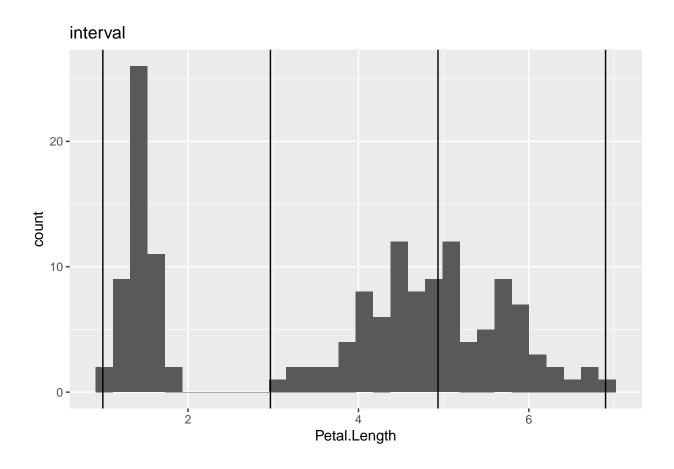
lista 2.

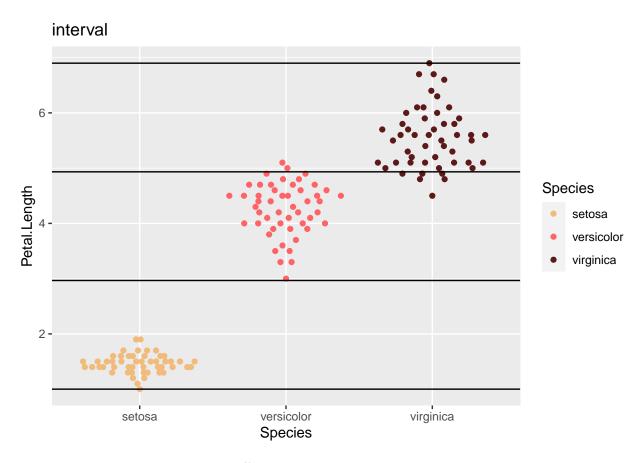
Mikołaj Langner, Marcin Kostrzewa

25.04.2021

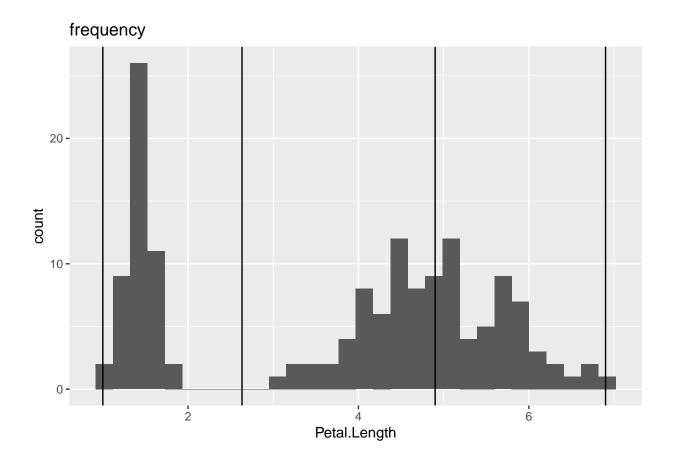
ZADANIE 1.

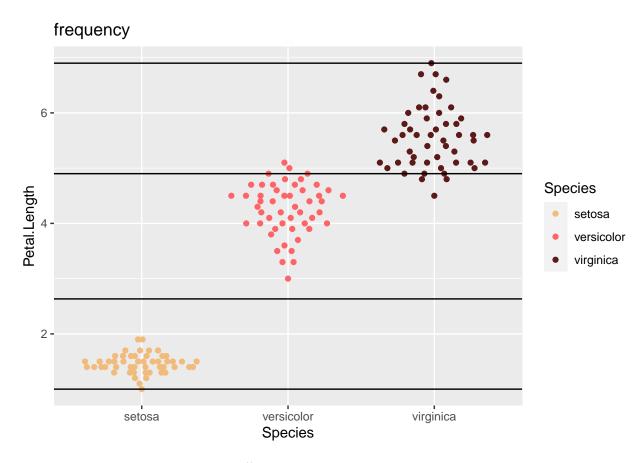
```
data(iris)
intervals <- c(min(iris$Petal.Length), 2, 5, max(iris$Petal.Length))</pre>
for (method in c("interval", "frequency", "cluster", "fixed")) {
  petal.length.discretized <- if (method != "fixed")</pre>
    discretize(iris$Petal.Length, method=method) else
    discretize(iris$Petal.Length, method=method, breaks=intervals)
  print(ggplot(iris, aes(Petal.Length)) +
          geom histogram() +
          geom_vline(xintercept=attributes(petal.length.discretized)$"discretized:breaks") +
          ggtitle(method))
  print(ggplot(iris, aes(Species, Petal.Length)) +
    geom_quasirandom(aes(col=Species)) +
    scale_color_manual(values=wes_palette("GrandBudapest1", 3)) +
    geom_hline(yintercept=attributes(petal.length.discretized)$"discretized:breaks") +
    ggtitle(method))
  discretized.table <- table(petal.length.discretized, iris$Species)</pre>
  matchClasses(discretized.table)
```



