STA 440 Final Project: Code Script

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Package Import & Data Cleaning

```r
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
```

```r
library(tidyr)
library(readr)
library(ggplot2)
```

```r
load("REE.RData")
```
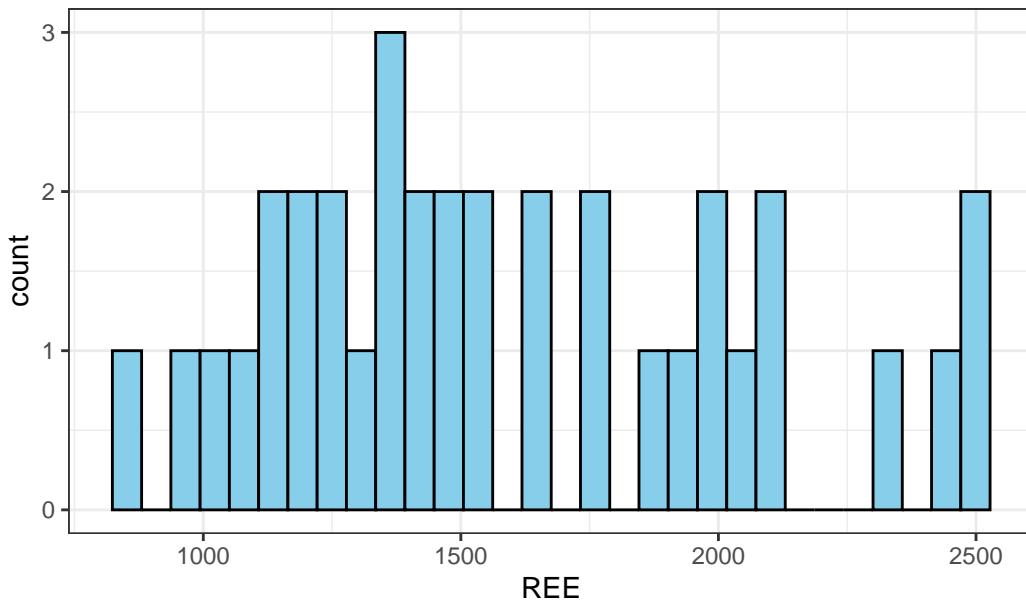
```r
REE <- REE %>%
  mutate(
    ID = factor(ID),
    Obese = factor(Obese, levels = c(0, 1)),
    Ventilator = factor(Ventilator, levels = c(0, 1)),
    ICUorSDU   = factor(ICUorSDU, levels = c("ICU", "SDU")),
    Measurement = as.numeric(Measurement)
  )
```

EDA

```
# Histogram of REE
ggplot(REE, aes(x = REE)) +
  geom_histogram(fill = "skyblue", color = "black") +
  labs(title = "Distribution of REE") +
  theme_bw()
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
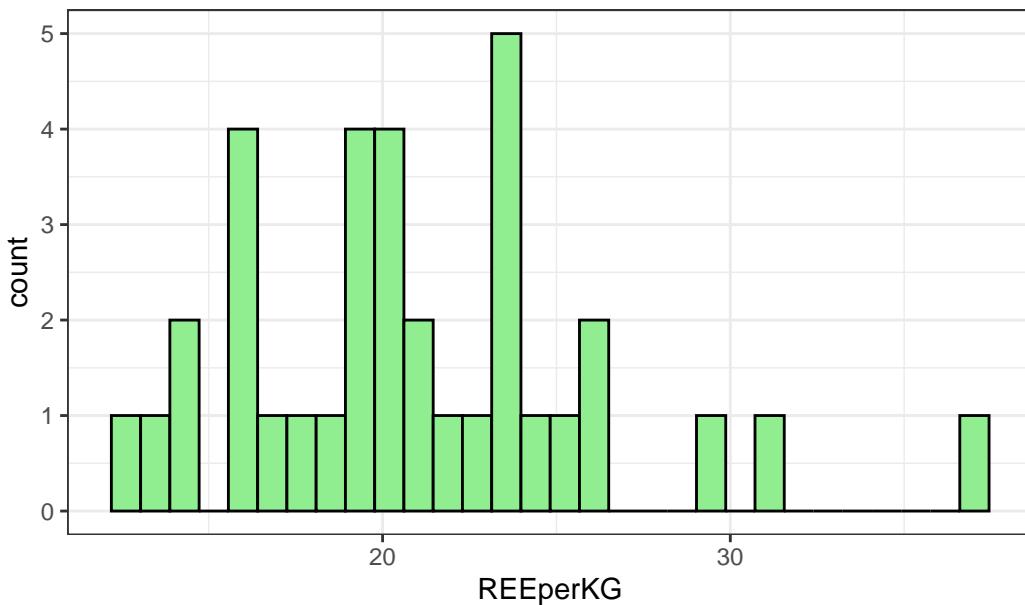
Distribution of REE


```
# Histogram of REE/kg
ggplot(REE, aes(x = REEperKG)) +
  geom_histogram(fill = "lightgreen", color = "black") +
  labs(title = "Distribution of REE per kg") +
  theme_bw()
```
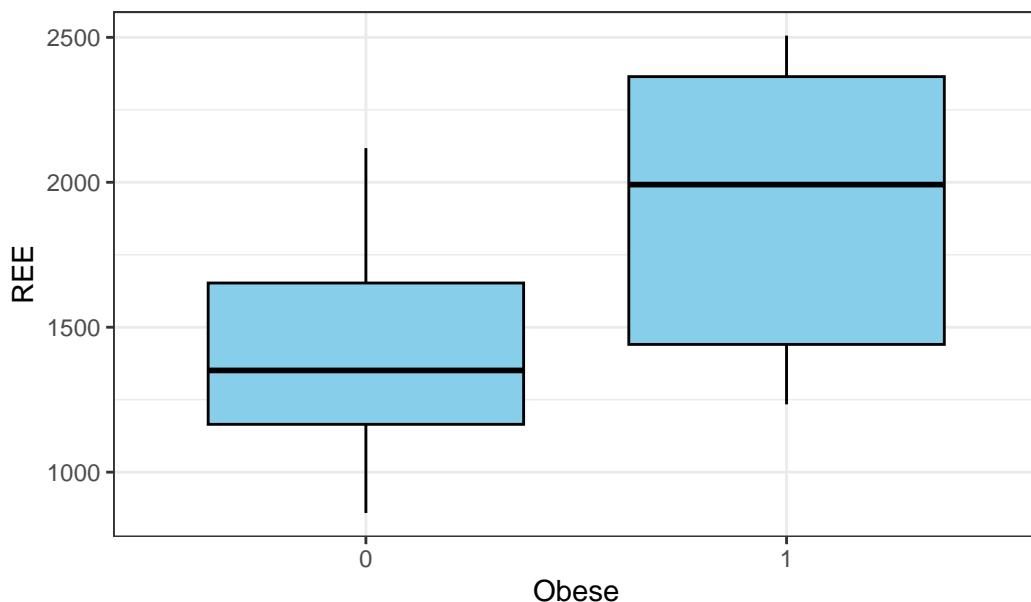
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

Distribution of REE per kg
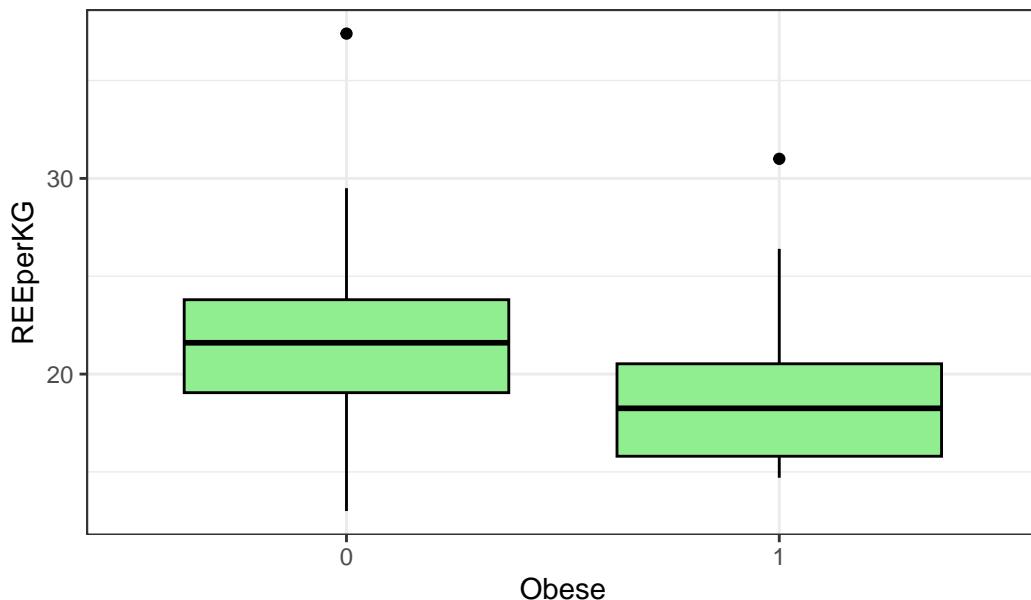

```r
ggplot(REE, aes(x = Obese, y = REE)) +
  geom_boxplot(fill = "skyblue", color = "black") +
  labs(title = "REE by Obesity") +
  theme_bw()
```

## REE by Obesity
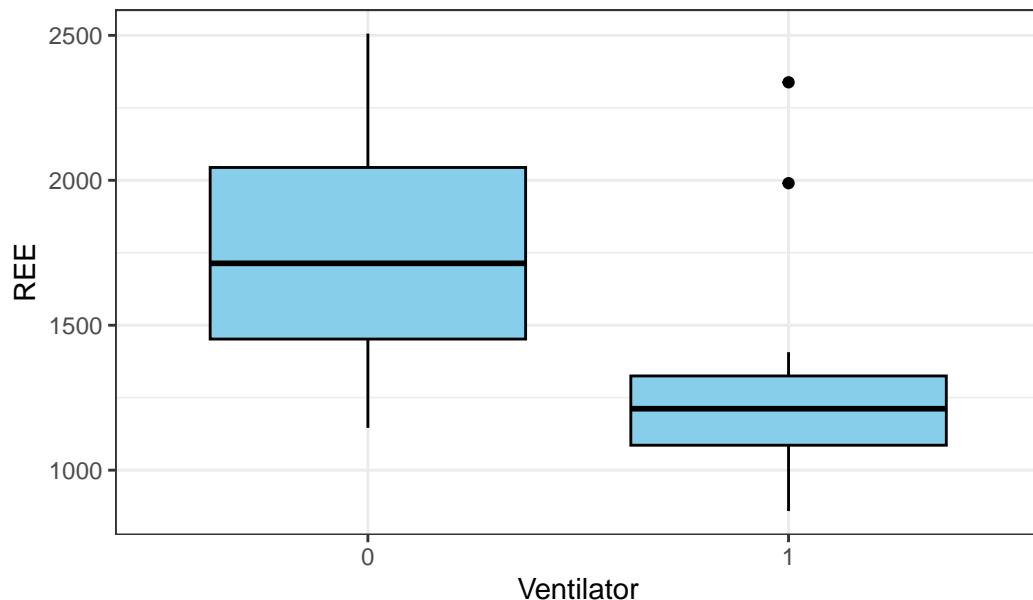


```r
ggplot(REE, aes(x = Obese, y = REEperKG)) +
  geom_boxplot(fill = "lightgreen", color = "black") +
  labs(title = "REE/kg by Obesity") +
  theme_bw()
```

REE/kg by Obesity
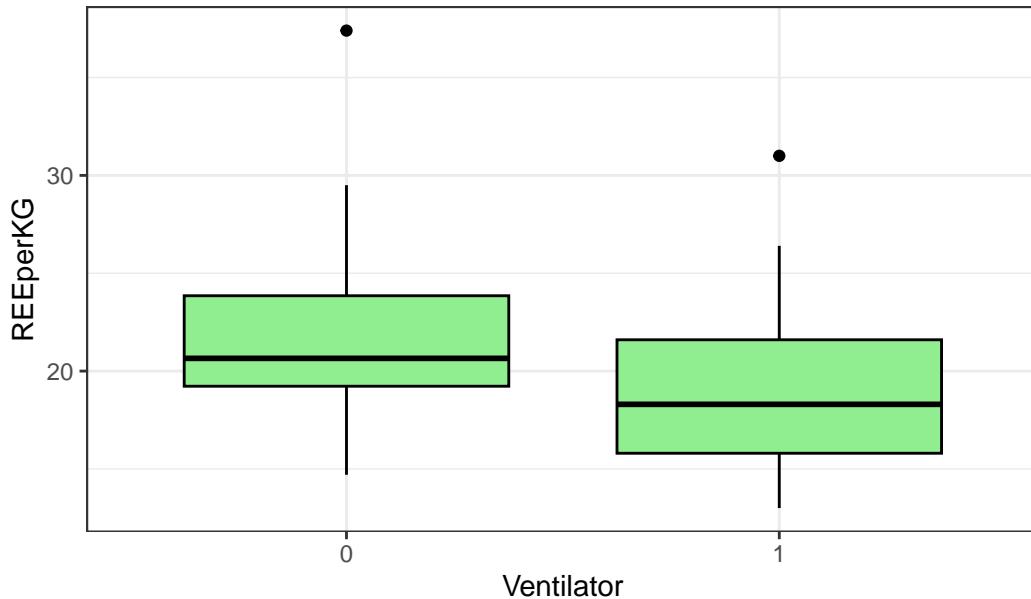

