Zadanie

```
library(tidyr)
library(tidyverse)
```

```
-- Attaching core tidyverse packages ---------------------- tidyverse 2.0.0 --
v dplyr     1.1.2      v purrr     1.0.1
v forcats   1.0.0      v readr     2.1.4
v ggplot2   3.4.4      v stringr   1.5.0
v lubridate 1.9.2      v tibble    3.2.1
-- Conflicts ----------------------------------------- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becor
```

```
library(ggplot2)
patients <- read_tsv("patient-data-cleaned.txt")
```

```
Rows: 100 Columns: 15
-- Column specification -------------------------------------------------------
Delimiter: "\t"
chr  (5): ID, Name, Sex, Smokes, State
dbl  (6): Height, Weight, Grade, Score, Age, BMI
lgl  (2): Died, Overweight
date (2): Birth, Date.Entered.Study

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
patients
```

```
# A tibble: 100 x 15
      ID       Name  Sex   Smokes Height Weight Birth      State Grade Died   Score
      <chr>    <chr> <chr> <chr>   <dbl>  <dbl> <date>     <chr> <dbl> <lgl> <dbl>
 1 AC/AH/001 Mich~ Male  Non-S~   183.   76.6 1972-02-06 Geor~     2 FALSE  0.01
 2 AC/AH/017 Derek Male  Non-S~   179.   80.4 1972-06-15 Colo~     2 FALSE -1.31
 3 AC/AH/020 Todd  Male  Non-S~   169.   75.5 1972-07-09 New ~     2 FALSE -0.17
 4 AC/AH/022 Rona~ Male  Non-S~   176.   94.5 1972-08-17 Colo~     1 FALSE -1.1
 5 AC/AH/029 Chri~ Fema~ Non-S~   164.   71.8 1973-06-12 Geor~     2 TRUE   1.42
 6 AC/AH/033 Dana  Fema~ Smoker   158.   69.9 1973-07-01 Indi~     2 FALSE  0.29
 7 AC/AH/037 Erin  Fema~ Non-S~   162.   68.8 1972-03-26 New ~     1 FALSE  0.16
 8 AC/AH/044 Rach~ Fema~ Non-S~   166.   70.4 1973-05-11 Colo~     1 FALSE -0.07
 9 AC/AH/045 Rona~ Male  Non-S~   181.   76.9 1971-12-31 Geor~     1 FALSE -1.43
10 AC/AH/048 Bryan Male  Non-S~   167.   79.1 1973-07-19 New ~     2 FALSE  0.54
# i 90 more rows
# i 4 more variables: Date.Entered.Study <date>, Age <dbl>, BMI <dbl>,
#   Overweight <lgl>
```
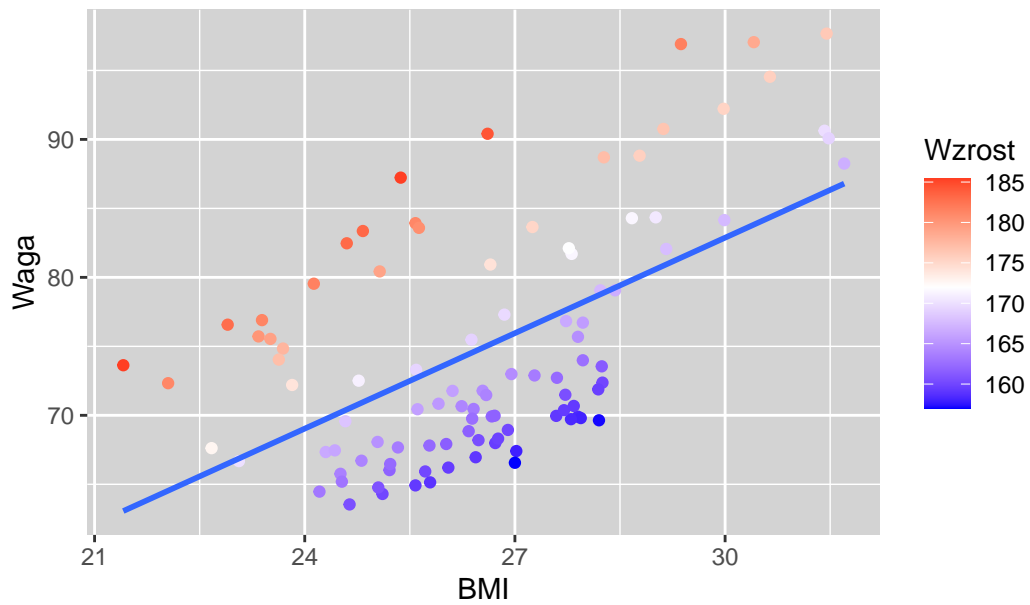