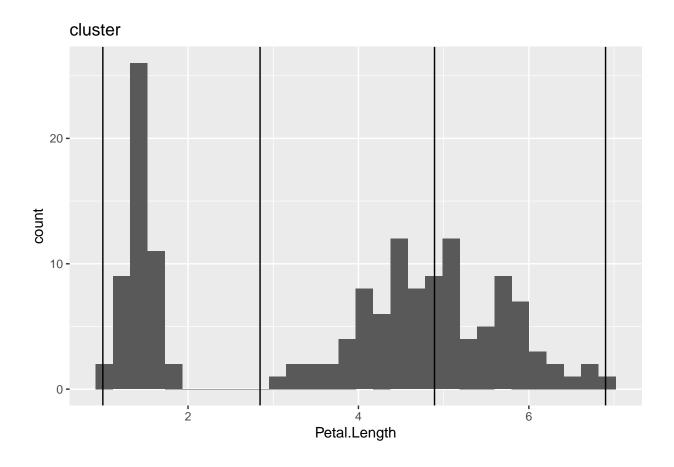


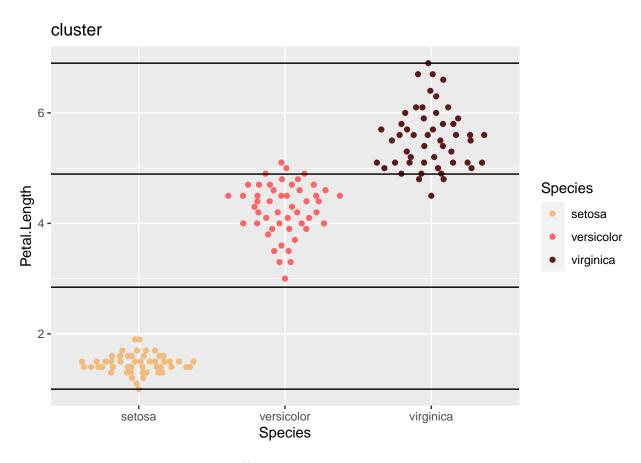
Cases in matched pairs: 94.67 %



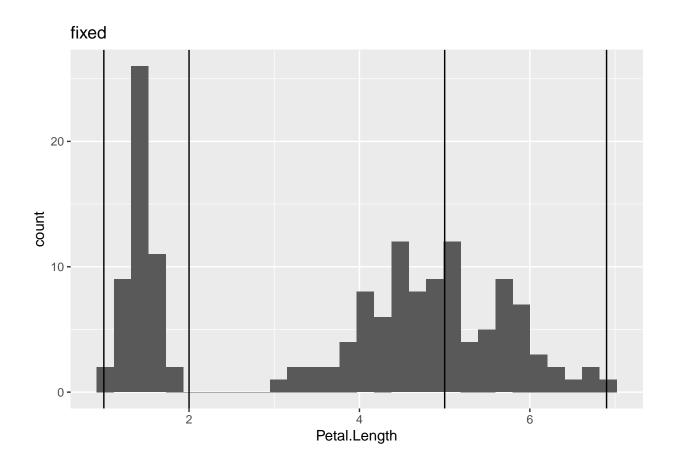


Cases in matched pairs: 95.33 %

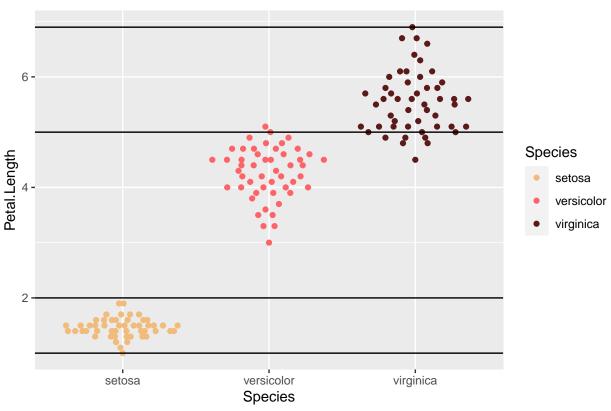




Cases in matched pairs: 95.33 %

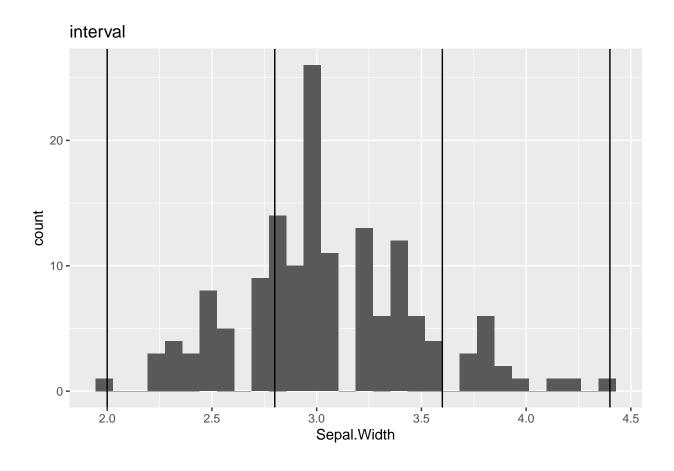


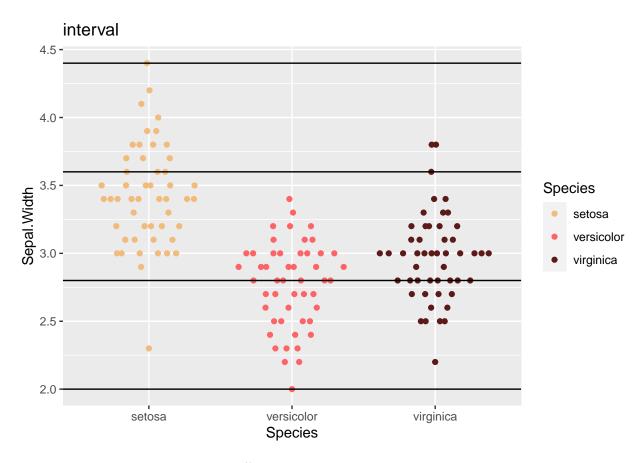
fixed



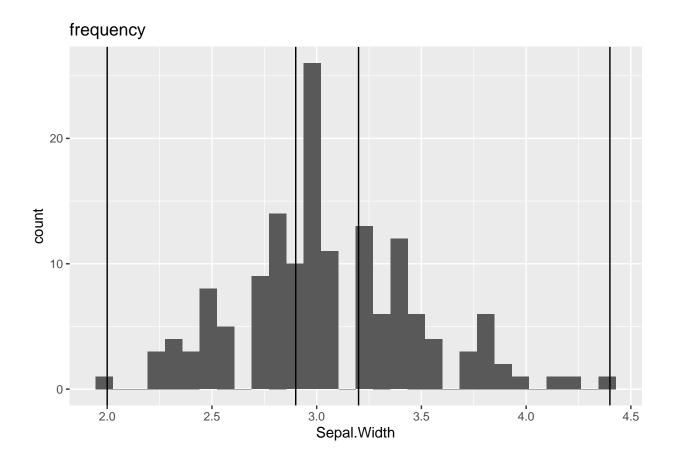
Cases in matched pairs: 94.67 %

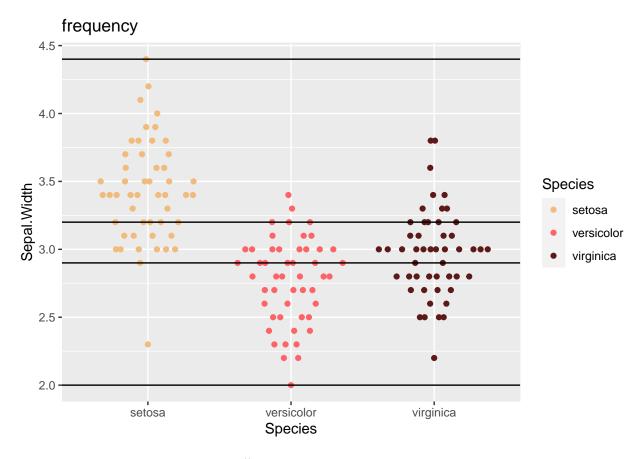
```
intervals <- c(min(iris$Sepal.Width), 2.5, 3, max(iris$Sepal.Width))</pre>
for (method in c("interval", "frequency", "cluster", "fixed")) {
  sepal.width.discretized <- if (method != "fixed")</pre>
   discretize(iris$Sepal.Width, method=method) else
    discretize(iris$Sepal.Width, method=method, breaks=intervals)
  print(ggplot(iris, aes(Sepal.Width)) +
          geom_histogram() +
          geom_vline(xintercept=attributes(sepal.width.discretized)$"discretized:breaks") +
          ggtitle(method))
  print(ggplot(iris, aes(Species, Sepal.Width)) +
   geom_quasirandom(aes(col=Species)) +
    scale_color_manual(values=wes_palette("GrandBudapest1", 3)) +
   geom_hline(yintercept=attributes(sepal.width.discretized)$"discretized:breaks") +
   ggtitle(method))
  discretized.table <- table(sepal.width.discretized, iris$Species)</pre>
  matchClasses(discretized.table)
}
```



