## Laboratorium 14 – Analiza i bazy danych

## Wprowadzenie do R-clustering.

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Programy realizujące zadania 1, 2 i 3 oraz ich wyniki.

```
library(magrittr)
      library(ggplot2)
     library(datasets)
     library(GGally)
     list_data <- c(1,2,3,4,5,6,7,8,9,10)
     list_data <- sqrt(sum(sin(log2(list_data))))</pre>
print (paste('Lista po wykonaniu odpowiednich obliczeń',list_data))
     data(iris)
     print(head(iris))
14 v agg <- iris %>%
          aggregate(. ~Species, .,mean)
     print(agg)
20 v a <- ggplot(iris, aes(x = Sepal.Width)) +
          geom_histogram(aes(fill=Species, color=Species), bins=20) +
          geom_vline(data=agg, aes(xintercept=Sepal.Width, color=Species), linetype="dashed") +
     labs(x='x_axis', y='y_axis', title='title')
     ggsave("/home/rplot.jpg", plot = a)
     a <- ggpairs(data = iris, aes(color = Species))</pre>
    ggsave("/home/rplot2.jpg", plot = a)
    x <- iris[, 1:4]
    y <- iris[,5]
    sum_sqr <-c()</pre>
        kmeans_result <- kmeans(x, i)</pre>
        sum_sqr <- append(sum_sqr, kmeans_result$tot.withinss)</pre>
    a <- ggplot(data.frame(iteration = 1:length(sum_sqr), value = sum_sqr), aes(x = iteration, y = sum_sqr)) +
    geom_line()
    ggsave("/home/rplot3.jpg", plot = a)
    kmeans_result <- kmeans(x, 3)</pre>
    a <- ggplot(iris, aes(x = Sepal.Width, y = Petal.Width, color= kmeans_result$cluster)) + geom_point()
    ggsave("/home/rplot4.jpg", plot = a)
46 a <- ggplot(iris, aes(x = Sepal.Width, y = Petal.Width, color = Species)) + geom_point()
47 ggsave("/home/rplot5.jpg", plot = a)
```