Geomy i estetyki

Wykresy punktowe (scatterplot)

```
BMIplot <-
  ggplot(patients, aes(x = BMI, y = Weight)) +
  geom_point(aes(color = Height)) +
  geom_smooth(method = "lm", formula = 'y ~ x', se = FALSE) +
  scale_colour_gradient2(low = "blue", high = "red", mid = "white", midpoint = 172) +
  labs(x = "BMI", y = "Waga", title = "Wykres punktowy BMI", color = "Wzrost") +
  theme(panel.background = element_rect(fill = "lightgray"))

BMIplot
```
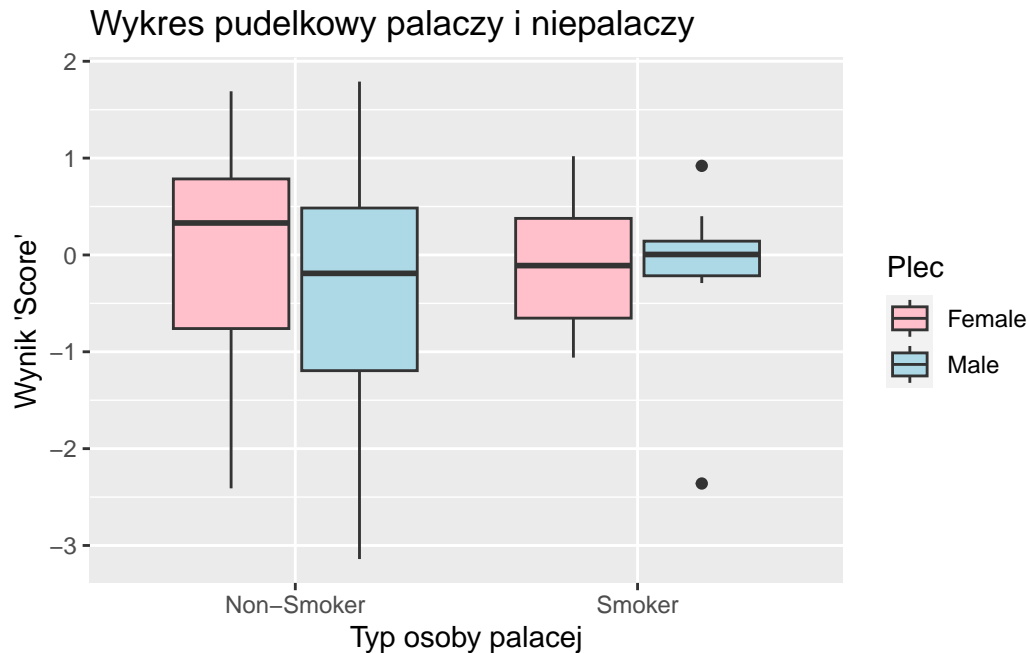
Wykres punktowy BMI

Wykresy pudełkowe

```
BMIplot <- ggplot(patients, aes(x = Smokes, y = Score, fill = Sex)) +
  geom_boxplot() +
  labs(x = "Typ osoby palacej", y = "Wynik 'Score'", fill = "Płeć", title = "Wykres pudełk
  scale_fill_manual(values = c("Male" = "lightblue", "Female" = "pink"))

BMIplot
```

Wykres pudelkowy palaczy i niepalaczy

Histogramy i estymatory jądrowe

```