```
ggplot(REE, aes(x = Ventilator, y = REE)) +
  geom_boxplot(fill = "skyblue", color = "black") +
  labs(title = "REE by Ventilator Use") +
  theme_bw()
```

REE by Ventilator Use
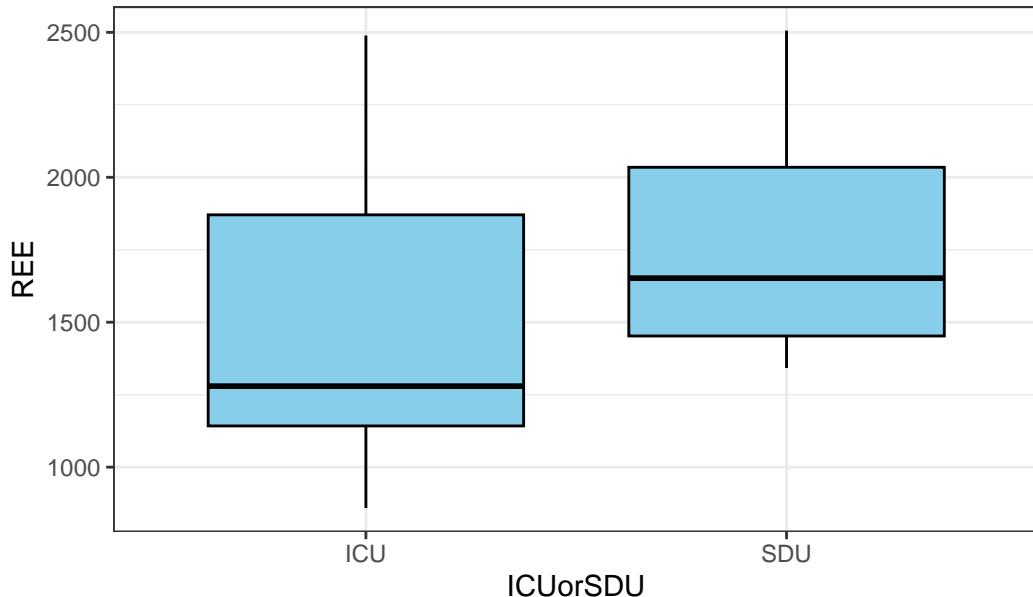

```
ggplot(REE, aes(x = Ventilator, y = REEperKG)) +
  geom_boxplot(fill = "lightgreen", color = "black") +
  labs(title = "REE/kg by Ventilator Use") +
  theme_bw()
```

REE/kg by Ventilator Use
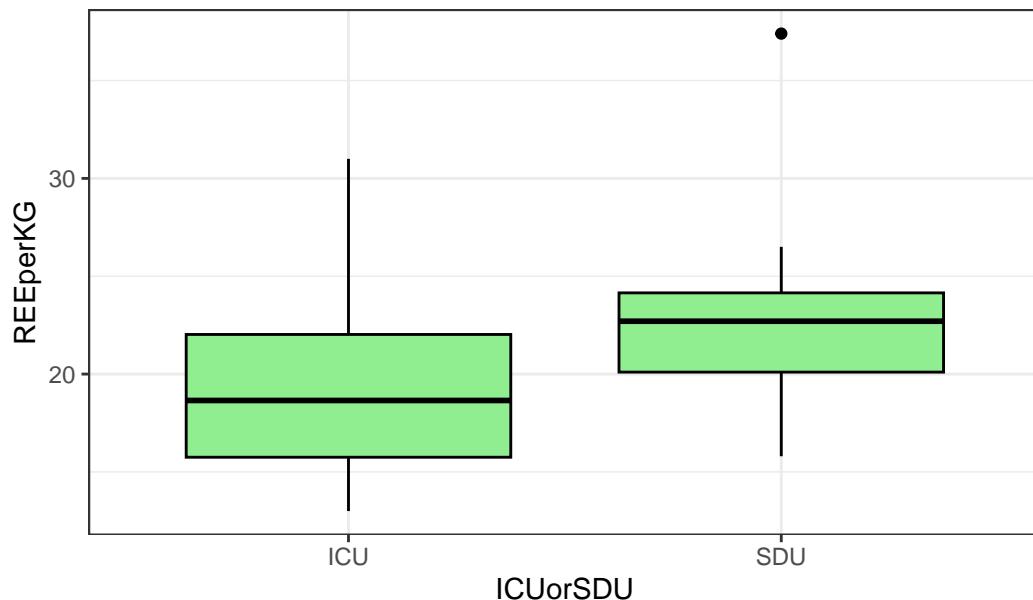

```
ggplot(REE, aes(x = ICUorSDU, y = REE)) +
  geom_boxplot(fill = "skyblue", color = "black") +
  labs(title = "REE by Location (ICU vs SDU)") +
  theme_bw()
```

REE by Location (ICU vs SDU)
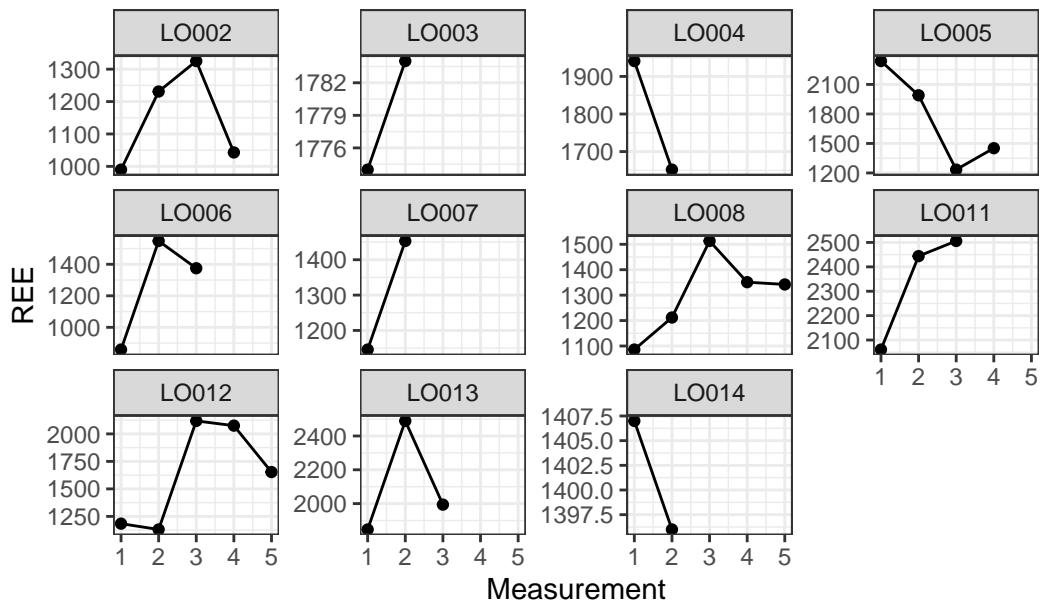

```
ggplot(REE, aes(x = ICUorSDU, y = REEperKG)) +
  geom_boxplot(fill = "lightgreen", color = "black") +
  labs(title = "REE/kg by Location (ICU vs SDU)") +
  theme_bw()
```

REE/kg by Location (ICU vs SDU)
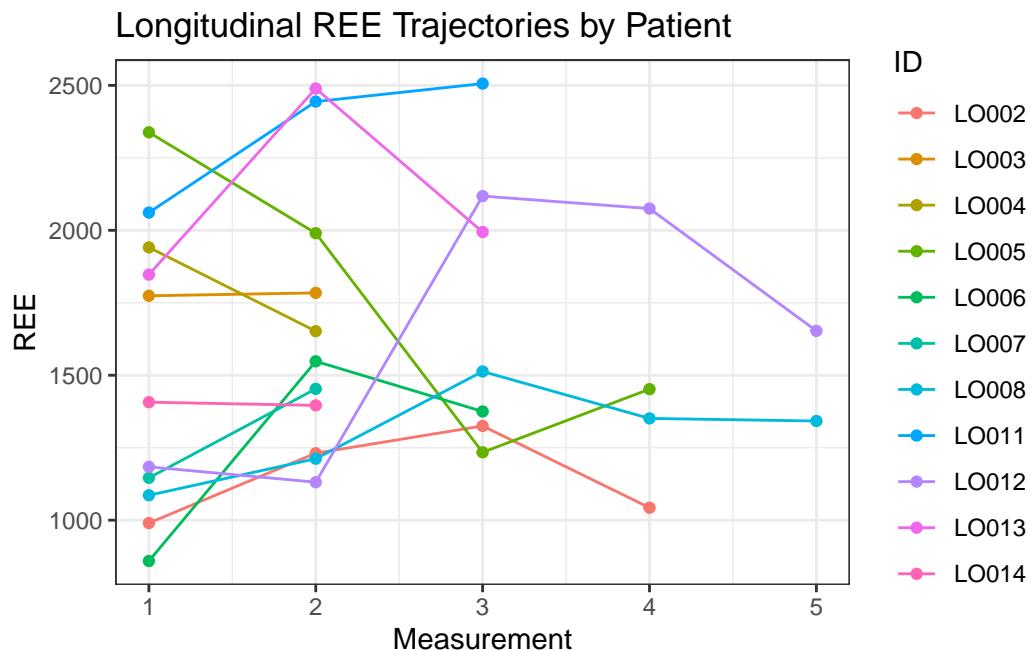

```
# Facet by patient: slope patterns
ggplot(REE, aes(x = Measurement, y = REE)) +
  geom_line() +
  geom_point() +
  facet_wrap(~ ID, scales = "free_y") +
  labs(title = "REE over Time for Each Patient") +
  theme_bw()
```

REE over Time for Each Patient
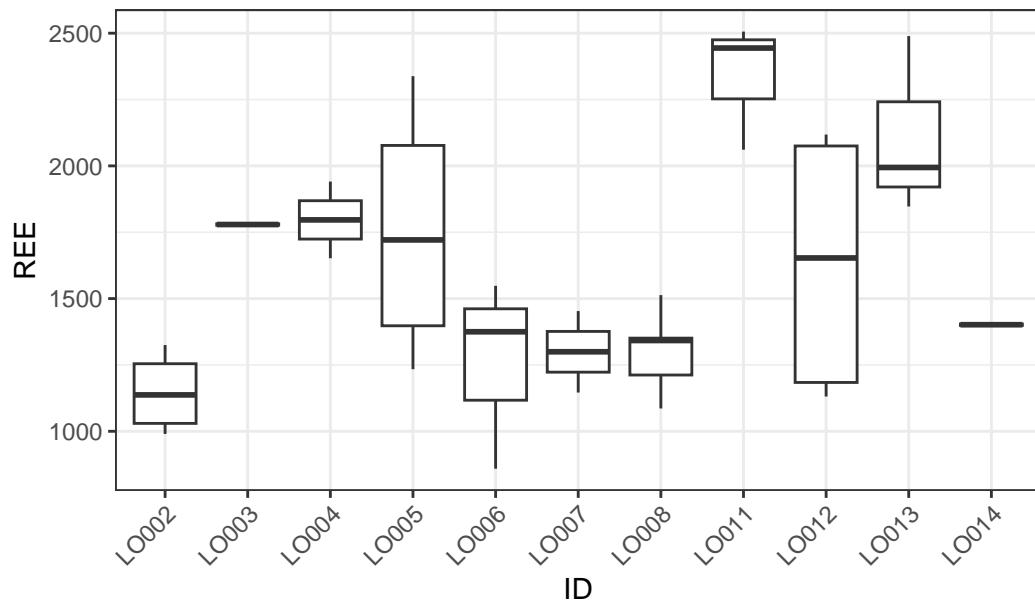

```
# Patient trajectories (spaghetti plot)
ggplot(REE, aes(x = Measurement, y = REE, group = ID, color = ID)) +
  geom_line() +
  geom_point() +
  labs(title = "Longitudinal REE Trajectories by Patient") +
  theme_bw() +
  theme(legend.position = "right")
```

Longitudinal REE Trajectories by Patient
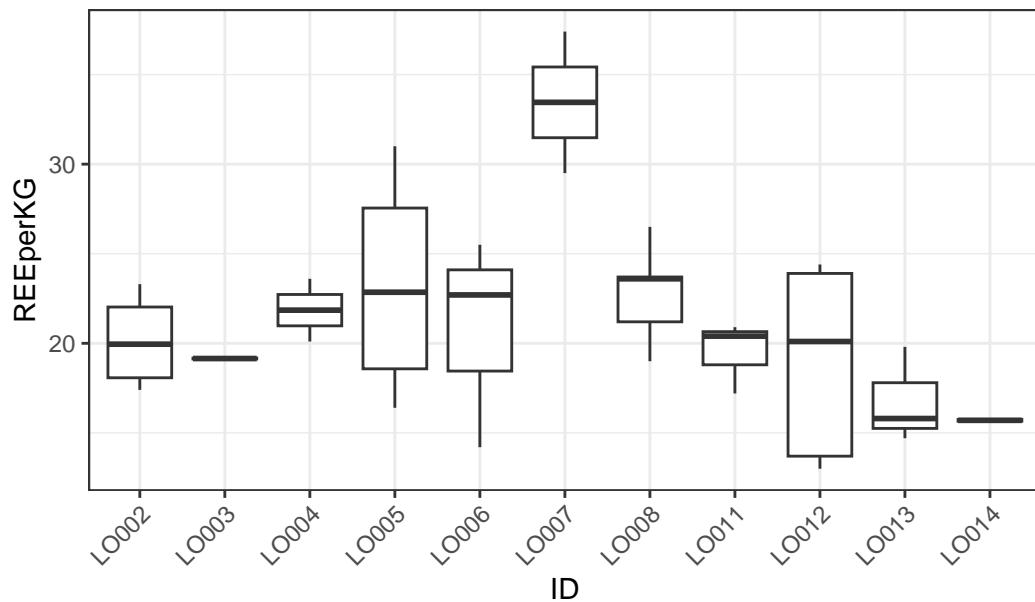
```
# Boxplot by patient
ggplot(REE, aes(x = ID, y = REE)) +
  geom_boxplot(outlier.colour = "red") +
  labs(title = "REE by Patient") +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

