Student 3000 Criminal Data : ggplot

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Working Data Loading

```
library(magrittr)
load("./crimtab.RData")
ls()
```

```
## [1] "crimtab_2"       "crimtab_df"      "crimtab_long"    "crimtab_long_df"
```

```
ls.str()
```

```
## crimtab_2 :  'table' int [1:42, 1:22] 0 0 0 0 0 0 1 0 0 0 ...
## crimtab_df : 'data.frame':   924 obs. of  3 variables:
##  $ finger: num  9.4 9.5 9.6 9.7 9.8 9.9 10 10.1 10.2 10.3 ...
##  $ height: num  56 56 56 56 56 56 56 56 56 56 ...
##  $ Freq  : int  0 0 0 0 0 0 1 0 0 0 ...
## crimtab_long :  num [1:3000, 1:2] 10 10.3 9.9 10.2 10.2 10.3 10.4 10.7 10 10.1 ...
## crimtab_long_df : 'data.frame':  3000 obs. of  2 variables:
##  $ finger: num  10 10.3 9.9 10.2 10.2 10.3 10.4 10.7 10 10.1 ...
##  $ height: num  56 57 58 58 58 58 58 58 59 59 ...
```

```
head(crimtab_long_df)
```

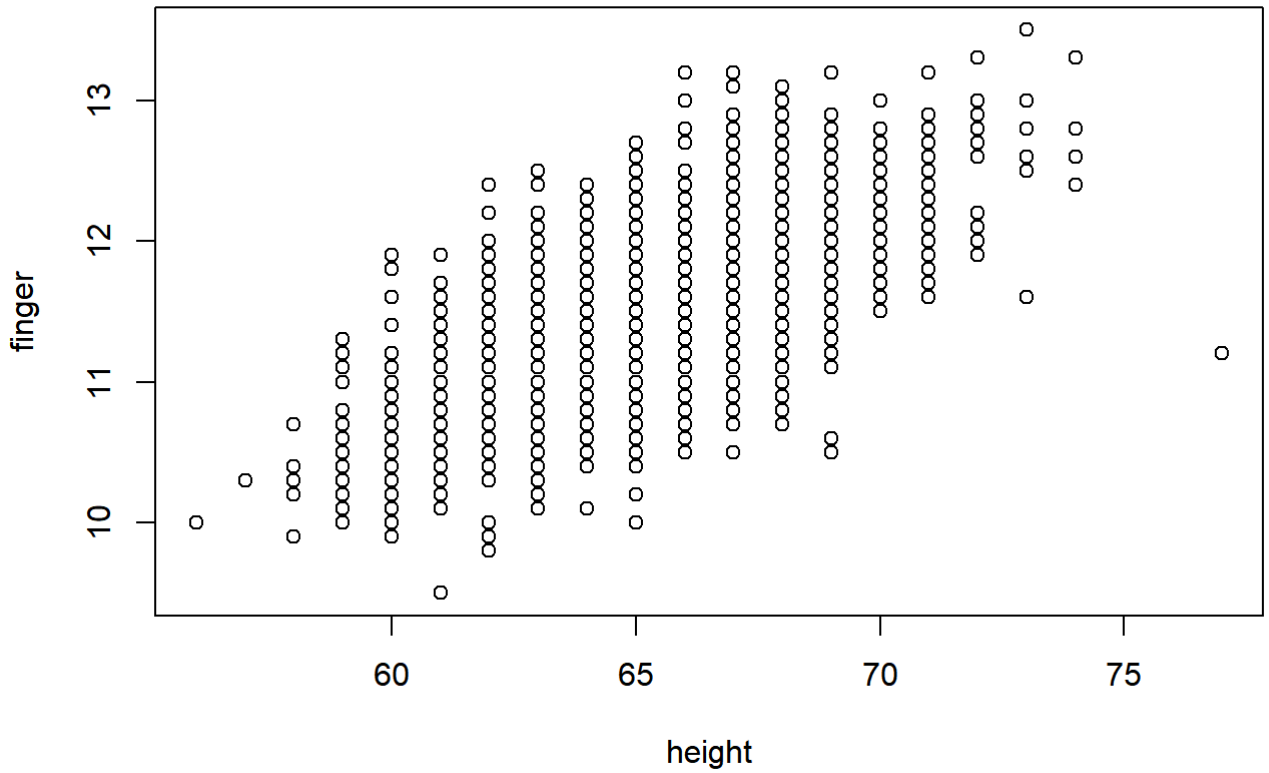
```
##   finger height
## 1   10.0     56
## 2   10.3     57
## 3    9.9     58
## 4   10.2     58
## 5   10.2     58
## 6   10.3     58
```

Graphic Representation

Base Graphics

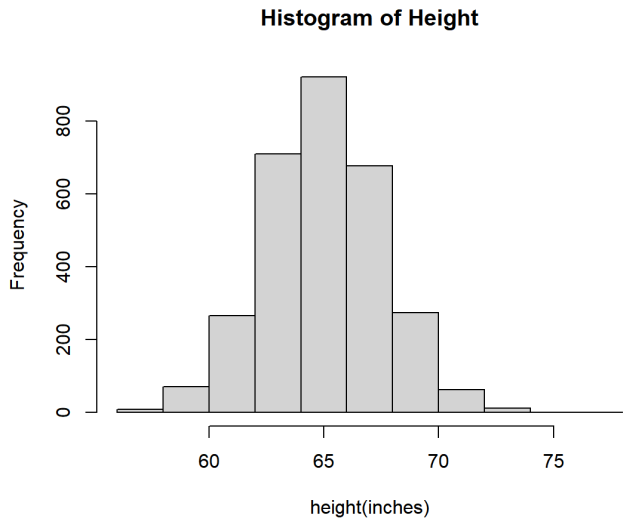
- 키와 손가락길이의 산점도

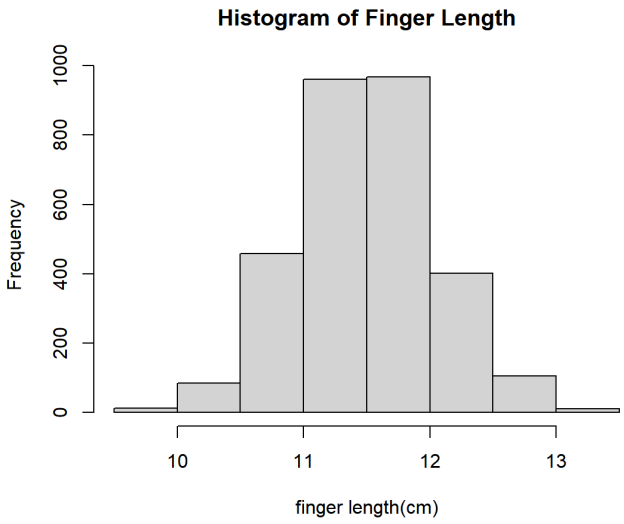
```
# plot(finger ~ height, data = crimtab_long_df)
crimtab_long_df[2:1] %>%
  plot()
plot(crimtab_long_df[, 2:1])
```



- 변수 각각의 히스토그램은?

```
par(mfrow = c(1, 2))
hist(crimtab_long_df$height,
     main = "Histogram of Height",
     xlab = "height(inches)")
hist(crimtab_long_df$finger,
     main = "Histogram of Finger Length",
     xlab = "finger length(cm)")
```






```
# hist(crimtab_long_df["height"],
#      main="Histogram of Height",
#      xlab="height(inches)")
# hist(crimtab_long_df["finger"],
#      main="Histogram of Finger Length",
#      xlab= "finger length(cm)")
```

- 평균과 표준편차를 한번에 구하려면 다음과 같이 anonymous function을 작성하고 `mapply()` 또는 `sapply()` 를 이용하는 게 편함. 이를 모수로 하는 정규곡선을 덧씌워 볼 것.
  - `mean_sd()` 도 `anonymous function` 으로 평균과 표준편차를 계산해서 출력하는 함수임. 이와 같은 함수를 저장해 놓으려면 `dump()` 를 이용함.
  - 이와 같이 계산한 평균과 표준편차를 모수로 하는 정규곡선을 덧씌워 볼 것.

```
mean_sd <- function(x) {
  mean <- mean(x, na.rm = TRUE)
  sd <- sd(x)
  c(mean = mean, sd = sd)
# list(mean = mean, sd = sd)
}
dump("mean_sd", file = "mean_sd.R")
```

```
# crimtab_long_df %>%
#   sapply(FUN = mean_sd)
crimtab_stat <- sapply(crimtab_long_df, FUN = mean_sd)
# crimtab_stat <- mapply(mean_sd, crimtab_long_df)
# apply(crimtab_long, 2, mean)
# apply(crimtab_long, 2, sd)
str(crimtab_stat)
```

```
##  num [1:2, 1:2] 11.547 0.549 65.473 2.558
##  - attr(*, "dimnames")=List of 2
##   ..$ : chr [1:2] "mean" "sd"
##   ..$ : chr [1:2] "finger" "height"
```

- `crimtab_stat` 이 어떤 성격을 갖는지 다음 질문과 추출 작업을 통해서 알아보자.

```
is.matrix(crimtab_stat)
```

```
## [1] TRUE
```

```
is.table(crimtab_stat)
```

```
## [1] FALSE
```

```
is.list(crimtab_stat)
```

```
## [1] FALSE
```

```
is.data.frame(crimtab_stat)
```

```
## [1] FALSE
```

```
crimtab_stat[, 1]
```

```
##       mean         sd
## 11.5473667  0.5487137
```

```
crimtab_stat[, "finger"]
```

```
##       mean         sd
## 11.5473667  0.5487137
```

```
crimtab_stat[, "finger"][1]
```

```
##     mean
## 11.54737
```

```
crimtab_stat[, "finger"][[1]]
```

```
## [1] 11.54737
```

```
crimtab_stat[1]
```

```
## [1] 11.54737
```

```
crimtab_stat[2:3]
```

```
## [1]  0.5487137 65.4730000
```

```
# crimtab_stat["finger"]
# crimtab_stat$finger
```

matrix 를 data frame 으로 변환하면

```
(crimtab_stat_df <- data.frame(crimtab_stat))
```

```
##          finger    height
## mean 11.5473667 65.473000
## sd    0.5487137  2.557757
```

```
is.matrix(crimtab_stat_df)
```

```
## [1] FALSE
```

```
is.table(crimtab_stat_df)
```

```
## [1] FALSE
```

```
is.list(crimtab_stat_df)
```

```
## [1] TRUE
```

```
is.data.frame(crimtab_stat_df)
```

```
## [1] TRUE
```

```
crimtab_stat_df[, 1]
```

```
## [1] 11.5473667  0.5487137
```

```
str(crimtab_stat_df[, 1])
```

```
##  num [1:2] 11.547 0.549
```

```
crimtab_stat_df[, "finger"]
```

```
## [1] 11.5473667  0.5487137
```

```
str(crimtab_stat_df[, "finger"])
```

```
##  num [1:2] 11.547 0.549
```

```
crimtab_stat_df[, "finger"][1]
```

```
## [1] 11.54737
```

```
str(crimtab_stat_df[, "finger"][1])
```

```
##  num 11.5
```

```
crimtab_stat_df[, "finger"][[1]]
```

```
## [1] 11.54737
```

```
str(crimtab_stat_df[, "finger"][[1]])
```

```
##  num 11.5
```

```
crimtab_stat_df[1]
```

```
##          finger
## mean 11.5473667
## sd    0.5487137
```

```
str(crimtab_stat_df[1])
```

```
## 'data.frame':    2 obs. of  1 variable:
##  $ finger: num  11.547 0.549
```

```
crimtab_stat_df["finger"]
```

```
##          finger
## mean 11.5473667
## sd    0.5487137
```

```
str(crimtab_stat_df["finger"])
```

```
## 'data.frame':    2 obs. of  1 variable:
##  $ finger: num  11.547 0.549
```

```
crimtab_stat_df["finger"][1]
```

```
##          finger
## mean 11.5473667
## sd    0.5487137
```

```
str(crimtab_stat_df["finger"][1])
```

```
## 'data.frame':    2 obs. of  1 variable:
##  $ finger: num  11.547 0.549
```

```
crimtab_stat_df["finger"][[1]]
```

```
## [1] 11.5473667  0.5487137
```

```
str(crimtab_stat_df["finger"][[1]])
```

```
##  num [1:2] 11.547 0.549
```

```
crimtab_stat_df$finger
```

```
## [1] 11.5473667  0.5487137
```

```
str(crimtab_stat_df$finger)
```

```
##  num [1:2] 11.547 0.549
```

```
crimtab_stat_df$finger[1]
```

```
## [1] 11.54737
```

```
str(crimtab_stat_df$finger[1])
```

```
##  num 11.5
```

```
crimtab_stat_df$finger[[1]]
```

```
## [1] 11.54737
```

