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Classification and Clustering: Models, Software and Applications

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Foreword and Acknowledgments

We are pleased to present the report on the 30th Fall Meeting of the working group “Data Analysis and Numerical Classification” (AG–DANK) of the German Classification Society. The meeting took place at the Weierstrass Institute for Applied Analysis and Stochastics (WIAS), Berlin, from Friday Nov. 14 till Saturday Nov. 15, 2008. Already 12 years ago, WIAS had hosted a traditional Fall Meeting with special focus on classification and multivariate graphics (Mucha and Bock, 1996). This time, the special topics were stability of clustering and classification, mixture decomposition, visualization, and statistical software.

The working group AG–DANK of the German Classification Society (“Gesellschaft für Klassifikation,” GfKl) deals with all statistical, mathematical, and computational aspects of data analysis and classification problems (clustering, discriminant analysis, supervised/unsupervised classification, pattern recognition, data mining) and with their applications in the sciences, the economy, engineering, archaeometry, and the administration. The GfKl, founded in the year 1977, is a transdisciplinary scientific society that aims at promoting methods of classification and data analysis in theory and application.

The editors and the working group AG–DANK would like to thank all who have contributed to this report. Our special thanks go to the head of WIAS for their active support and thorough preparation of the event.

Gunter Ritter
Chair of AG-DANK

Hans-Joachim Mucha
Local organizer

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Preface

During the 30th Fall Meeting of the working group AG-DANK a dozen talks were presented. Among them, three discussion papers dealt with statistical analyses of special data sets issued in advance. All in all 16 participants contributed to the meeting with talks and discussions, see the Appendix (Part III below). Here follows the list of the talks and analyses.

Part I: Talks

- Peter Kurz, TNS Infratest, München: Stability of “clustering on clusters”- methods in the field of marketing
- Hans-Joachim Mucha, WIAS Berlin: ClusCorr98® for Excel 2007: Clustering, Multivariate Visualization, and Validation
- Gunter Ritter, Uni Passau: Resolving ambiguity in segmentation problems by the method of variants
- Hans-Georg Bartel, Humboldt-Universität zu Berlin: Archäometrische Daten römischer Ziegel aus *Germania Superior*
- Marcus Weber, ZIB Berlin: Spectral Clustering
- Susanna Röblitz, ZIB Berlin: Clustering of high-dimensional data by domain decomposition methods
- Christian Hennig, University College London: Merging Gaussian mixture components - an overview
- Florian Meyer, Uni Marburg: Interpretable models of leptokurtic distributions
- Anne Spickenheuer, BGFA an der Ruhr-Universität Bochum: Classification of workers with different exposure levels to fumes of bitumen

Part II: Data Analyses

- Roman Tiles Data Set
 - Gerhard Pöppel and Reinhard Schachtner, Infineon, Regensburg: Analysis I by Projection Pursuit
 - Gunter Ritter: Analysis II by Model Based Clustering
 - Susanna Röblitz and Marcus Weber: Analysis III by Spectral Clustering
 - Hans-Georg Bartel, Hans-Joachim Mucha and Jens Dolata: Comparison of Results for the the Tiles Data

- Synthetic Data Set 1
 - Gunter Ritter: Structure of the synthetic data set Berlin08_synth1
 - Gerhard Pöppel: Analysis A by MCLUST
 - Susanna Röblitz and Marcus Weber: Analysis B by Spectral Clustering
 - Gunter Ritter and Hans-Joachim Mucha: Comparison of Results
- Synthetic Data Set 2
 - Gunter Ritter: Structure of the synthetic data set Berlin08_synth2
 - Gerhard Pöppel and Reinhard Schachtner: Analysis by Projection Pursuit
 - Gunter Ritter and Hans-Joachim Mucha: Comparison of Results

The present publication does not cover all talks presented at the Fall Meeting, but only a selection of contributions. They are listed in the order of their presentation at WIAS.

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Part I

Papers of Talks

1 ClusCorr98[®] for Excel 2007: Clustering, Multivariate Visualization, and Validation

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Abstract

Really, in Excel 2007, you get much more because it now supports 1 048 576 rows and 16 384 columns. Such an Excel 2007 “Big Grid” spreadsheet is both the distinguished repository for data/distances and the perfect plotting board for multivariate graphics that can be composed in VBA-code (examples are dendograms, plot-dendograms, scatterplot matrices, density plots, principal components analysis plots,...), or can be obtained by “playing” with the properties of cells in cell-based graphics (pixel graphics) like the heat plot of a proximity matrix. Pairwise data clustering, and furthermore restricted in terms of the two simplest Gaussian model-based cluster analyses, will be considered in more detail here. That means, the usual estimation of expectation values of clusters is no more necessary. By using special randomized weights one can perform built-in validations of cluster analysis results by bootstrapping techniques [13].

Keywords: Cluster analysis, dimension reduction, statistical software, dendrogram, Excel, Visual Basic for Applications

Introduction

The Excel 2007 “Big Grid”: spreadsheets with 64 times more columns ($= 16\,536$) than before and about 1 million rows. Now a huge $I \times I$ proximity matrix can be stored directly in an Excel sheet for further usage (clustering, visualization,...). (Proximities are a general term for pairwise distances, similarities,...) Thus, the huge number of cells ($=$ “pixels” in cell-based graphics) is up to now often far beyond the technical limits of screens and printers. Therefore one has to navigate inside the big pictures to look for interesting areas.

Concerning cluster analysis, the main focus here is on simple Gaussian model-based methods that can be generalized by (adaptive) weighting of the variables and/or the observations. It should be noted that the simple models are essential with respect to the subsequent use of complex Gaussian models because of an appropriate initialization of parameters and partitions [19]. In the following, pairwise distances are the starting point for cluster analysis, but also for appropriate multivariate

graphics of data and clusters by applying methods of projection, such as principal components analysis and multidimensional scaling.

Another main focus is on validation. The proposed built-in validation techniques can verify the results of the two most important families of methods, the hierarchical and partitional cluster analysis. The finding of the appropriate number of clusters, as the main task of model selection, is the ultimate aim here. The built-in validation evaluates additionally the stability of each cluster and the degree of membership of each observation to its cluster.

This paper outlines the complete life cycle of cluster analysis starting from raw data up to ending with both the validated results and the multivariate graphics. Some of the most successful applications come from quite different fields such as archaeometry (see below in Sect. 3 and Sect. 7 in this report, [16], [17]), computational linguistics [18], ecology ([19], [21]), economics [13], chemometrics [15], and demography (see Fig. 18 below).

1.1 The Statistical Software ClusCorr98[®]

ClusCorr98[®] is based on the programming environment Visual Basic for Application (VBA) in the host application Excel. One does not forget about the “A”: sorting, removing duplicates, pivot tables, SQL for querying a database, working with ranges (= matrices, e.g. “ $\mathbf{X} = \text{selection.value}$ ” gets you a data matrix \mathbf{X} , and “ $\text{selection.value} = \mathbf{D}$ ” saves a distance matrix \mathbf{D})... would be much faster than any VB code or C++ code anyone could write. ClusCorr98[®] is much more than can be presented here, that is, this paper is designed as a kind of introduction only.

The statistical software performs exploratory data analysis mainly by using adaptive methods of cluster analysis, classification, and multivariate visualization. The main focus is on simple, stable models accompanied by appropriate multivariate (graphical) methods like principal components plots and informative dendrograms (binary trees). The “Big Grid” sheets are also a perfect plotting board for scatter-plot matrices whose support often has been of value for the search of an appropriate cluster analysis model. Cell-based graphic is another kind of visualization in spreadsheets. Examples are heat plots (see Fig. 3 below), colored dendrograms (Fig. 16), or informative dendrograms (Fig. 20) that show the results of validation of clusters.

The software ClusCorr98[®] comes in an Excel 2003 format. However it can make use of the “Big Grid” spreadsheets of Excel 2007 by the VBA programming language. Moreover, there are new or improved built-in graphic tools of Excel 2007 which can do a lot for you, for a better understanding of the data at hand.

