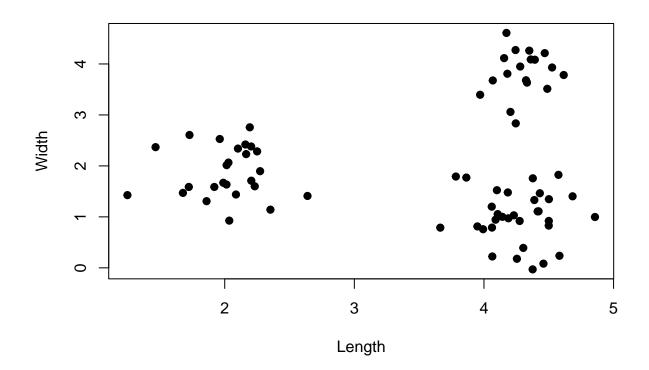
Exam: 2021/06/18

Marco Scarpelli

06 giugno, 2024

Dataset exploration

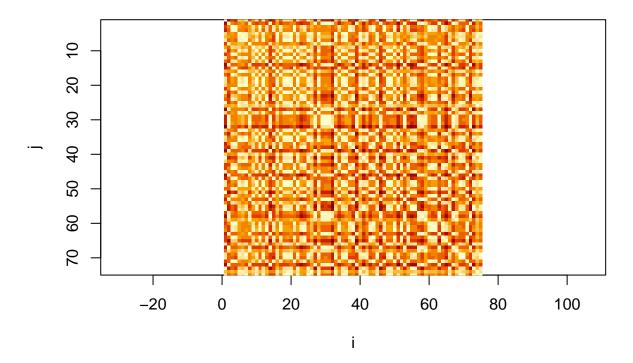
```
## Length Width
## Site_1 4.4590 0.0823
## Site_2 4.2797 3.9496
## Site_3 2.2500 2.2847
## Site_4 1.9620 2.5277
## Site_5 4.1843 1.4793
## Site_6 4.5748 1.8245
```



Point A

We report the dissimilarity matrix:

Dissimilarity matrix

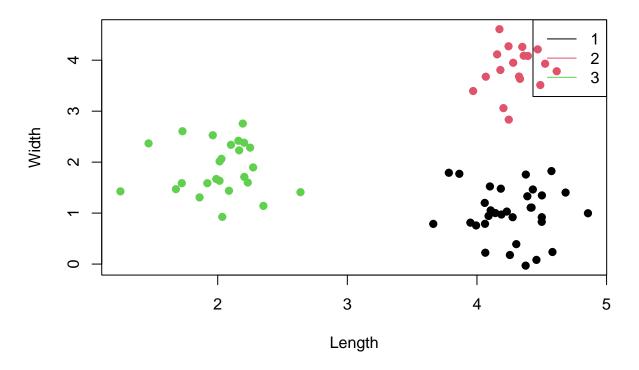


We run the clustering algorithm and provide the dendrogram. From it, it seems that the correct amount of clusters is 3, since there is a great height since the two-to-three split and the next one. We hence highlight the cut at three clusters:

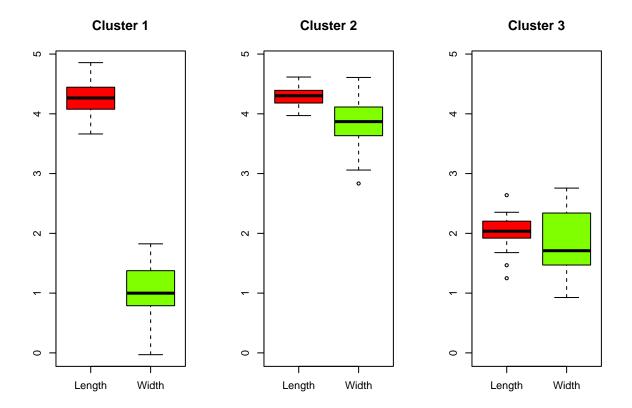
Dendrogram



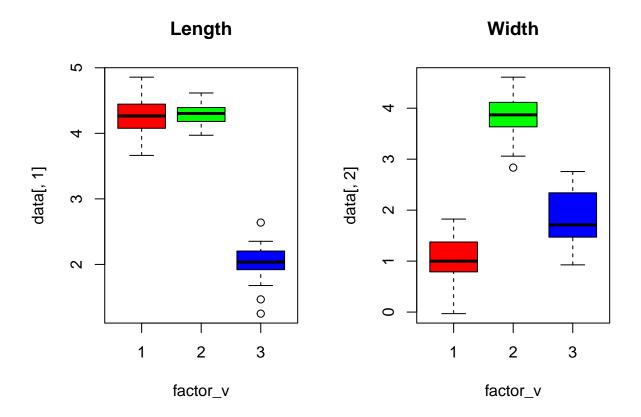
We report the resulting clustering:



And other plots, by cluster:



and feature:



Point B

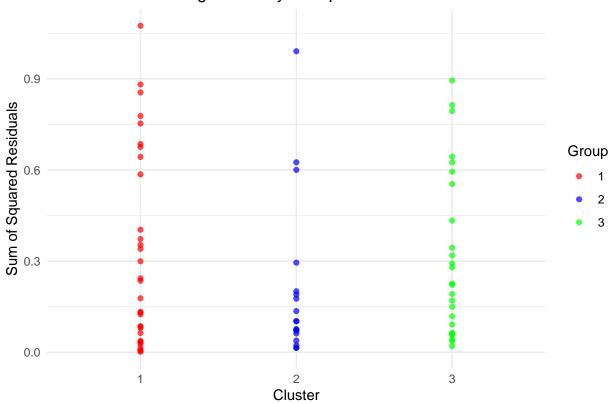
Let us check whether the three clusters have the same covariance structure; we will check the residuals after fitting the model. We will check the three covariance matrices and verify that no element on the diagonal is larger than 10 times (10 is specific for MANOVA, usually it is 4) any other element on the diagonals:

```
##
                Length
                               Width
## Length 0.071160980 -0.008768262
## Width -0.008768262 0.258558836
##
              Length
                           Width
## Length 0.02705947 0.01211026
## Width 0.01211026 0.19607752
##
                Length
                               Width
## Length 0.0848463042 0.0009094381
## Width 0.0009094381 0.2500743862
The test has positive results; we may proceed.
##
             Df
                    Wilks approx F num Df den Df
                                                      Pr(>F)
## factor_v
              2 0.0083476
                             353.05
                                          4
                                               142 < 2.2e-16 ***
## Residuals 72
## ---
                   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Signif. codes:
```

The summary reports that the membership to a cluster does indeed have an effect on the mean features of a stone flake, as the p-value is practically 0.

Let us check whether the residuals are homoscedastic:





```
## Length Width
## Length 0.071160980 -0.008768262
## Width -0.008768262 0.258558836

## Length Width
## Length 0.02705947 0.01211026
## Width 0.01211026 0.19607752

## Length Width
## Length 0.0848463042 0.0009094381
## Width 0.0009094381 0.2500743862
```

The homoscedasticity does not seem to be respected too well.

Point C

```
## $`diff 1-2`
## inf12 sup12
## Length -0.2216299 0.1474938
## Width -3.1823644 -2.4733238
##
## $`diff 2-3`
## inf23 sup23
## Length 2.084059 2.471340
## Width 1.584009 2.327927
##
```

```
## $ diff 1-3 sup13
## Length 2.073422 2.4078408
## Width -1.193064 -0.5506875
```

Only the interval on length between the first and second clusters constains 0, which means that these two clusters could likely have the same mean. All other combinations of clusters have means that differ, some with more confidence than others.