

lac

Håvard Crantz Lorentzen

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```
library(tidyverse)
library(readxl)
library(ggplot2)

lactate <- read_excel("data til laktatprofil.xlsx", na="NA")

lactate1 <- lactate %>%
  # Select columns needed for analysis
  select(FP, time, lac.75:lac.300) %>%
  # Only one participant and time-point
  filter(time == "pre", FP == 6) %>%
  # Pivot to long format data using the lactate columns
  pivot_longer(names_to = "watt",
               values_to = "lactate",
               names_prefix = "lac.",
               names_transform = list(watt = as.numeric),
               cols = lac.75:lac.300) %>%
  # Remove NA (missing) values to avoid warning/error messages.
  filter(!is.na(lactate))

# fit "straight line" model
m1 <- lm(lactate ~ watt, data = lactate1)

# fit second degree polynomial
m2 <- lm(lactate ~ poly(watt, 2, raw = TRUE), data = lactate1)

# fit third degree polynomial
m3 <- lm(lactate ~ poly(watt, 3, raw = TRUE), data = lactate1)

# fit forth degree polynomial
m4 <- lm(lactate ~ poly(watt, 4, raw = TRUE), data = lactate1)

# Store all residuals as new variables
lactate1$resid.m1 <- resid(m1)
lactate1$resid.m2 <- resid(m2)
lactate1$resid.m3 <- resid(m3)
lactate1$resid.m4 <- resid(m4)

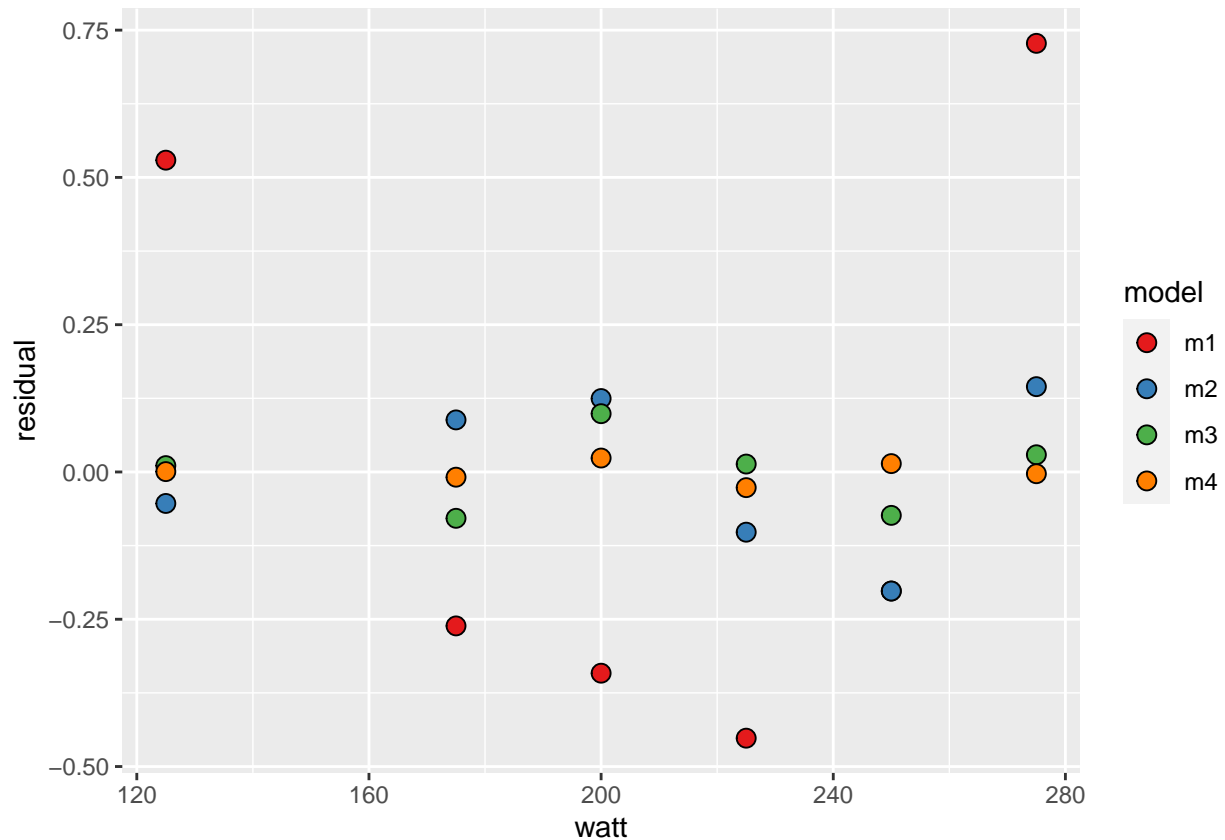
lactate1 %>%
  # gather all the data from the models
  pivot_longer(names_to = "model",
               values_to = "residual",
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names_prefix = "resid.",
names_transform = list(residual = as.numeric),
cols = resid.m1:resid.m4) %>%
# Plot values with the observed watt on x axis and residual values at the y
ggplot(aes(watt, residual, fill = model)) + geom_point(shape = 21, size = 3) +

# To set the same colors/fills as above we use scale fill manual
scale_fill_manual(values = c("#e41a1c", "#377eb8", "#4daf4a", "#ff7f00"))

```



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#new data data frame
ndf <- data.frame(watt = seq(from = 125, to = 275, by = 0.1)) # high resolution, we can find the nearest

ndf$predictions <- predict(m4, newdata = ndf)

lactate_threshold4 <- ndf %>%
  filter(abs(predictions - 4) == min(abs(predictions - 4)))

lactate_threshold2 <- ndf %>%
  filter(abs(predictions - 2) == min(abs(predictions - 2)))

lactate <- read_excel("data til laktatprofil.xlsx", na="NA")

lactate2 <- lactate %>%
  select(FP, time, lac.75:lac.300) %>%
  pivot_longer(names_to = "watt",

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      values_to = "lactate",
      names_prefix = "lac.",
      names_transform = list(watt = as.numeric),
      cols = lac.75:lac.300) %>%
filter(FP == 6,
      time == "pre",
      !is.na(lactate)) %>% # Remove NA values
print()