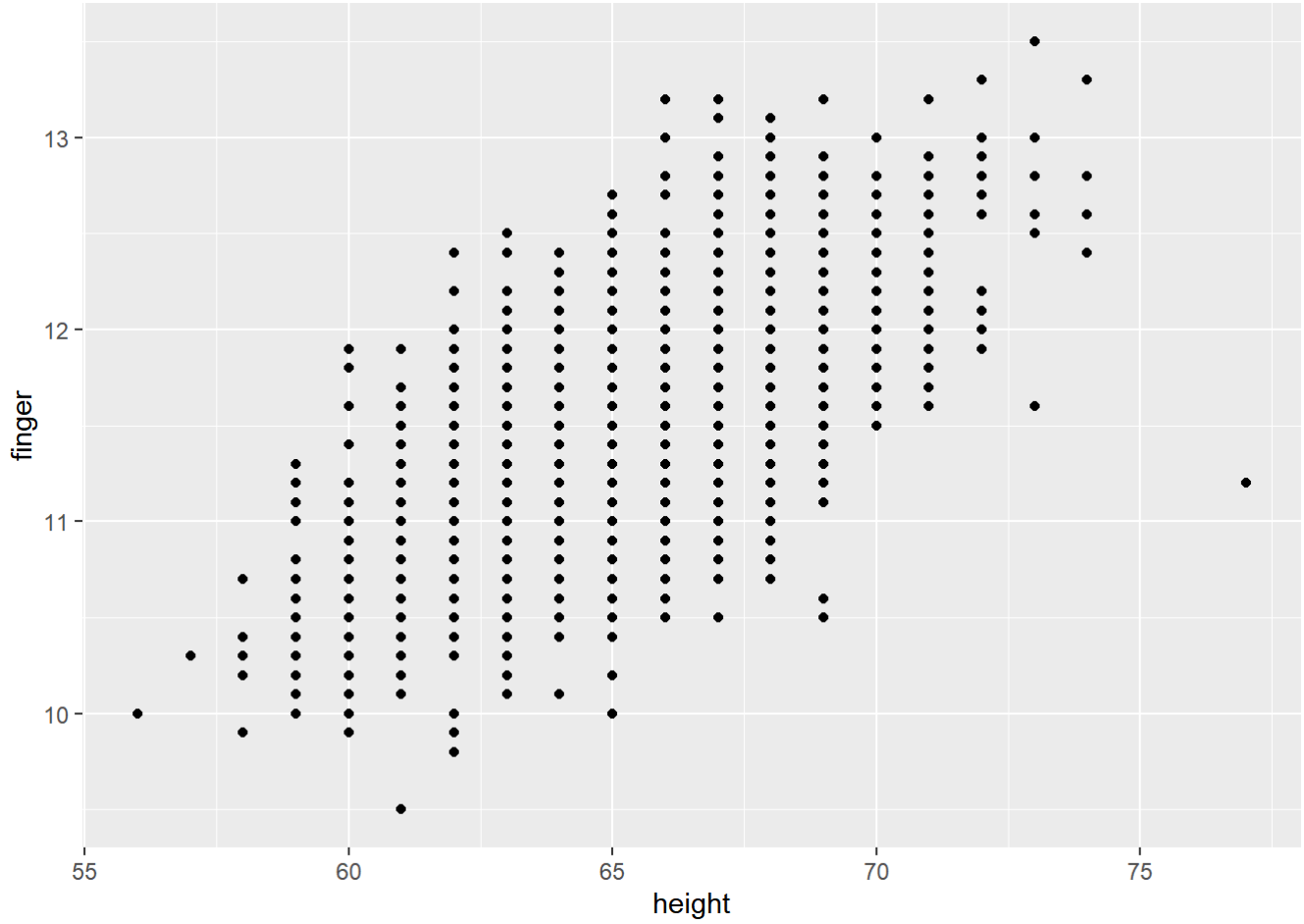
```
str(crimtab_stat_df$finger[[1]])
```

```
##  num 11.5
```

ggplot

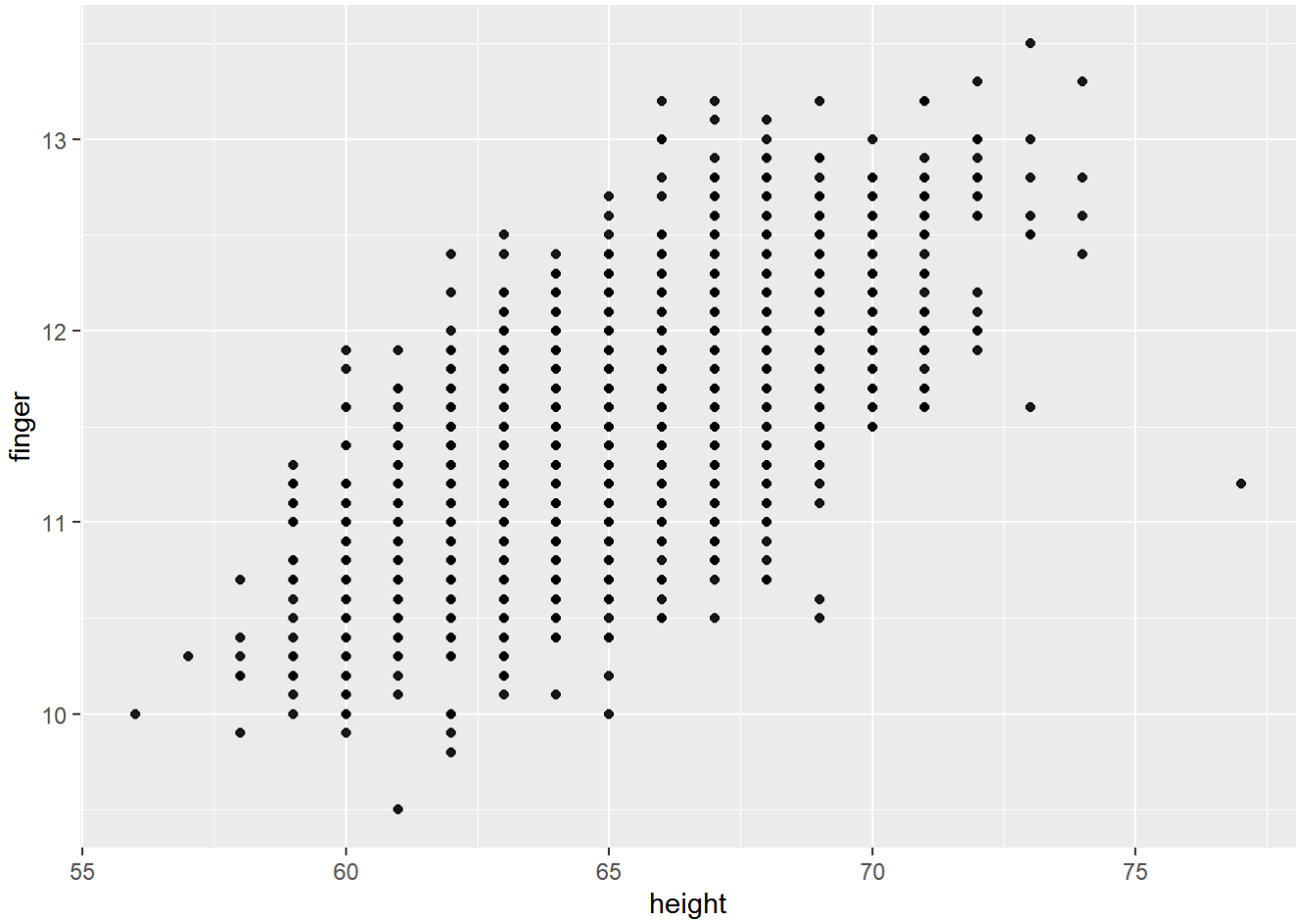
- 키와 손가락 길이의 산점도

```
library(ggplot2)
g1 <- ggplot(data = crimtab_long_df,
             mapping = aes(x = height, y = finger))
g2 <- g1 +
  geom_point()
g2
```



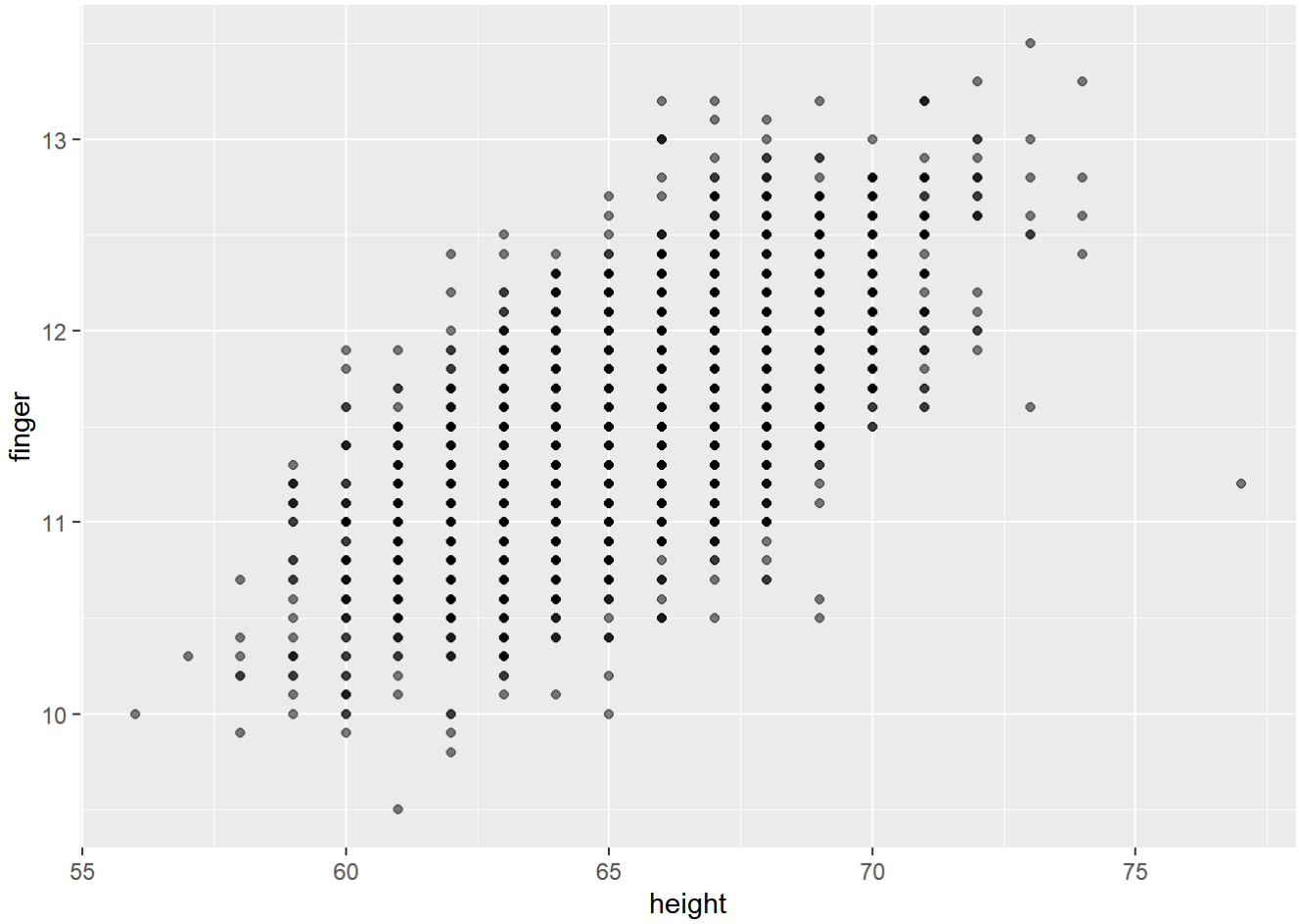
- 투명도 변경 : `alpha = 0.9`

```
g2_2 <- g1 +
  geom_point(alpha = 0.9)
g2_2
```



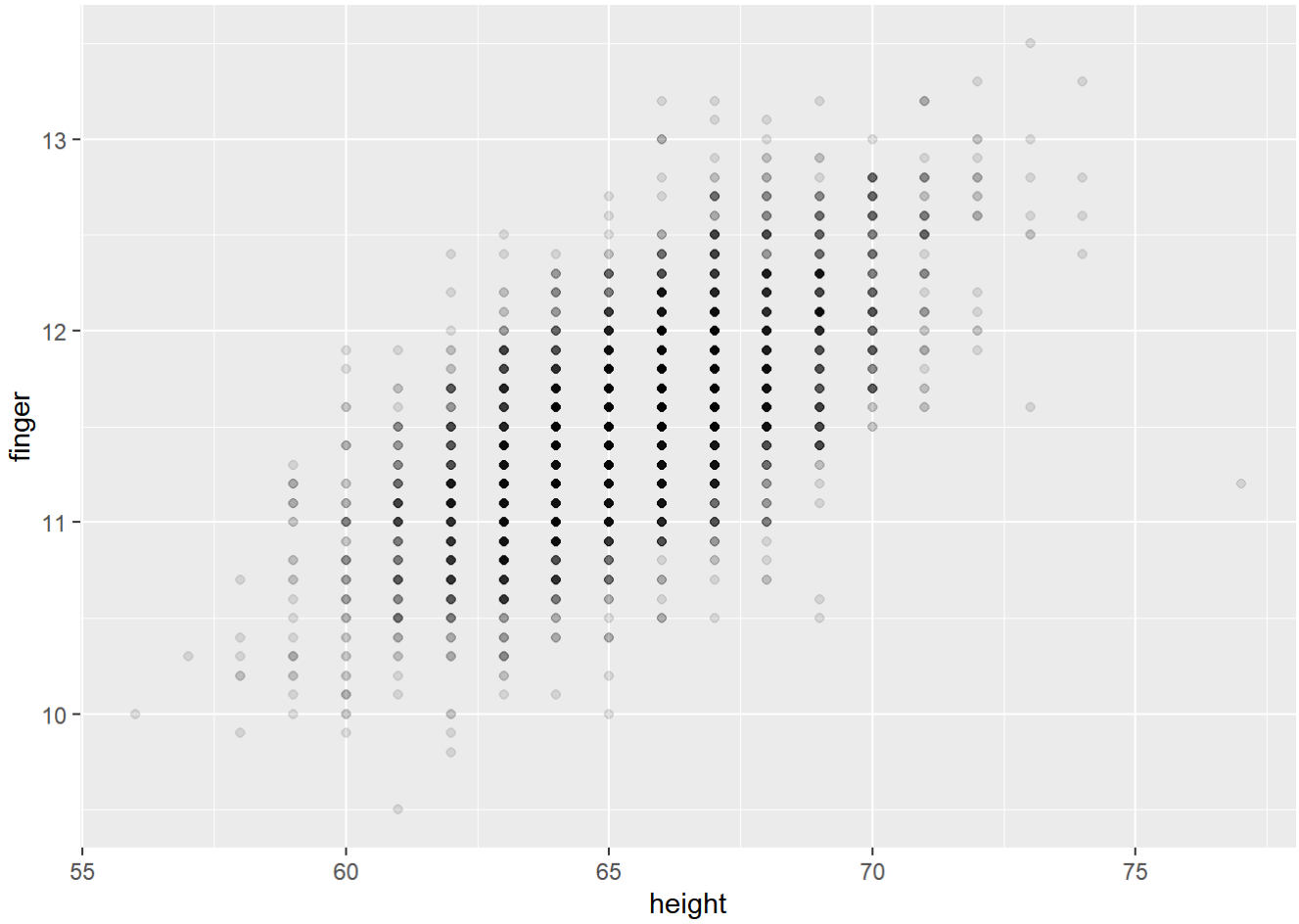
- 투명도 변경 : `alpha = 0.5`

```
g2_3 <- g1 +
  geom_point(alpha = 0.5)
g2_3
```