Figure 1: From a data matrix \mathbf{X} to a distance matrix \mathbf{D} .

1.2 Pairwise Distances

Let us introduce into the problem of finding clusters (groups, subsets) of observations (objects) based on pairwise distances. Pairwise distances play also an important role in Sect. 3, Sect. 4, and Sect. 5 in this report. Without loss of generality the focus here is on clustering the observations. Clustering the variables can be done often in a similar way, for instance, in the case of binary data or contingency tables (see Fig. 10 below).

Let a sample of I independent observations (objects) is given in R^J and denote by $\mathbf{X} = (x_{ij})$ the corresponding data matrix consisting of I rows and J columns (variables), where the element x_{ij} provides a value for the j th variable describing the i th object. Objects can be species of plants, animals, individuals, archaeological findings, countries, enterprises, and so on. Further, let $\mathcal{C} = \{\mathbf{x}_1, \dots, \mathbf{x}_i, \dots, \mathbf{x}_I\}$ denote the finite set of the I objects (see at the outer left hand side of Fig. 1). Alternatively, let us write shortly $\mathcal{C} = \{1, \dots, i, \dots, I\}$.

Generally, the clusters that we are looking for should be as homogeneous as possible in some sense. Usually, cluster analysis techniques are applied in order to reach this aim. Fig. 1 presents two dimensional toy data and introduces both the data matrix $\mathbf{X} = (x_{ij})$ and the corresponding distance matrix $\mathbf{D} = (d_{ih})$ with the element $d_{ih} = (x_{i1} - x_{h1})^2 + (x_{i2} - x_{h2})^2$ (that is the usual squared Euclidean distance in R^2). In some applications the distance matrix \mathbf{D} (or a proximity matrix) may arise directly. Therefore, and because of its more general meaning, a distance matrix will be our preferable starting point for practical cluster analysis. Usually, \mathbf{D} is symmetric with $d_{ih} = d_{hi}$.

For a distance matrix, filled with real numbers and stored in an Excel spreadsheet, a so-called fingerprint (or heat plot) can be created easily. Fig. 2 shows such a heat plot of a 250×250 distance matrix \mathbf{D} . One can clearly see the pixels that become a color that is dependent on the distance value of the corresponding cell

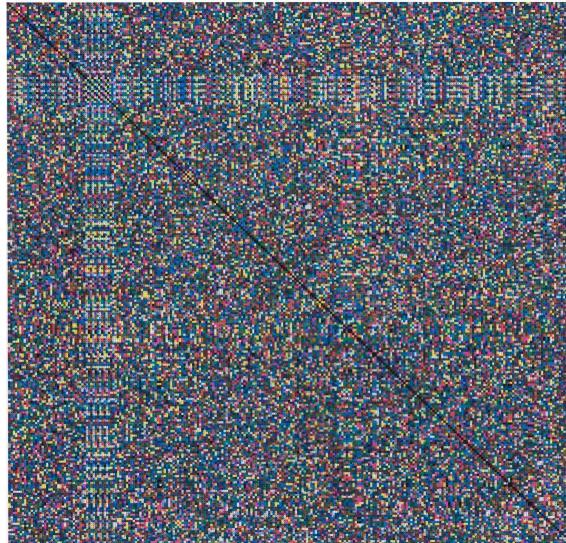


Figure 2: Heat plot of a distance matrix of randomly generated multivariate data.

in the spreadsheet. Here the distances are computed from a multivariate randomly generated data set \mathbf{X} , where the number of dimensions is $J = 20$. Obviously the random number generator does not do a good job because the result looks systematic in some regions of \mathbf{D} . Hence, such a heat plot seems to be an easy way to verify your random number generator, especially in the case of very high dimensions. Whatever the number of original variables J is (10, 100, 1000, or much more) the size of the corresponding distance matrix remains the same. Of course, it can become very dangerous to compute one single real number d_{ih} (i.e., the distance value) from two “arbitrary” high-dimensional observations \mathbf{x}_i and \mathbf{x}_h because the true statistical distance is unknown in practice usually. From this point of view, the “appropriate” computation of distances seems to be the most critical point in cluster analysis.

For the next figures, Fig. 3 and Fig. 5, Excel 2007 is required. They show two fragments of the heat plot of a huge 4000×4000 distance matrix \mathbf{D} that contains Euclidean distances: see Fig. 4 for the corresponding schematic view of \mathbf{D} (grey background color) and the legend of relations of color and distance. Here, at the left hand side and at bottom, the clusters are indicated by their number. The lower left rectangle in Fig. 3 presents the pairwise distances between observations of class 3 (last 1300 rows) and class 1 (first 1100 columns). Great distances are located at the lower left corner (in blue, light blue, green to yellow). These are distances between pairs of objects coming from cluster 3 and cluster 1, respectively. The smaller the distances the darker become the red and brown color. For instance, the distances inside class 2 (see at the right top in Fig. 3 and at left and middle in Fig. 5 (1585 rows and first 1585 columns)) seem to be very small compared with the inter-class distances mentioned above. The heat plots suggest that there may be a structure in the data. The entire heat plot cannot be presented because of technical limitations of both the screen and the printer. Each figure is composed of 3 591 610 (= 1585×2266) pixels. The data behind \mathbf{D} is a 4000×2 data matrix \mathbf{X} consisting of the

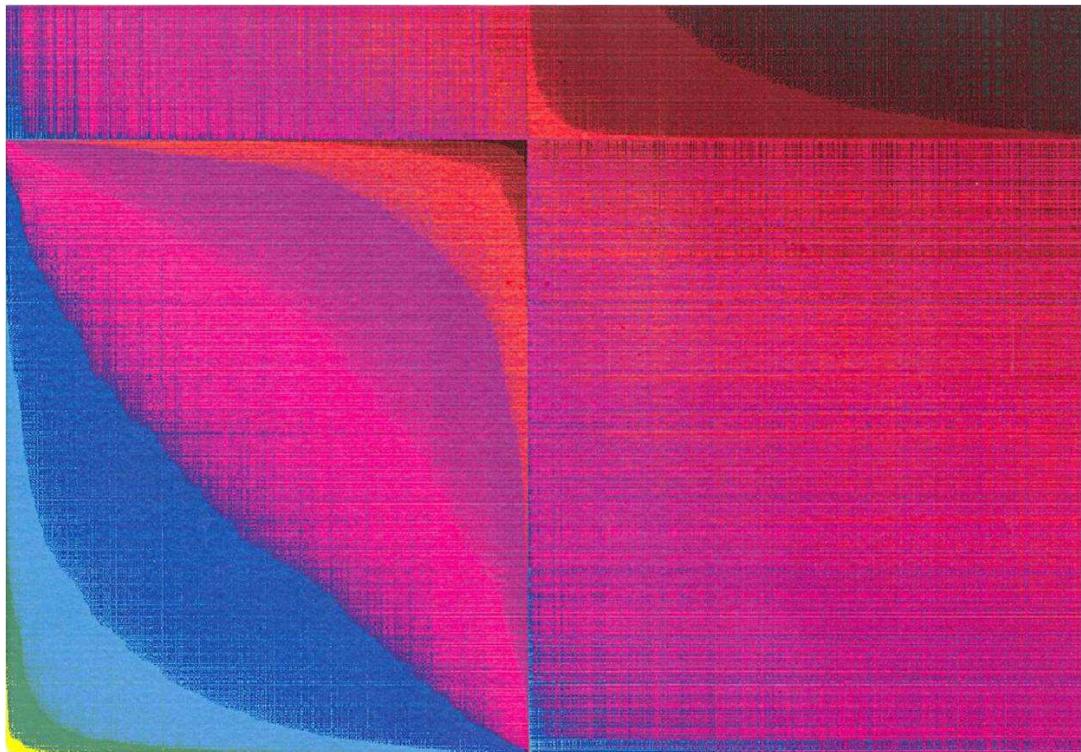


Figure 3: Heat plot of a distance matrix (lower left subarea) of the three-class data

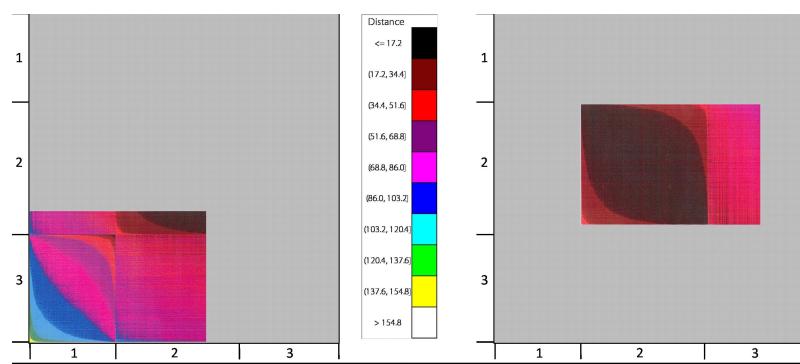


Figure 4: Location of the subareas that are presented in Fig. 3 and Fig. 5.