```

```

## # A tibble: 6 x 4
##   FP time   watt lactate
##   <dbl> <chr> <dbl>   <dbl>
## 1     6 pre    125     1.48
## 2     6 pre    175     1.67
## 3     6 pre    200     2.08
## 4     6 pre    225     2.46
## 5     6 pre    250     3.2
## 6     6 pre    275     4.62

```

```

# Fit the model
model <- lm(lactate ~ watt + I(watt^2) + I(watt^3), data = lactate2)

# Predict lactate values over all observed watt values
# calculate the smallest distance from the fixed lactate value

new_data <- data.frame(watt = seq(from = min(lactate2$watt), to = max(lactate2$watt), by = 0.1))

new_data$dist <- abs(predict(model, newdata = new_data) - 4)

# Find the smallest value of predicted - fixed lactate value
new_data %>%
  filter(dist == min(dist)) # Where the dist value equals the minimum dist value

```

```

##   watt      dist
## 1 265.1 0.002391221

```

```

lt <- function(data) {

  # Fit a 3 degree polynomial model
  m <- lm(lactate ~ watt + I(watt^2) + I(watt^3), data = data)

  # Store a data frame with exercise intensities
  new_data <- data.frame(watt = seq(from = min(data$watt), to = max(data$watt), by = 0.01))

  # Predict using the new data, predicting lactate values at each
  new_data$pred <- predict(m, newdata = new_data)

  # calculate deviation from the lactate value of interest
  new_data$watt.4mmol <- abs(new_data$pred - 4)
  new_data$watt.2mmol <- abs(new_data$pred - 2)

```

```

# Create a results data frame
results <- data.frame(watt.4mmol = new_data[which.min(new_data$watt.4mmol),1], watt.2mmol = new_data[

# Return the data frame
return(results)

}

lactate3 <- lactate %>%
  select(FP, time, lac.75:lac.300) %>%
  pivot_longer(names_to = "watt",
               values_to = "lactate",
               names_prefix = "lac.",
               names_transform = list(watt = as.numeric),
               cols = lac.75:lac.300) %>%
  filter(!is.na(lactate)) %>% # Remove NA values
  group_by(time, FP) %>%
  mutate(n = n()) %>%
  filter(n >= 4) %>%
  # Use group_modify to apply the function to all participants per time-point (and group)
  group_modify(~ lt(.)) %>%
  print()

```

```

## # A tibble: 12 x 4
## # Groups:   time, FP [12]
##   time    FP watt.4mmol watt.2mmol
##   <chr> <dbl>      <dbl>      <dbl>
## 1 post     1      172.        75
## 2 post     2      297.       239.
## 3 post     3      135.       96.8
## 4 post     4      169.       75.7
## 5 post     5      205.       125
## 6 post     6      279.       197.
## 7 post     7      130.        75
## 8 pre      1      126.       78.3
## 9 pre      2      275.       215.
## 10 pre     4      157.       119.
## 11 pre     5      241.       144.
## 12 pre     6      265.       201.

```

```

lactate4 <- lactate3 %>%
  group_by(FP) %>%
  mutate(n = n()) %>%
  filter(n == 2) %>%
  pivot_wider(names_from = time, values_from = c(watt.4mmol, watt.2mmol)) %>%
  print()

```

```

## # A tibble: 5 x 6
## # Groups:   FP [5]
##   FP      n watt.4mmol_post watt.4mmol_pre watt.2mmol_post watt.2mmol_pre
##   <dbl> <int>          <dbl>          <dbl>          <dbl>          <dbl>

```

## 1	1	2	172.	126.	75	78.3
## 2	2	2	297.	275	239.	215.
## 3	4	2	169.	157.	75.7	119.
## 4	5	2	205.	241.	125	144.
## 5	6	2	279.	265.	197.	201.

```
TE4 <- lactate4 %>%
  mutate(diff = watt.4mmol_post - watt.4mmol_pre) %>%
  ungroup() %>%
  # Change/difference score
  summarise(s = sd(diff, na.rm = TRUE), # Summarize to calculate sd, and...
            m = mean(c(watt.4mmol_post, watt.4mmol_pre)), # mean
            te = s / sqrt(2), 1, # the typical error.
            cv = 100 * (te / m), 1,
            L = qt(0.975, 4) * s) %>% # Calculate as a percentage of the mean
  print()
```

```
## # A tibble: 1 x 6
##       s      m    te   '1'    cv     L
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1  29.7  219.  21.0     1  9.59  82.4
```

```
TE2 <- lactate4 %>%
  mutate(diff = watt.2mmol_post - watt.2mmol_pre) %>%
  ungroup() %>% # Change/difference score
  summarise(s = sd(diff), # Summarize to calculate sd, and...
            m = mean(c(watt.2mmol_post, watt.2mmol_pre)), # mean
            te = s / sqrt(2), 1, # the typical error.
            cv = 100 * (te / m), 1,
            L = qt(0.975, 4) * s) # Calculate as a percentage of the mean

cv4 <- round(TE4$cv, 2)
cv2 <- round(TE2$cv, 2)
```

Resultater

Typefeil er ved 4mmol laktat er 9.59% og ved 2mmol laktat er den 11.8%