# BMIplot <- ggplot(patients, aes(x = BMI)) +
#   geom_histogram(binwidth = 2 * IQR(patients$BMI) / (length(patients$BMI) ^ (1 / 3)), co
#   labs(x = "BMI", y = "Liczba pacjentów", title = "Histogram BMI") +
#   theme(panel.background = element_rect(fill = "#efefef"))
#
# BMIplot
```
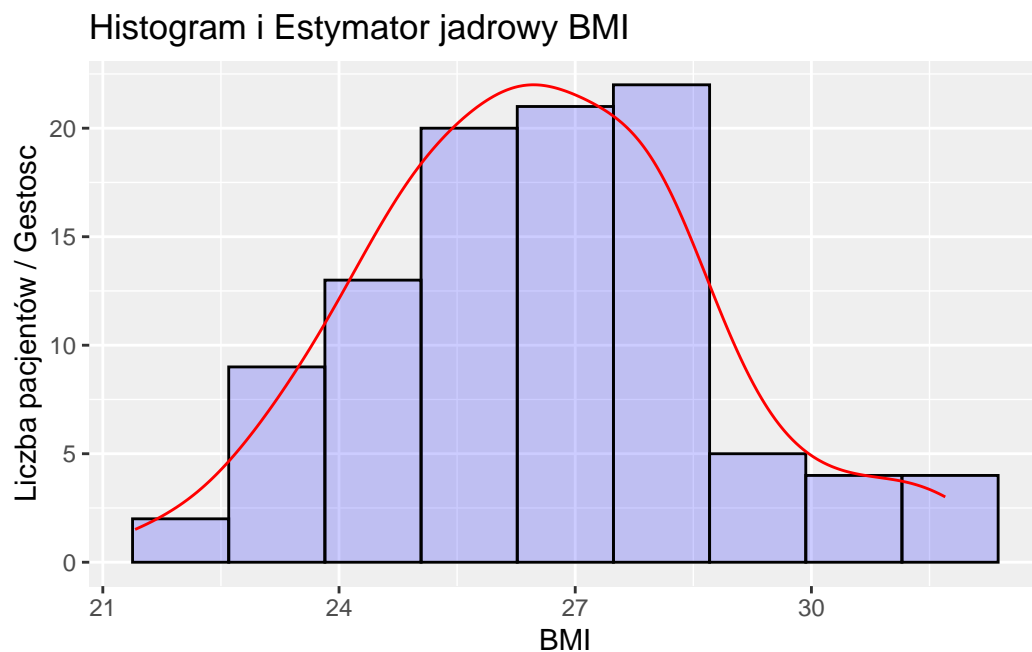
```
# BMIplot <- ggplot(patients, aes(x = BMI)) +
#   geom_density(color = "black", fill='blue') +
#   labs(x = "BMI", y = "Gęstość", title = "Estymator jądrowy BMI") +
#   theme(panel.background = element_rect(fill = "#efefef"))
#
#
# BMIplot
```

```
max.hist.heigth <- max(hist(patients$BMI, plot = FALSE)$counts)

BMIplot <- ggplot(patients, aes(x = BMI)) +
```

```
geom_histogram(binwidth = 2 * IQR(patients$BMI) / (length(patients$BMI) ^ (1 / 3)), colo
geom_density(mapping = aes(y = after_stat(scaled) * max.hist.heigth), color = "red", fil
labs(x = "BMI", y = "Liczba pacjentów / Gęstość", title = "Histogram i Estymator jądrowy
theme(panel.background = element_rect(fill = "#efefef"))
```
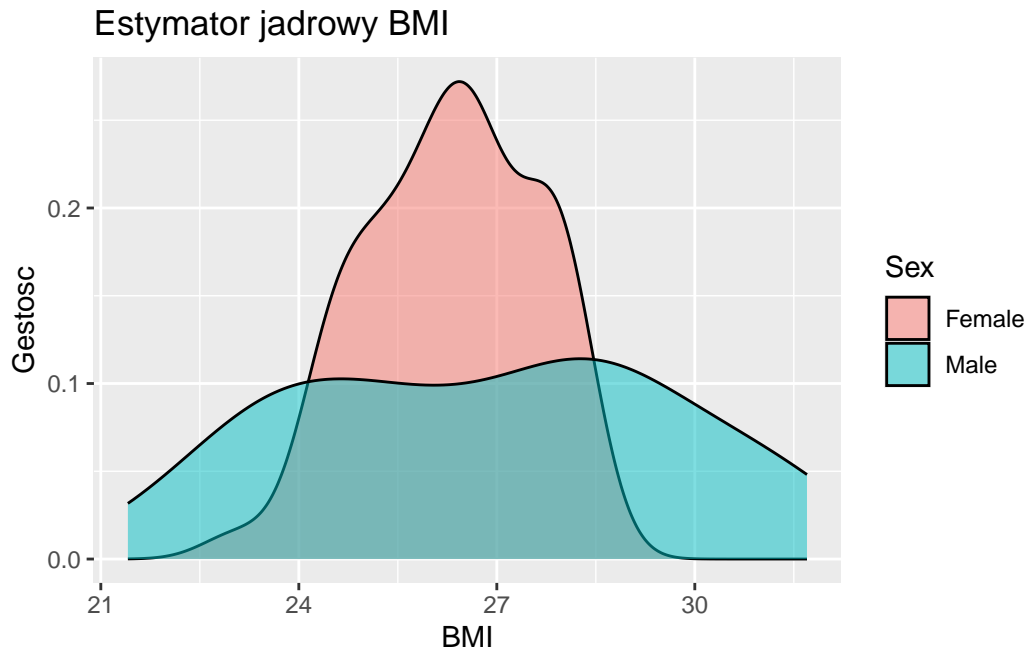
BMIplot