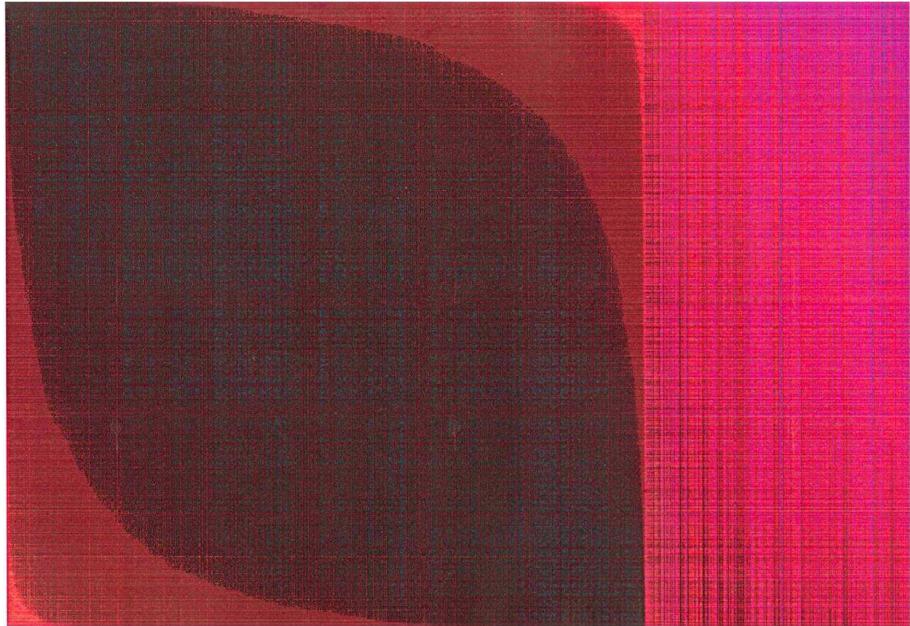


Figure 5: Heat plot of a distance matrix (middle part) of the three-class data.

following three spherical, randomly generated Gaussian classes of sizes 1100, 1600, and 1300, respectively, with the following different mean values $(-3, 3)$, $(0, 0)$, $(3, 3)$ and different standard deviations $(1, 1)$, $(0.7, 0.7)$, and $(1.2, 1.2)$. The values (x_{ij}) were generated simply by using the `rand()` function of VBA that delivers randomly generated uniformly distributed values r_1 and r_2 coming from $[0,1)$:

$$x_{ij} = \sigma_j \sqrt{-2 \ln r_1} \cos(2\pi r_2) + \mu_j .$$

Here σ_j and μ_j are the standard deviations and mean values of variable j , respectively. This data set is presented in Fig. 6 (scatterplot).

However, more information about the classes is given by histograms as shown in Fig. 7 (scatterplot-histogram). The univariate histogram of the first variable (that is projected onto the wall at the left hand side and estimates the corresponding marginal distribution) reflects the three-class structure much better than the one of the second variable. Also, one can see that cluster \mathcal{C}_2 at the right hand side has much less deviations from mean as compared to the other two clusters. Thus, the cluster \mathcal{C}_2 is most compact. A smooth and much more impressive version of Fig. 7 can be obtained by non-parametric density estimation. Fig. 8 (density-plot) shows such a bivariate density surface of the two-dimensional three-class data. It is obvious to expect that cluster analysis should be successful in dividing (decomposing) into smaller subsets (clusters) here.

As one might suppose correctly, the ordering of objects plays an important role in heat plots, see for instance [16]. Really, the observations in Fig. 3 to Fig. 5 are ordered first by classes 1, 2, and 3 and then by the scores of the first principal component.

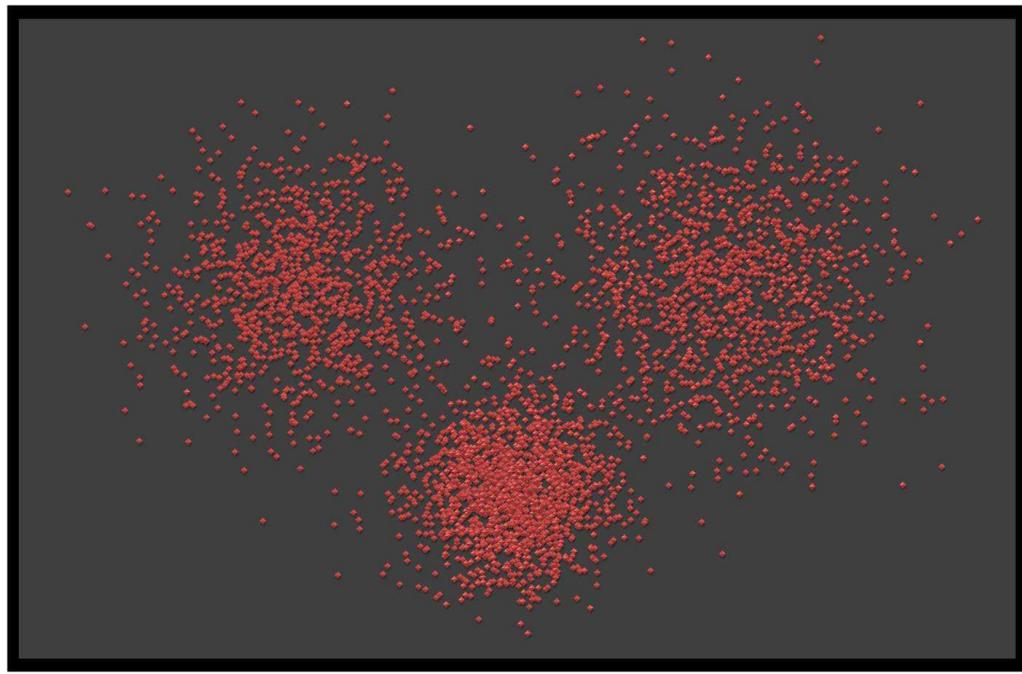


Figure 6: Scatterplot of the three-class data.

