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Cross-sectional Analysis 3 Clustering Methods

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- In case of clustering the data contain no output variable and we want to find a group structure in the data, such that the observations in the groups are rather homogeneous with respect to the variables
- Data N observations in p variables

Variables:
$$\vec{X} = (X_1, X_2, ..., X_p)$$

Observations:
$$\vec{x} = (x_1, x_2, ..., x_p)$$

- Main prerequisite for clustering is a distance between observations
- Most important distance for quantitative variables is the Euclidean distance:

$$d^{2}(\vec{x}, \vec{z}) = \sum_{i=1}^{p} (x_{i} - z_{i})^{2}$$

Alternatives:

- Absolute deviation
$$d_1(\vec{x}, \vec{z}) = \sum_{i=1}^{p} |x_i - z_i|$$

- Maximum distance:
$$d_s(\vec{x}, \vec{z}) = \max_p |x_i - z_i|$$

- In case of binary variables the Hamming distance is frequently used, which is defined by the number of different values in the variables
 - The Hamming distance is equivalent to the Euclidean distance

- Another measure frequently used is the Cosine similarity defined by the angle between two vectors
 - The cosine defines a similarity of two vectors; if the have the same direction, the similarity is 1, if the vectors are orthogonal the similarity is 0, if the vectors have opposite direction the similarity is -1
 - Cosine similarity is frequently used if the vectors are binary vectors

- In case qualitative variables on can reduce the problem to a problem for binary variables by defining indicator variables for each attribute value
 - -q different values lead to $ln_2(q)$ binary variables
- Combination of qualitative and quantitative variables: procedure daisy in R

- For more complex structures like string variables (text) or graphs the distance calculation can be based on kernels
 - String kernels: based on counting the simultaneous occurrence of substrings of certain length

- An important issue is many times standardization of the variables
 - All variables are standardized with zero and variance 1
 - All variables are standardized such that the values are in the interval [0, 1], or [-1, 1]

- Main goals in clustering:
 - Find homogeneous groups, i.e., variability of observation within groups is explanation of observation, distance between groups measures separation of groups
- Main analysis tasks
 - Determine the number of clusters
 - Assign observations to clusters
 - Find representative objects in the groups (vector quantization)

- Evaluation of clusters
 - Homogeneity measures for groups
 - Validation with a test sample
 - Validity of the solution with respect to a subject matter explanation
- Types of cluster algorithms
 - Hierarchical methods
 - Partitioning Methods
 - Combination of the methods
 - Model based clustering

- Most frequently used is agglomerative clustering
- Basic outline of an agglomerative cluster algorithm:

Algorithm 4: Agglomerative clustering

```
1 Define clusters C_k, 1 \le k \le N by the observations, N_{cl} = N;

2 for k = 1 to N - 1 do

3 Merge clusters C_r and C_s for which d(C_r, C_s) = \min_{(l,k)} D((C_l, C_k));

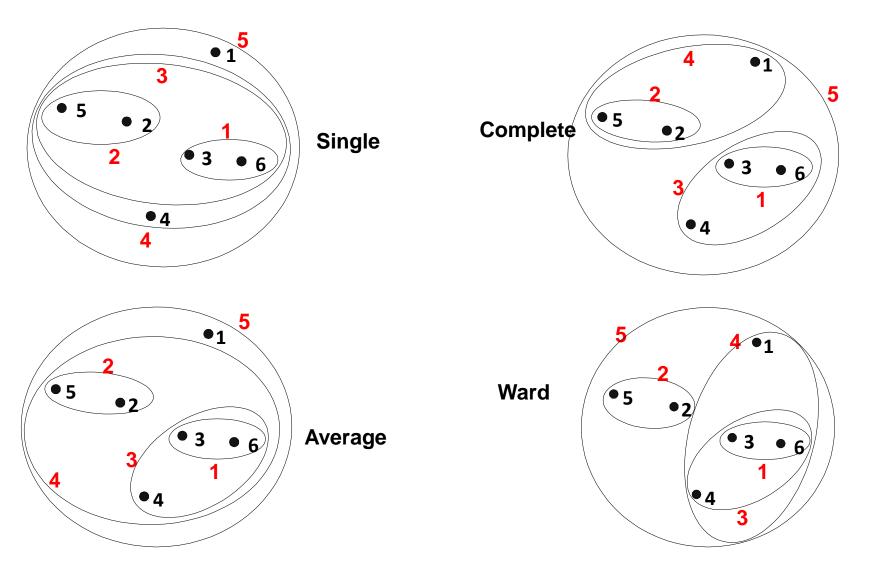
4 N_{cl} = N_{cl} - 1;

5 end
```