Histogram i Estymator jadrowy BMI

```
BMIplot <- ggplot(patients, aes(x = BMI, fill = Sex)) +
  geom_density(alpha = 0.5) +
  labs(x = "BMI", y = "Gęstość", title = "Estymator jądrowy BMI")
```
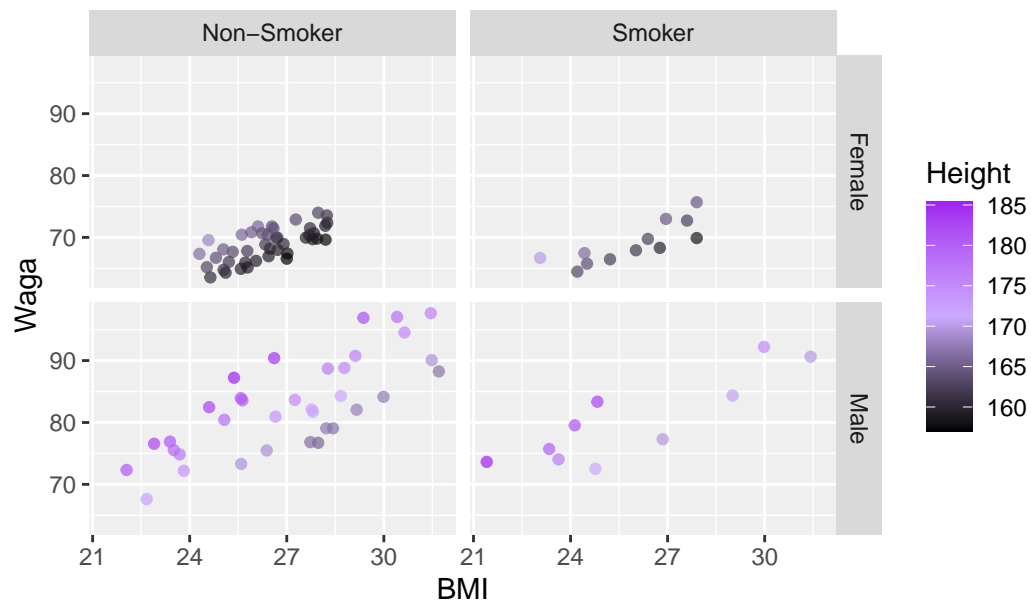
BMIplot

Estymator jadrowy BMI

Kafelki

```r
BMIplot <- ggplot(patients, aes(x = BMI, y = Weight, color = Height)) +
  geom_point(alpha = 0.7) +
  scale_colour_gradient2(low = "black", high = "purple", mid = "#ccaaff", midpoint = (max(
  labs(x = "BMI", y = "Waga", title = "Wykres punktowy BMI wagi pacjenta") +
  theme(panel.background = element_rect(fill = "#efefef")) +
  facet_grid(Sex ~ Smokes)

BMIplot
```
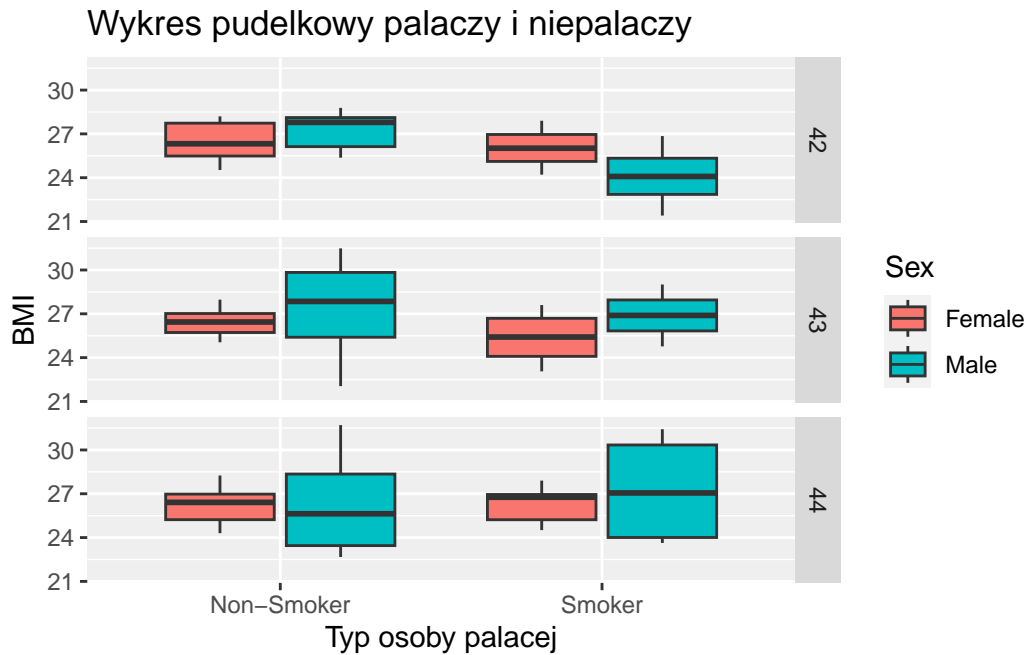
Wykres punktowy BMI wagi pacjenta


```r
BMIplot <- ggplot(patients, aes(x = Smokes, y = BMI, fill = Sex)) +
  geom_boxplot() +
  labs(x = "Typ osoby palacej", y = "BMI", title = "Wykres pudełkowy palaczy i niepalaczy"
  theme(panel.background = element_rect(fill = "#efefef")) +
  facet_grid(Age ~ .)