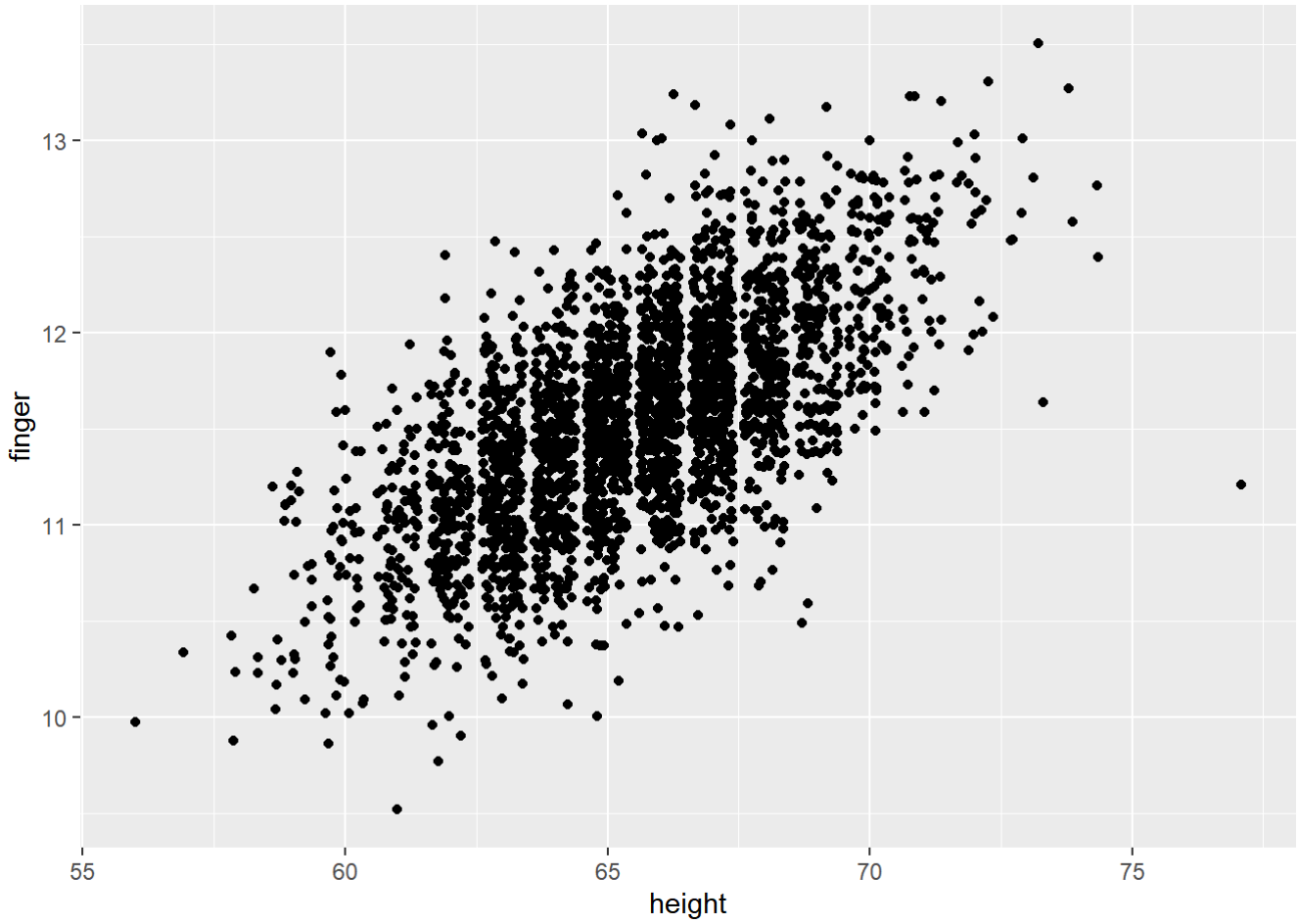
- 투명도 변경 : `alpha = 0.1`

```
g2_4 <- g1 +
  geom_point(alpha = 0.1)
g2_4
```



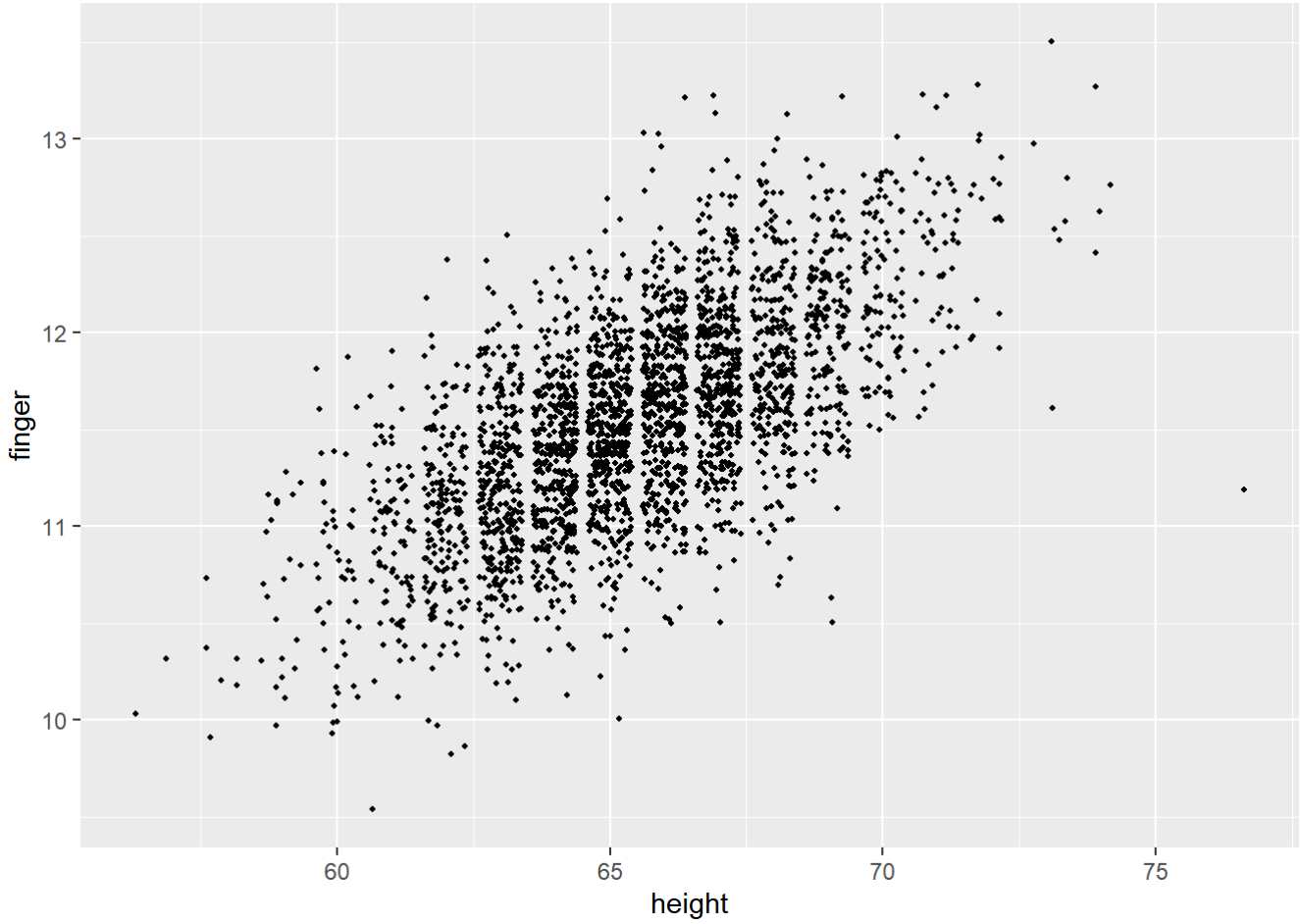
- 중복점 흐트러놓기 : `position = jitter`

```
g2_5 <- g1 +
  geom_point(position = "jitter")
g2_5
```



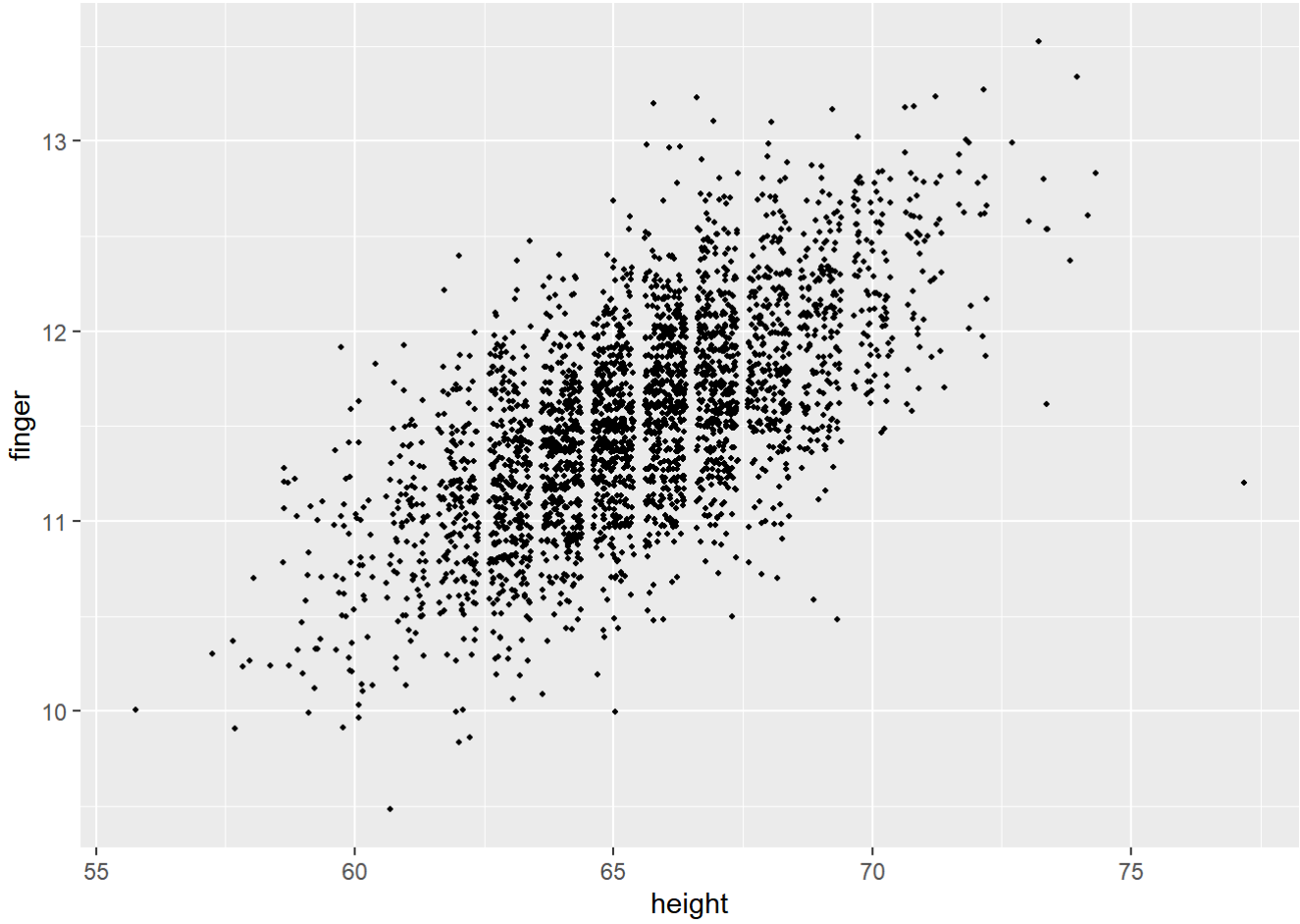
- 점의 크기를 줄이고 중복점 흐트러놓기 : `position = jitter, size = 0.7`

```
g2_6 <- g1 +
  geom_point(position = "jitter", size = 0.7)
g2_6
```



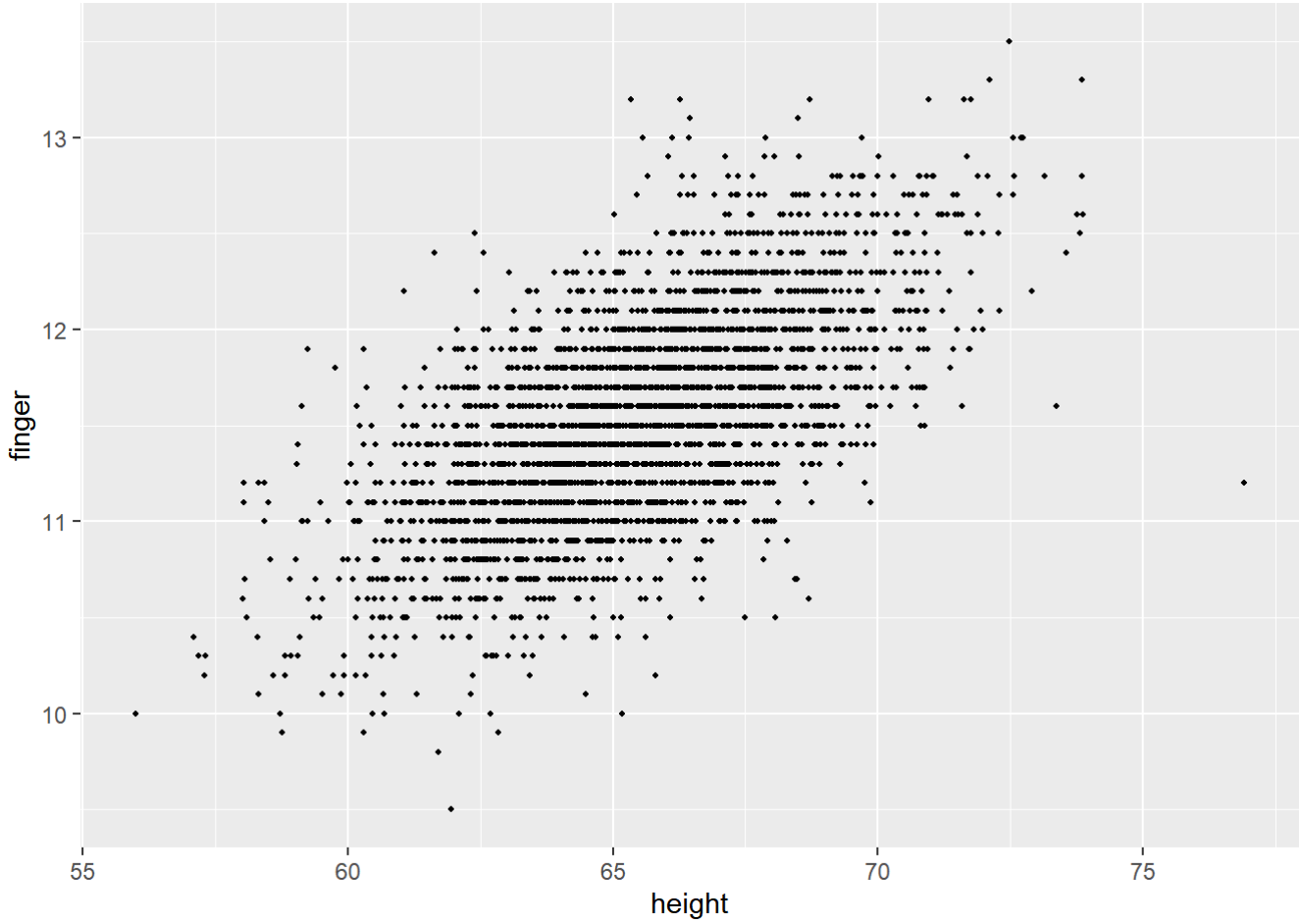
- 동일한 효과 : `position = position_jitter(), size = 0.7`

```
g2_7 <- g1 +
  geom_point(position = position_jitter(), size = 0.7)
g2_7
```