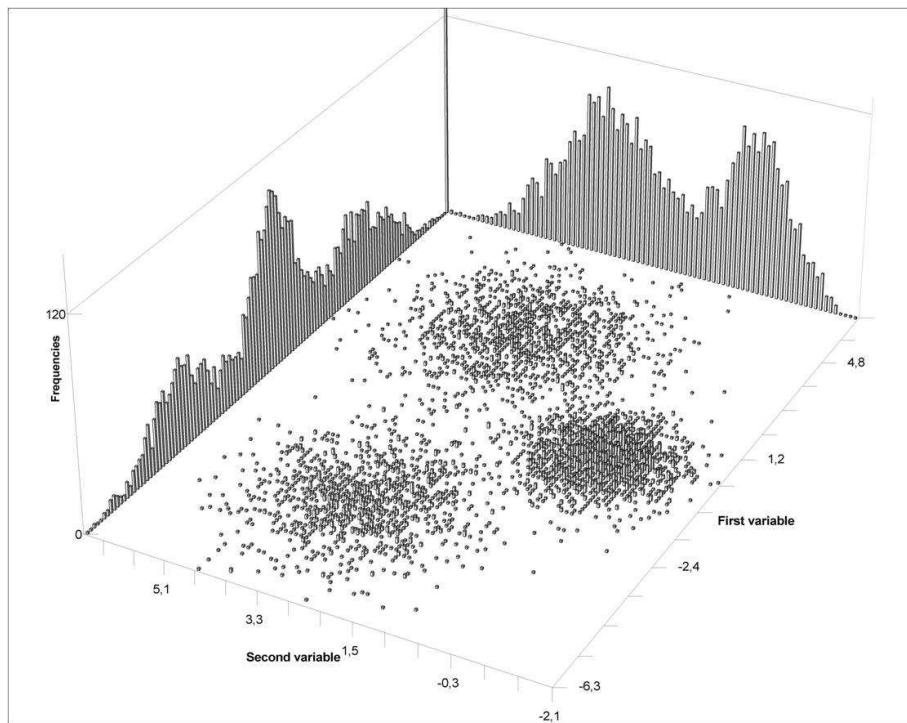


Figure 7: Plot of several histograms of the three-class data.

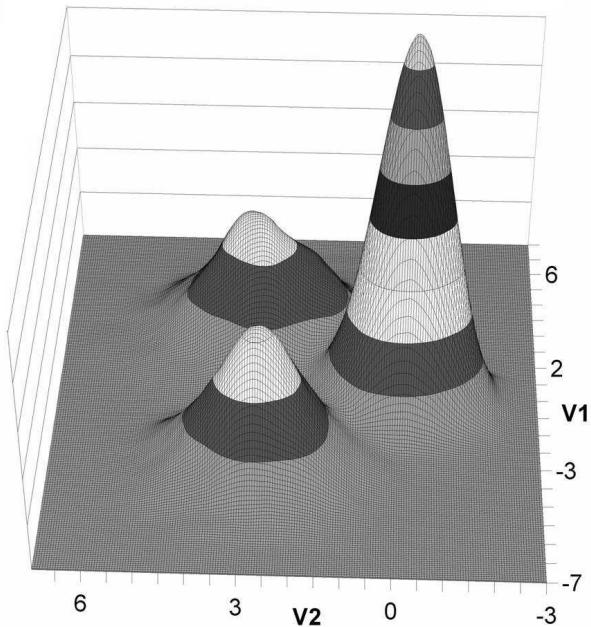


Figure 8: Density plot of the three-class data.

Heat plots offer an easy way to detect structures, also in other matrices such as a data matrix \mathbf{X} (see Fig. 46 in Sect. 3) or a correlation matrix. However, the elements of the matrices should be ordered in an optimum way before.

1.3 From Distances to Partitions and Hierarchies

But now to our basic problem: finding clusters. In the following, the focus is on model-based Gaussian clustering of observations in its simplest setting that results in the sum of squares and logarithmic sum of squares methods. It should be mentioned that both methods can be extended to adaptive techniques ([11], [12]). These simple methods can become a little bit flexible by weighting objects and/or variables, and thus they get more practical relevance. The general model-based Gaussian clustering approach was described first in [1] in all its glory. Because we will make use only of the simple model-based Gaussian clustering based on pairwise distances in this paper, we briefly introduce first some general underlying facts and notations.

Above we introduced the starting points of cluster analysis. Now let us formalize the simplest (elementary) solution to the clustering problem with a fixed number of clusters K : the Boolean assignment matrix $\mathbf{G} \in \{0, 1\}^{I \times K}$ (that is, $\mathbf{G} = (g_{ik})$) with the restriction of uniqueness and exhaustive assignment (completeness) $\sum_{k=1}^K g_{ik} = 1$ for every object i . Formally, the mapping is,

$$G : \mathcal{C} \times \{1, 2, \dots, K\} \longrightarrow \{0, 1\}$$

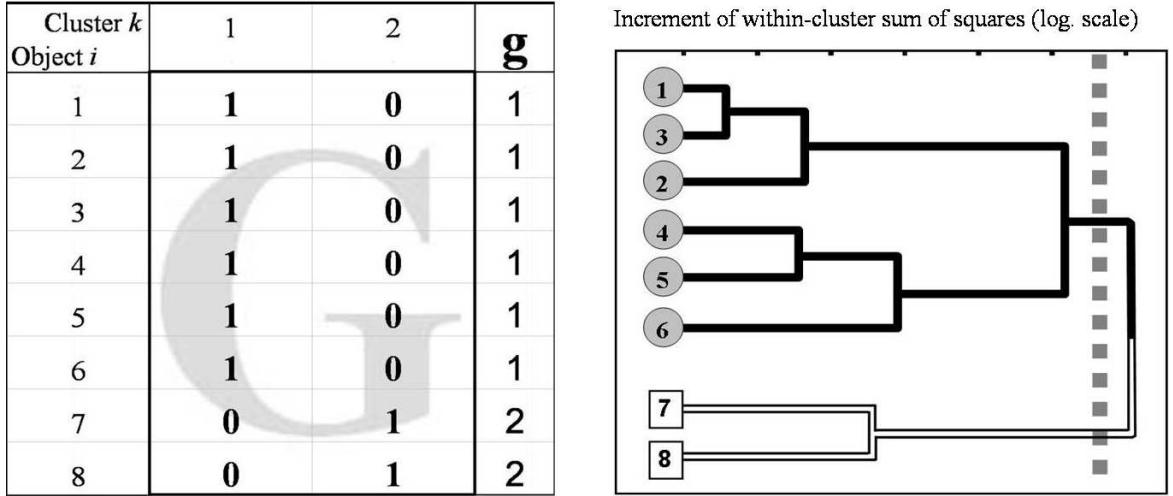


Figure 9: The Boolean assign matrix \mathbf{G} , the vector \mathbf{g} of cluster labels, and the corresponding partition in the dendrogram.

with

$$g_{ik} = \begin{cases} 1 & \text{if } i \text{ comes from the cluster (subset) } \mathcal{C}_k \\ 0 & \text{otherwise.} \end{cases}$$

Indeed, the cluster mapping G induces a partition $\{\mathcal{C}_1, \dots, \mathcal{C}_K\}$ of \mathcal{C} . Hereby

$$\bigcup_{k=1}^K = \mathcal{C}$$

and

$$\mathcal{C}_k \cap \mathcal{C}_l = \emptyset$$

for every pair of clusters \mathcal{C}_k and \mathcal{C}_l , $k, l = 1, 2, \dots, K, k \neq l$. This cluster mapping yields exactly K clusters (subsets), where the numbering of the clusters is arbitrary because it usually depends on the applied clustering algorithm itself. Alternatively, let $\mathbf{g} = (g_1, \dots, g_I)^T$ denote the identifying labels for the clustering and thus for the cluster mapping G , where $g_i = k$ if the i th object \mathbf{x}_i comes from the k th cluster. One can understand \mathbf{g} as a categorical variable or partition variable with K different nominal states $\{1, 2, \dots, K\}$. Formally, $\mathbf{g} = \mathbf{Ge}$, where the vector $\mathbf{e} = (1, 2, 3, \dots, K)^T$ has K entities.