- Main problem is the definition of the distance between the clusters based on the distance between the objects, and determination of number of clusters
- The distance is called the linkage of the clusters
- Different specifications are possible
 - Single linkage: Distance between clusters is the distance of the closest points (minimum spanning tree)
 - Complete linkage: Distance between clusters is the distance of the farthest points

- Average linkage: mean distance between all the point sin the two clusters
- Ward distance: difference between the total within cluster sum of squares for the two clusters separately, and the within cluster sum of squares resulting from merging the two clusters in cluster
- In general average linkage and Ward's method are recommended
- Single linkage is not useful in most cases because the clusters are forming chains

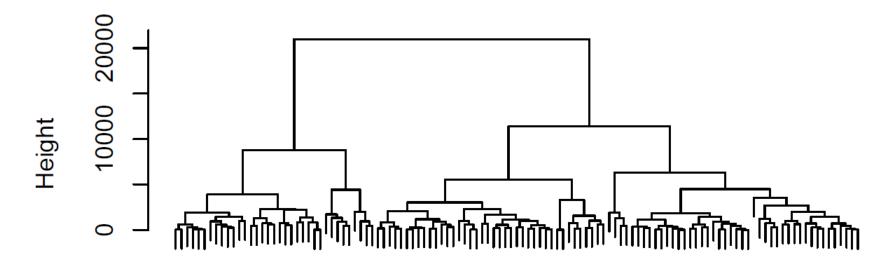
Hierarchical Clustering, Comparison of Linkages



- Determination of the number of clusters is done by visual inspection of the distance of the clusters which are merged
- Most popular method is using the dendrogram
 - A dendrogram is a visual representation of the aggregation process as a tree
 - The leaves of the tree are defined by the objects
 - Other nodes are formed according to the aggregation process
 - The heights of branches is given by the distance

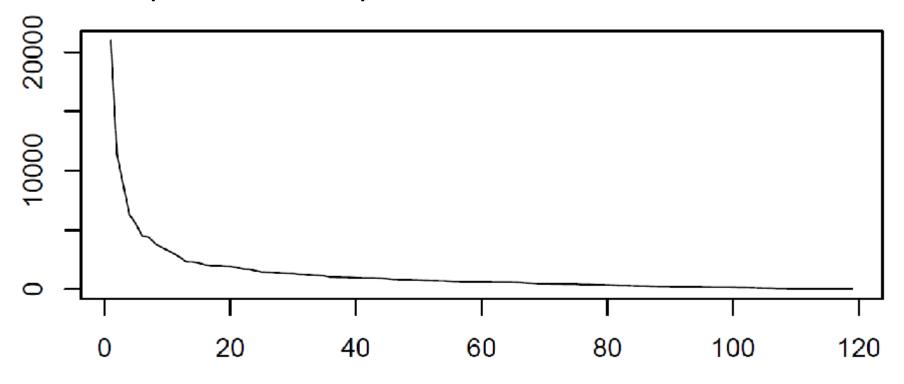
Example of a dendrogram

Dendrogramm, complete linkage



- An alternative to the dendrogram is a scree plot of the distance between the merged classes in dependence of the number of classes
- The decision about the number of classes is defined by the elbow of the scree plot