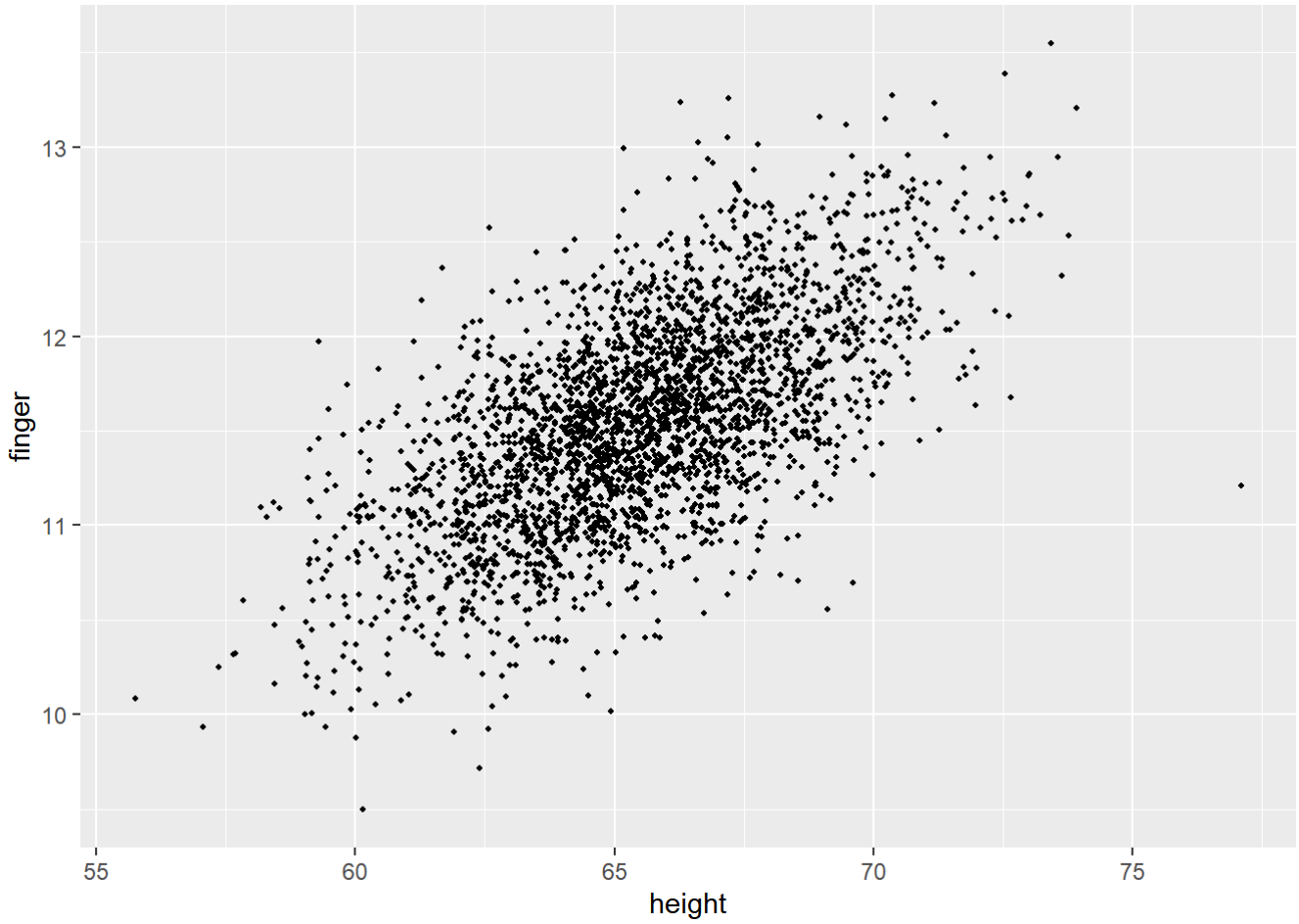
- 흐트러놓는 폭 조절 : `width = 1, height = 0, size = 0.7`

```
g2_8 <- g1 +
  geom_point(position = position_jitter(width = 1, height = 0),
             size = 0.7)
g2_8
```



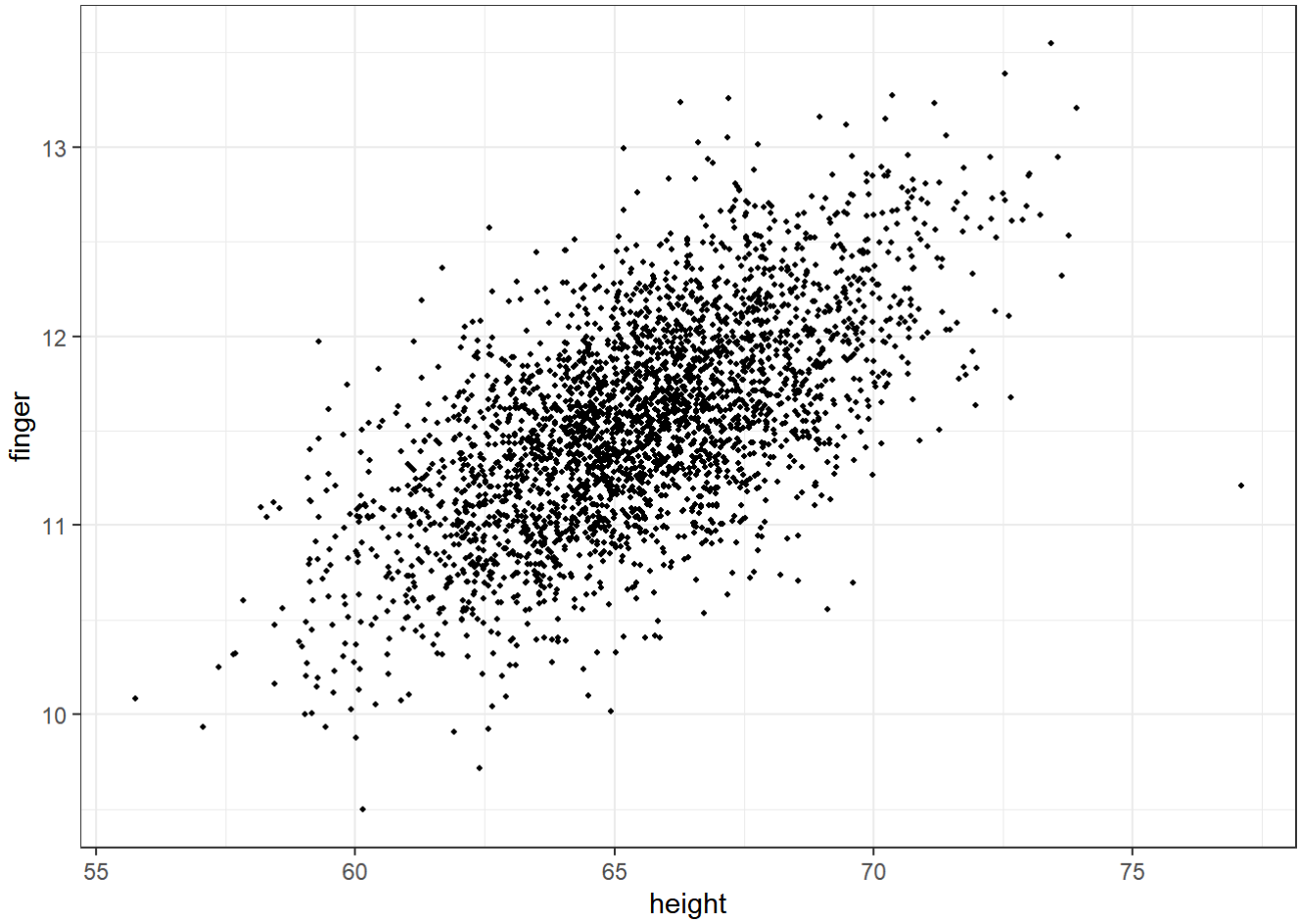
- 흐트러놓는 폭과 높이 조절 : `width = 1, height = 0.1, size = 0.7`

```
g2_9 <- g1 +
  geom_point(position = position_jitter(width = 1, height = 0.1),
             size = 0.7)
g2_9
```