Fig. 9 (at the left hand side) illustrates both an example of the Boolean assignment matrix $\mathbf{G} = (g_{ik})$ that maps the I object into $K = 2$ clusters and the corresponding partition \mathbf{g} of the data that is given above in Fig. 1. Here \mathbf{G} gives the optimum K -means cluster analysis solution that is shown in Fig. 11. Typically, a partition is the result of a partitional cluster analysis method like K -means. Such a partition can be obtained also by cutting a dendrogram at a certain level of cluster distance (as it is indicated by the dashed vertical line at the right hand side of Fig. 9). By the way, here the hierarchical cluster analysis method finds the same optimum partition into $K = 2$ clusters as the partitional $D_{ih}Ex$ method does (see below for details on

the methods). This dendrogram is the result of hierarchical clustering by Ward's incremental sum of squares method based on the distance matrix \mathbf{D} in Fig. 1. By cutting a dendrogram at several different levels of cluster distances one gets a set of partitions.

Banfield and Raftery [1] developed a model-based framework for clustering by parameterizing the covariance matrix in terms of its eigenvalue decomposition. In the following the focus is on a special assumption about the covariance structure. When the covariance matrix is constrained to be diagonal and uniform across all K assumed clusters, the sum of within-clusters sum of squares criterion (shortly: sum of squares = SS)

$$W_K(\mathbf{G}) = \sum_{k=1}^K \text{tr}(\mathbf{W}_k) \quad (1)$$

has to be minimized with respect to \mathbf{G} for a fixed K . Herein

$$\mathbf{W}_k = \sum_{i=1}^I g_{ik} (\mathbf{x}_i - \bar{\mathbf{x}}_k)(\mathbf{x}_i - \bar{\mathbf{x}}_k)^T \quad (2)$$

is the sample cross-product matrix for the k th cluster \mathcal{C}_k , and

$$\bar{\mathbf{x}}_k = \frac{1}{g_{.k}} \sum_{i=1}^I g_{ik} \mathbf{x}_i \quad (3)$$

is the usual maximum likelihood estimate of expectation values in cluster \mathcal{C}_k . Further, $g_{.k}$ is the cardinality of cluster \mathcal{C}_k , that is, $g_{.k} = \sum_i g_{ik}$. The SS is fundamental for inferential statistics and descriptive statistics, not only in cases $K > 1$. When scaling the SS (or more precisely the sum of the squared deviations) and the cross product matrix for the number of degrees of freedom in the case $K = 1$, it becomes the variance and the covariance matrix, respectively. In (1), no pairwise distances occur directly in the case of Gaussian distribution, but indirectly they are introduced via the corresponding density function. It is well known that criterion (1) can be written in the following equivalent form without the explicit specification of cluster centers (centroids) $\bar{\mathbf{x}}_k$

$$W_K(\mathbf{G}) = \sum_{k=1}^K \frac{1}{2g_{.k}} \sum_{i=1}^I \sum_{h=1}^I g_{ik} g_{hk} d_{ih} , \quad (4)$$

and

$$d_{ih} = d(\mathbf{x}_i, \mathbf{x}_h) = (\mathbf{x}_i - \mathbf{x}_h)^T (\mathbf{x}_i - \mathbf{x}_h) = \|\mathbf{x}_i - \mathbf{x}_h\|^2 \quad (5)$$

is the squared Euclidean distance between two objects i and h . It is also well known that this criterion is dependent on the scales of the variables. Different scales can be formalized by introducing weights of variables. Behind this special use, the variables can be weighted generally by giving important variables more weight (i.e., to gain

in importance). Taking into account weights of the variables the squared weighted Euclidean distance

$$d_{ih} = d_Q(\mathbf{x}_i, \mathbf{x}_h) = (\mathbf{x}_i - \mathbf{x}_h)^T \mathbf{Q} (\mathbf{x}_i - \mathbf{x}_h) , \quad (6)$$

generalizes formulae (4), where the $J \times J$ matrix \mathbf{Q} is restricted to be diagonal. With $\mathbf{Q} = \text{diag}(q_1, q_2, \dots, q_J)$, where $q_j (=q_{jj})$ denotes the weight of the j th variable, we can write simply

$$d_{ih} = \sum_{j=1}^J q_j (x_{ij} - x_{hj})^2 .$$

In doing so, at least scaling problems can be handled fashionably without any data preprocessing step such as the standardization of variables. Moreover adaptive weights of variables can be used that are estimated during the iteration process of clustering. (For details, also in the frame of principal components analysis (PCA) and in terms of the sample cross-product matrices (2), see [12].) Another approach of assigning weights to variables is clustering of objects with regard to subsets of variables (see Friedman and Meulman [5]). Of course, the statistical distance (6) with a positive definite matrix \mathbf{Q} can be generalized further to cluster specific statistical distances, where instead of \mathbf{Q} the K inverse within-cluster covariance matrices \mathbf{Q}_k are used [22].

Now we are able to forget (2) and thus the corresponding estimates (3). Keep in mind, pairwise distances \mathbf{D} are more general as starting point for (exploratory) cluster analysis and data analysis than a data matrix \mathbf{X} . However, the criterion (4) presents practical problems of storage and computation time for increasing I because of their quadratic increase, as Späth [22] pointed out. Meanwhile, a new generation of computers can deal easily with both problems also for $I > 10\,000$. And, the Excel 2007 “Big Grid” spreadsheet is coming in the nick of time.

In order to cluster a practically unlimited number of objects based on criterion (4), let us generalize further by introducing positive weights of objects $u_i, i = 1, 2, \dots, I$ that will be called here also masses. Instead of dealing with millions of objects directly in (4), their appropriate representatives are clustered subsequent to a preprocessing step of data aggregation. Usually, an aggregation is like smoothing and it has a stabilizing effect. Especially the influence of outliers can be handled in this way to some degree. Obviously, the estimates (3) are affected by masses, but the distances (6) are independent of masses. That means, from the computational point of view, that distances are most suitable for simulation studies (see next Section) because they need to be figured out only ones. The criterion (4) becomes the generalized form

$$W_K^*(\mathbf{G}) = \sum_{k=1}^K \frac{1}{2U_k} \sum_{i=1}^I u_i \sum_{h=1}^I g_{ik} g_{hk} u_h d_{ih} \quad (7)$$

that has to be minimized by incorporating positive masses (weights of objects) and weighted distances (6), where $U_k = \sum_i g_{ik} u_i$ and u_i denote the mass of cluster \mathcal{C}_k

and the mass of object i , respectively. In the case of weighted observations, the sample cross-product matrix for the k th cluster \mathcal{C}_k (2) becomes

$$\mathbf{W}_k^* = \sum_{i=1}^I g_{ik} u_i (\mathbf{x}_i - \bar{\mathbf{x}}_k^*) (\mathbf{x}_i - \bar{\mathbf{x}}_k^*)^T$$

with

$$\bar{\mathbf{x}}_k^* = \frac{1}{U_k} \sum_{i=1}^I g_{ik} u_i \mathbf{x}_i .$$

As already mentioned above, the principle of weighting the observations is a key idea for handling cores (representatives) and outliers. In the case of outliers one has to downweight them in some way in order to reduce their influence. In the case of representatives of cores, one has to weight them, for example, proportionally to the cardinality of the cores (for details and applications see [19]). Moreover, in [19], concerning the *K-means* algorithm, one will find conditions of exchange of an observation i from cluster k into cluster g that has to be fulfilled for minimizing (7).

Fig. 10 give you an impression about the flexibility of the simplest model-based criterion (7) when using both special weights of rows u_i and special weights of columns q_j in (6). In doing so, the decomposition of the chi-square statistic of a contingency table is obtained that is of special interest (see [6] for details). In Fig. 10, the data at hand counts the world's largest merchant fleets by country of owner, i.e. all self-propelled oceangoing vessels 1,000 gross tons and greater (as of July 1, 2003, published by CIA World Factbook [3]). The data matrix consists of 20 observations (countries) with the three variables Full Container (abbr.: Cont), Dry Bulk (Bulk), and Tanker (Tank).