BMIplot
```

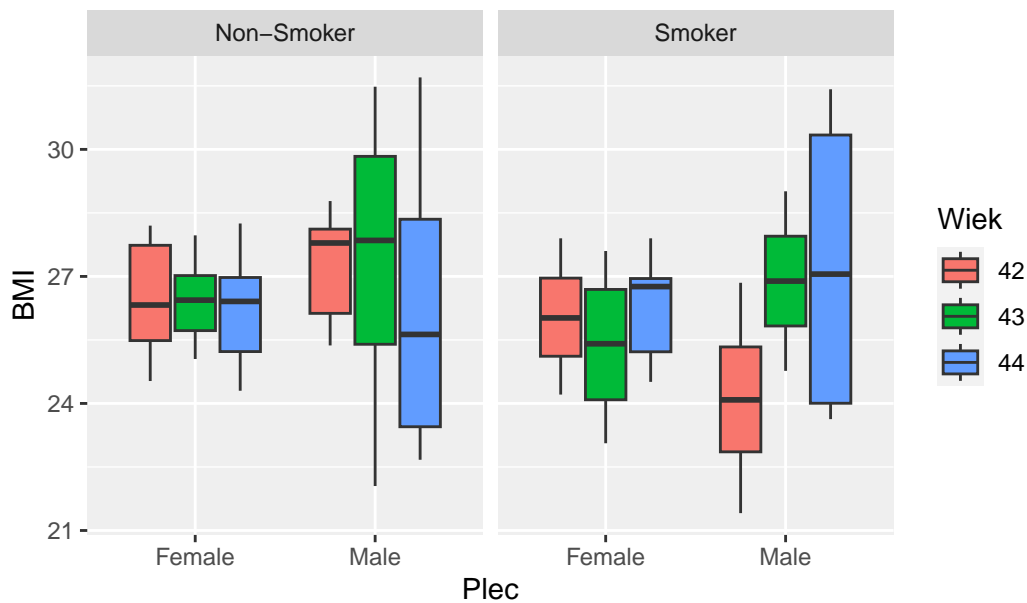# Wykres pudelkowy palaczy i niepalaczy


```
patients$Age <- as.factor(patients$Age)

BMIplot <- ggplot(patients, aes(x = Sex, y = BMI, fill = Age)) +
  geom_boxplot() +
  labs(x = "Płeć", y = "BMI", title = "Wykres pudełkowy palaczy i niepalaczy", fill = "Wie
  theme(panel.background = element_rect(fill = "#efefef")) +
  facet_grid(. ~ Smokes)

BMIplot
```
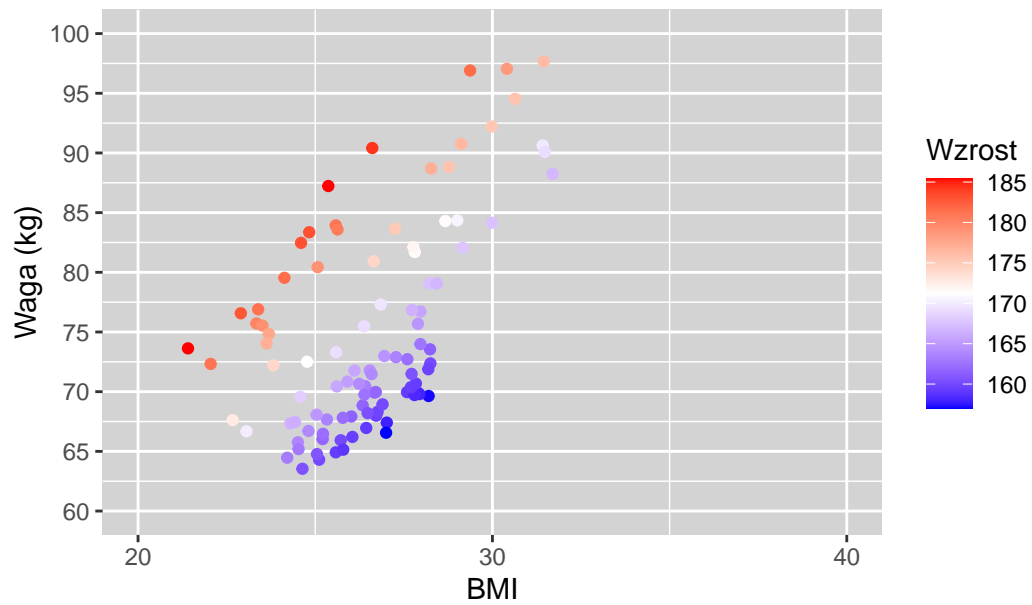
Wykres pudelkowy palaczy i niepalaczy

Skale i tematy

Skale

```
BMIplot <-
  ggplot(patients, aes(x = BMI, y = Weight)) +
  geom_point(aes(color = Height)) +
  scale_colour_gradient2(low = "blue", high = "red", mid = "white", midpoint = (max(patien
  labs(title = "Wykres punktowy BMI", color = "Wzrost") +
  theme(panel.background = element_rect(fill = "lightgray")) +
  scale_x_continuous(breaks = c(20, 30, 40), limits = c(20, 40), name = "BMI") +