REE by Patient
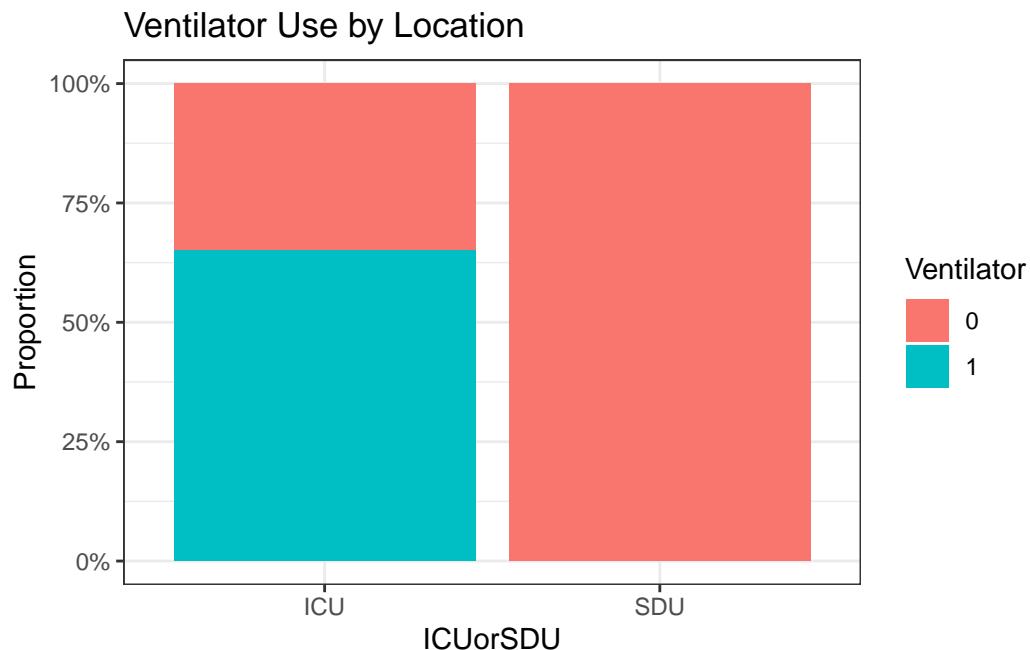

```
# Boxplot by patient
ggplot(REE, aes(x = ID, y = REEperKG)) +
  geom_boxplot(outlier.colour = "red") +
  labs(title = "REE/kg by Patient") +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

REE/kg by Patient
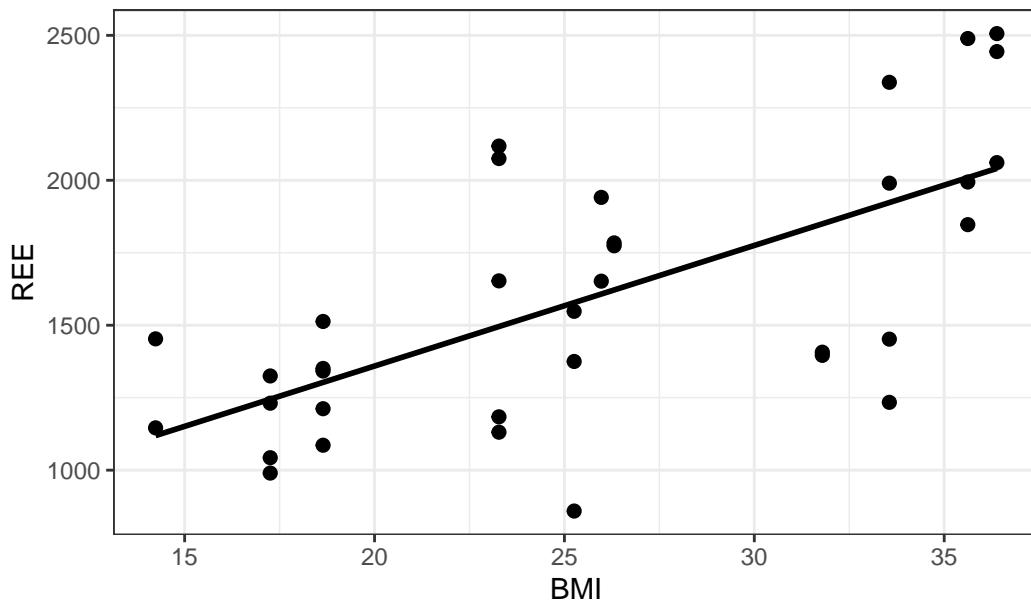

```r
# Proportion of Ventilation by Location
ggplot(REE, aes(x = ICUorSDU, fill = Ventilator)) +
  geom_bar(position = "fill") +
  scale_y_continuous(labels = scales::percent) +
  labs(y = "Proportion", title = "Ventilator Use by Location") +
  theme_bw()
```

Ventilator Use by Location


```
# REE vs BMI
ggplot(REE, aes(x = BMI, y = REE)) +
  geom_point(size = 2) +
  geom_smooth(method = "lm", se = FALSE, colour = "black") +
  labs(title = "REE vs BMI") +
  theme_bw()
```
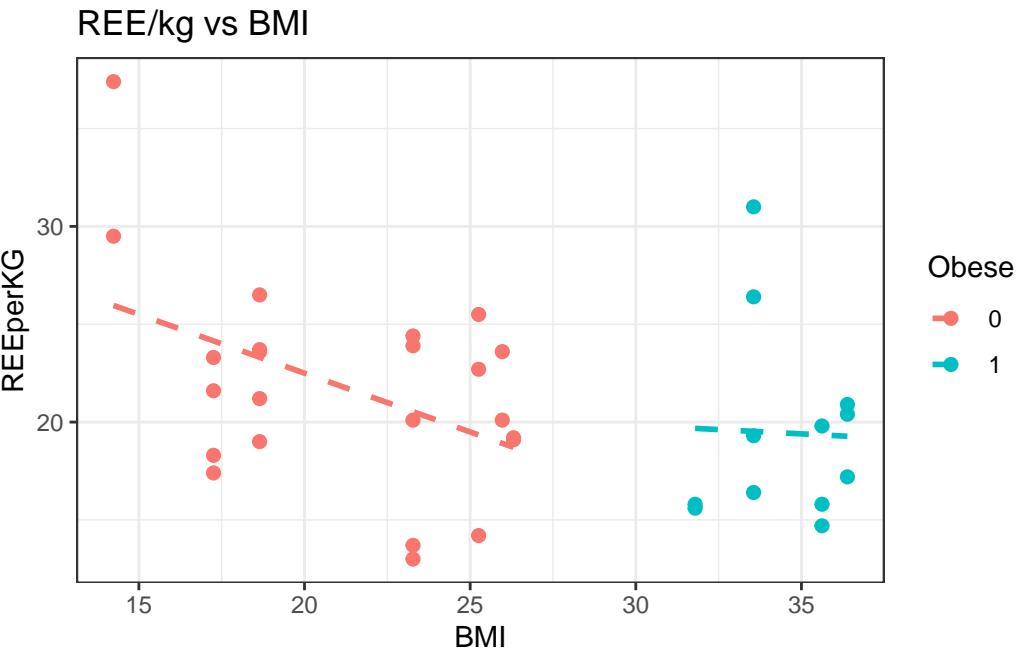
`geom_smooth()` using formula = 'y ~ x'

REE vs BMI


```r
# REE/kg vs BMI
ggplot(REE, aes(x = BMI, y = REEperKG, colour = Obese)) +
  geom_point(size = 2) +
  geom_smooth(method = "lm", se = FALSE, linetype = "dashed") +
  labs(title = "REE/kg vs BMI") +
  theme_bw()
```

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

REE/kg vs BMI

Initial Model

```
library(lme4)
```

```
Loading required package: Matrix
```

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

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

    expand, pack, unpack
```

```
Warning in check_dep_version(): ABI version mismatch:
lme4 was built with Matrix ABI version 2
Current Matrix ABI version is 1
Please re-install lme4 from source or restore original 'Matrix' package
```

```
model_REEperKG <- lmer(
  REEperKG ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator + (1 | ID),
  data = REE
)

summary(model_REEperKG)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula:
REEperKG ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator +
    (1 | ID)
   Data: REE

REML criterion at convergence: 178.9

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.4128 -0.6014 -0.1273  0.5621  1.5307

Random effects:
 Groups   Name        Variance Std.Dev.
 ID       (Intercept) 20.83    4.564
 Residual             11.14    3.338
Number of obs: 35, groups:  ID, 11

Fixed effects:
                         Estimate Std. Error t value
(Intercept)               21.0144     2.9073   7.228
Obese1                     4.2462     4.0805   1.041
Measurement                0.3738     1.0875   0.344
ICUorSDUSDU                6.5742     3.6543   1.799
Ventilator1               -3.0581     2.2974  -1.331
Obese1:Measurement        -3.5279     1.2526  -2.816
Measurement:ICUorSDUSDU   -1.2072     1.4533  -0.831

Correlation of Fixed Effects:
            (Intr) Obese1 Msrmnt ICUSDU Vntlt1 Obs1:M
Obese1      -0.508
Measurement -0.557  0.166
ICUorSDUSDU -0.307  0.128  0.318
Ventilator1 -0.445  0.097 -0.036  0.010
Obs1:Msrmnt  0.289 -0.641 -0.285 -0.155 -0.072
```
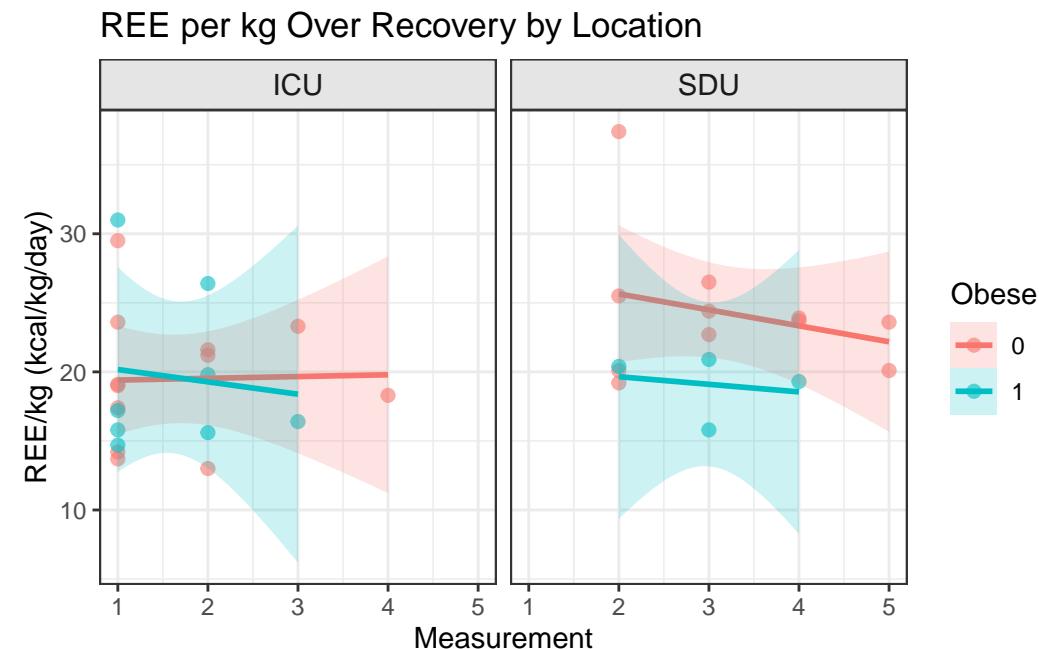
```
M:ICUSDUSDU  0.247 -0.038 -0.642 -0.812  0.314  0.080
```

```
ggplot(REE, aes(x = Measurement, y = REEperKG, color = Obese)) +
  geom_point(size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = TRUE,
              aes(fill = Obese), alpha = 0.2) +
  facet_wrap(~ ICUorSDU) +
  labs(title = "REE per kg Over Recovery by Location",
       y = "REE/kg (kcal/kg/day)") +
  theme_bw() +
  theme(strip.background = element_rect(fill="grey90"),
        strip.text = element_text(size=11))
```