By the way, going from pairwise squared Euclidean distances d_{ih} to within-cluster sum of squares w of the two objects i and h means generally

$$w\{i, h\} = \frac{u_i u_h}{u_i + u_h} d_{ih} ,$$

and in particular

$$w\{i, h\} = \frac{1}{2} d_{ih}$$

in the case of unit masses $u_i = u_h = 1$. This way is correct in the case of the assumption of the simplest Gaussian model. The advantage of distances are that they are fixed forever independent on weighting the corresponding objects. This is in contrast to the sample cross product matrices (2) and the cluster centers (3) that are affected by changing the weights of objects. Therefore, “soft bootstrapping” by random weighting the objects or subsampling can be performed with an unchanged distance matrix \mathbf{D} . For example, one can think about weighting the objects like doubling the sample ($u_i = 2, i = 1, 2, \dots, I$). In this special case, where the distances become the sum of squares of the set consisting of a pair of objects, the result of clustering should be unchanged. SPSS gives you the opportunity to double a sample easily by a click. However afterwards, SPSS cluster analysis comes up with different

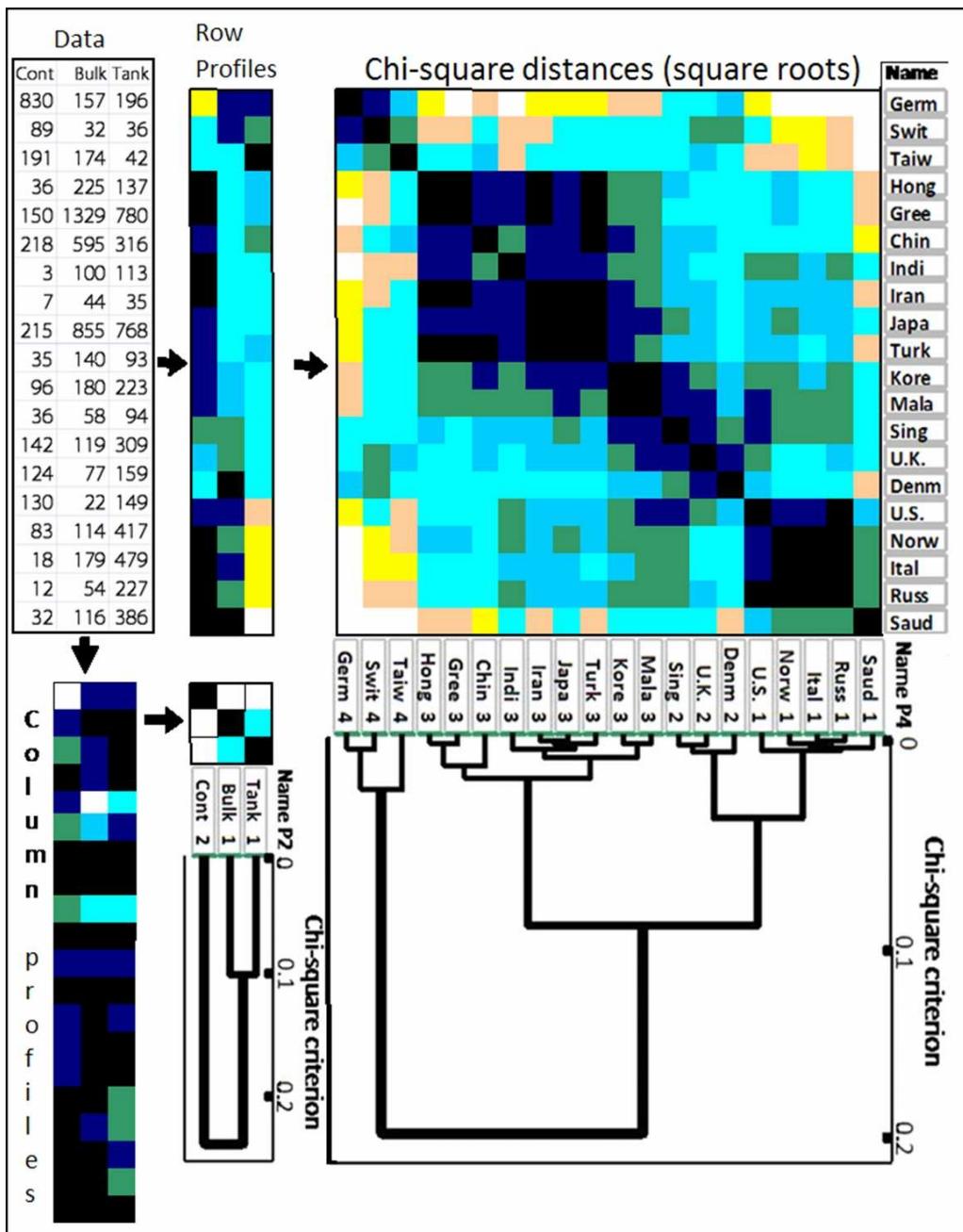


Figure 10: From distances to hierarchies: cluster analysis of a contingency table.

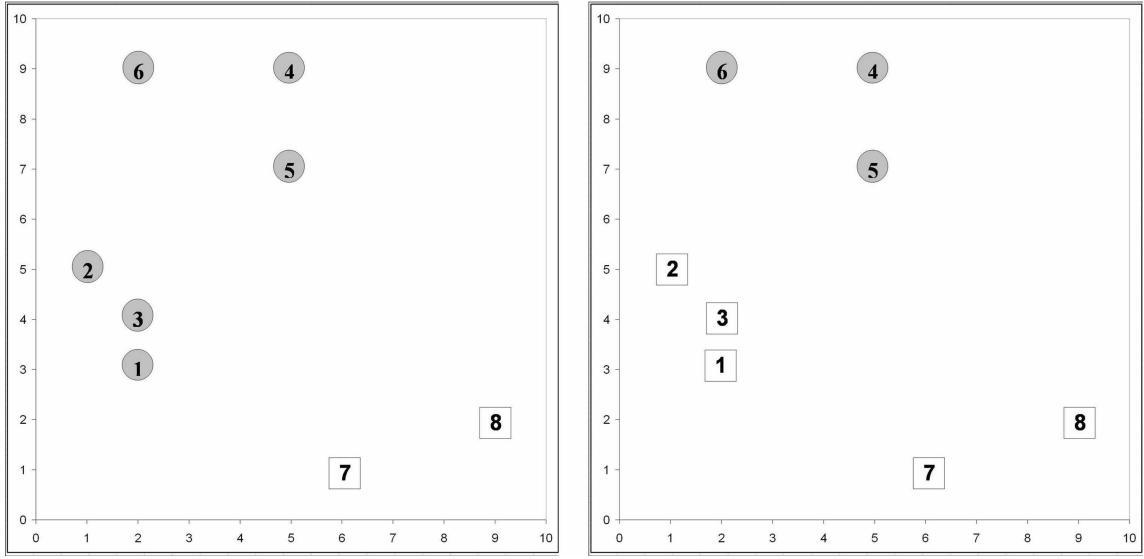


Figure 11: Clustering into two clusters by $D_{ih}Ex$ method (optimum solution) and *Quickcluster* of SPSS (at the right hand side).

results! Correct statistical analysis of weighted objects seems to be a serious problem for some software ...

There are at least two well-known clustering techniques for minimizing the sum of squares criterion based on pairwise distances: the partitional $D_{ih}Ex$ method minimizes the criterion (4) for a single partition \mathbf{G} by exchanging objects between clusters ([22], [2]), and the hierarchical *Ward's* clustering minimizing (4) in a stepwise manner by agglomerative grouping [10]. The well-known K -means method becomes a special case of the $D_{ih}Ex$ method in the framework of pairwise clustering based on squared Euclidean distances without using centroids anymore. Also one usual definition out of many possible definitions of the most typical object (MTO) of a cluster can be: a MTO is that object that is the most similar one to the centroid, becomes more general in pairwise clustering (see also [10]). Here the typical object of a cluster is the one that minimizes the sum of the (pairwise) distances to the other members of the cluster. Of course, in the case of Gaussian normals, this general most typical object is located usually nearby the expectation value, i.e. the centroid, of the cluster.