- 흑백 테마 : `theme_bw()`

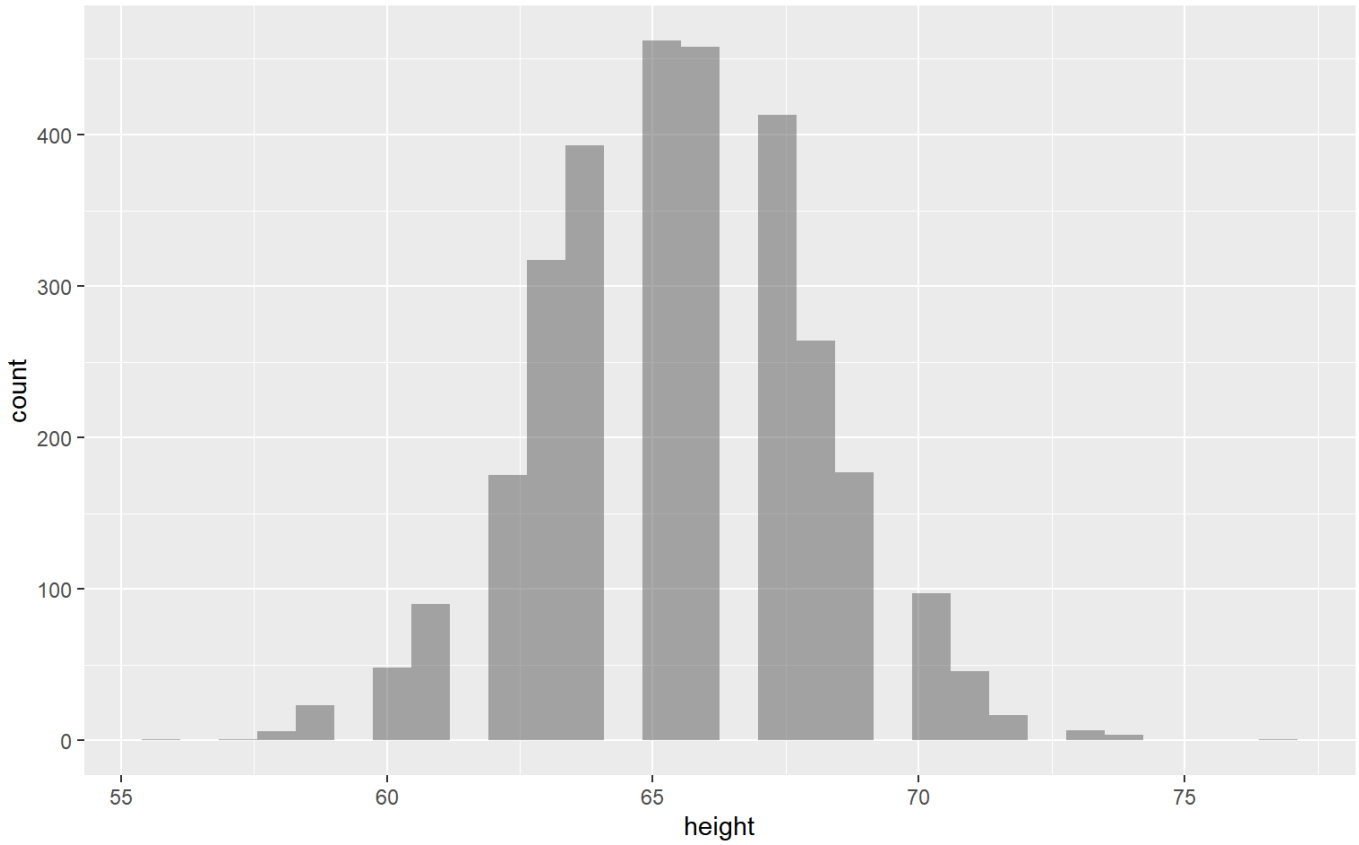
```
g3 <- g2_9 +
  theme_bw()
g3
```



히스토그램

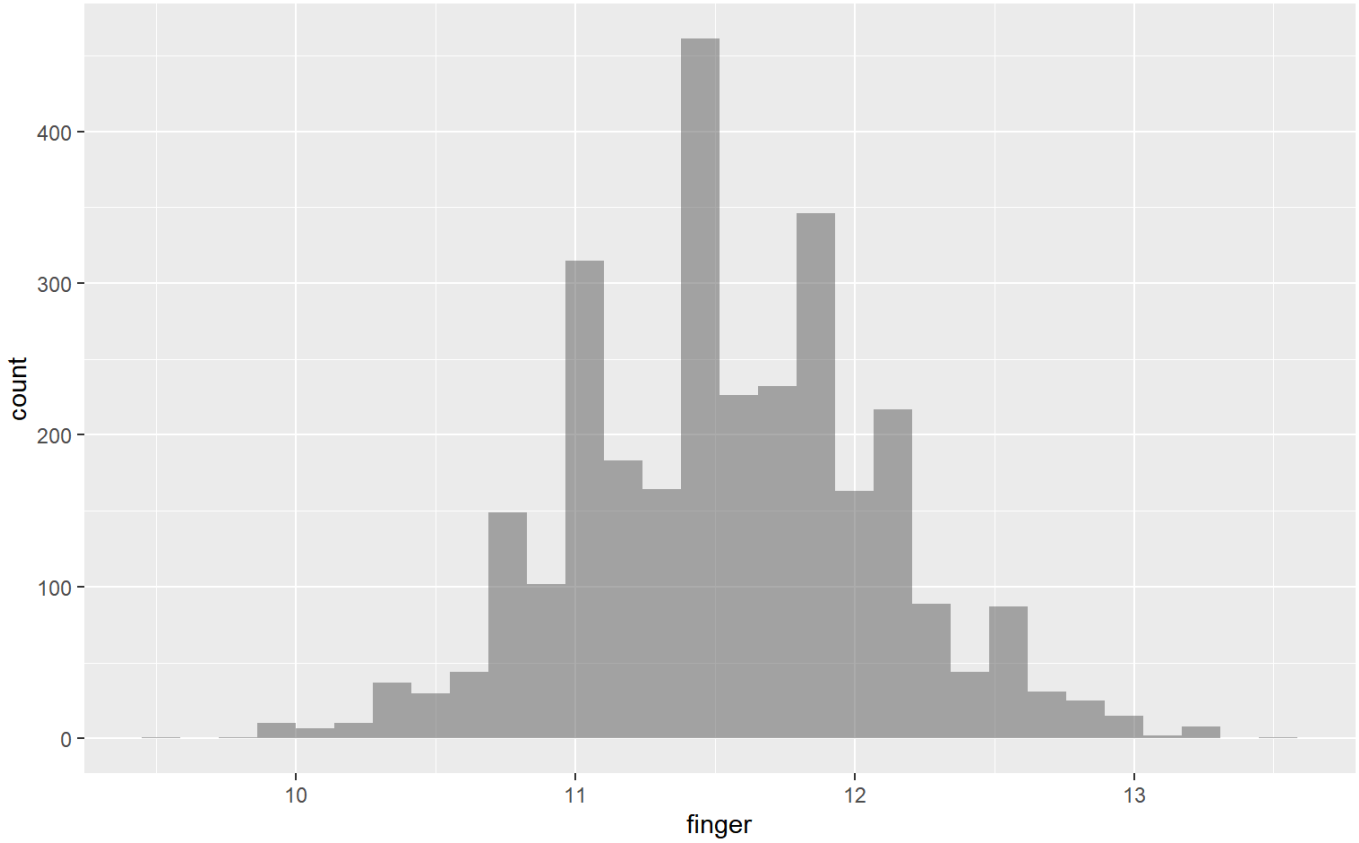
```
h1 <- ggplot(data = crimtab_long_df,
             mapping = aes(x = height))
h1 + geom_histogram(alpha = 0.5)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

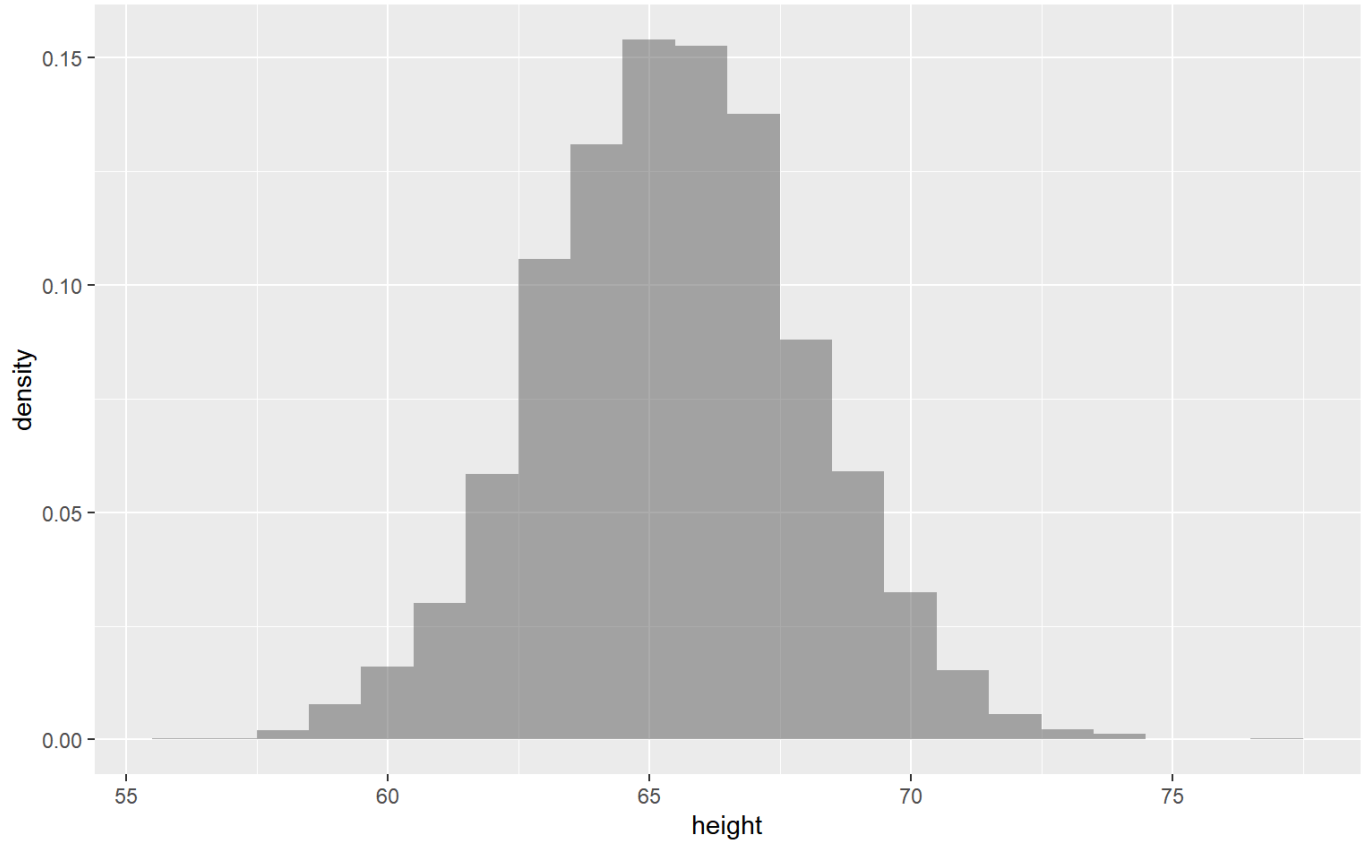


```
f1 <- ggplot(data = crimtab_long_df,
             mapping = aes(x = finger))
f1 + geom_histogram(alpha = 0.5)
```

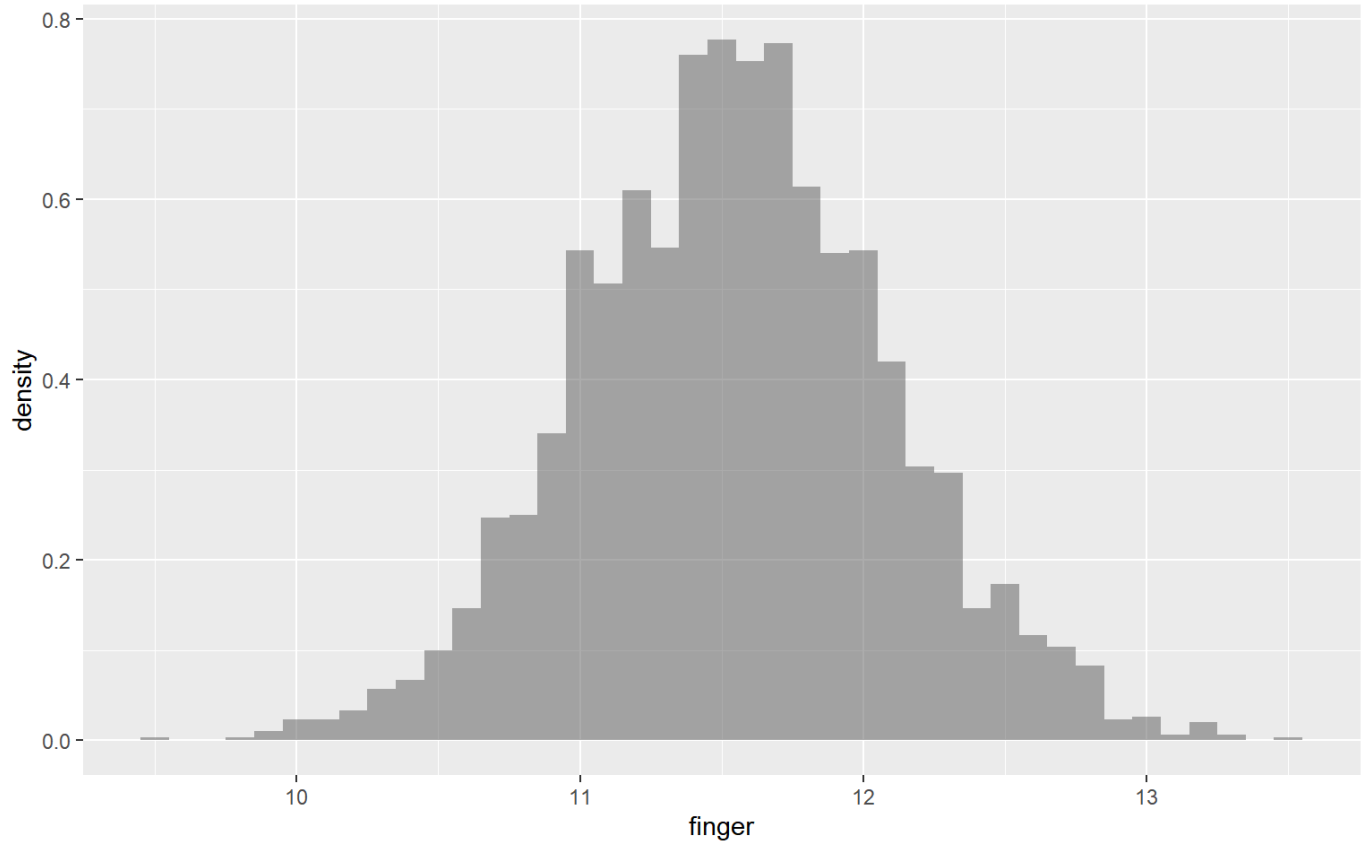
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



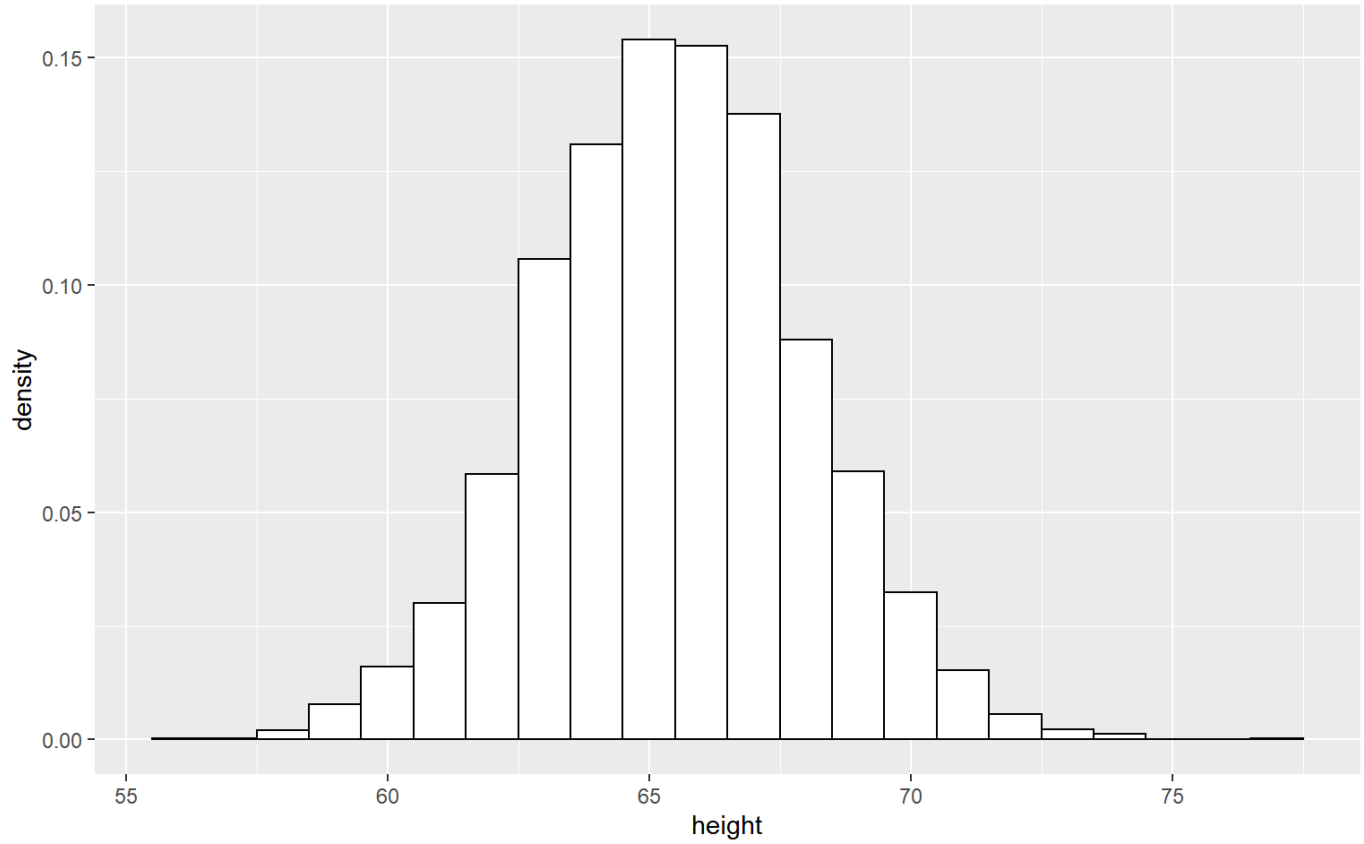

