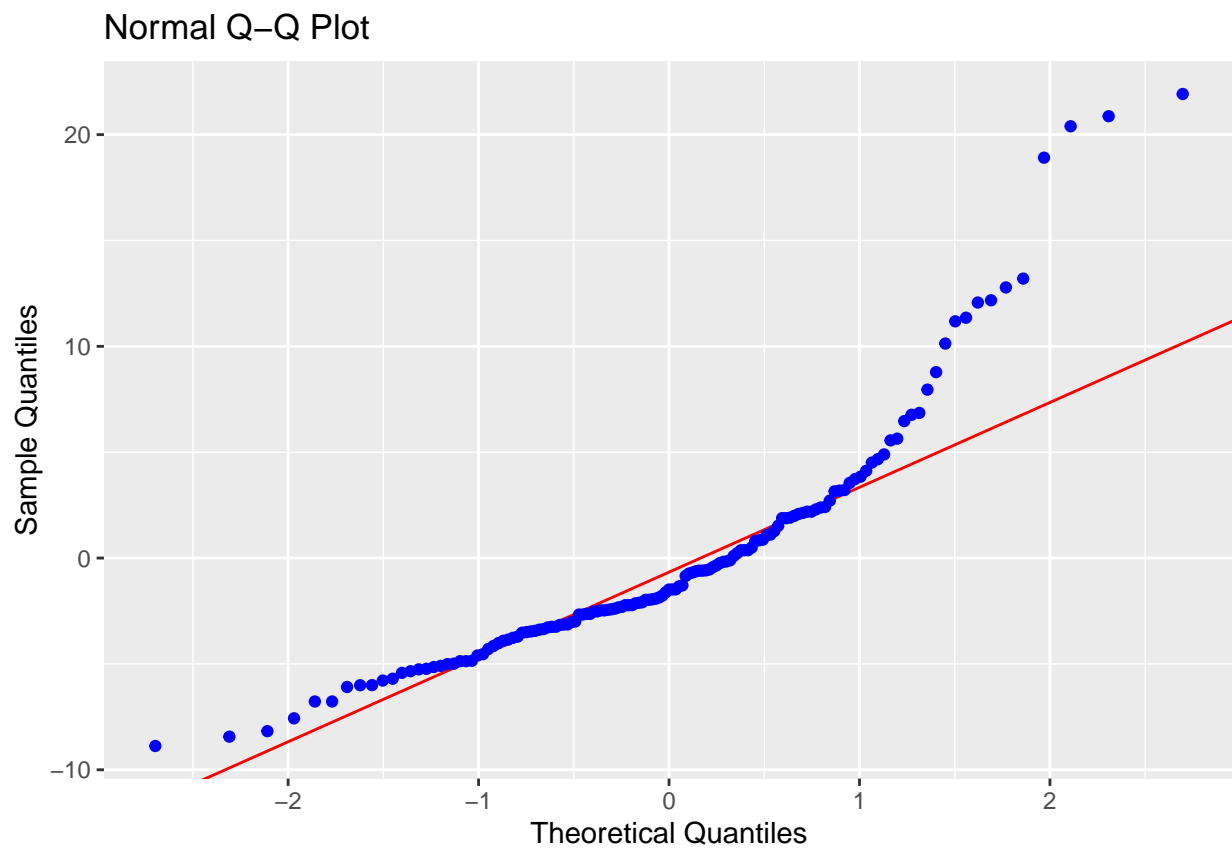
```r
#Q3 piecewise linear regression of Cortisol

cortdat0<-cortdat[cortdat$minWakeBook<=30,]

cortdat1<-cortdat[cortdat$minWakeBook>30,]


modknot1 <- lm((Cortisol..nmol.L.)~ minWakeBook, data=cortdat0)

modknot2 <- lm((Cortisol..nmol.L.)~ minWakeBook, data=cortdat1)


ols_plot_resid_qq(modknot1)
```
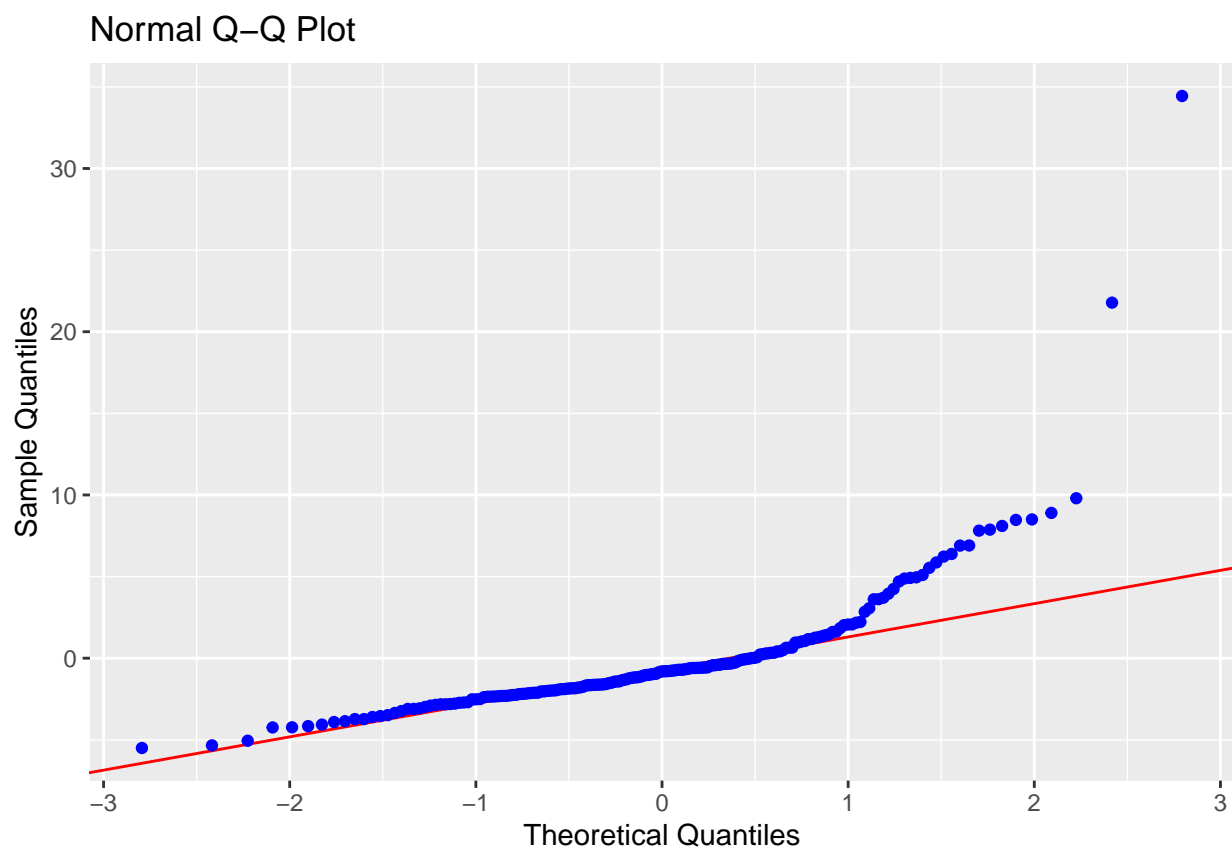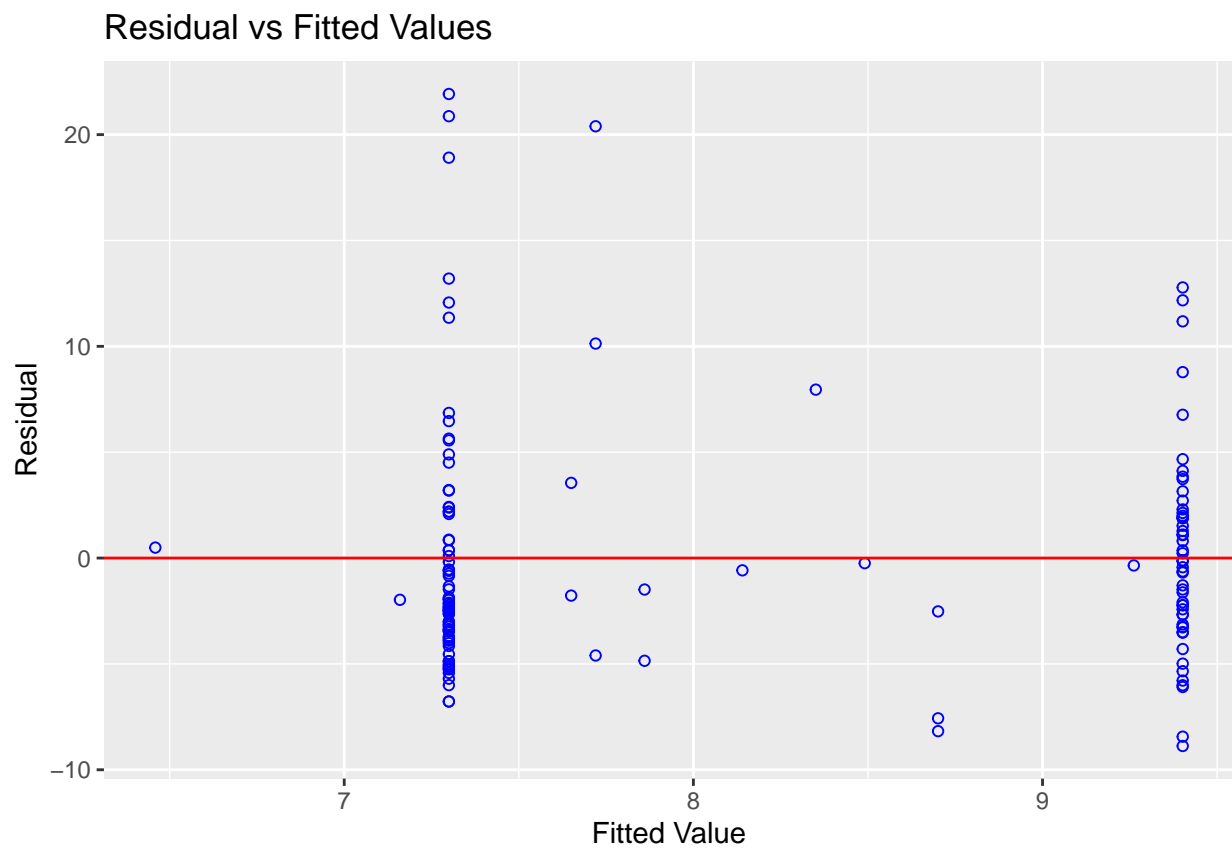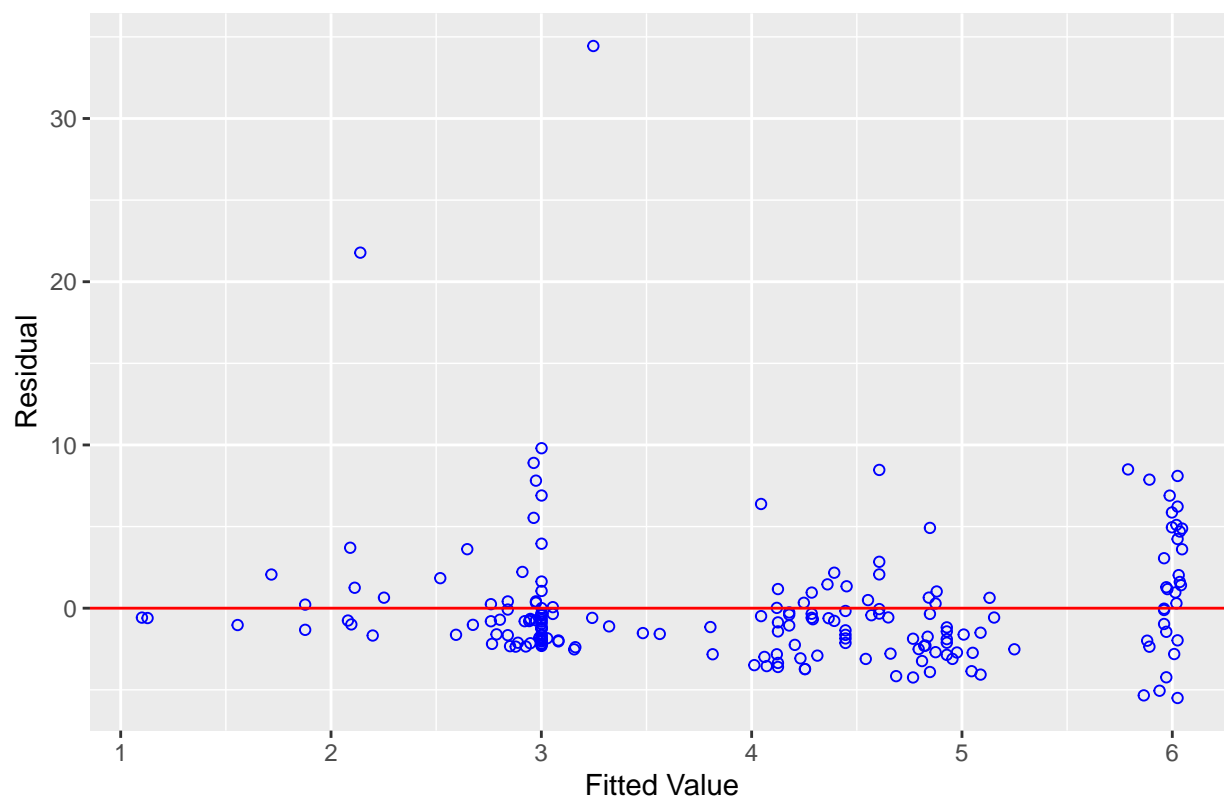
Normal Q–Q Plot

```
ols_plot_resid_qq(modknot2)
```

Normal Q–Q Plot


```r
