

Body temperature investigation

DAPR1 staff

1 Introduction

The data available at <https://uoepsy.github.io/data/BodyTemp.csv> comprise measurements of the body temperature (**BodyTemp**, in Celsius) and pulse rate (**Pulse**) for a random sample of 50 healthy individuals. We are interested in estimating the mean body temperature for all healthy humans and testing whether this is different from the commonly thought value of 37 °C. As such, for the purpose of this investigation, we will only focus on the variable **BodyTemp**.

2 Analysis

Figure 1 shows that the body temperatures of the sample of 50 healthy individuals follow roughly a bell-shaped distribution, with most values between 36.5 and 37.5 °C and fewer in the tails of the distribution. No values were lower than 35.75 or larger than 38.22. The average body temperature in the sample was 36.81 °C, see Table 1, with a SE of 0.06 and 95% CI [36.69, 36.93]. Hence, we are 95% confident that the average body temperature for a healthy individual is between 36.69 °C and 36.93 °C.

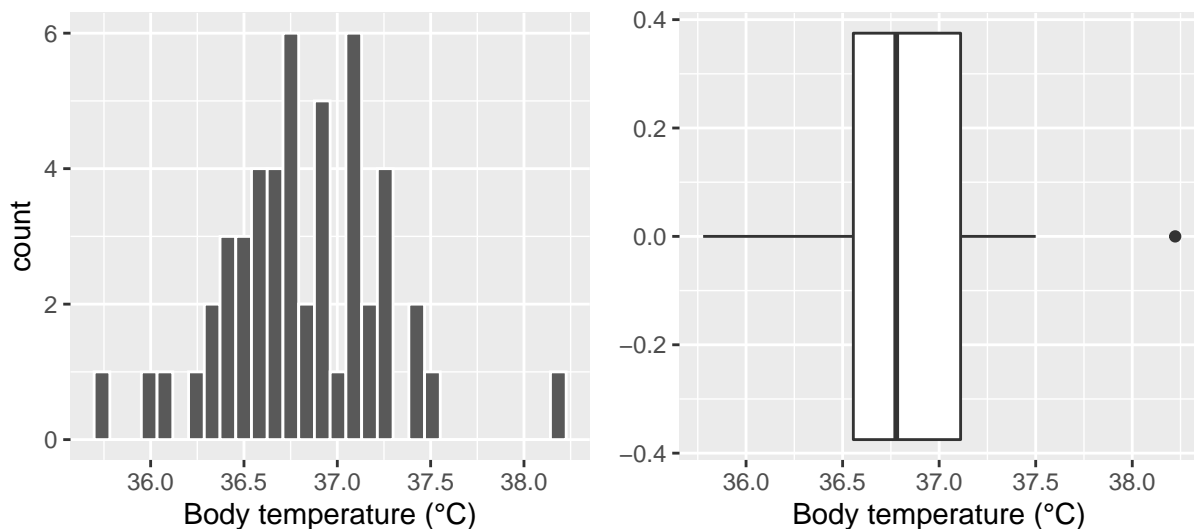


Figure 1: Distribution of body temperatures (°C)

At the 5% significance level, we tested whether the average body temperature of all healthy individuals was significantly different from the commonly thought value of 37 °C. The sample data provide very strong evidence against the null hypothesis and in favour of the alternative one that the mean body temperature is different from the hypothesised value of 37 °C, $t(49) = -3.14, p = .003$, two-sided.

Table 1: Descriptive statistics of body temperatures (°C)

n	M	SD	Min	Max
50	36.81	0.43	35.78	38.22

3 Discussion

Will be added in the next weeks during the live R...

3.1 Appendix

```
knitr::opts_chunk$set(echo = FALSE, message = FALSE, warning = FALSE)
# week 1 code
library(tidyverse)
library(patchwork)
library(kableExtra)

temp_data <- read_csv("https://uoepsy.github.io/data/BodyTemp.csv")

temp_data <- temp_data %>%
  select(BodyTemp)

dim(temp_data)
head(temp_data)
glimpse(temp_data) # str()
summary(temp_data)

plt.h <- ggplot(temp_data, aes(x = BodyTemp)) +
  geom_histogram(color = 'white') +
  labs(x="Body temperature (°C)")
plt.h

plt.d <- ggplot(temp_data, aes(x = BodyTemp)) +
  geom_density() +
  labs(x="Body temperature (°C)")
plt.d

plt.b <- ggplot(temp_data, aes(x = BodyTemp)) +
  geom_boxplot() +
  labs(x="Body temperature (°C)")
plt.b

plt.h | plt.b

# Option 1: with a descriptives table
stats <- temp_data %>%
  summarise(
    n = n(),
    M = mean(BodyTemp),
    SD = sd(BodyTemp),
```

```

    Min = min(BodyTemp),
    Max = max(BodyTemp)
  )
stats

tstar <- qt(c(0.025, 0.975), df = stats$n - 1)
stats$M + tstar * (stats$SD / sqrt(stats$n))

# Option 2: creating each variable
xbar <- mean(temp_data$BodyTemp)
n <- nrow(temp_data)
s <- sd(temp_data$BodyTemp)
se <- s / sqrt(n)
tstar <- qt(c(0.025, 0.975), df = n - 1)
xbar + tstar * se

# week 2 code

# Step 1. Specify null and alternative hypotheses
# H0 :  $\mu = 37$ 
# H1 :  $\mu$  not equal to 37

# Step 2. Compute t-statistic
#  $t_{obs} = (xbar - \mu_0) / SE$  where  $SE = s / \sqrt{n}$ 

t_obs <- (stats$M - 37) / (stats$SD / sqrt(stats$n))
t_obs

# Step 3. Compute the p-value
pvalue <- 2 * pt(abs(t_obs), df = stats$n - 1, lower.tail = FALSE)
pvalue

# Step 4. Make a decision by comparing the p-value to alpha (significance level)
# - Reject H0 if pvalue <= alpha
# - Do not reject H0 if pvalue > alpha

pvalue <= 0.05

# Step 5. Writing up
plt.h | plt.b
kbl(stats, booktabs = TRUE, digits = 2,
     caption = "Descriptive statistics of body temperatures (°C)")

```