```
h1 + geom_histogram(aes(y = ..density..),
                    binwidth = 1,
                    alpha = 0.5)
```



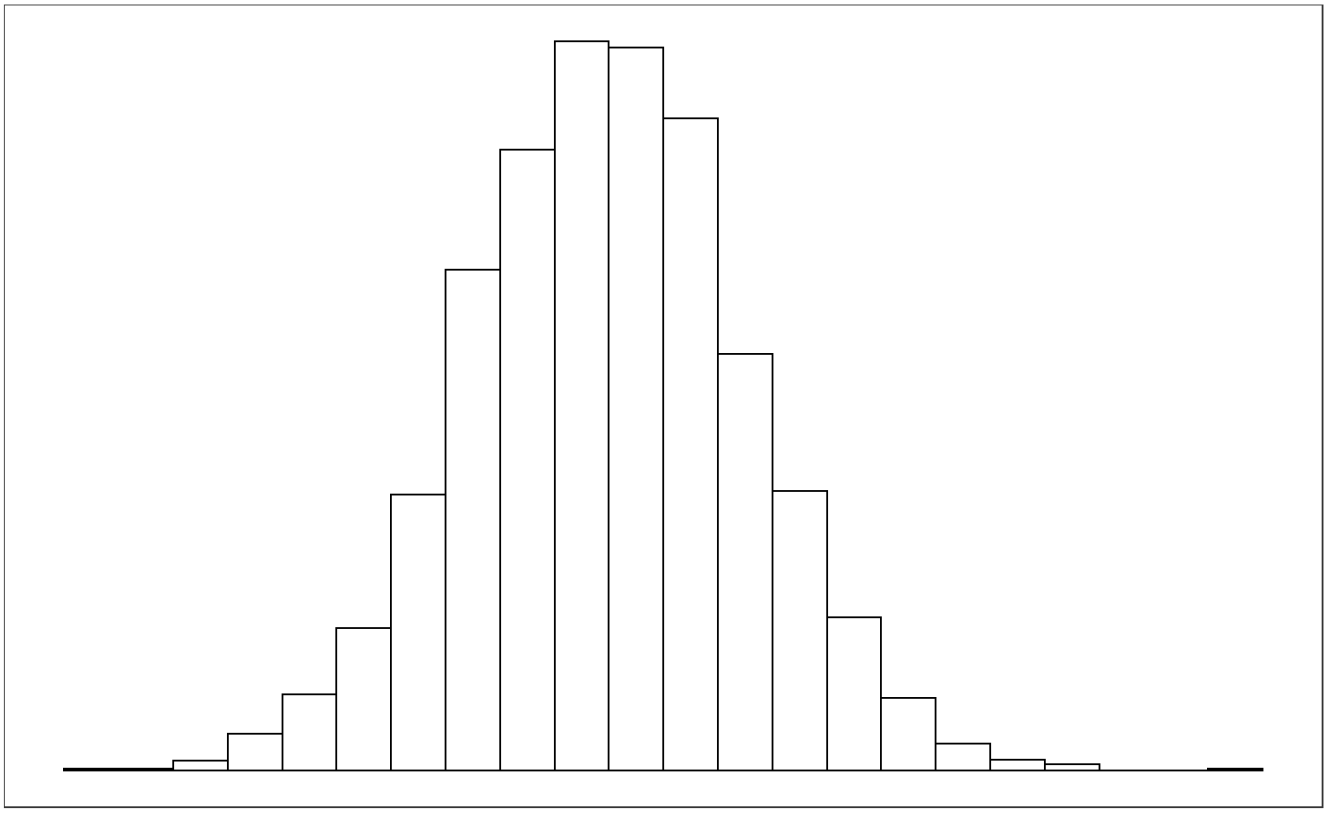

```
f1 + geom_histogram(aes(y = ..density..),
                    binwidth = 0.1,
                    alpha = 0.5)
```



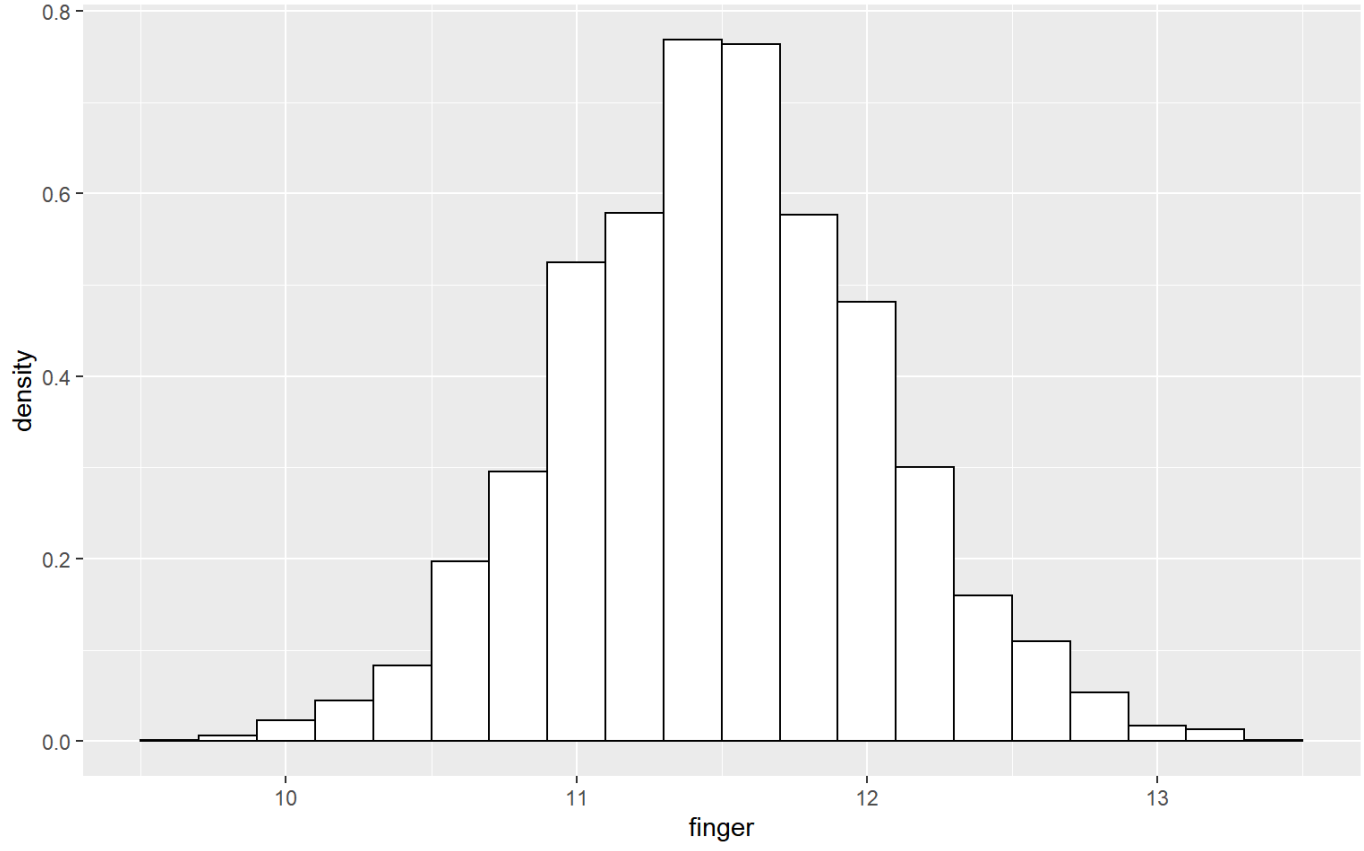
```
(g_h_1 <- h1 +
   geom_histogram(aes(y = ..density..),
                  binwidth = 1,
                  fill = "white",
                  colour = "black"))
```



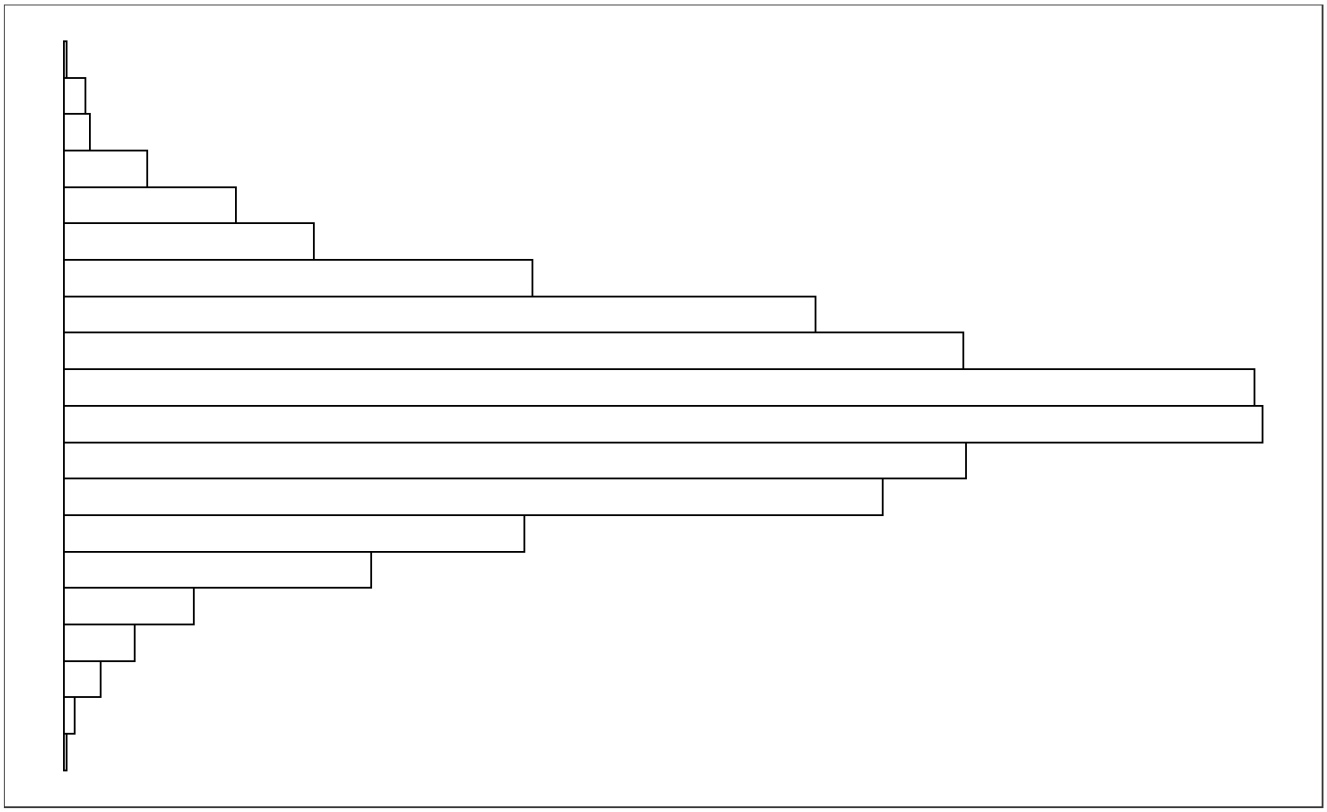

```
(g_h <- g_h_1 +
   theme_bw() +
   scale_x_continuous(name = "",
                      breaks = NULL) +
   scale_y_continuous(name = "",
                      breaks = NULL))
```



```
(g_f_1 <- f1 +
   geom_histogram(aes(y = ..density..),
                  binwidth = 0.2,
                  fill = "white",
                  colour = "black"))
```



```
(g_f <- g_f_1 +
   theme_bw() +
   scale_x_continuous(name = "",
                      breaks = NULL) +
   scale_y_continuous(name = "",
                      breaks = NULL) +
   coord_flip())
```



평균 위치를 화살표로 나타내려면

```
library(grid)
(mean_finger <- crimtab_stat[, 1][[1]])
```

```
## [1] 11.54737
```

```
(sd_finger <- crimtab_stat[, 1][[2]])
```

```
## [1] 0.5487137
```

```
(mean_height <- crimtab_stat[, 2][[1]])
```

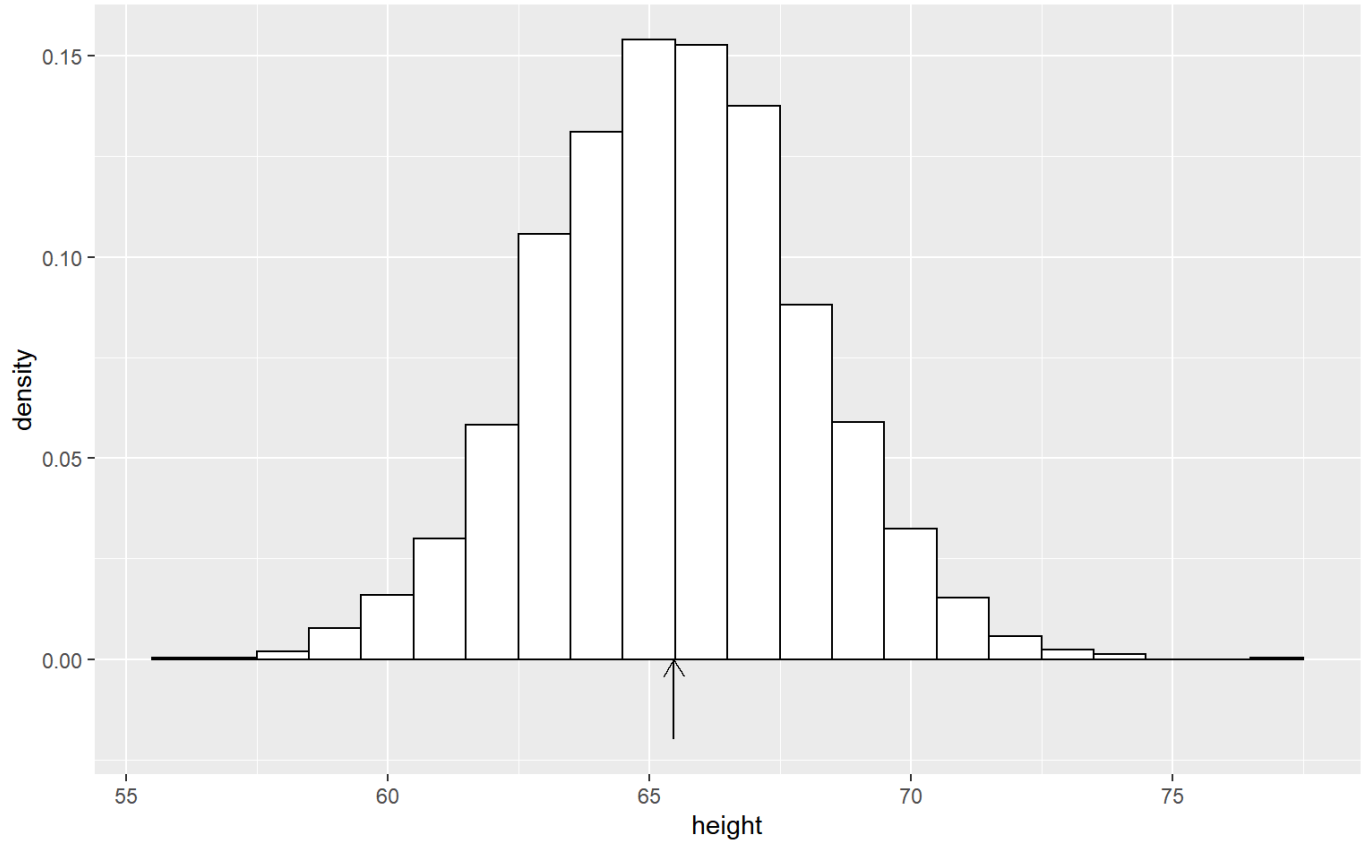
```
## [1] 65.473
```

