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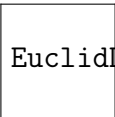
1 Review of Last Class

- Cluster analysis is a convenient method for identifying homogenous groups of objects called clusters. Objects (or cases, observations) in a specific cluster share many characteristics, but are very dissimilar to objects not belonging to that cluster.
- There are three cluster analysis approaches: hierarchical methods, partitioning methods (more precisely, *k*-means), and two-step clustering, which is largely a combination of the first two methods. In the last class we looked at hierarchical clustering analysis.
- Each of these procedures follows a different approach to grouping the most similar objects into a cluster and to determining each object's cluster membership.
- Some approaches – most notably hierarchical methods – require us to specify how similar or different objects are in order to identify different clusters. Most software packages, such as SPSS, calculate a measure of (dis)similarity by estimating the distance between pairs of objects. Objects with smaller distances between one another are more similar, whereas objects with larger distances are more dissimilar.
- An important problem in the application of cluster analysis is the decision regarding how many clusters should be derived from the data. This question is explored in the next step of the analysis. Sometimes, however, number of segments that have to be derived from the data will be known in advance.
- By choosing a specific clustering procedure, we determine how clusters are to be formed. (This always involves optimizing some kind of criterion, such as minimizing the within-cluster variance (i.e., the clustering variable's overall variance of objects in a specific cluster), or maximizing the distance between the objects or clusters). The procedure could also address the question of how to determine the (dis)similarity between objects in a newly formed cluster and the remaining objects in the dataset.
- Hierarchical clustering procedures are characterized by the tree-like structure established in the course of the analysis. Most hierarchical techniques fall into a category called agglomerative clustering. In this category, clusters are consecutively formed from objects. Initially, this type of procedure starts with each object representing an individual cluster. These clusters are then sequentially merged according to their similarity. First, the two most similar clusters (i.e., those with the smallest distance between them) are merged to form a new cluster at the bottom of the hierarchy. In the next step, another pair of clusters is merged and linked to a higher level of the hierarchy, and so on. This allows a hierarchy of clusters to be established from the bottom up.
- A cluster hierarchy can also be generated top-down. In this divisive clustering, all objects are initially merged into a single cluster, which is then gradually split up. Divisive procedures are quite rarely used in practice. We therefore concentrate on the agglomerative clustering procedures.
- This means that if an object is assigned to a certain cluster, there is no possibility of reassigning this object to another cluster. This is an important distinction between these types of clustering and partitioning methods such as *k*-means.

- There are various measures to express (dis)similarity between pairs of objects. A straightforward way to assess two objects proximity is by drawing a straight line between them. This type of distance is also referred to as ***Euclidean distance*** (or straight-line distance) and is the most commonly used type when it comes to analyzing ratio or interval-scaled data.


 EuclidDistance1.jpg

The Euclidean distance is the square root of the sum of the squared differences in the variables values. Suppose B and C were positioned as (7, 6) and (6, 5) respectively.

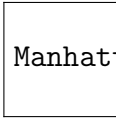

 EuclidDistance2.jpg

This distance corresponds to the length of the line that connects objects B and C. In this case, we only used two variables but we can easily add more under the root sign in the formula. However, each additional variable will add a dimension to our research problem (e.g., with ten clustering variables, we have to deal with ten dimensions), making it impossible to represent the solution graphically.

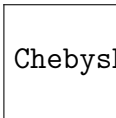
- The ***Squared Euclidean distance*** uses the same equation as the Euclidean distance metric, but does not take the square root. In the previous example, the squared Euclidean distance between B and C is 2. As a result, clustering with the Squared Euclidean distance is computationally faster than clustering with the regular Euclidean distance.
- We can compute the distance between all other pairs of objects. All these distances are usually expressed by means of a ***distance matrix***. In this distance matrix, the non-diagonal elements express the distances between pairs of objects and zeros on the diagonal (the distance from each object to itself is, of course, 0). In our example, the distance matrix is an 8×8 table with the lines and rows representing the objects under consideration.