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


REE per kg Over Recovery by Location

```
ggplot(REE, aes(x = Measurement, y = REEperKG, color = ICUorSDU)) +
  geom_point(size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = TRUE,
              aes(fill = ICUorSDU), alpha = 0.2) +
  facet_wrap(~ Obese) +
  labs(title = "REE per kg Over Recovery by Obesity Status",
```
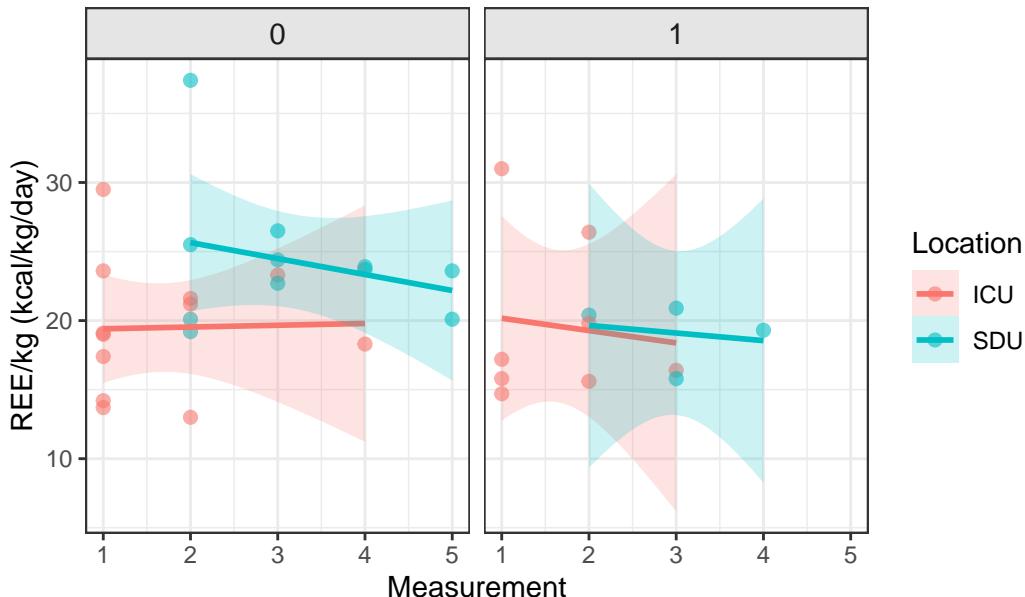
```
        y = "REE/kg (kcal/kg/day)",
        color = "Location",
        fill = "Location") +
  theme_bw() +
  theme(strip.background = element_rect(fill="grey90"),
        strip.text = element_text(size=11))
```

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

REE per kg Over Recovery by Obesity Status

```
model_REE <- lmer(
  REE ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator + (1 | ID),
  data = REE
)

summary(model_REE)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: REE ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator +
    (1 | ID)
   Data: REE
```

```
REML criterion at convergence: 418.9

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.3155 -0.5735 -0.2568  0.5738  1.6933

Random effects:
 Groups   Name        Variance Std.Dev.
 ID       (Intercept) 36139    190.1
 Residual             79976    282.8
Number of obs: 35, groups:  ID, 11

Fixed effects:
                        Estimate Std. Error t value
(Intercept)             1448.707    197.797   7.324
Obese1                   932.125    272.028   3.427
Measurement                3.954     87.954   0.045
ICUorSDUSDU              432.998    299.913   1.444
Ventilator1             -319.944    167.986  -1.905
Obese1:Measurement      -212.845    103.909  -2.048
Measurement:ICUorSDUSDU  -79.188    117.350  -0.675

Correlation of Fixed Effects:
            (Intr) Obese1 Msrmnt ICUSDU Vntlt1 Obs1:M
Obese1      -0.494
Measurement -0.631  0.216
ICUorSDUSDU -0.439  0.176  0.365
Ventilator1 -0.437  0.127 -0.157  0.102
Obs1:Msrmnt  0.352 -0.809 -0.291 -0.180 -0.065
M:ICUSDUSDU  0.365 -0.064 -0.698 -0.809  0.270  0.104
```
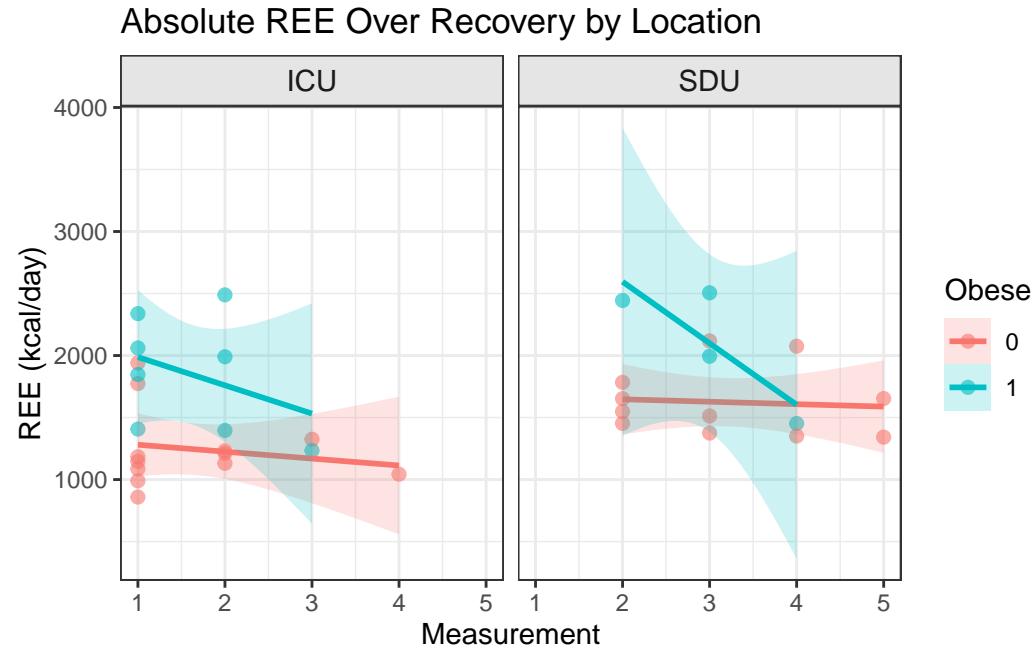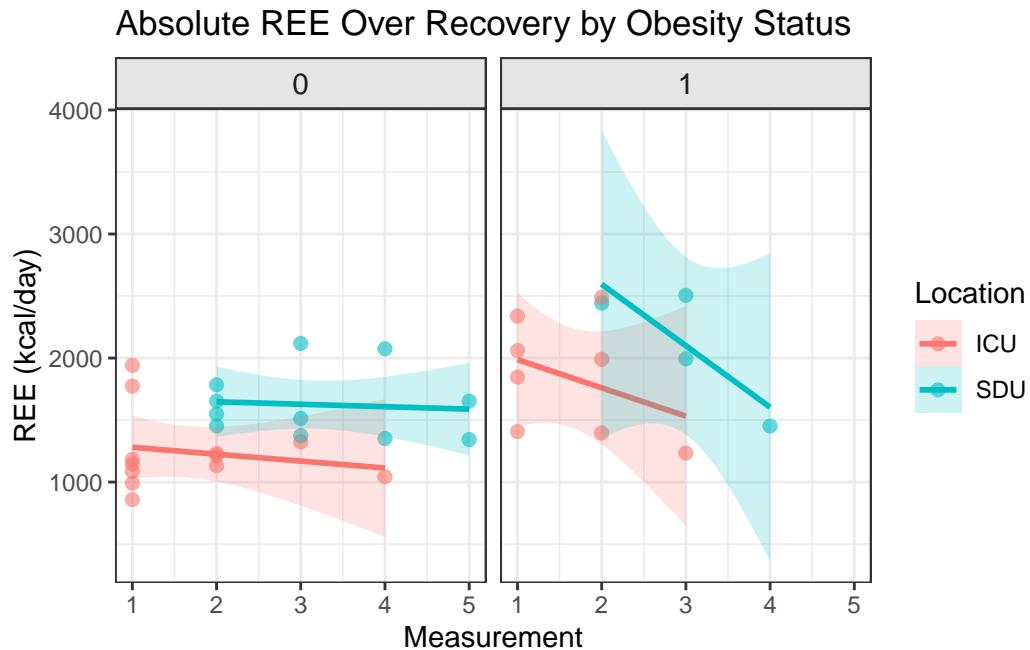
```r
ggplot(REE, aes(x = Measurement, y = REE, color = Obese)) +
  geom_point(size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = TRUE,
              aes(fill = Obese), alpha = 0.2) +
  facet_wrap(~ ICUorSDU) +
  labs(title = "Absolute REE Over Recovery by Location",
       y = "REE (kcal/day)") +
  theme_bw() +
  theme(strip.background = element_rect(fill="grey90"),
        strip.text = element_text(size=11))
```

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

Absolute REE Over Recovery by Location



```
ggplot(REE, aes(x = Measurement, y = REE, color = ICUorSDU)) +
  geom_point(size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = TRUE,
              aes(fill = ICUorSDU), alpha = 0.2) +
  facet_wrap(~ Obese) +
  labs(title = "Absolute REE Over Recovery by Obesity Status",
       y = "REE (kcal/day)",
       color = "Location",
       fill = "Location") +
  theme_bw() +
  theme(strip.background = element_rect(fill="grey90"),
        strip.text = element_text(size=11))
```

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

Absolute REE Over Recovery by Obesity Status
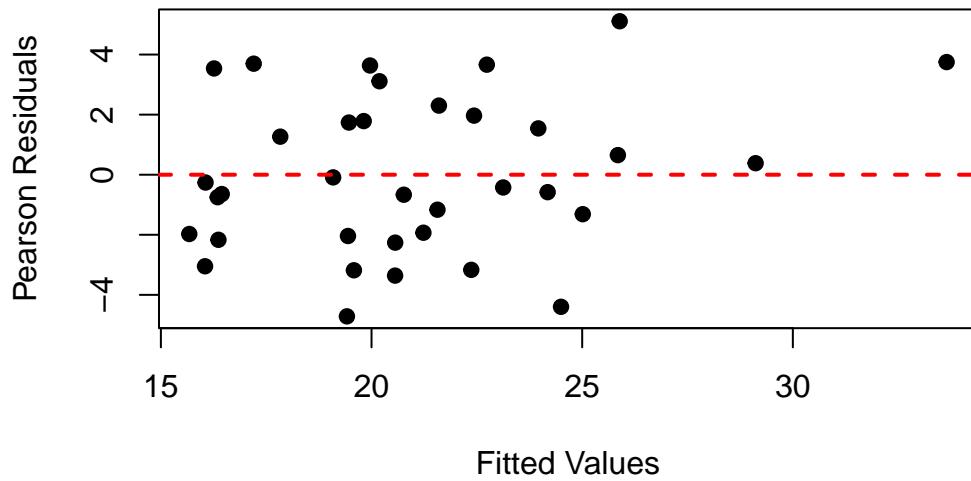
Initial Model Diagnostics
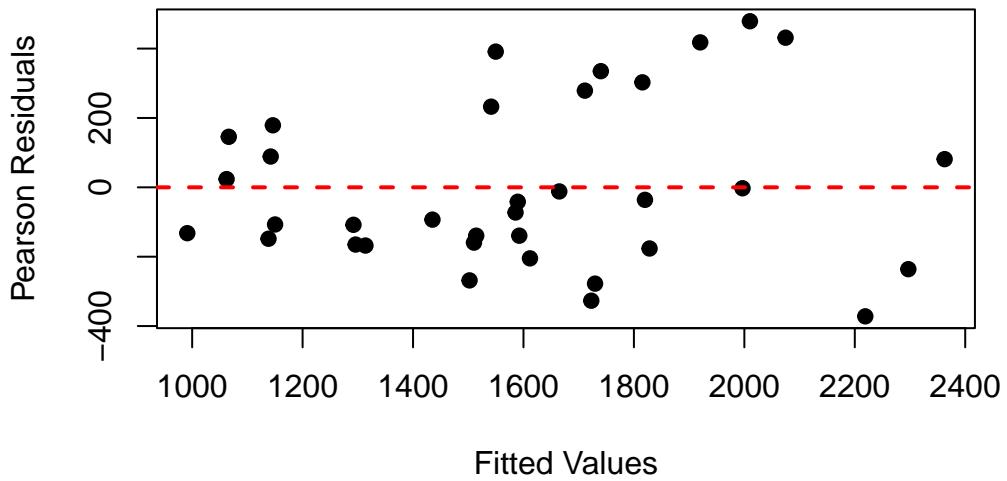
```
# Residual plots
plot(
  fitted(model_REEperKG),
  resid(model_REEperKG, type = "pearson"),
  pch = 19, col = "black",
  xlab = "Fitted Values",
  ylab = "Pearson Residuals",
  main = "Residuals vs Fitted: REEperKG"
)
abline(h = 0, col = "red", lty = 2, lwd = 2)
```

