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Section: [Numerical classification](#)

## Evaluation of classification results

### silhouette (library cluster)

Evaluates, if the sample has appropriate group membership. Samples with high  $s$  value are well clustered,  $s$  value around zero means that the sample is between two clusters, and negative  $s$  value means that the sample has been misclassified.

For example, we will use results of *beta flexible* numerical classification of `vltava.spe` data (see [agnes \(library cluster\)](#)):

```
## Example of silhouette function

## Following code is not necessary, if you already used examples above...
# library (cluster)
# dis <- vegdist (sqrt (vltava.spe), method = 'bray') # percentage cover
data are transformed by square root
# cluster.flexible <- agnes (x = dis, method = 'flexible', par.method =
0.625)
# cluster.flexible.hclust <- as.hclust (cluster.flexible)

cl <- cutree (cluster.flexible.hclust, k = 5)
si <- silhouette (cl, dis)
plot (si)

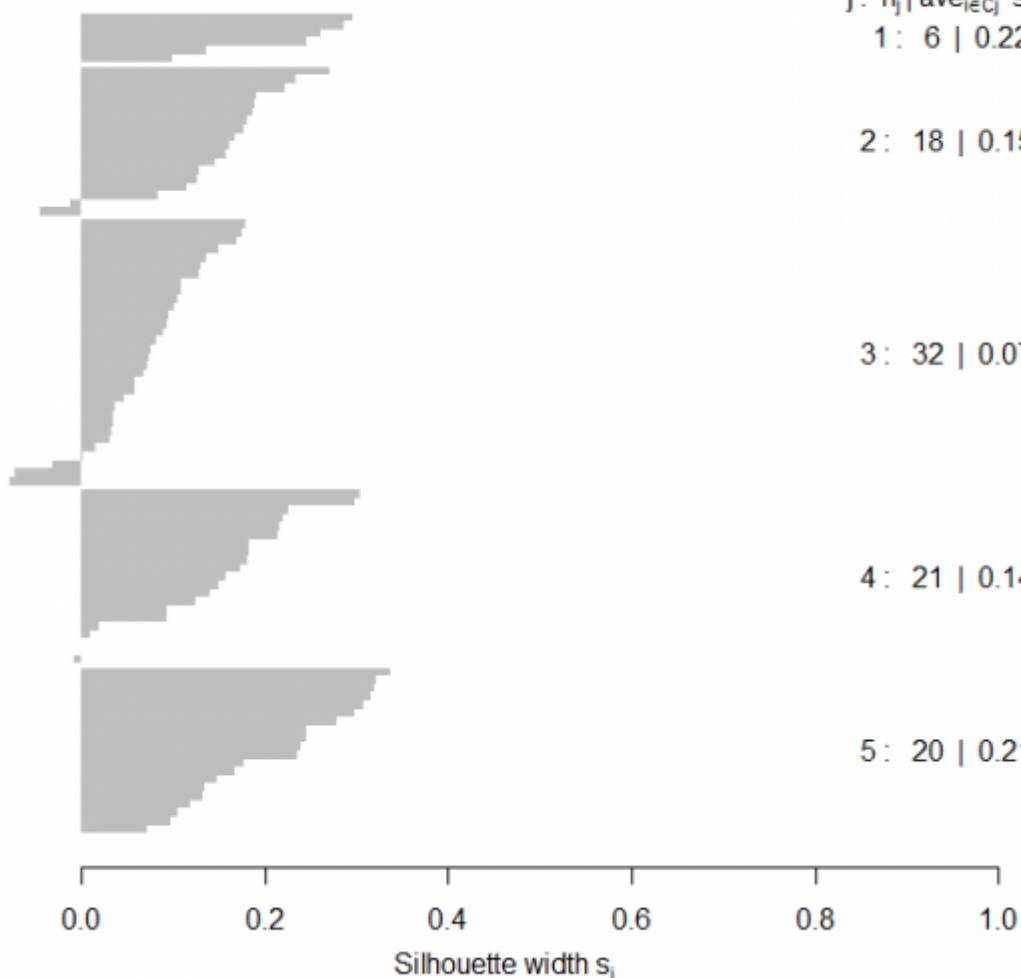
# Group 3 has the highest number of missclassified samples, on the other
hand groups 1, 2 and 5 are well defined.
```

### Silhouette plot of (x = cl, dist = dis)

n = 97

5 clusters  $C_j$

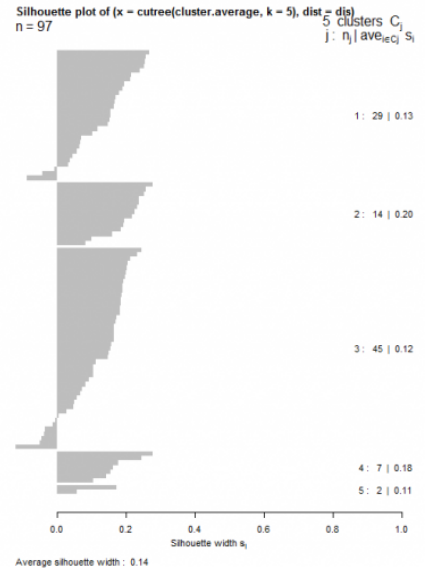
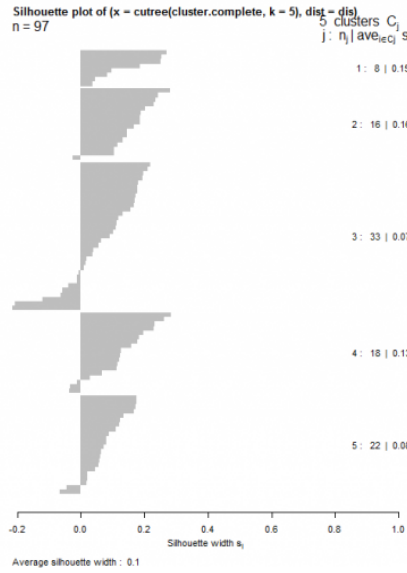
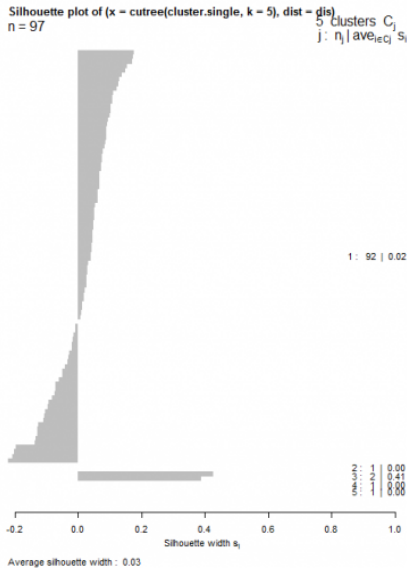
j	$n_j$	$\text{ave}_{i \in C_j} s_i$
1	6	0.22
2	18	0.15
3	32	0.07
4	21	0.14
5	20	0.21



Average silhouette width : 0.14

```
# Comparison of silhouettes for single linkage, complete average linkage
method.
# dis <- vegdist (sqrt (vltava.spe), method = 'bray') # percentage cover
data are transformed by square root
# cluster.single <- hclust (d = dis, method = 'single')
# cluster.complete <- hclust (dis, 'complete')
# cluster.average <- hclust (dis, 'average')

par (mfrow = c(1,3))
plot (silhouette (cutree (cluster.single, k = 5), dis))
plot (silhouette (cutree (cluster.complete, k = 5), dis))
plot (silhouette (cutree (cluster.average, k = 5), dis))
```



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