 DistanceMatrix.jpg

- There are also alternative distance measures: The ***Manhattan distance*** or city-block distance uses the sum of the variables absolute differences. This is often called the Manhattan metric as it is akin to the walking distance between two points in a city like New Yorks Manhattan district, where the distance equals the number of blocks in the directions North-South and East-West. Using the points B and C that we used previously, the manhattan distance is computed as follows:


 Manhattan.jpg

- When working with metric (or ordinal) data, researchers frequently use the ***Chebyshev distance***, which is the maximum of the absolute difference in the clustering variables values. For B and C, this result is:

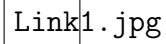

 Chebyshev.jpg

- There are other distance measures such as the Angular, Canberra or Mahalanobis distance. In many situations, the ***Mahalanobis distance*** is desirable as this measure compensates for ***multi-collinearity*** between the clustering variables. However, it is unfortunately not menu-accessible in SPSS.
- In statistics, the occurrence of several variables in a multiple regression model are ***closely correlated*** to one another, and carrying the same information, more or less. Multi-collinearity can cause strange results when attempting to study how well individual independent variables contribute to an understanding of the dependent variable, often undermining the analysis.
- In many analysis tasks, the variables under consideration are measured on different scales or levels. This would clearly distort any clustering analysis results. We can resolve this problem by ***standardizing*** the data prior to the analysis.
- Different standardization methods are available, such as the simple ***z standardization***, which re-scales each variable to have a mean of 0 and a standard deviation of 1.
- In most situations, however, ***standardization by range***(e.g., to a range of 0 to 1 or -1 to 1) is preferable. We recommend standardizing the data in general, even though this procedure can potentially reduce or inflate the variables influence on the clustering solution.
- A commonly used approach in hierarchical clustering is ***Wards linkage method***. This approach does not combine the two most similar objects successively. Instead, those objects whose merger increases the overall within-cluster variance to the smallest possible degree, are combined. If you expect somewhat equally sized clusters and the data set does not include outliers, you should always use Wards method.

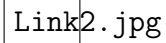
We will use the Ward's linkage method for laboratory exercises.

- Other most popular agglomerative clustering procedures include the following:

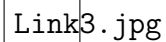
Single linkage (nearest neighbor) : The distance between two clusters corresponds to the shortest distance between any two members in the two clusters.

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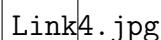
Complete linkage (furthest neighbor) : The oppositional approach to single linkage assumes that the distance between two clusters is based on the longest distance between any two members in the two clusters.

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Average linkage : The distance between two clusters is defined as the average distance between all pairs of the two clusters members.

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Centroid : In this approach, the geometric center (centroid) of each cluster is computed first. The distance between the two clusters equals the distance between the two centroids.

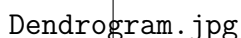
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Each of these linkage algorithms can yield totally different results when used on the same data set, as each has its specific properties. As the single linkage algorithm is based on minimum distances, it tends to form one large cluster with the other clusters containing only one or few objects each. We can make use of this *chaining effect* to detect outliers, as these will be merged with the remaining objects usually at very large distances in the last steps of the analysis. Generally, single linkage is considered the most versatile algorithm.

Conversely, the complete linkage method is strongly affected by outliers, as it is based on maximum distances. Clusters produced by this method are likely to be rather compact and tightly clustered. The average linkage and centroid algorithms tend to produce clusters with rather low within-cluster variance and similar sizes. However, both procedures are affected by outliers, though not as much as complete linkage.

An understanding of linkage method's other than than Ward method will be expected in the end of year examination.

- A common way to visualize the cluster analysis progress is by drawing a dendrogram, which displays the distance level at which there was a combination of objects and clusters. Here is an example of a dendrogram (which corresponds to the example in the next section of material).

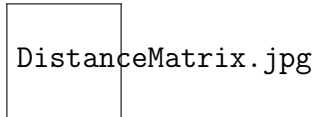
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- An important question is how to decide on the number of clusters to retain from the data. Unfortunately, hierarchical methods provide only very limited guidance for making this decision. The only meaningful indicator relates to the distances at which the objects are combined. Similar to factor analysis scree plot, we can seek a solution in which an additional combination of clusters or objects would occur at a greatly increased distance. This raises the issue of what a great distance is, of course. For this purpose, we can make use of the dendrogram.
- In constructing the dendrogram, SPSS rescales the distances to a range of 025; that is, the last merging step to a one-cluster solution takes place at a (rescaled) distance of 25. The rescaling often lengthens the merging steps, thus making breaks occurring at a greatly increased distance level more obvious. Despite this, this distance-based decision rule does not work very well in all cases.