Residuals vs Fitted: REEperKG
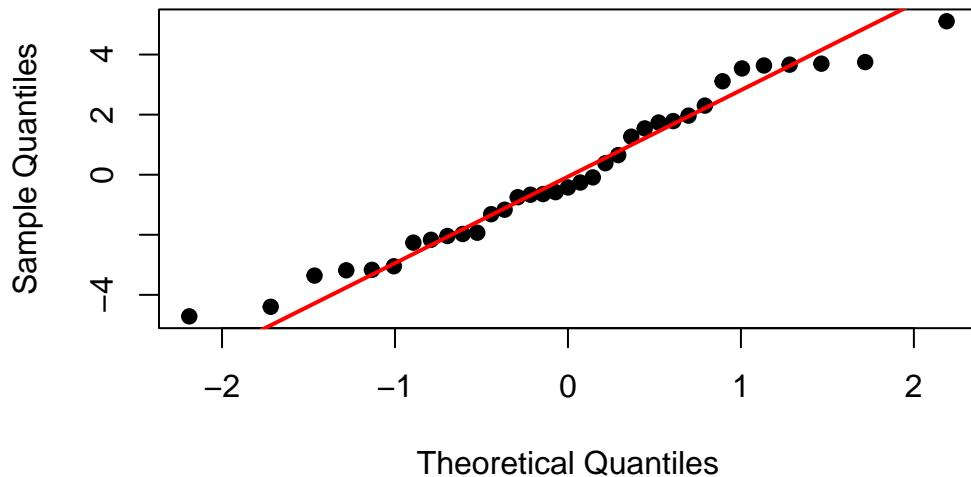

```r
plot(
  fitted(model_REE),
  resid(model_REE, type = "pearson"),
  pch = 19, col = "black",
  xlab = "Fitted Values",
  ylab = "Pearson Residuals",
  main = "Residuals vs Fitted: REE"
)
abline(h = 0, col = "red", lty = 2, lwd = 2)
```

Residuals vs Fitted: REE
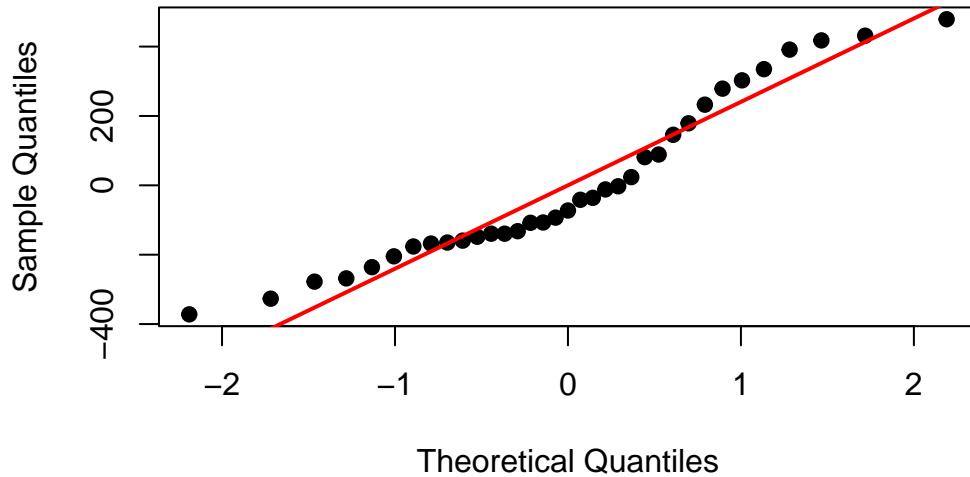

```
# QQ plots: residuals
qqnorm(resid(model_REEperKG),
       main = "Q-Q Plot of Residuals: REEperKG",
       pch = 19, col = "black")
qqline(resid(model_REEperKG), col = "red", lwd = 2)
```

Q–Q Plot of Residuals: REEperKG


```
qqnorm(resid(model_REE),
       main = "Q-Q Plot of Residuals: REE",
       pch = 19, col = "black")
qqline(resid(model_REE), col = "red", lwd = 2)
```
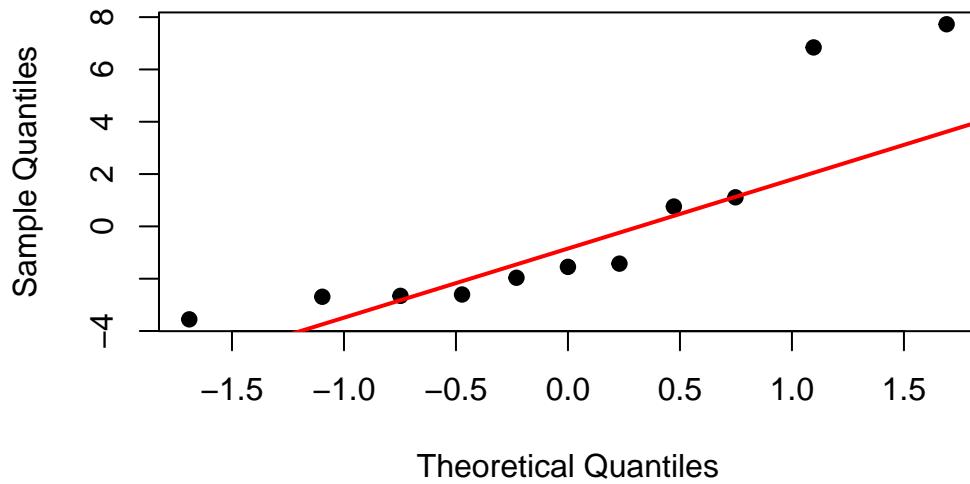
Q–Q Plot of Residuals: REE


```
## QQ plots: random effects
re_REEperKG <- ranef(model_REEperKG)$ID[[1]]
re_REE      <- ranef(model_REE)$ID[[1]]

qqnorm(re_REEperKG,
       main = "Q-Q Plot of Random Intercepts: REEperKG",
       pch = 19, col = "black")
qqline(re_REEperKG, col = "red", lwd = 2)
```
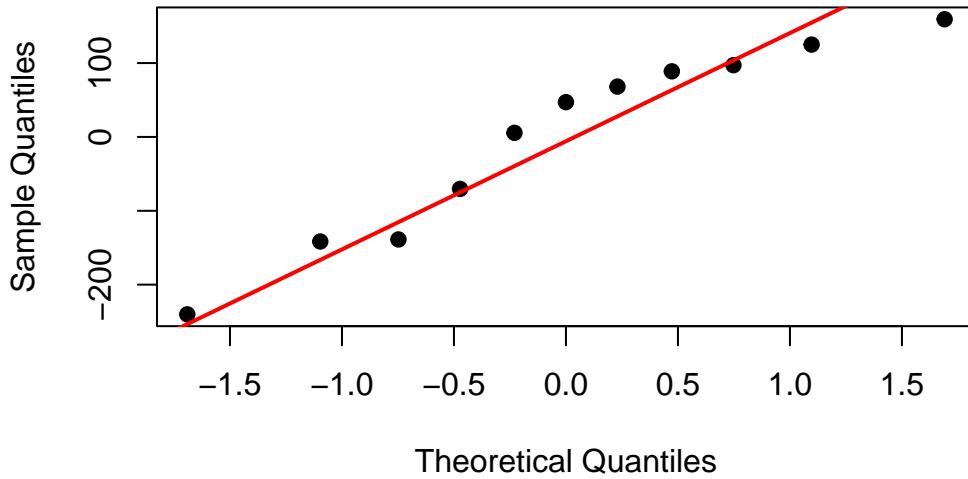
Q–Q Plot of Random Intercepts: REEperKG


```
qqnorm(re_REE,
       main = "Q-Q Plot of Random Intercepts: REE",
       pch = 19, col = "black")
qqline(re_REE, col = "red", lwd = 2)
```

Q–Q Plot of Random Intercepts: REE


```r
# REEperKG: Ratio test
model_REEperKG_full_ML <- update(model_REEperKG, REML = FALSE)

## Drop ICU x Measurement
model_REEperKG_no_locInt <- lmer(
  REEperKG ~ Obese * Measurement + ICUorSDU + Measurement + Ventilator + (1 | ID),
  data = REE,
  REML = FALSE
)

## Drop Obese x Measurement
model_REEperKG_no_obInt <- lmer(
  REEperKG ~ Obese + Measurement + ICUorSDU * Measurement + Ventilator + (1 | ID),
  data = REE,
  REML = FALSE
)

## Drop both interactions (main-effects only)
model_REEperKG_main <- lmer(
  REEperKG ~ Obese + Measurement + ICUorSDU + Ventilator + (1 | ID),
  data = REE,
  REML = FALSE
)
```

```
## AIC & BIC
AIC(model_REEperKG_full_ML, model_REEperKG_no_locInt, model_REEperKG_no_obInt, model_REEperK
```

```
                         df      AIC
model_REEperKG_full_ML    9 214.7266
model_REEperKG_no_locInt  8 213.5626
model_REEperKG_no_obInt   8 220.1186
model_REEperKG_main       7 218.4164
```

```
BIC(model_REEperKG_full_ML, model_REEperKG_no_locInt, model_REEperKG_no_obInt, model_REEperK
```

```
                         df      BIC
model_REEperKG_full_ML    9 228.7248
model_REEperKG_no_locInt  8 226.0054
model_REEperKG_no_obInt   8 232.5613
model_REEperKG_main       7 229.3039
```

```
## Likelihood ratio tests
anova(model_REEperKG_full_ML, model_REEperKG_no_locInt)
```

```
Data: REE
Models:
model_REEperKG_no_locInt: REEperKG ~ Obese * Measurement + ICUorSDU + Measurement + Ventilato
model_REEperKG_full_ML: REEperKG ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator
                         npar    AIC     BIC  logLik deviance Chisq Df
model_REEperKG_no_locInt    8 213.56 226.00 -98.781   197.56
model_REEperKG_full_ML      9 214.73 228.72 -98.363   196.73 0.836  1
                         Pr(>Chisq)
model_REEperKG_no_locInt
model_REEperKG_full_ML       0.3606
```

```
anova(model_REEperKG_full_ML, model_REEperKG_no_obInt)
```

```
Data: REE
Models:
model_REEperKG_no_obInt: REEperKG ~ Obese + Measurement + ICUorSDU * Measurement + Ventilator
model_REEperKG_full_ML: REEperKG ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator
                         npar    AIC     BIC   logLik deviance  Chisq Df
model_REEperKG_no_obInt     8 220.12 232.56 -102.059   204.12
```

```
model_REEperKG_full_ML       9 214.73 228.72  -98.363    196.73 7.3919  1
                              Pr(>Chisq)
model_REEperKG_no_obInt
model_REEperKG_full_ML        0.006552 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
anova(model_REEperKG_full_ML, model_REEperKG_main)
```

```
Data: REE
Models:
model_REEperKG_main: REEperKG ~ Obese + Measurement + ICUorSDU + Ventilator + (1 | ID)
model_REEperKG_full_ML: REEperKG ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator
                        npar    AIC    BIC   logLik deviance  Chisq Df
model_REEperKG_main        7 218.42 229.30 -102.208    204.42
model_REEperKG_full_ML     9 214.73 228.72  -98.363    196.73 7.6898  2
                          Pr(>Chisq)
model_REEperKG_main
model_REEperKG_full_ML      0.02139 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# REE: Ratio test
model_REE_full_ML <- update(model_REE, REML = FALSE)

# Drop ICU x Measurement
model_REE_no_locInt <- lmer(
  REE ~ Obese * Measurement + ICUorSDU + Measurement + Ventilator + (1 | ID),
  data = REE,
  REML = FALSE
)

# Drop Obese x Measurement
model_REE_no_obInt <- lmer(
  REE ~ Obese + Measurement + ICUorSDU * Measurement + Ventilator + (1 | ID),
  data = REE,
  REML = FALSE
)

# Drop both interactions (main-effects only)
model_REE_main <- lmer(
  REE ~ Obese + Measurement + ICUorSDU + Ventilator + (1 | ID),
```

```
  data = REE,
  REML = FALSE
)

# AIC & BIC
AIC(model_REE_full_ML, model_REE_no_locInt, model_REE_no_obInt, model_REE_main)
```

```
                     df      AIC
model_REE_full_ML     9 514.1467
model_REE_no_locInt   8 512.6707
model_REE_no_obInt    8 516.2957
model_REE_main        7 514.4486
```

```
BIC(model_REE_full_ML, model_REE_no_locInt, model_REE_no_obInt, model_REE_main)
```

```
                     df      BIC
model_REE_full_ML     9 528.1449
model_REE_no_locInt   8 525.1134
model_REE_no_obInt    8 528.7385
model_REE_main        7 525.3360
```

```
# Likelihood ratio tests
anova(model_REE_full_ML, model_REE_no_locInt)
```

```
Data: REE
Models:
model_REE_no_locInt: REE ~ Obese * Measurement + ICUorSDU + Measurement + Ventilator + (1 |
model_REE_full_ML: REE ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator + (1 | ID)
                    npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
model_REE_no_locInt    8 512.67 525.11 -248.34   496.67
model_REE_full_ML      9 514.15 528.14 -248.07   496.15 0.5239  1     0.4692
```

```
anova(model_REE_full_ML, model_REE_no_obInt)
```

```
Data: REE
Models:
model_REE_no_obInt: REE ~ Obese + Measurement + ICUorSDU * Measurement + Ventilator + (1 | ID
model_REE_full_ML: REE ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator + (1 | ID)
                  npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
```

```
model_REE_no_obInt    8 516.30 528.74 -250.15    500.30
model_REE_full_ML     9 514.15 528.14 -248.07    496.15 4.1489  1    0.04166 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

anova(model_REE_full_ML, model_REE_main)

```
Data: REE
Models:
model_REE_main: REE ~ Obese + Measurement + ICUorSDU + Ventilator + (1 | ID)
model_REE_full_ML: REE ~ Obese * Measurement + ICUorSDU * Measurement + Ventilator + (1 | ID)
                 npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
model_REE_main      7 514.45 525.34 -250.22    500.45
model_REE_full_ML   9 514.15 528.14 -248.07    496.15 4.3019  2     0.1164
```

Final Model