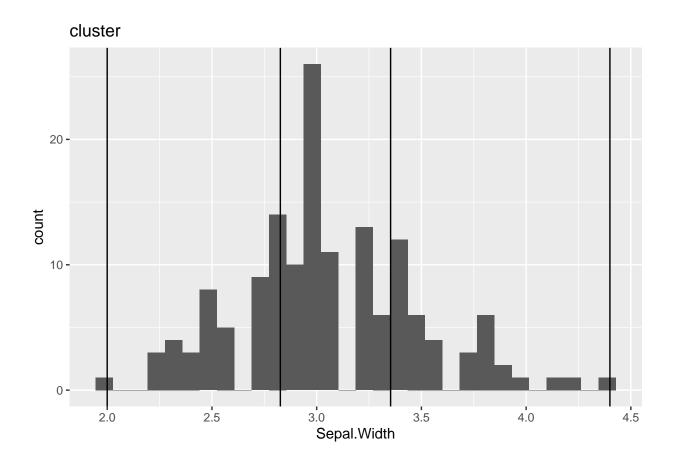


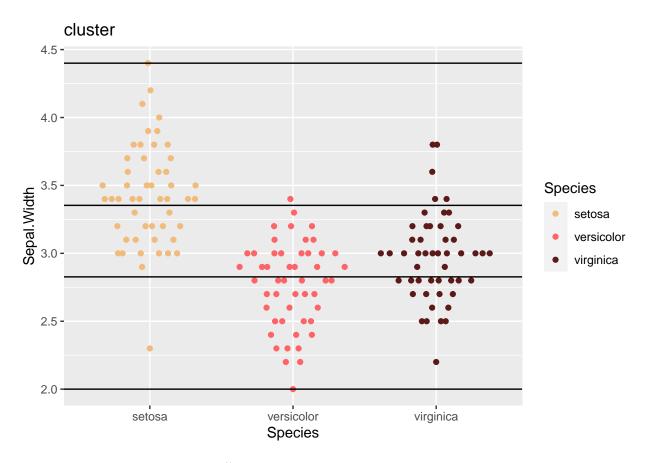
Cases in matched pairs: 50.67 %



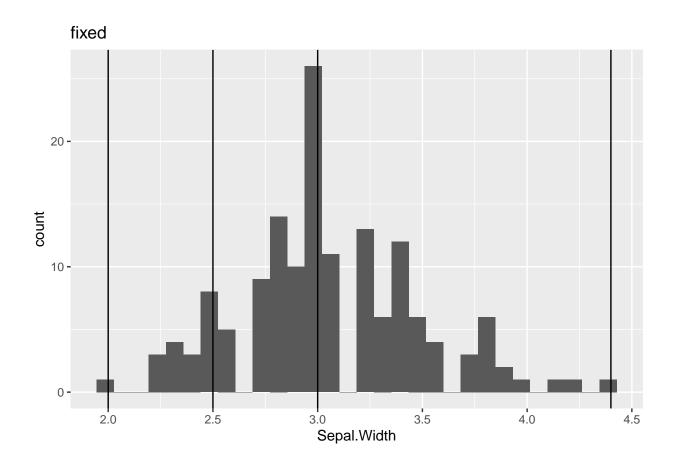


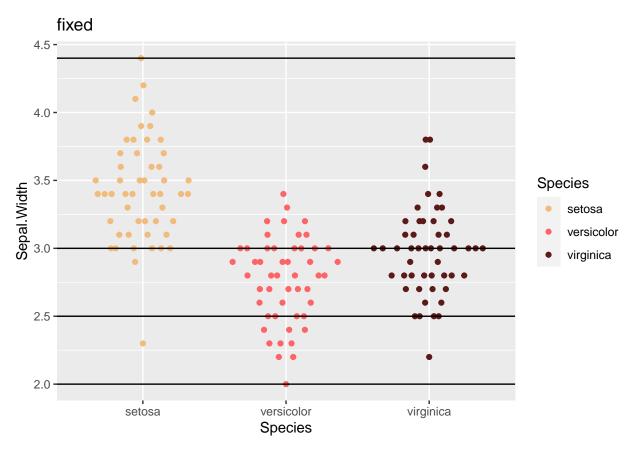
Cases in matched pairs: 55.33 %



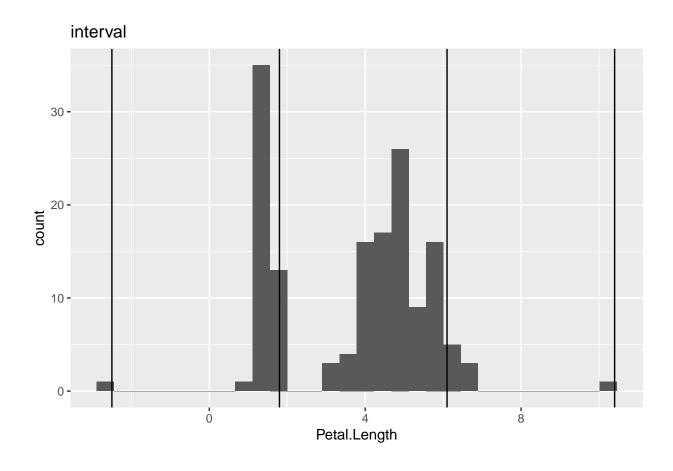


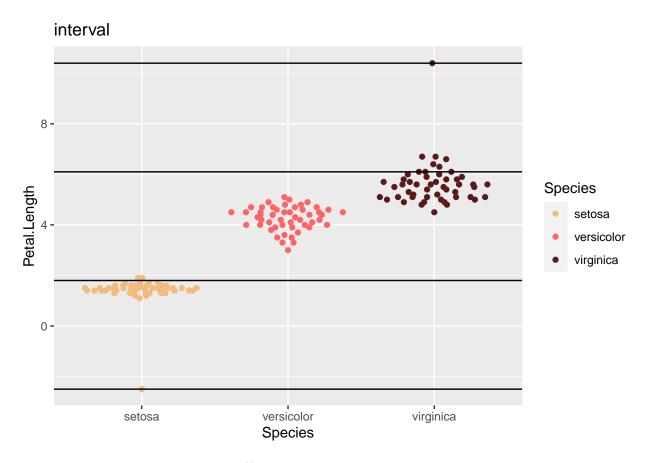
Cases in matched pairs: 56 %



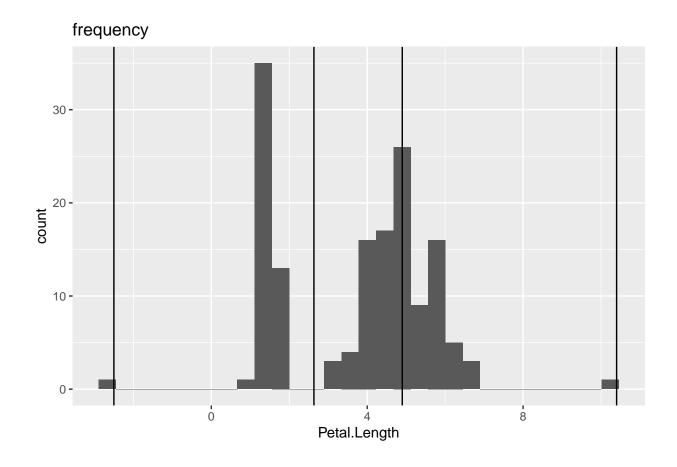


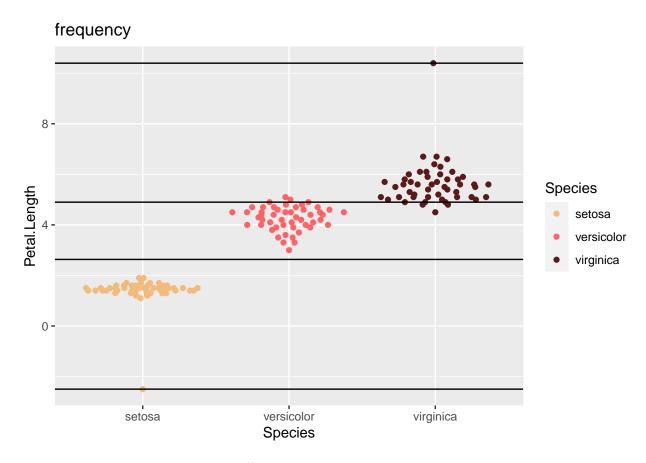
```
## Cases in matched pairs: 54.67 \%
iris$Petal.Length[which.min(iris$Petal.Length)] <- min(iris$Petal.Length) - IQR(iris$Petal.Length)</pre>
iris$Petal.Length[which.max(iris$Petal.Length)] <- max(iris$Petal.Length) + IQR(iris$Petal.Length)</pre>
intervals <- c(min(iris$Petal.Length), 2, 5, max(iris$Petal.Length))</pre>
for (method in c("interval", "frequency", "cluster", "fixed")) {
  petal.length.discretized <- if (method != "fixed")</pre>
    discretize(iris$Petal.Length, method=method) else
    discretize(iris$Petal.Length, method=method, breaks=intervals)
  print(ggplot(iris, aes(Petal.Length)) +
          geom_histogram() +
          geom_vline(xintercept=attributes(petal.length.discretized)$"discretized:breaks") +
          ggtitle(method))
  print(ggplot(iris, aes(Species, Petal.Length)) +
    geom_quasirandom(aes(col=Species)) +
    scale_color_manual(values=wes_palette("GrandBudapest1", 3)) +
    geom_hline(yintercept=attributes(petal.length.discretized)$"discretized:breaks") +
    ggtitle(method))
  discretized.table <- table(petal.length.discretized, iris$Species)</pre>
  matchClasses(discretized.table)
```