In Fig. 11 two different results of clustering are given that divide the toy data of Fig. 1 into two clusters. The plot at the left hand side shows the optimum result with regard to minimum sum of within-cluster sum of squares ($= 52.667$, see below (1)) that should be easy to find by appropriate methods like the well-known K -means clustering which looks for optimum K centroids (means). However, this result here is obtained by the $D_{ih}Ex$ method (speak Dihex, it is based on the exchange algorithm, for details see [2]) that is a partitional clustering method (based on the pairwise distances $\mathbf{D} = (d_{ih})$). In our statistical software ClusCorr98[®], a generalized method [2] is used that goes back to Späth [22] who called it TIHEXM. Furthermore,

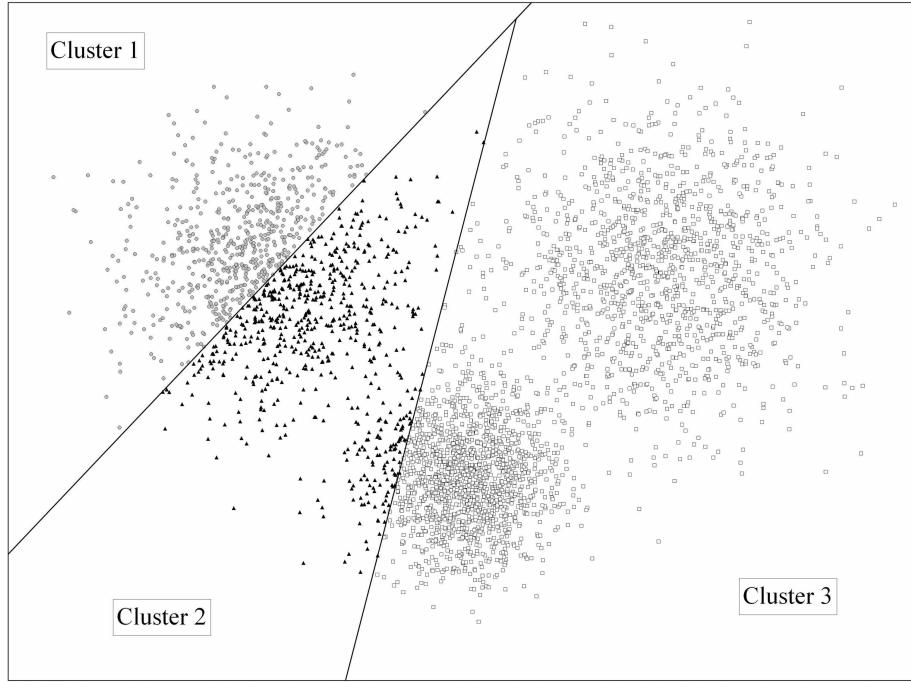


Figure 12: Result of *Quickcluster* of SPSS (same data as in Fig. 7).

our algorithms work with random access to the observations. At the right hand of Fig. 11 a bad sub-optimum solution ($= 64.667$, see the plot) is found by the K -means clustering procedure *Quickcluster* of SPSS¹ using the running means option. This option means nothing more than exchange method. Moreover, the *Quickcluster*-iterations failed to converge! That is to say, the iterations stopped only when the maximum number of iterations was performed. If one repeats the run, the result remains the very same.

Fig 12 shows a quite bad result of clustering the three randomly generated normal subpopulations. Here the procedure *Quickcluster* of SPSS is applied again with the option running means: the clusters are updated after each object is assigned to a new cluster. The main reason for this failure is that the underlying algorithm depends on the sequence of objects. What, if one can not check the validity of cluster analysis results visually by eye? (Here in R^2 a graphical inspection is both easy to do and very powerful.) There is a need for a validation approach that works in almost all situations (see the next subsection).

Therefore, let us generalize the validation by comparing two partitions \mathbf{f} and \mathbf{g} into M and K clusters (categories), respectively. Well-known measures of correspondence between such categorical variables are based on the contingency table $\mathbf{N} = (n_{mk})$ that is obtained by crossing the vectors \mathbf{f} and \mathbf{g} . A contingency table, also referred to as pivot table, can be established easily in Excel. Alternatively, such a contingency

¹Here release SPSS 17 for Windows is used for the tests (see also Fig. 12). Some of the problems which have occurred will be mentioned below. Almost all have been well known for a long time.

		Partition g				g (Ward's method)			g ($D_{ih}Ex$ method)			
		Cluster k	1	2	3	Sum	1	2	3	1	2	3
Partition f (true)	Class m	1	596	501	3	1100	1089	9	2	5	0	1095
	2	2	0	130	1470	1600	7	1587	6	1595	0	5
	3	3	0	8	1292	1300	5	21	1274	31	1255	14
	Sum		596	639	2765	4000	1101	1617	1282	1631	1255	1114

Figure 13: A contingency table \mathbf{N} that is obtained by crossing two partitions \mathbf{f} and \mathbf{g} , and two other tables of results.

table \mathbf{N} can be formulated by simple matrix notation

$$\mathbf{N} = \mathbf{F}^T \mathbf{G}$$

based on the corresponding two Boolean assignment matrices \mathbf{F} and \mathbf{G} . Fig. 13 shows at the left hand side the contingency table that comes from crossing the true partition of the simulated data set of 4000 objects with the cluster analysis result of *Quickcluster* of SPSS (see Fig. 12). At the right hand side two other contingency tables are presented that come from *Ward's* clustering and $D_{ih}Ex$ clustering (outside right), respectively. The last two results are based on pairwise clustering using the squared Euclidean distances (5). A comparison of the performance of the three methods on clustering the three-class data says: *Ward's* method performs slightly better (50 errors only) than the $D_{ih}Ex$ clustering with 55 misclassifications. It has to be mentioned that the criterion (1) that is minimized here by the three methods is not the most appropriate one for this data. The right one is the logarithmic sum of squares (see below).

Almost all (exploratory) clustering techniques detect clusters, even on data without any cluster structure. Often, clustering techniques are applied for finding (practical useful) segmentations of data such as vector quantization by using K -means clustering. Fig. 14 shows the cluster membership of 4000 points into 15 clusters that is obtained by the hierarchical Ward method. This is an example of a data set without any cluster structure. The randomly generated data in R^2 come from a bivariate Gaussian distribution $N_2(\mu, \Sigma)$ with parameters μ (mean vector) and Σ (covariance matrix). Here one standard normal population is generated with $\mu = 0$ and $\Sigma = \mathbf{I}_J$, where \mathbf{I}_J is the $J \times J$ identity matrix. The centers of the clusters “C1”, …, “C15” are marked by an asterisk (“Cs” in the legend). Fig. 15 shows the clusters that are obtained by the $D_{ih}Ex$ method, that is, by the K -means method.

Even though both clustering techniques, the hierarchical Ward and the partitional K -means method, have the same underlying statistical model and minimize the same criterion (4), but in another way, the results are usually different. The last one

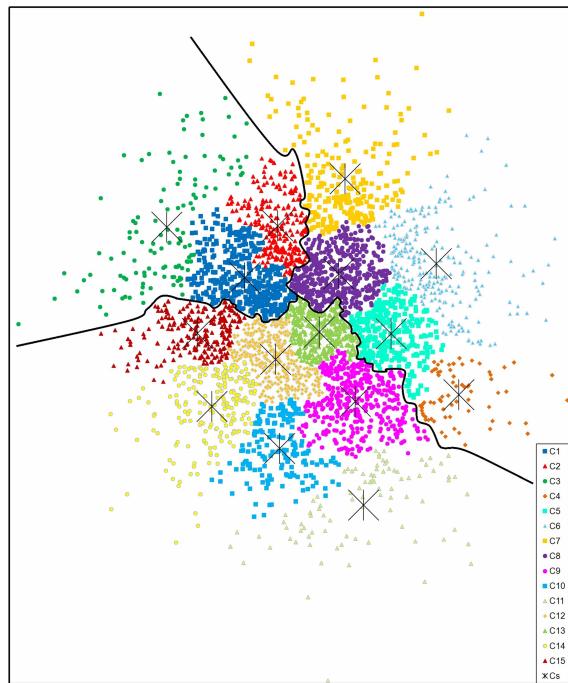


Figure 14: Ward's clustering of no-structure data into 15 and 3 clusters, respectively.