```
REEperKG_model <- lmer(
  REEperKG ~ Obese * Measurement + ICUorSDU + Ventilator + (1 | ID),
  data = REE
)

summary(REEperKG_model)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: REEperKG ~ Obese * Measurement + ICUorSDU + Ventilator + (1 |      ID)
   Data: REE

REML criterion at convergence: 182.2

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.4489 -0.7006 -0.1305  0.6526  1.4366

Random effects:
 Groups   Name        Variance Std.Dev.
 ID       (Intercept) 20.74    4.554
 Residual             11.00    3.317
Number of obs: 35, groups:  ID, 11
```

```
Fixed effects:
                    Estimate Std. Error t value
(Intercept)          21.6132     2.8047   7.706
Obese1                4.1214     4.0599   1.015
Measurement          -0.2068     0.8289  -0.250
ICUorSDUSDU           4.1105     2.1200   1.939
Ventilator1          -2.4634     2.1690  -1.136
Obese1:Measurement   -3.4471     1.2407  -2.778


Correlation of Fixed Effects:
             (Intr) Obese1 Msrmnt ICUSDU Vntlt1
Obese1       -0.515
Measurement  -0.536  0.184
ICUorSDUSDU  -0.188  0.166 -0.454
Ventilator1  -0.568  0.114  0.228  0.477
Obs1:Msrmnt   0.278 -0.639 -0.305 -0.155 -0.102
```

```
REE_model <- lmer(
  REE ~ Obese * Measurement + ICUorSDU + Ventilator + (1 | ID),
  data = REE
)
summary(REE_model)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: REE ~ Obese * Measurement + ICUorSDU + Ventilator + (1 | ID)
   Data: REE

REML criterion at convergence: 430.8

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.3502 -0.6189 -0.1831  0.6726  1.8067

Random effects:
 Groups   Name        Variance Std.Dev.
 ID       (Intercept) 35224    187.7
 Residual             78575    280.3
Number of obs: 35, groups:  ID, 11

Fixed effects:
                Estimate Std. Error t value
(Intercept)      1497.43     182.35   8.212
```

```
Obese1                    920.25      268.87   3.423
Measurement               -37.48       62.38  -0.601
ICUorSDUSDU               269.18      174.54   1.542
Ventilator1              -289.40      160.20  -1.806
Obese1:Measurement  -205.42          102.42  -2.006


Correlation of Fixed Effects:
            (Intr) Obese1 Msrmnt ICUSDU Vntlt1
Obese1       -0.506
Measurement -0.565  0.240
ICUorSDUSDU -0.264  0.213 -0.476
Ventilator1 -0.598  0.150  0.045  0.567
Obs1:Msrmnt  0.340 -0.809 -0.307 -0.163 -0.097
```
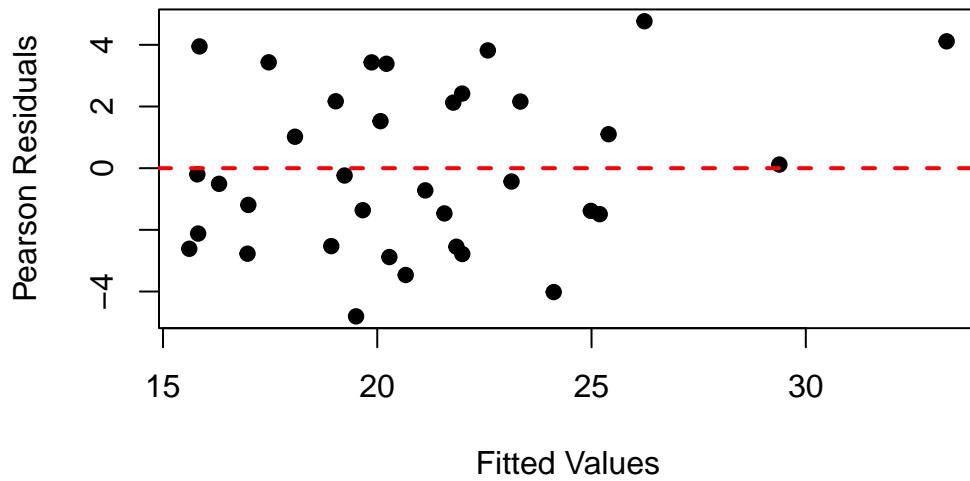
Final Model Assessment
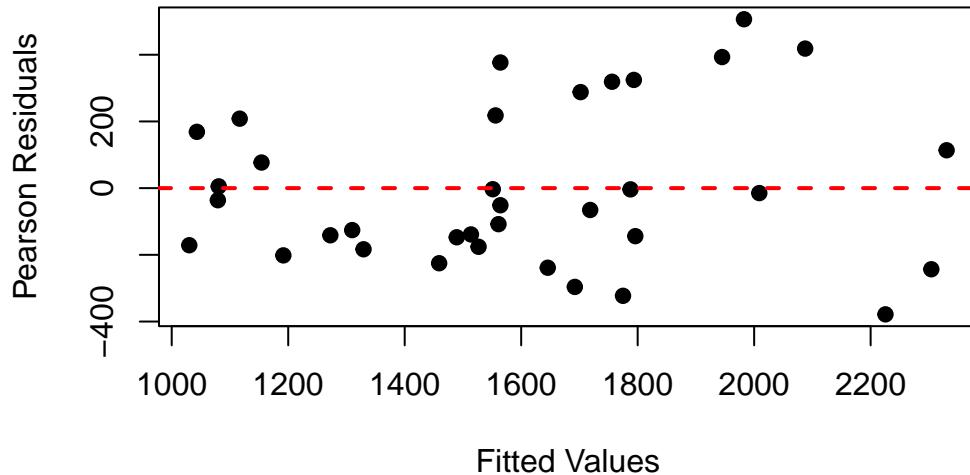
```
# Residual plots
plot(
  fitted(REEperKG_model),
  resid(REEperKG_model, type = "pearson"),
  pch = 19, col = "black",
  xlab = "Fitted Values",
  ylab = "Pearson Residuals",
  main = "Residuals vs Fitted: REEperKG"
)
abline(h = 0, col = "red", lty = 2, lwd = 2)
```

Residuals vs Fitted: REEperKG
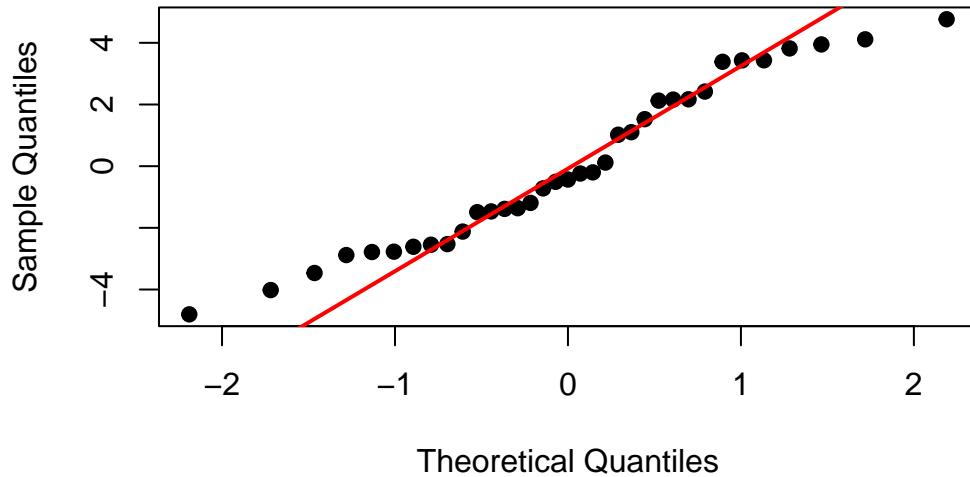

```r
plot(
  fitted(REE_model),
  resid(REE_model, type = "pearson"),
  pch = 19, col = "black",
  xlab = "Fitted Values",
  ylab = "Pearson Residuals",
  main = "Residuals vs Fitted: REE"
)
abline(h = 0, col = "red", lty = 2, lwd = 2)
```

**Residuals vs Fitted: REE**
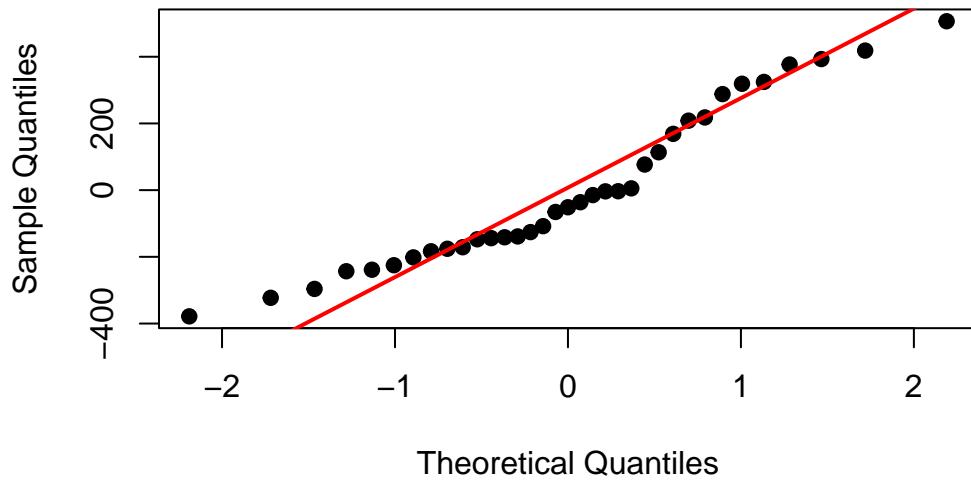

```
# QQ plots: residuals
qqnorm(resid(REEperKG_model),
       main = "Q-Q Plot of Residuals: REEperKG",
       pch = 19, col = "black")
qqline(resid(REEperKG_model), col = "red", lwd = 2)
```

Q–Q Plot of Residuals: REEperKG


```
qqnorm(resid(REE_model),
       main = "Q-Q Plot of Residuals: REE",
       pch = 19, col = "black")
qqline(resid(REE_model), col = "red", lwd = 2)
```
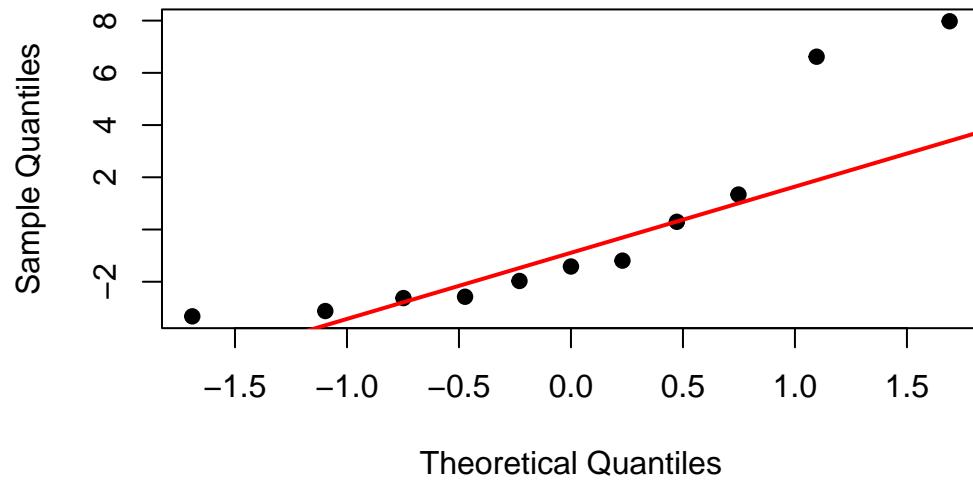
Q–Q Plot of Residuals: REE


```
## QQ plots: random effects
REEperKG_re <- ranef(REEperKG_model)$ID[[1]]
REE_re      <- ranef(REE_model)$ID[[1]]

qqnorm(REEperKG_re,
       main = "Q-Q Plot of Random Intercepts: REEperKG",
       pch = 19, col = "black")
qqline(REEperKG_re, col = "red", lwd = 2)
```
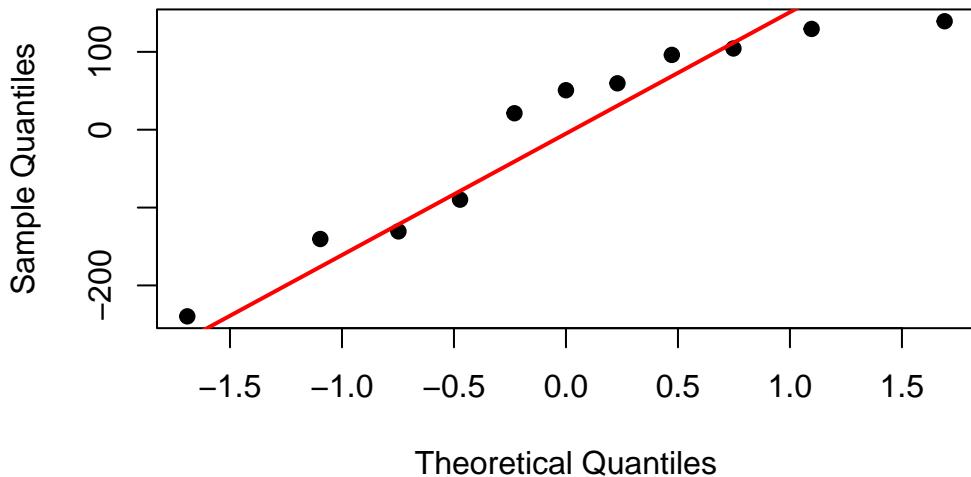
Q–Q Plot of Random Intercepts: REEperKG