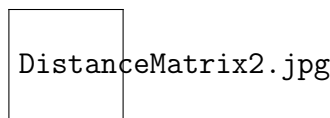
It is often difficult to identify where the break actually occurs. This is also the case in our example above. By looking at the dendrogram, we could justify a two-cluster solution ($[A,B,C,D,E,F]$ and $[G]$), as well as a five-cluster solution ($[B,C,E]$, $[A]$, $[D]$, $[F]$, $[G]$).

2 Clustering Algorithm

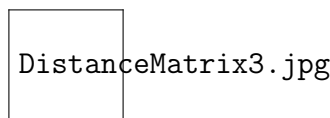
To better understand how a clustering algorithm works, let's manually examine some of the single linkage procedure calculation steps. We start off by looking at the initial (Euclidean) distance matrix displayed previously.



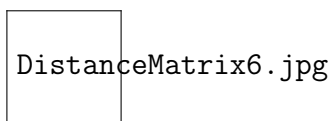
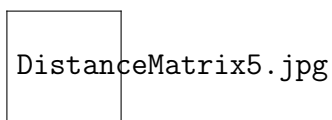
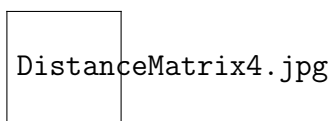
- In the very first step, the two objects exhibiting the smallest distance in the matrix are merged. Note that we always merge those objects with the smallest distance, regardless of the clustering procedure (e.g., single or complete linkage). (N.B. In the following example, ties will be broken at random.)
- As we can see, this happens to two pairs of objects, namely B and C ($d(B, C) = 1.414$), as well as C and E ($d(C, E) = 1.414$). In the next step, we will see that it does not make any difference whether we first merge the one or the other, so let's proceed by forming a new cluster, using objects B and C.



- Having made this decision, we then form a new distance matrix by considering the single linkage decision rule as discussed above. According to this rule, the distance from, for example, object A to the newly formed cluster is the minimum of $d(A, B)$ and $d(A, C)$. As $d(A, C)$ is smaller than $d(A, B)$, the distance from A to the newly formed cluster is equal to $d(A, C)$; that is, 2.236.
- We also compute the distances from cluster [B,C] (clusters are indicated by means of squared brackets) to all other objects (i.e. D, E, F, G) and simply copy the remaining distances such as $d(E, F)$ that the previous clustering has not affected.



- Continuing the clustering procedure, we simply repeat the last step by merging the objects in the new distance matrix that exhibit the smallest distance (in this case, the newly formed cluster [B, C] and object E) and calculate the distance from this cluster to all other objects.



- We continue in the same fashion until one cluster is left. By following the single linkage procedure, the last steps involve the merger of cluster [A,B,C,D,E,F] and object G at a distance of 3.162.

3 K-Means Clustering

- Hierarchical clustering requires a distance or similarity matrix between all pairs of cases. That's an extremely large matrix if you have tens of thousands of cases in your data file.
- A clustering method that doesn't require computation of all possible distances is k-means clustering. It differs from hierarchical clustering in several ways. You have to know in advance the number of clusters you want. You can't get solutions for a range of cluster numbers unless you rerun the analysis for each different number of clusters.
- The algorithm repeatedly reassigns cases to clusters, so the same case can move from cluster to cluster during the analysis. In agglomerative hierarchical clustering, on the other hand, cases are added only to existing clusters. They are forever captive in their cluster, with a widening circle of "neighbours".
- The algorithm is called **k-means**, where **k** is the number of clusters you want, since a case is assigned to the cluster for which its distance to the cluster mean is the smallest.
- The k-means algorithm follows an entirely different concept than the hierarchical methods discussed before. This algorithm is not based on distance measures such as Euclidean distance or city-block distance, but uses the ***within-cluster variation*** as a measure to form homogenous clusters. Specifically, the procedure aims at segmenting the data in such away that the within-cluster variation is minimized. Consequently, we do not need to decide on a distance measure in the first step of the analysis.
- The action in the algorithm centers around finding the k-means. You start out with an initial set of means and classify cases based on their distances to the centers.
- Next, you compute the cluster means again, using the cases that are assigned to the cluster; then, you reclassify all cases based on the new set of means. You keep repeating this step until cluster means don't change much between successive steps.
- Finally, you calculate the means of the clusters once again and assign the cases to their permanent clusters.