  scale_y_continuous(breaks = seq(60, 100, by = 5), limits = c(60, 100), name = "Waga (kg)

BMIplot
```
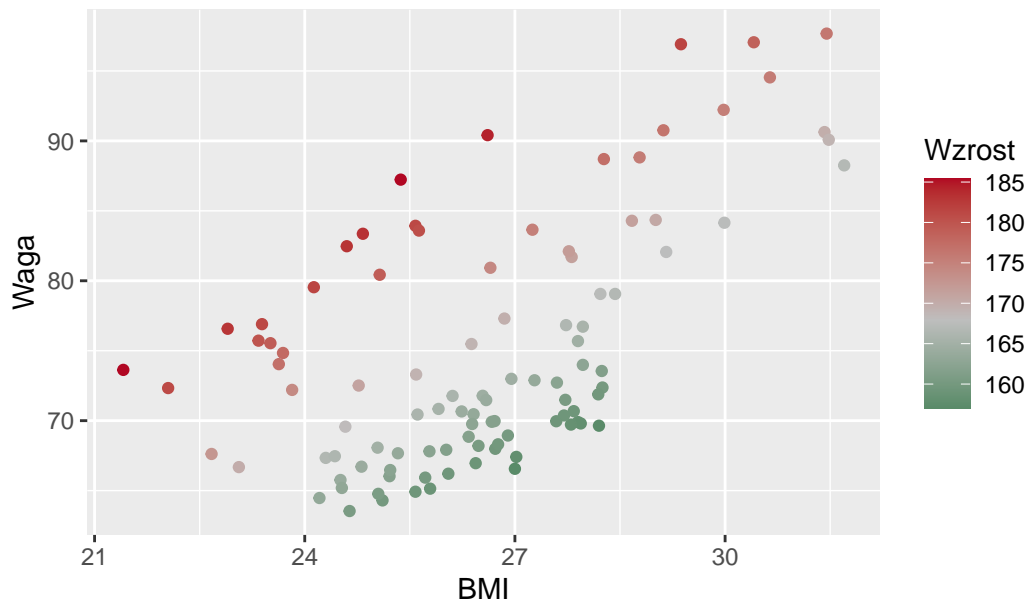
Wykres punktowy BMI


```
BMIplot <-
  ggplot(patients, aes(x = BMI, y = Weight)) +
  geom_point(aes(color = Height)) +
  scale_colour_gradient2(low = "#006B38", high = "#B10723", mid = "grey", midpoint = mean(
  labs(x = "BMI", y = "Waga", title = "Wykres punktowy BMI", color = "Wzrost")

BMIplot
```

Wykres punktowy BMI

Motywy

```r
BMIplot <- ggplot(patients, aes(x = BMI, y = Weight, color = Height)) +
  geom_point() +
  geom_smooth(aes(group = Height), method = "lm", formula = 'y ~ x', se = FALSE) +
  labs(x = "BMI", y = "Waga", title = "Wykres punktowy BMI") +
  theme(panel.background = element_rect(fill = "white")) +
  theme(legend.key = element_rect(fill = "white")) +
  theme(legend.position = "bottom") +