```
qqnorm(REE_re,
       main = "Q-Q Plot of Random Intercepts: REE",
       pch = 19, col = "black")
qqline(REE_re, col = "red", lwd = 2)
```

Q–Q Plot of Random Intercepts: REE


```
# Pearson residuals
REE$resid_REEkg <- resid(REEperKG_model, type = "pearson")

ggplot(REE, aes(x = Measurement, y = resid_REEkg)) +
  geom_point(color = "black", alpha = 0.75, size = 2) +
  geom_hline(yintercept = 0, linetype = "dotted", color = "red", linewidth = 1) +
  geom_smooth(method = "loess", se = FALSE, color = "blue", linewidth = 1) +
  labs(
    title = "Residuals vs Measurement: REE per kg Model",
    x = "Measurement (Recovery Day Index)",
    y = "Pearson Residuals"
  ) +
  theme_bw()
```
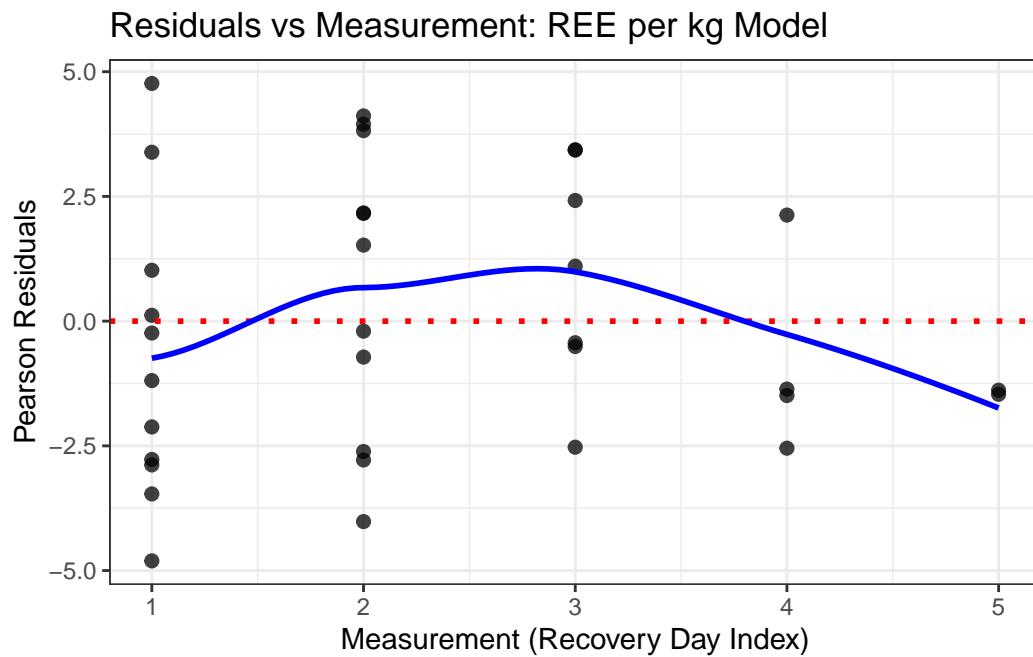
`geom_smooth()` using formula = 'y ~ x'

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: pseudoinverse used at 0.98

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: neighborhood radius 2.02

```
Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: reciprocal condition number 5.1453e-17
```

```
Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: There are other near singularities as well. 1
```


Residuals vs Measurement: REE per kg Model

```
REE$resid_REE <- resid(REE_model, type = "pearson")

ggplot(REE, aes(x = Measurement, y = resid_REE)) +
  geom_point(color = "black", alpha = 0.75, size = 2) +
  geom_hline(yintercept = 0, linetype = "dotted", color = "red", linewidth = 1) +
  geom_smooth(method = "loess", se = FALSE, color = "blue", linewidth = 1) +
  labs(
    title = "Residuals vs Measurement: Absolute REE Model",
    x = "Measurement (Recovery Day Index)",
    y = "Pearson Residuals"
  ) +
  theme_bw()
```
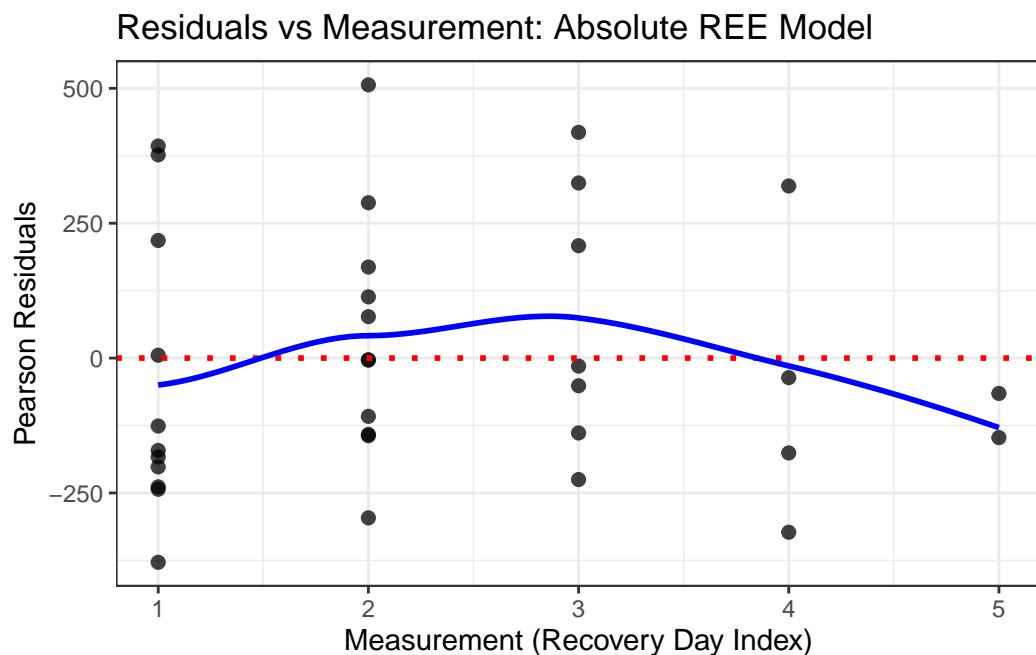
```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: pseudoinverse used at 0.98

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: neighborhood radius 2.02

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: reciprocal condition number 5.1453e-17

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: There are other near singularities as well. 1
```

Residuals vs Measurement: Absolute REE Model


```r
plot_residual_vs <- function(model, var, title) {
  res_df <- data.frame(
    Resid = resid(model, type = "pearson"),
    Var = REE[[var]]
  )

  # Detect categorical vs numeric
  if (is.factor(res_df$Var) || is.character(res_df$Var)) {
    ggplot(res_df, aes(x = Var, y = Resid)) +
```

```r
      geom_boxplot(fill = "grey85", color = "black", alpha = 0.6) +
      geom_jitter(width = 0.1, alpha = 0.6, size = 2) +
      geom_hline(yintercept = 0, linetype = "dotted",
                 color = "red", linewidth = 1) +
      labs(x = var, y = "Pearson Residuals", title = title) +
      theme_bw(base_size = 13)
  } else {
    ggplot(res_df, aes(x = Var, y = Resid)) +
      geom_point(color = "black", alpha = 0.7, size = 2) +
      geom_smooth(method = "loess", se = FALSE,
                  color = "blue", linewidth = 1) +
      geom_hline(yintercept = 0, linetype = "dotted",
                 color = "red", linewidth = 1) +
      labs(x = var, y = "Pearson Residuals", title = title) +
      theme_bw(base_size = 13)
  }
}
```

```r
plot_residual_vs(REE_model, "Measurement",
                 "Residuals vs Measurement: Absolute REE Model")
```

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

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: pseudoinverse used at 0.98

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: neighborhood radius 2.02

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: reciprocal condition number 5.1453e-17

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: There are other near singularities as well. 1

Residuals vs Measurement: Absolute REE Mode

```
plot_residual_vs(REE_model, "Obese",
                 "Residuals vs Obesity Status: Absolute REE Model")
```


Residuals vs Obesity Status: Absolute REE Mode
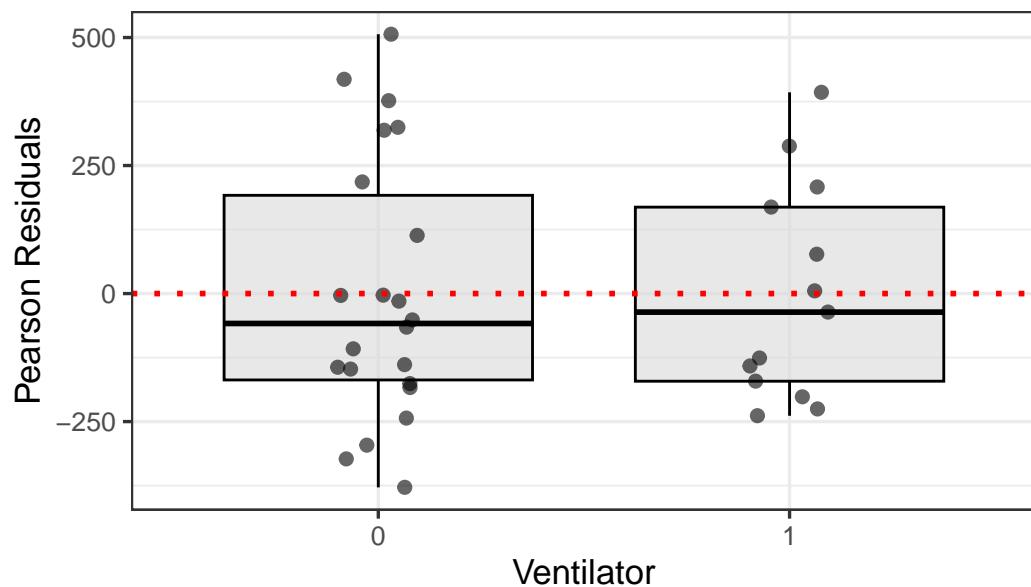
```
plot_residual_vs(REE_model, "ICUorSDU",
                 "Residuals vs ICU/SDU: Absolute REE Model")
```

Residuals vs ICU/SDU: Absolute REE Model


```
plot_residual_vs(REE_model, "Ventilator",
                 "Residuals vs Ventilation: Absolute REE Model")
```
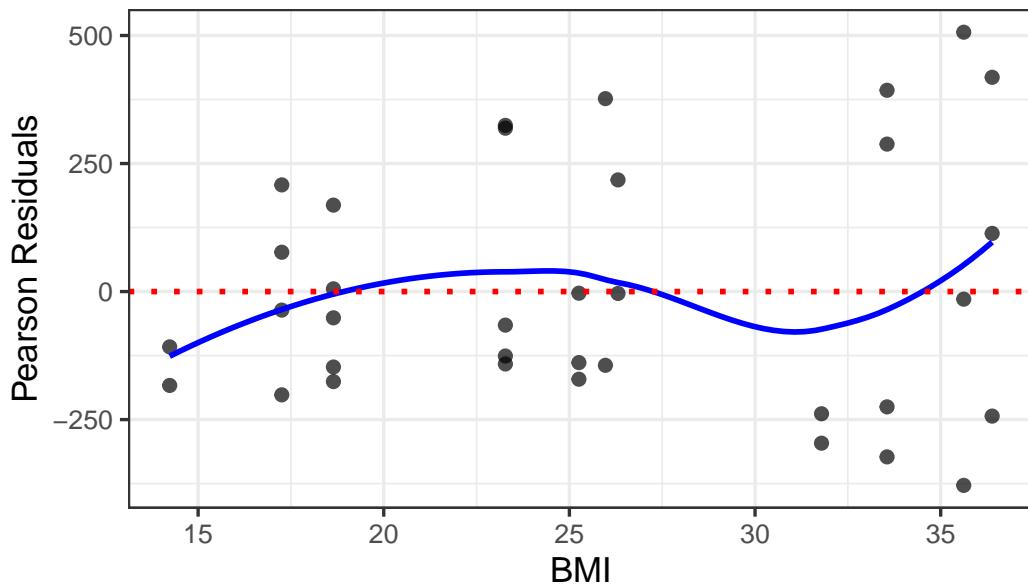
Residuals vs Ventilation: Absolute REE Model


```r
plot_residual_vs(REE_model, "BMI",
                 "Residuals vs BMI: Absolute REE Model")
```

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

Residuals vs BMI: Absolute REE Model