Example of a scree plot

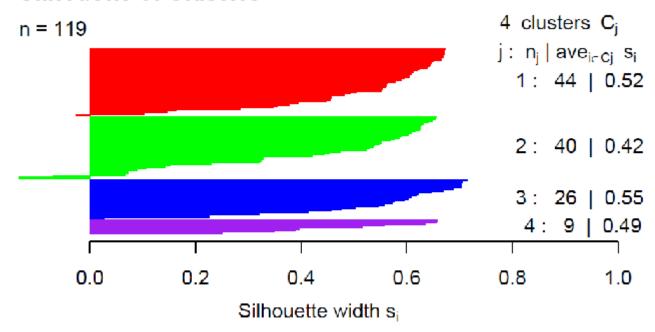


Number of Classes

- A method for evaluation of the cluster solution is the silhouette plot
 - The silhouette shows for each point how well the point is located in the cluster
 - A value close to 1 shows that the point is well located in the cluster
 - A negative value indicates that the point is not well assigned
- The silhouette can be used also for comparing different cluster solutions

Example of a silhouette

Silhouette of Clusters



Average silhouette width: 0.49

- Properties of Hierarchical clustering
 - Good visualization of the solution
 - Decision about the numbers of clusters can be done after analysis
 - Limited to small number of observations
 - The decision about the cluster assignment cannot be changed in the algorithm

- Partitioning methods define in an iterative way a cluster solution for the observations given the number of clusters in advance
- The most popular method is k-means clustering, where k stands for the number of clusters

Basic algorithm

Algorithm 5: k-Means Algorithm

Data: Observation matrix \mathbf{X} and distance for the objects; number of clusters K.

Result: Cluster solution for observations

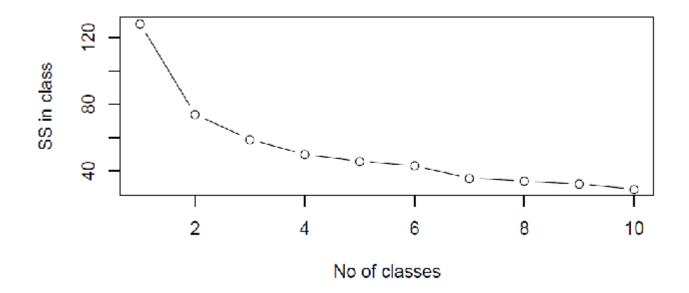
1 begin

- Define an initial solution for the cluster centers (c_1, c_2, \dots, c_k) ;
- 3 Assign each observation x to the cluster which center is closest to the observation;
- 4 Compute new centers for the clusters as means of the assigned observations;
- 5 Repeat steps 2 and 3 as long as there is no significant change in the centers;

6 end

- Main points in application
 - Decision about the number of clusters
 - Finding initial centers of the clusters
- Determination of the number of clusters can be based on a visualization of the sum of squares within the clusters for a solution in dependence of the number of clusters
 - This is similar to the idea of variance decomposition in case of analysis of variance

 Usually the plot shows a shape similar to a scree plot and the decision is based on the elbow criterion



- With respect to the initial solution the standard procedure is choosing the centers randomly and try different solutions
- Properties of k-means clustering
 - Procedure is fast from computational point of view
 - Applicable for large data sets (parallel implementations exist)
 - A found solution can be applied to new observations (cf. nearest neighbor classification)

Other Methods

- There exist numerous clustering algorithms for specific problems
 - Self organizing maps (SOM) are clustering methods based on the idea of a neural net. They can be understood as a kmeans clustering defined on a distorted grid
 - Two stage clustering combine the ideas of hierarchical clustering with the ideas of k-means (IBM/SPSS) by using a cluster-feature tree
 - Model based clustering looks at the problem from a more theoretical perspective and defines a model for the data by a mixture of normal distributions