  theme(axis.line = element_line(linewidth = 0.2)) +
  theme(axis.ticks = element_line(linewidth = 0.2)) +
  theme(axis.title = element_text(size = 10)) +
  theme(axis.text = element_text(size = 8)) +
  theme(legend.text = element_text(size = 8)) +
  theme(legend.title = element_blank()) +
  theme(panel.grid = element_blank()) +
  theme(panel.grid.minor = element_blank()) +
  theme(legend.background = element_rect(fill = "white")) +
  theme(legend.box.background = element_rect(fill = "white")) +
  theme(legend.box.margin = margin(0, 0, 0, 0)) +
  theme(legend.margin = margin(0, 0, 0, 0)) +
```

```
    theme(legend.key.size = unit(0.5, "cm")) +
    theme(plot.title = element_text(size = 12)) +
    theme(plot.margin = margin(1, 1, 1, 1))
```

BMIplot
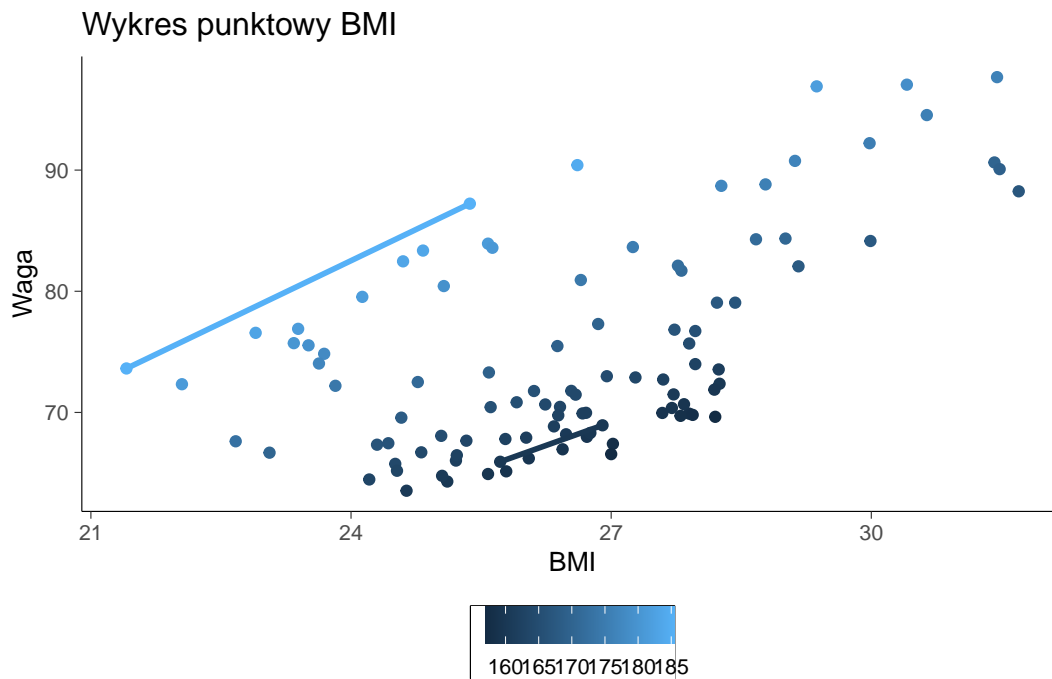

```
ggsave("BMIplot.png", plot = BMIplot, width = 16, height = 16, units = "cm")
```