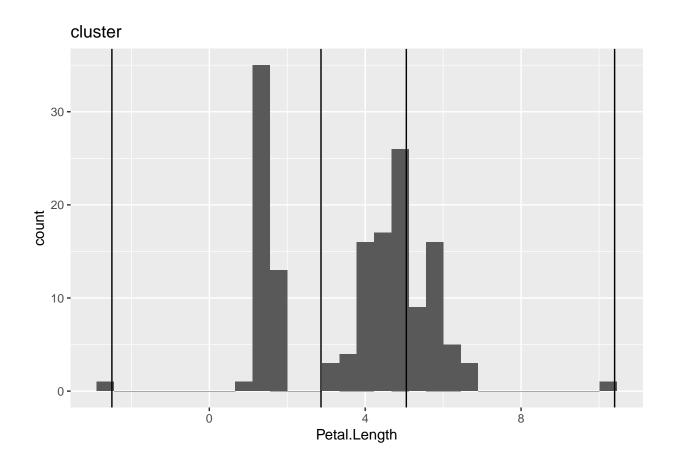


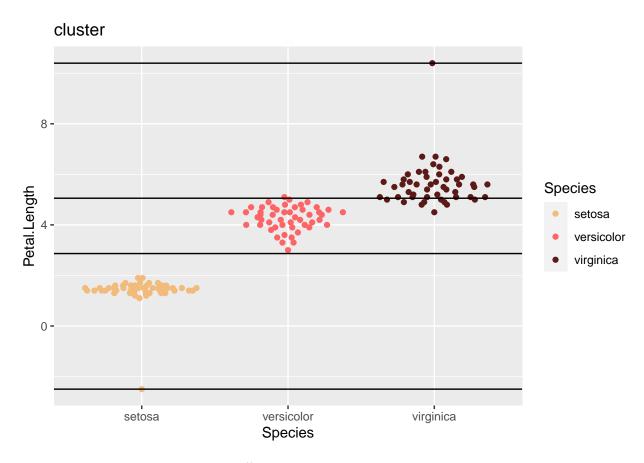
Cases in matched pairs: 71.33 %



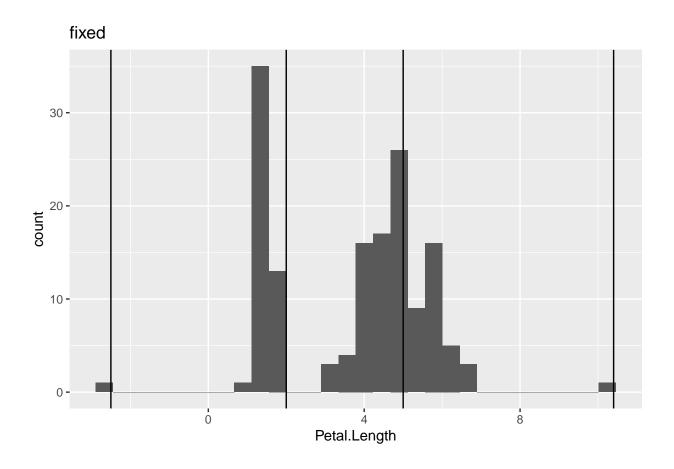


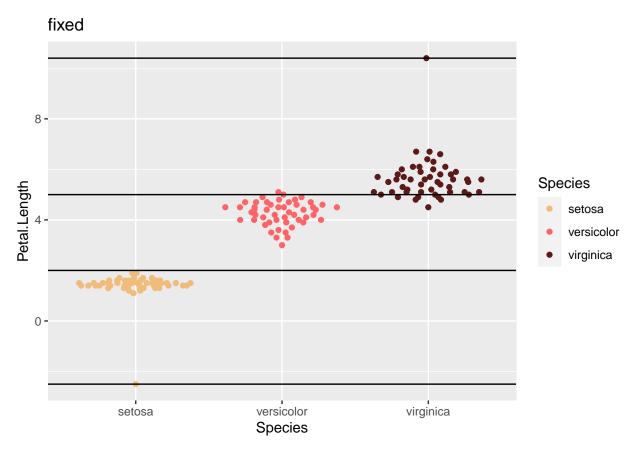
Cases in matched pairs: 95.33 %



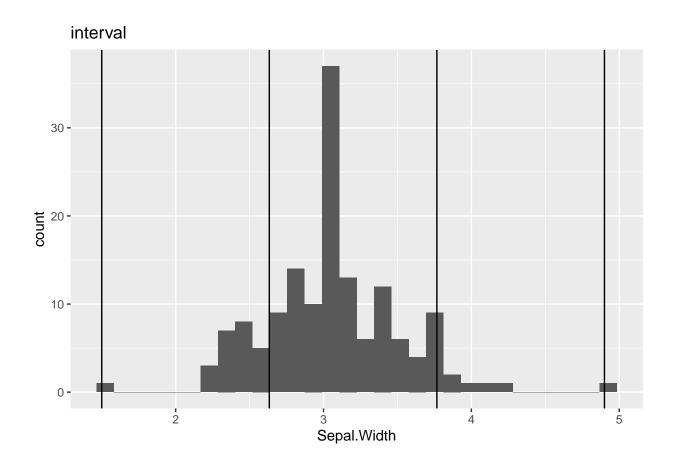


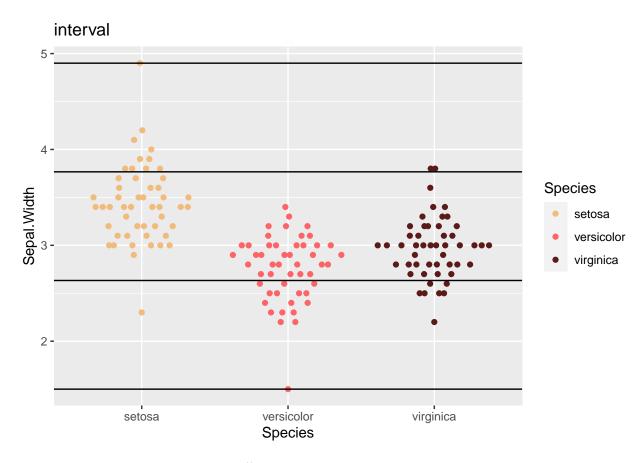
Cases in matched pairs: 93.33 %



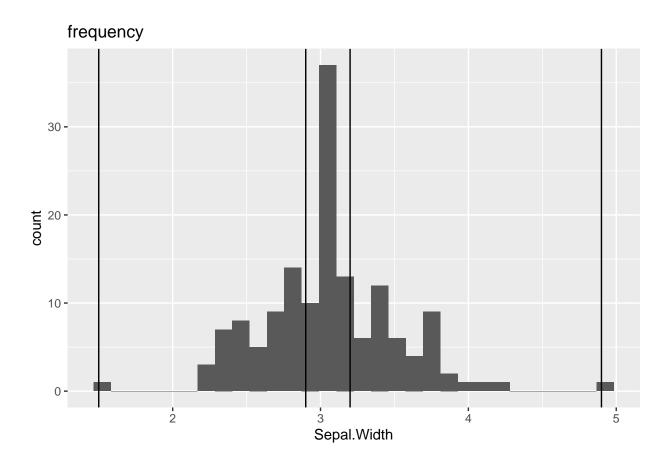


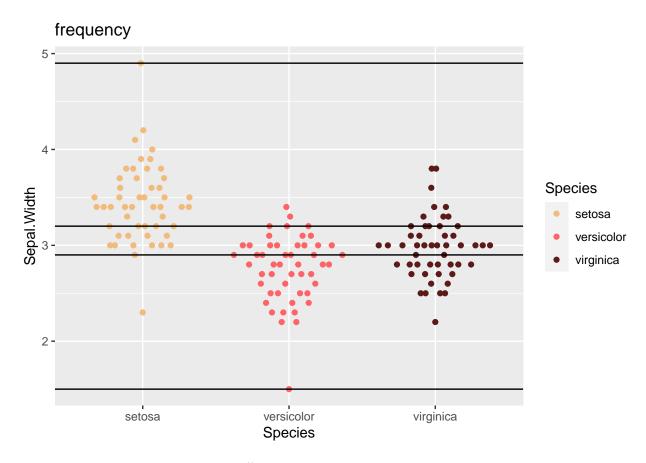
```
## Cases in matched pairs: 94.67 \%
iris$Sepal.Width[which.min(iris$Sepal.Width)] <- min(iris$Sepal.Width) - IQR(iris$Sepal.Width)</pre>
iris$Sepal.Width[which.max(iris$Sepal.Width)] <- max(iris$Sepal.Width) + IQR(iris$Sepal.Width)</pre>
intervals <- c(min(iris$Sepal.Width), 2.5, 3, max(iris$Sepal.Width))</pre>
for (method in c("interval", "frequency", "cluster", "fixed")) {
  sepal.width.discretized <- if (method != "fixed")</pre>
    discretize(iris$Sepal.Width, method=method) else
    discretize(iris$Sepal.Width, method=method, breaks=intervals)
  print(ggplot(iris, aes(Sepal.Width)) +
          geom_histogram() +
          geom_vline(xintercept=attributes(sepal.width.discretized)$"discretized:breaks") +
          ggtitle(method))
  print(ggplot(iris, aes(Species, Sepal.Width)) +
    geom_quasirandom(aes(col=Species)) +
    scale_color_manual(values=wes_palette("GrandBudapest1", 3)) +
    geom_hline(yintercept=attributes(sepal.width.discretized)$"discretized:breaks") +
    ggtitle(method))
  discretized.table <- table(sepal.width.discretized, iris$Species)</pre>
  matchClasses(discretized.table)
```