```
(sd_height <- crimtab_stat[, 2][[2]])
```

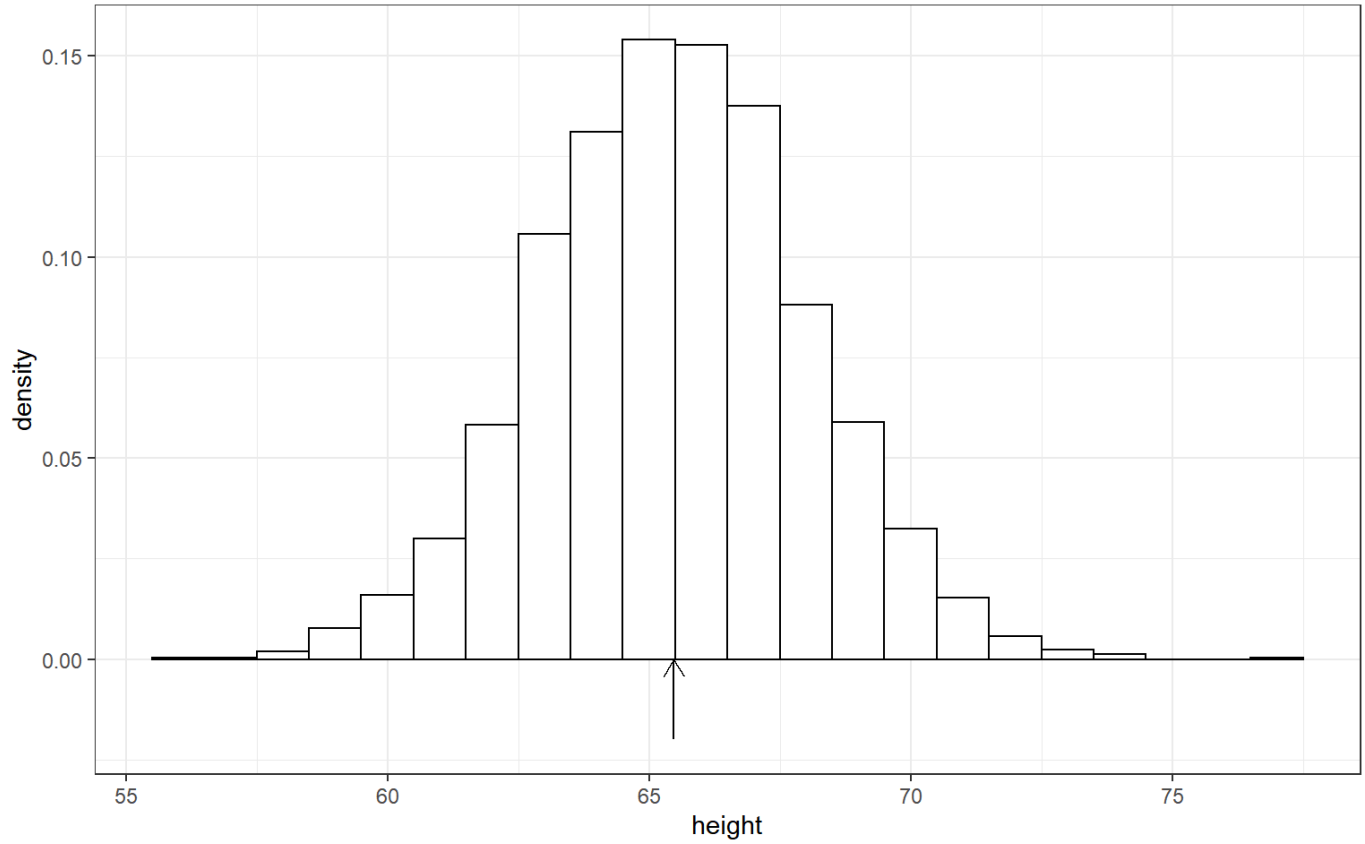
```
## [1] 2.557757
```

```
x_finger <- seq(9.5, 13.5,
                length.out = 3000)
y_finger <- dnorm(x_finger,
                  mean = mean_finger,
                  sd = sd_finger)
x_height <- seq(56, 77,
                length.out = 3000)
y_height <- dnorm(x_height,
                  mean = mean_height,
                  sd = sd_height)
```

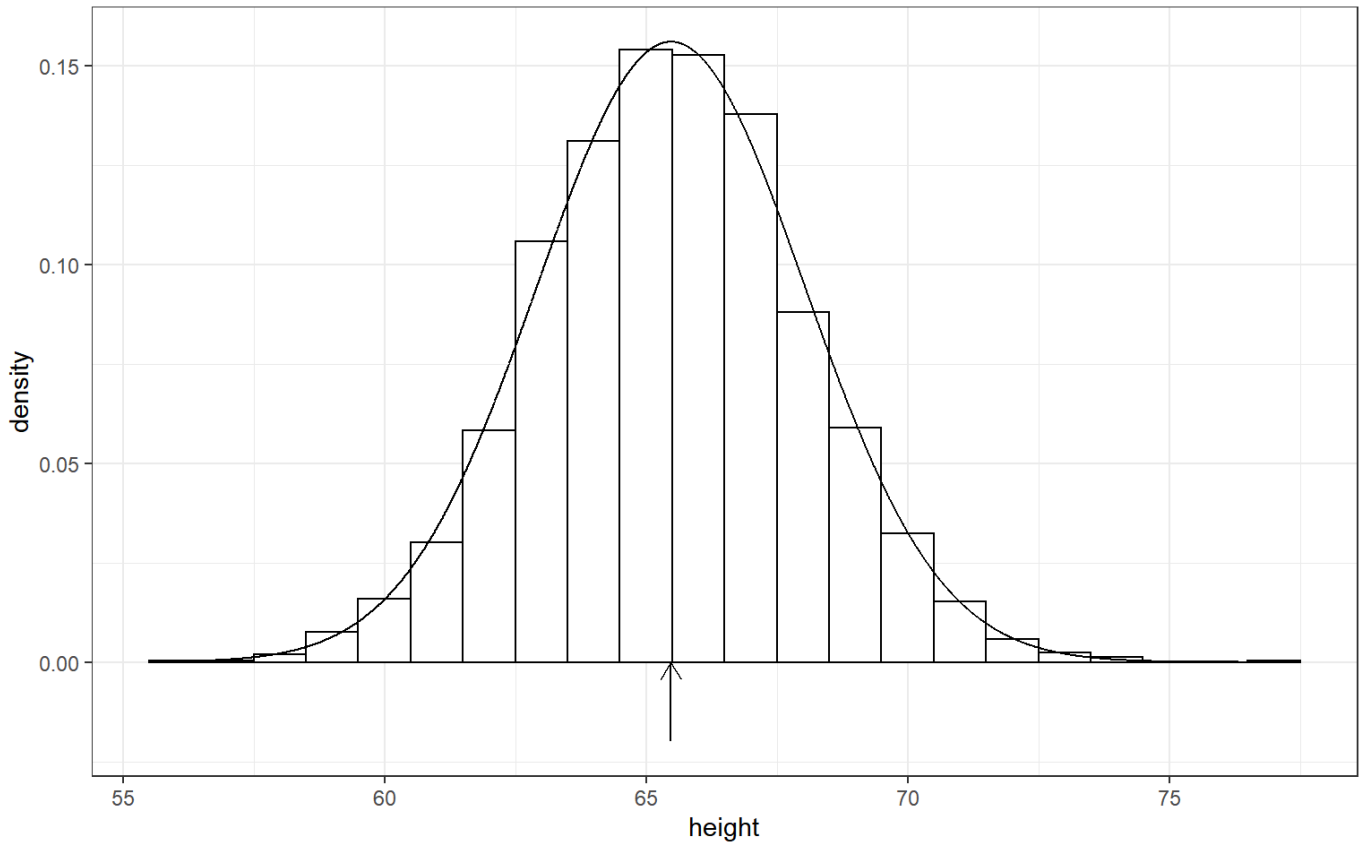
```
(g_h_2 <- g_h_1 +
    annotate("segment",
             x = mean_height,
             xend = mean_height,
             y = -0.02,
             yend = 0,
             arrow = arrow(length = unit(0.3, "cm"))))
```



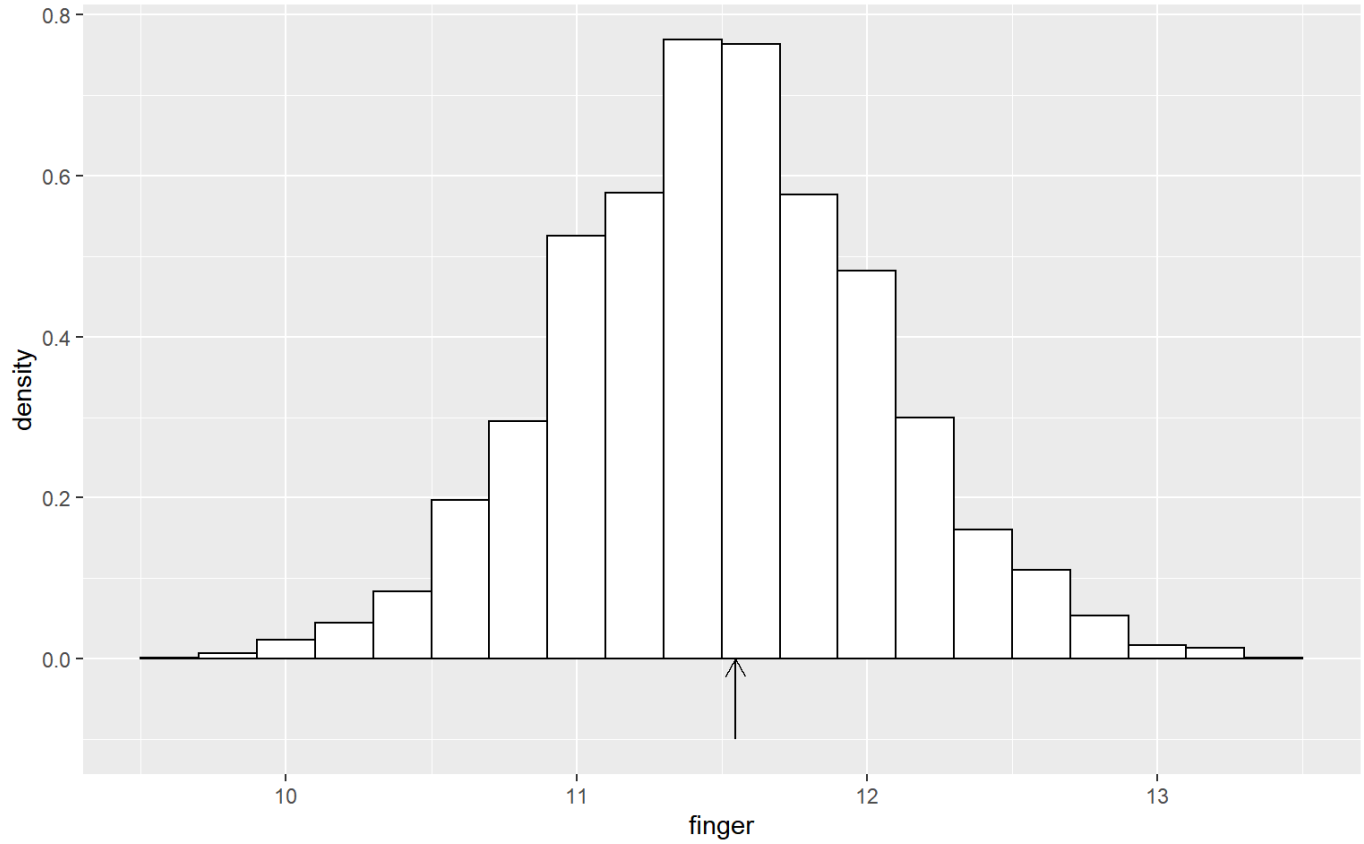