ols_plot_resid_fit(modknot1)
```

Residual vs Fitted Values

```r
ols_plot_resid_fit(modknot2)
```

Residual vs Fitted Values


```
#residual plots show that using the log of cortisol is better!
```

```
library(lme4)
```

```
## Loading required package: Matrix
```

```
##
```

```
## Attaching package: 'Matrix'
```

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

```
##
```

```
##     expand, pack, unpack
```

```r
library(splines)


q3_mod <- lmer(log(Cortisol..nmol.L.)~bs(minWakeBook, knots=c(30),
↪  degree=1)+(1|SubjectID),
               data=cortdat)
summary(q3_mod)
```

```
## Linear mixed model fit by REML ['lmerMod']

## Formula: log(Cortisol..nmol.L.) ~ bs(minWakeBook, knots = c(30), degree = 1) +

##     (1 | SubjectID)

##    Data: cortdat

##

## REML criterion at convergence: 805.1

##

## Scaled residuals:

##     Min      1Q  Median      3Q     Max

## -3.3140 -0.5084  0.0531  0.5756  3.7601

##

## Random effects:

##  Groups     Name        Variance Std.Dev.

##  SubjectID (Intercept) 0.1045   0.3233
```

```
##   Residual                      0.5790    0.7609

## Number of obs: 335, groups:   SubjectID, 31

##

## Fixed effects:

##                                    Estimate Std. Error t value

## (Intercept)                          1.6555     0.1339  12.365

## bs(minWakeBook, knots = c(30), degree = 1)1   0.1683     0.1570   1.072

## bs(minWakeBook, knots = c(30), degree = 1)2  -1.7648     0.1658 -10.645

##

## Correlation of Fixed Effects:

##                     (Intr) b(WB,k=c(30),d=1)1

## b(WB,k=c(30),d=1)1 -0.800

## b(WB,k=c(30),d=1)2 -0.574   0.413
```