3.1 Initial Cluster Centres

The first step in k-means clustering is finding the k centres. This is done iteratively. You start with an initial set of centres and then modify them until the change between two iterations is small enough.

If you have good guesses for the centres, you can use those as initial starting points; otherwise, you can let SPSS find k cases that are well separated and use these values as initial cluster centers. (i.e. The clustering process starts by randomly assigning objects to a number of clusters).

K-means clustering is very sensitive to outliers, since they will usually be selected as initial cluster centers. This will result in outliers forming clusters with small numbers of cases. Before you start a cluster analysis, screen the data for outliers and remove them from the initial analysis. The solution may also depend on the order of the cases in the data.


After the initial cluster centers have been selected, each case is assigned to the closest cluster, based on its distance from the cluster centers. After all of the cases have been assigned to clusters, the cluster centers are recomputed, based on all of the cases in the cluster.

The cases are then successively reassigned to other clusters to minimize the within-cluster variation, which is basically the (squared) distance from each observation to the center of the associated cluster. If the reallocation of an case to another cluster decreases the within-cluster variation, this case is reassigned to that cluster.


Case assignment is done again, using these updated cluster centers. You keep assigning cases and recomputing the cluster centers until no cluster center changes appreciably or the maximum number of iterations (10 by default) is reached.

3.2 Demonstration of k-means

In this example, two cluster centers are randomly initiated, which CC1 (first cluster) and CC2 (second cluster). Euclidean distances are computed from the cluster centers to every single




kmeans1.jpg




kmeans2.jpg

object. Each object is then assigned to the cluster center with the shortest distance to it.

In this example, objects A, B, and C are assigned to the first cluster, whereas objects D, E, F, and G are assigned to the second. We now have our initial partitioning of the objects into two clusters. Based on this initial partition, each clusters geometric center (i.e., its centroid) is computed (third step). This is done by computing the mean values of the objects contained in the cluster (e.g., A, B, C in the first cluster) regarding each of the variables (in this example: price consciousness and brand loyalty). Both clusterscenters now shift into new positions (CC1



kmeans3.jpg



kmeans4.jpg

for the first and CC2 for the second cluster). In the fourth step, the distances from each object to the newly located cluster centers are computed and objects are again assigned to a certain cluster on the basis of their minimum distance to other cluster centers (CC1 and CC2).

Since the cluster centers position changed with respect to the initial situation in the first step, this could lead to a different cluster solution. This is also true of our example, as object E is now unlike in the initial partition closer to the first cluster center (CC1) than to the second (CC2). Consequently, this object is now assigned to the first cluster. The k-means procedure now repeats the third step and re-computes the cluster centers of the newly formed clusters, and so on. In other words, steps 3 and 4 are repeated until a predetermined number of iterations are reached, or convergence is achieved (i.e., there is no change in the cluster affiliations).

3.3 Performance of k-means clustering

Generally, k-means is superior to hierarchical methods as it is less affected by outliers and the presence of irrelevant clustering variables. Furthermore, k-means can be applied to very large data sets, as the procedure is less computationally demanding than hierarchical methods. In fact, we suggest definitely using k-means for sample sizes above 500, especially if many clustering

variables are used. From a strictly statistical viewpoint, k-means should only be used on interval or ratio-scaled data as the procedure relies on Euclidean distances. However, the procedure is routinely used on ordinal data as well, even though there might be some distortions.

One problem associated with the application of k-means relates to the fact that the researcher has to pre-specify the number of clusters to retain from the data. This makes k-means less attractive to some and still hinders its routine application in practice.