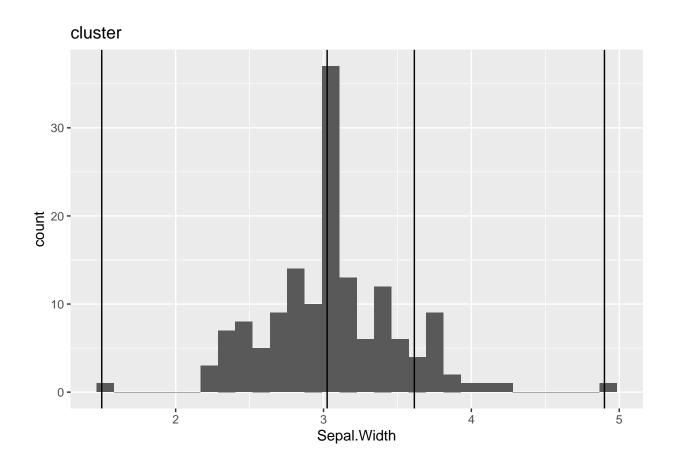


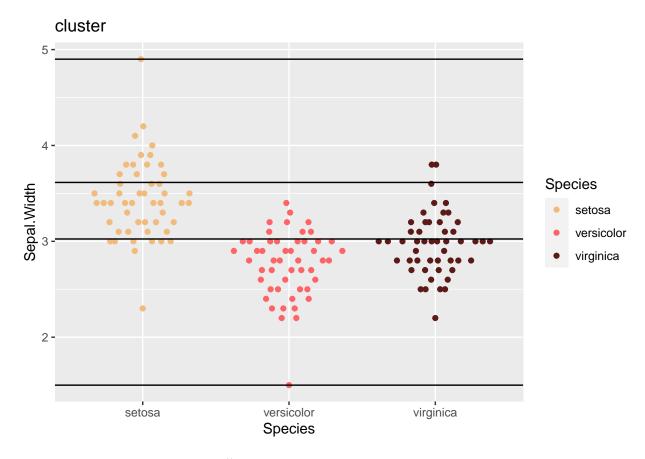
Cases in matched pairs: 44.67 %



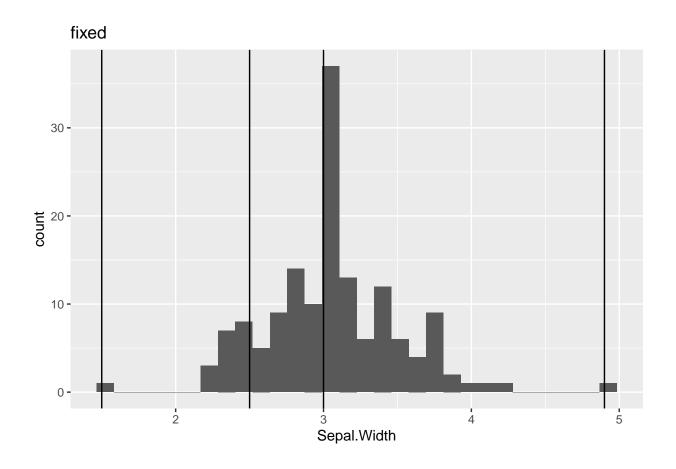


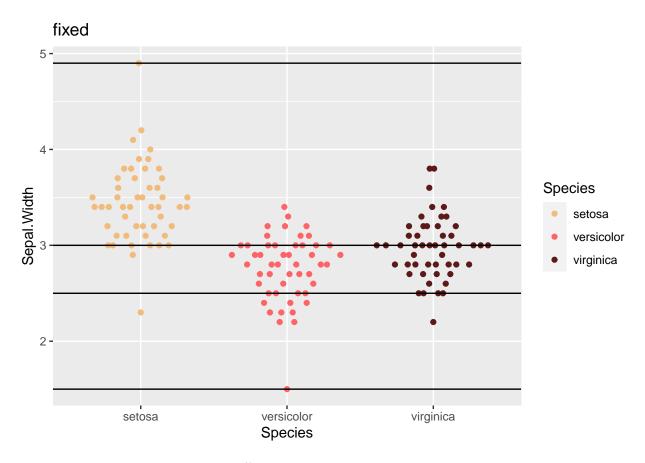
Cases in matched pairs: 55.33 %





Cases in matched pairs: 56 %

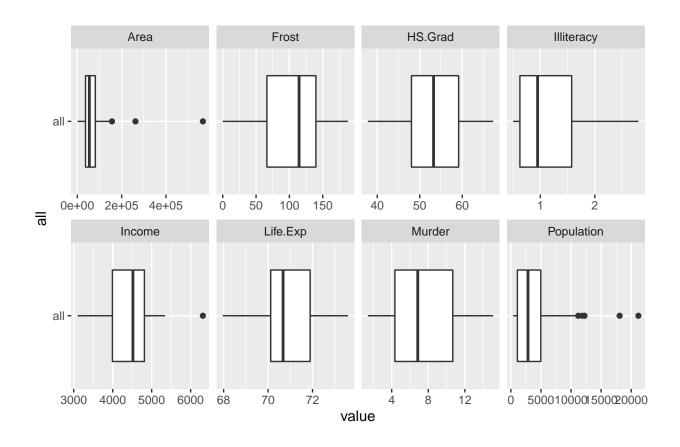




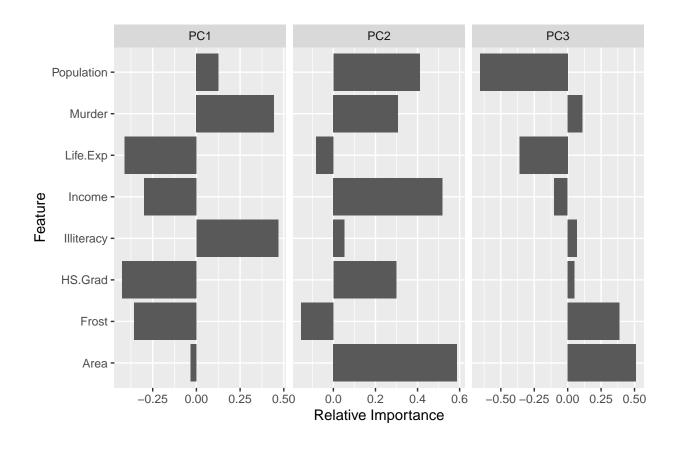
Cases in matched pairs: 54.67 %

ZADANIE 2.

```
data(state)
state <- as.data.frame(state.x77)
plot_boxplot(data.frame(state, all="all"), by="all")</pre>
```



```
sapply(state, function(X) c(sd=sd(X), cv=cv(X)))
                        Income Illiteracy Life Exp
##
       Population
                                                          Murder
                                                                   HS Grad
                                                                                 Frost
## sd 4464.491433 614.4699392 0.6095331 1.34239355 3.6915397 8.0769978 51.9808481
         1.051354
                     0.1385252 \quad 0.5209685 \ 0.01893934 \ 0.5003442 \ 0.1520863 \quad 0.4976149
##
             Area
## sd 85327.29962
## cv
          1.20628
p <- plot_prcomp(state, prcomp_args=list(scale=TRUE, center=TRUE), variance_cap=0.8)[2]</pre>
print(p)
```



p <- plot_prcomp(state, prcomp_args=list(scale=TRUE, center=TRUE), variance_cap=1)[1]
print(p)</pre>

% Variance Explained By Principal Components (Note: Labels indicate cumulative % explained variance)