```
plot_residual_vs(REEperKG_model, "Measurement",
                 "Residuals vs Measurement: REE/kg Model")
```

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

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: pseudoinverse used at 0.98

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: neighborhood radius 2.02

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: reciprocal condition number 5.1453e-17

Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
: There are other near singularities as well. 1
```
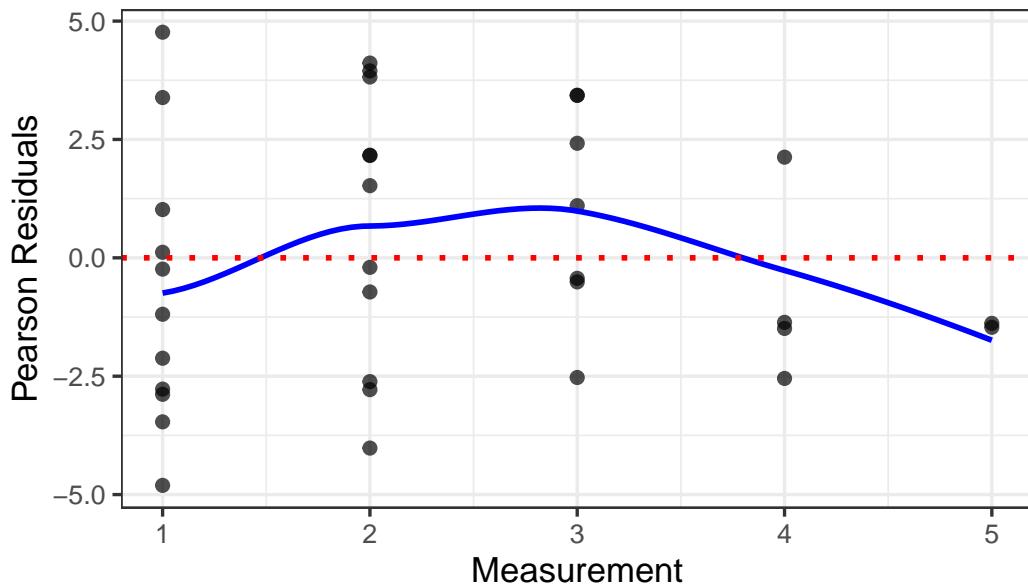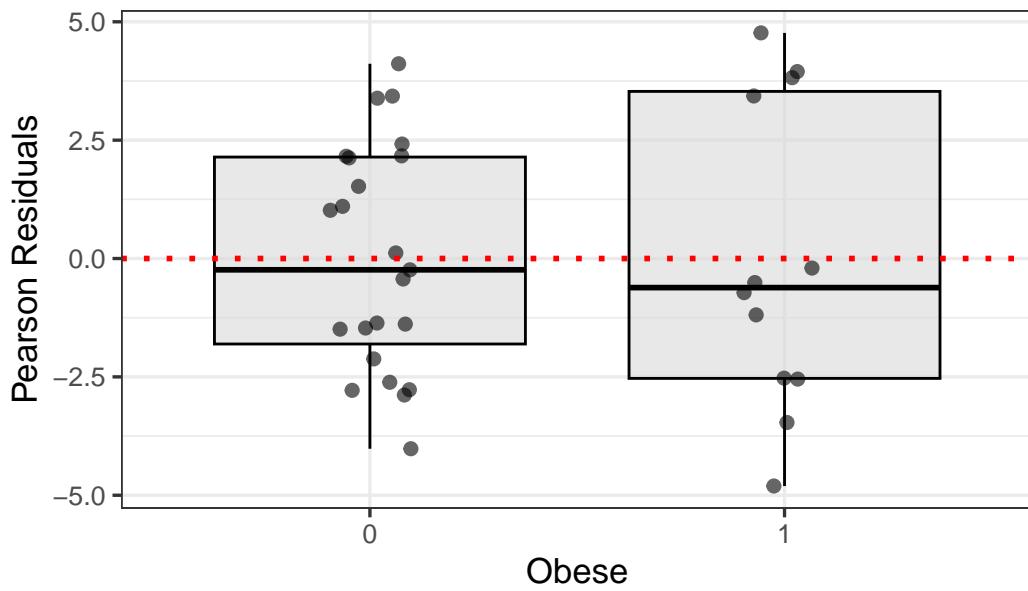
Residuals vs Measurement: REE/kg Model
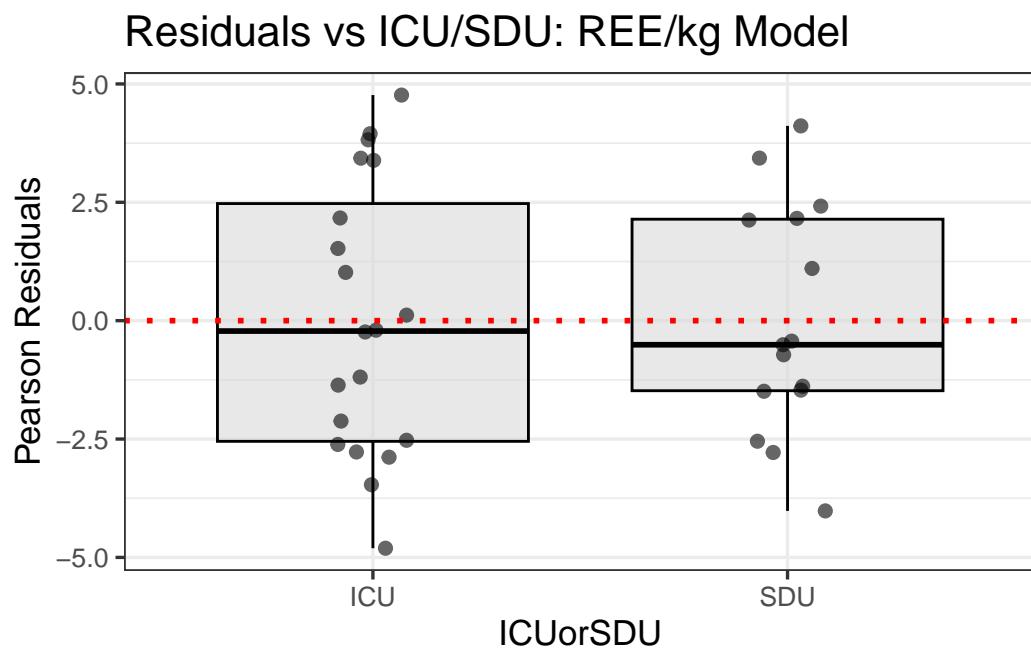
```
plot_residual_vs(REEperKG_model, "Obese",
                 "Residuals vs Obesity Status: REE/kg Model")
```


Residuals vs Obesity Status: REE/kg Model
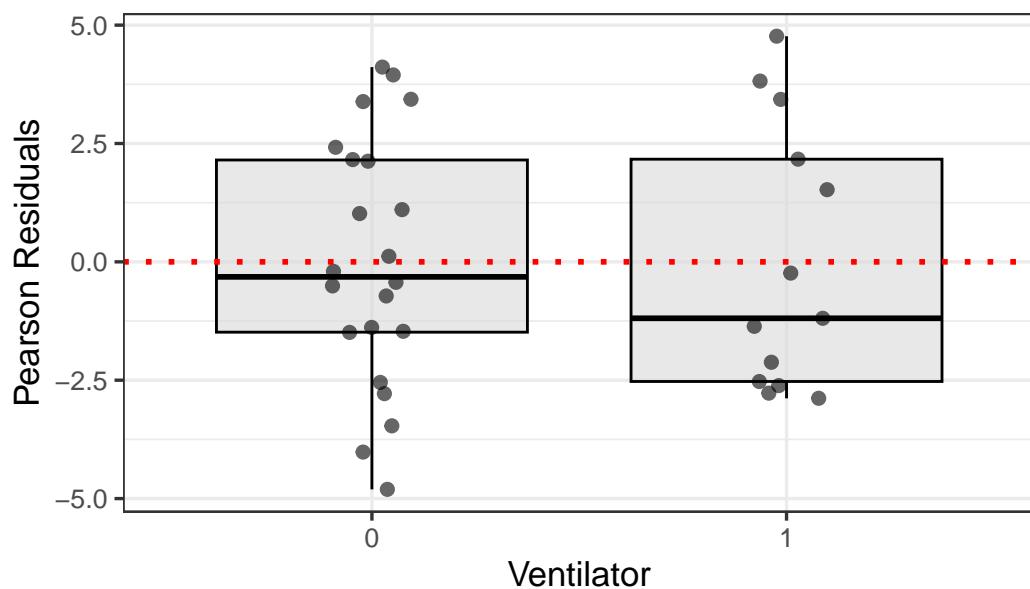
```r
plot_residual_vs(REEperKG_model, "ICUorSDU",
                 "Residuals vs ICU/SDU: REE/kg Model")
```

Residuals vs ICU/SDU: REE/kg Model


```r
plot_residual_vs(REEperKG_model, "Ventilator",
                 "Residuals vs Ventilation: REE/kg Model")
```
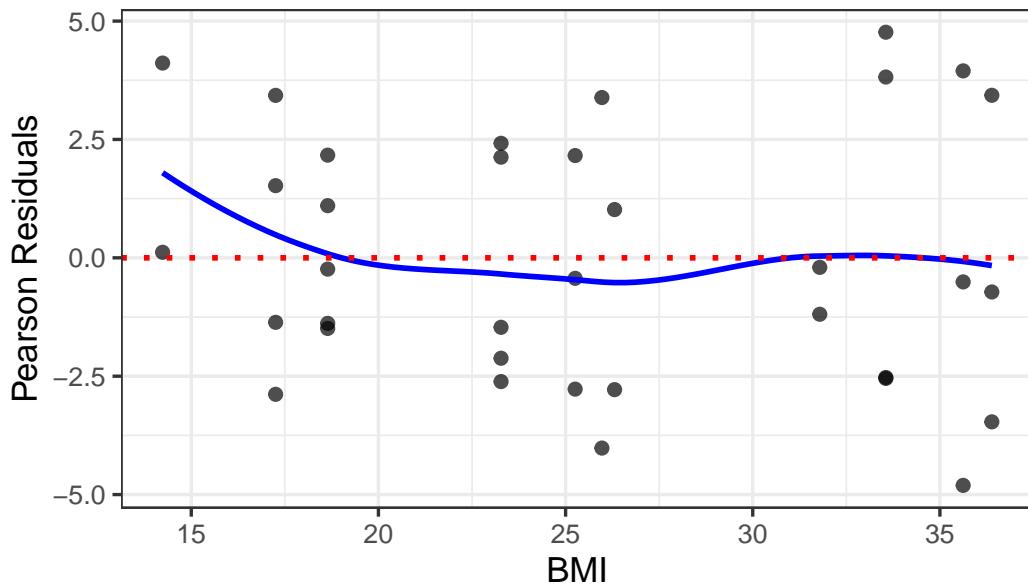
Residuals vs Ventilation: REE/kg Model


```
plot_residual_vs(REEperKG_model, "BMI",
                 "Residuals vs BMI: REE/kg Model")
```

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

Residuals vs BMI: REE/kg Model


```r
library(lmerTest)
```

```
Attaching package: 'lmerTest'

The following object is masked from 'package:lme4':

    lmer

The following object is masked from 'package:stats':

    step
```

```r
# Refit your models using lmerTest::lmer()
REE_model <- lmer(
  REE ~ Obese * Measurement + ICUorSDU + Ventilator + (1 | ID),
  data = REE
)

REEperKG_model <- lmer(
  REEperKG ~ Obese * Measurement + ICUorSDU + Ventilator + (1 | ID),
```

```
   data = REE
)

summary(REE_model)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: REE ~ Obese * Measurement + ICUorSDU + Ventilator + (1 | ID)
   Data: REE

REML criterion at convergence: 430.8

Scaled residuals:
    Min   1Q Median   3Q   Max
-1.3502 -0.6189 -0.1831 0.6726 1.8067

Random effects:
 Groups   Name   Variance Std.Dev.
 ID   (Intercept) 35224   187.7
 Residual   78575   280.3
Number of obs: 35, groups: ID, 11

Fixed effects:
                   Estimate Std. Error   df t value Pr(>|t|)
(Intercept)   1497.43   182.35   24.00   8.212 1.98e-08 ***
Obese1   920.25   268.87   28.10   3.423 0.00192 **
Measurement   -37.48   62.38   28.98 -0.601 0.55257
ICUorSDUSDU   269.18   174.54   23.25   1.542 0.13651
Ventilator1   -289.40   160.20   28.82 -1.806 0.08130 .
Obese1:Measurement -205.42   102.42   22.87 -2.006 0.05686 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) Obese1 Msrmnt ICUSDU Vntlt1
Obese1   -0.506
Measurement -0.565 0.240
ICUorSDUSDU -0.264 0.213 -0.476
Ventilator1 -0.598 0.150 0.045 0.567
Obs1:Msrmnt 0.340 -0.809 -0.307 -0.163 -0.097
```

```
summary(REEperKG_model)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: REEperKG ~ Obese * Measurement + ICUorSDU + Ventilator + (1 | ID)
   Data: REE

REML criterion at convergence: 182.2

Scaled residuals:
    Min   1Q Median   3Q   Max
-1.4489 -0.7006 -0.1305 0.6526 1.4366

Random effects:
 Groups   Name   Variance Std.Dev.
 ID   (Intercept) 20.74   4.554
 Residual   11.00   3.317
Number of obs: 35, groups: ID, 11

Fixed effects:
                  Estimate Std. Error   df t value Pr(>|t|)
(Intercept)   21.6132   2.8047 21.9337   7.706 1.11e-07 ***
Obese1   4.1214   4.0599 20.1379   1.015   0.3221
Measurement   -0.2068   0.8289 26.8246 -0.250   0.8048
ICUorSDUSDU   4.1105   2.1200 21.2548   1.939   0.0659 .
Ventilator1   -2.4634   2.1690 27.6083 -1.136   0.2658
Obese1:Measurement -3.4471   1.2407 21.1459 -2.778   0.0112 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) Obese1 Msrmnt ICUSDU Vntlt1
Obese1   -0.515
Measurement -0.536 0.184
ICUorSDUSDU -0.188 0.166 -0.454
Ventilator1 -0.568 0.114 0.228 0.477
Obs1:Msrmnt 0.278 -0.639 -0.305 -0.155 -0.102