```
(g_h_3 <- g_h_2 +
   theme_bw())
```


0.15
0.10
0.05
0.00
density
55
60
65
70
75
height

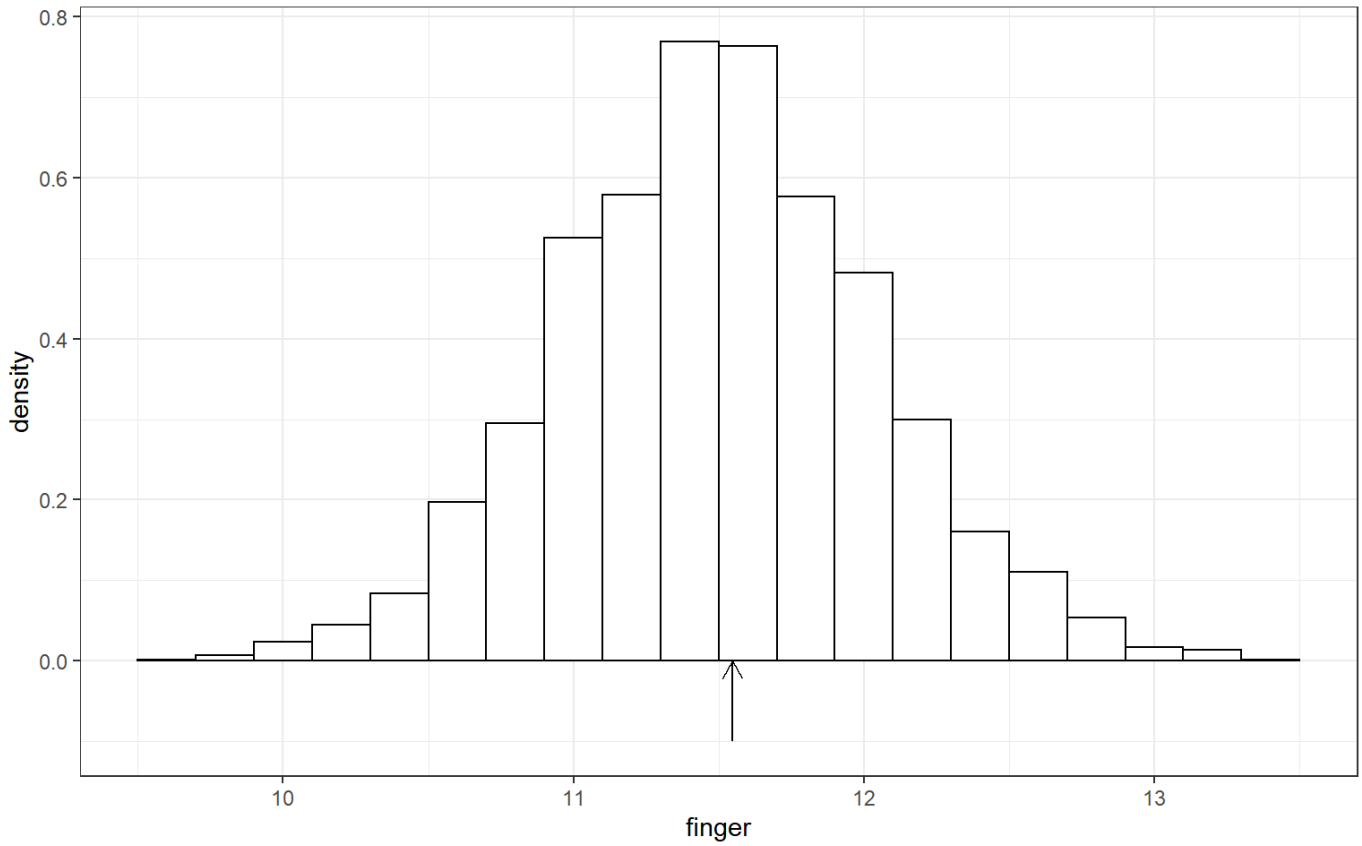
```
(g_h_4 <- g_h_3 +
   geom_line(aes(x = x_height, y = y_height)))
```



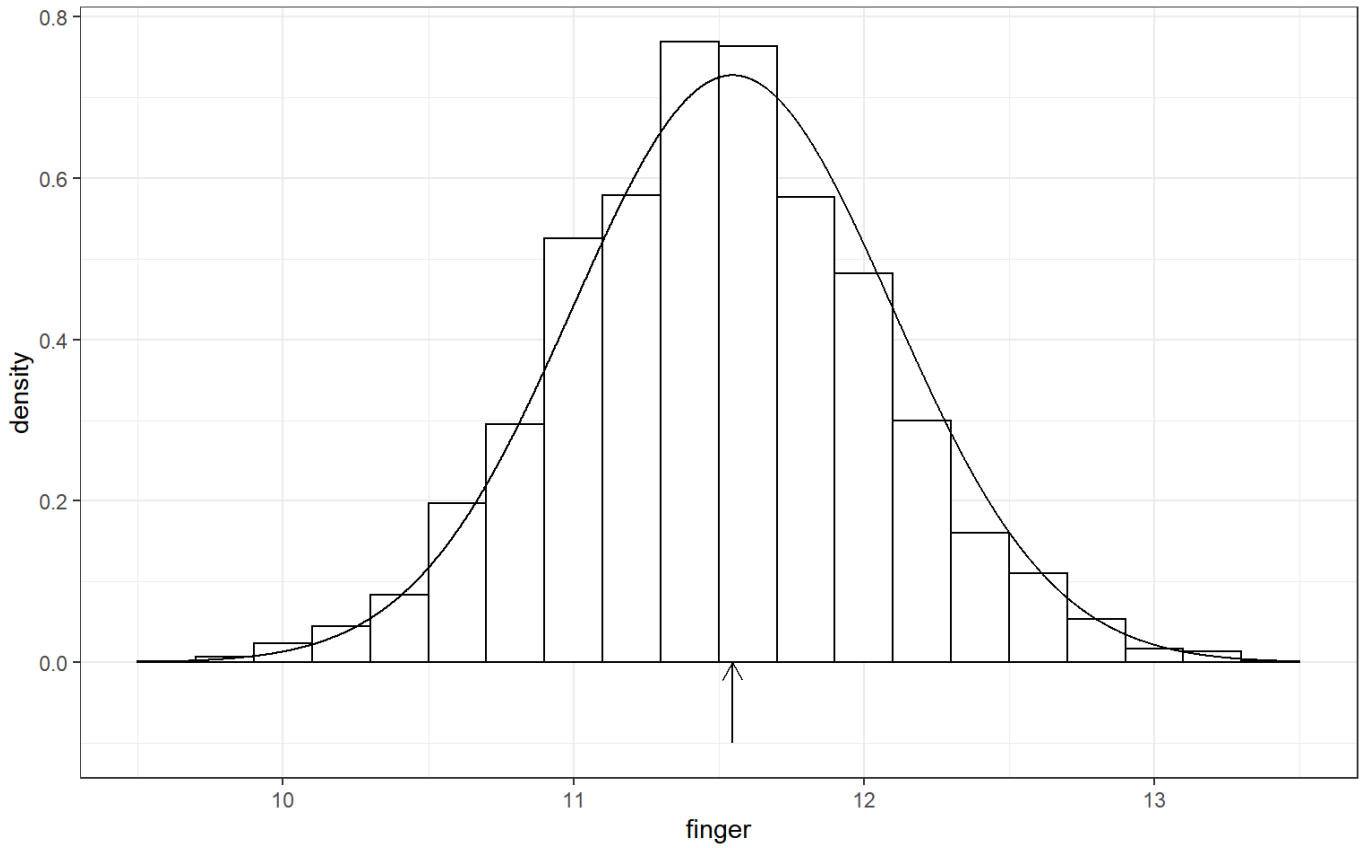

```
(g_f_2 <- g_f_1 +
   annotate("segment",
            x = mean_finger,
            xend = mean_finger,
            y = -0.1,
            yend = 0,
            arrow = arrow(length = unit(0.3, "cm"))))
```


0.8
0.6
0.4
0.2
0.0
density
10
11
12
13
finger

```
(g_f_3 <- g_f_2 +
   theme_bw())
```



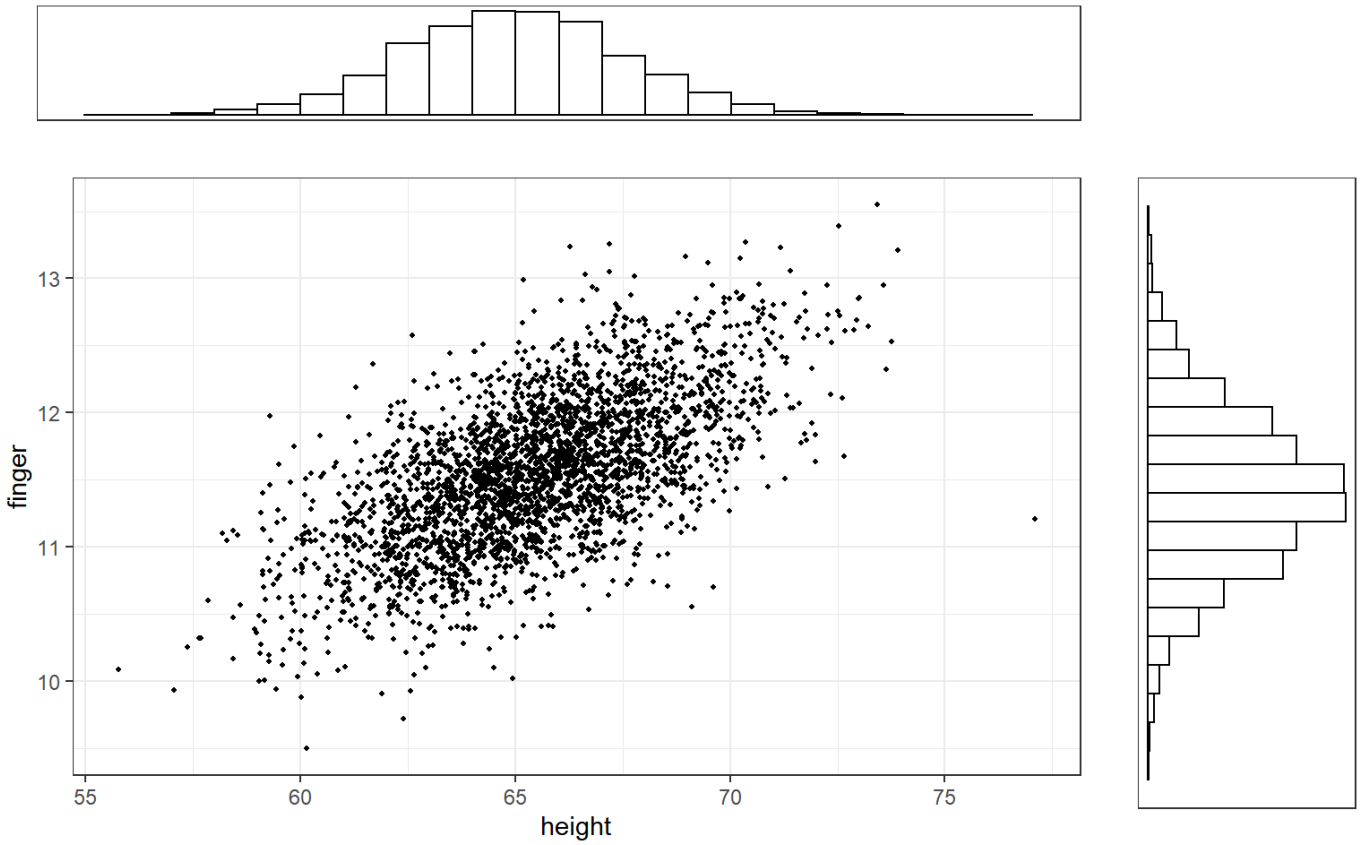

```
(g_f_4 <- g_f_3 +
   geom_line(aes(x = x_finger, y = y_finger)))
```



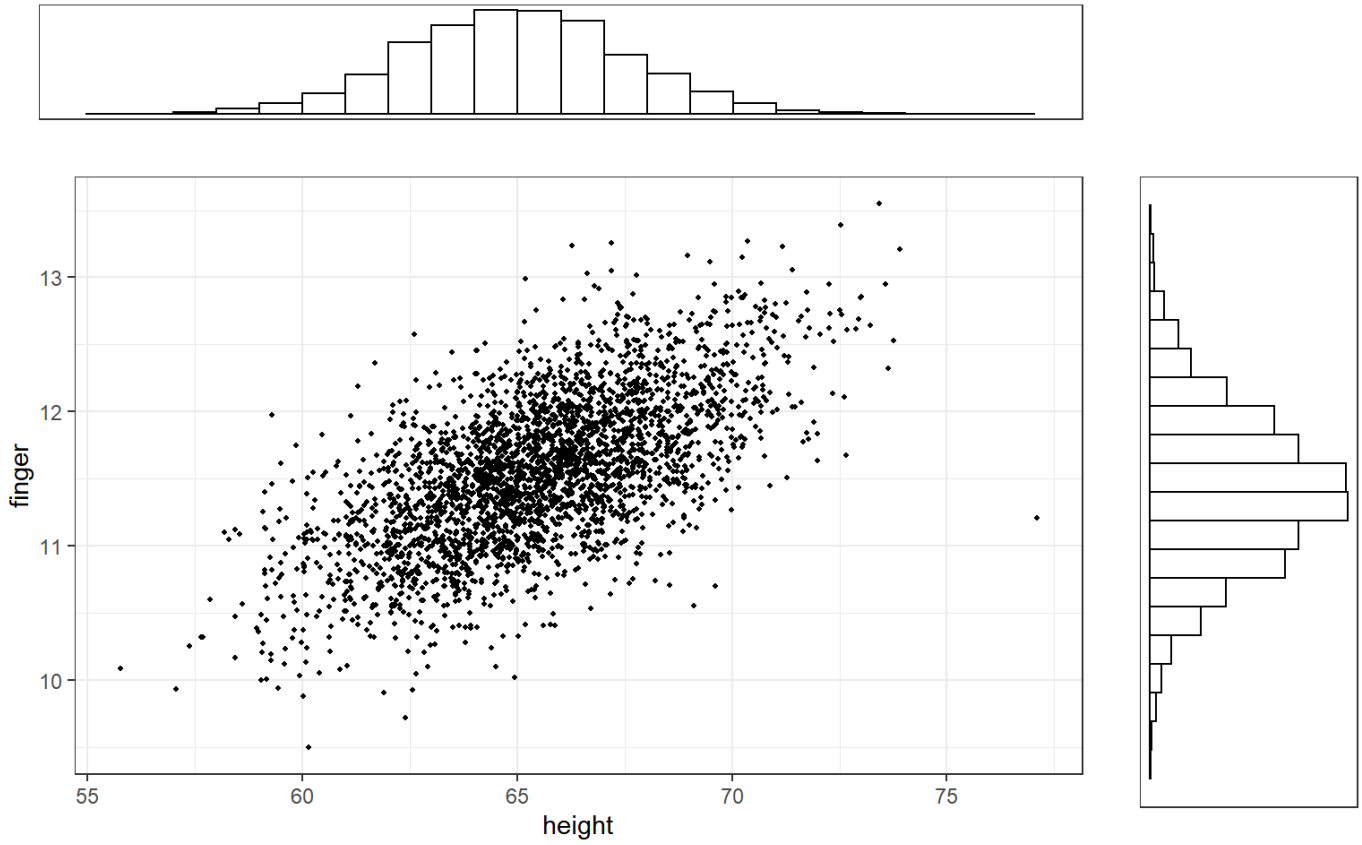
산점도와 히스토그램 함께 배열하기

grid 및 gridExtra 패키지와 함께 blank Grob 설정이 핵심. grid.arrange 사용법에 유의.

```
library(gridExtra)
grid.rect(gp = gpar(col = "white"), draw = FALSE) %>%
grid.arrange(g_h, ., g3, g_f,
             ncol = 2,
             widths = c(4, 1),
             heights = c(1, 4))
```




```
blank <- grid.rect(gp = gpar(col = "white"), draw = FALSE)
grid.arrange(g_h, blank, g3, g_f,
             ncol = 2,
             widths = c(4, 1),
             heights = c(1, 4))
```


13
12
11
10
finger
55
60
65
70
75
height

Comments

이번시간에는 ggplot2를 이용하여 키와손가락길이의 관계를 그래프로 나타내는방법을 알 수 있었습니다. hist(crimtab_long_df[“height”] / hist(crimtab_long_df[, “height”] 두개를 보면서 차이를 확인할 수 있게되었는데 뒤에껀 vector라 그림이 나온다는 것을 알게되었습니다. position_jiter()라는 함수를통해 중복점을 흐트러놓는법을 새로 알게되었습니다. 또, sapply를통해 그전에 만들어둔 평균과 표준편차를 확인할 수 있었습니다. ggplot2를 사용해 산점도와 히스토그램 함께 배열하는 방법을 배울수 있었는데, 산점도를 그리고 기존에 만들었던것을 순서대로 배치시킬수 있게 되었습니다.