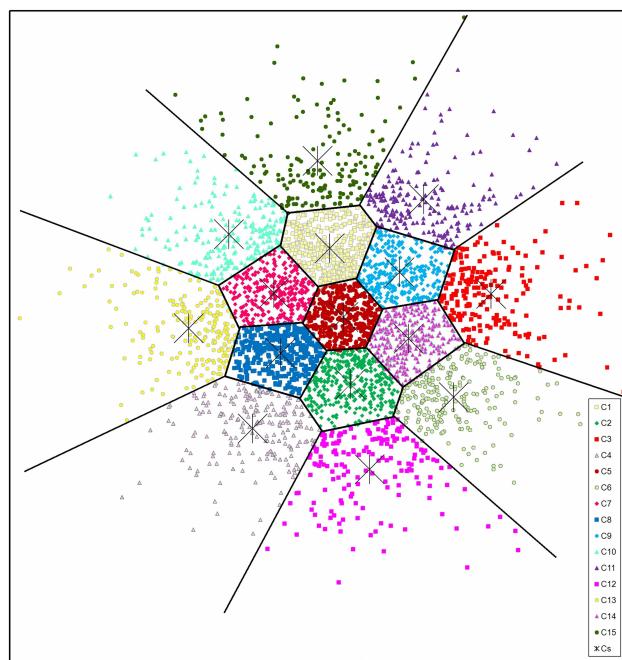


Figure 15: $D_{ih}Ex$ clustering of no-structure data into 15 clusters.

is leading to the well-known Voronoi tessellation, where the objects have minimum distance to their centroid and thus, the borderlines between clusters are hyperplanes. By contrast, the Ward method does not necessarily have to creates hyperplanes as borderlines between clusters, as Fig. 14 shows for the three-cluster solution.

When the covariance matrix of each cluster C_k ($k = 1, 2, \dots, K$) is constrained to be diagonal, but otherwise allowed to vary between groups, the logarithmic sum-of-squares criterion

$$V_K(\mathbf{G}) = \sum_{k=1}^K g_{\cdot k} \log \text{tr} \frac{\mathbf{W}_k}{g_{\cdot k}} . \quad (8)$$

Once again the following equivalent formulation can be derived

$$V_K(\mathbf{G}) = \sum_{k=1}^K g_{\cdot k} \log \left(\sum_{i=1}^I \sum_{h=1}^I \frac{g_{ik} g_{hk}}{2g_{\cdot k}^2} d_{il} \right) . \quad (9)$$

Considering formulae (9) (and (8) in the case of formulation with sample cross product matrices, respectively) and weights of observations u_i , the logarithmic sum-of-squares criterion can be generalized to

$$V_K^*(\mathbf{G}) = \sum_{k=1}^K U_k \log \left(\sum_{i=1}^I \sum_{h=1}^I \frac{u_i u_h}{2U_k^2} g_{ik} g_{hk} d_{il} \right) . \quad (10)$$

According to this logarithmic sum-of-squares criterion, the partitional *K-means*-like clustering algorithm is also referred to as *Log-K-means* and the hierarchical *Ward*-like agglomerative method as *LogWard*, respectively [19]. Concerning the hierarchical algorithms there are special treatments of observations with low weights in use (see, for example, [19]). Such special tricks are essential because the original Ward's hierarchical agglomerative clustering is based on minimum incremental of sum of squares, and therefore all observations with zero (or quasi-zero) weight would be merged together into one cluster, whatever the level of distance values may be. By the way, *K-means* and *Log-K-means* based on pair-wise distances (6) are also more general because they never require an $(I \times J)$ -data matrix \mathbf{X} . The pixel graphic of Fig. 16 shows the result of hierarchical clustering based on the criterion (10) when using both special weights of rows u_i and special weights of columns q_j in (6).

1.4 Built-in Validation of Cluster Analysis Results

As already shown above, more often than not clustering techniques always detect clusters. Moreover, hierarchical clustering presents all the clusters that are established during the agglomeration or the division process. In Fig. 17 the amalgamation process of 13 points is illustrated. The points are located at the real line and their values can be taken from the picture. Each point is a terminal node in the tree. It is marked by a dark circle with its value given below. Here the *weighted pair-group method using centroids* (called also *Median method*) is applied [11]. Each non-trivial

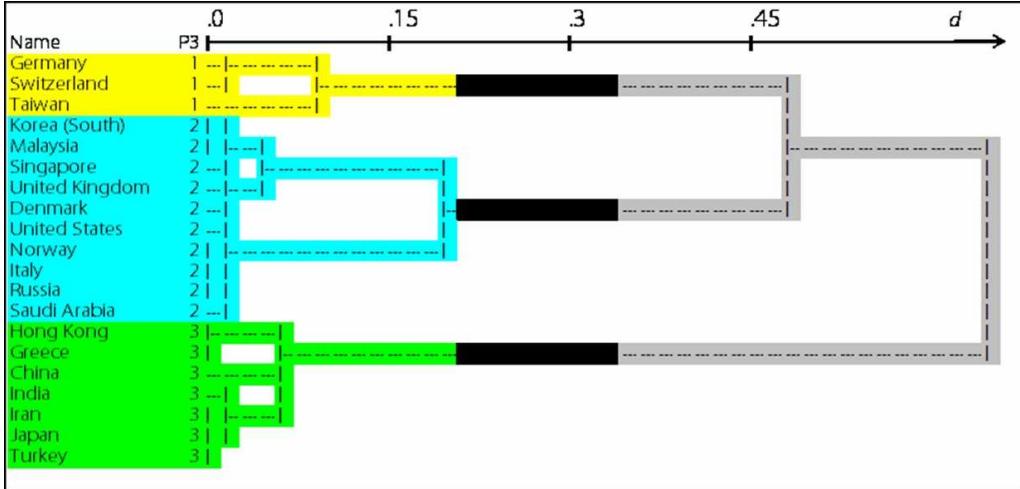


Figure 16: Colored dendrogram of *LogWard*-clustering of the table of Fig. 10.

cluster (non-terminal node) is marked by a light circle. Most of all clusters are characterized by their centroids additionally. Obviously, in every agglomeration step an increasing amount of information is lost. A better visual impression can be obtained by a plot-dendrogram, that is a dendrogram projected onto a plane. Fig. 18 shows a hierarchy of 227 countries based on demographic variables. The main question is: how many clusters are there? Or, in other words, when should the agglomeration process stops? Or, in terms of the density estimation in Fig. 19, what is the right cut-off density level for fixing clusters? Another outfit of this figure is presented below in Sect. 3 in Fig. 44.

There are so many different clustering algorithms and new ones occur daily in the literature. More often than not they do their job and usually, they present a solution in almost all cases. As from now let us suppose that they do a good (accurate) job (because otherwise the validation can give the right answer to the wrong question). Then the main question arises: is there really a cluster structure in the data? Therefore, in this section a validation of clustering results based on resampling techniques is highly recommended that can be considered as a three level assessment of stability. The first, most general level is decision making about the appropriate number of clusters. Second, the stability of each individual cluster is assessed based on measures of similarity between sets. From many applications it is known that it makes sense to investigate the specific stability of clusters. In the third and most detailed level of validation, the reliability of the cluster membership of each individual object can be assessed.

In any case, it is highly recommended that the stability of the obtained clusters has to be assessed by using validation techniques ([9], [11], [7]). Concretely, here a built-in validation of clustering results based on resampling or subsampling techniques (bootstrapping) is highly recommended that can be considered as a three level assessment of stability. An alternative way beside bootstrapping is disturbing the data by randomly generated errors (noise). The first and most general level is

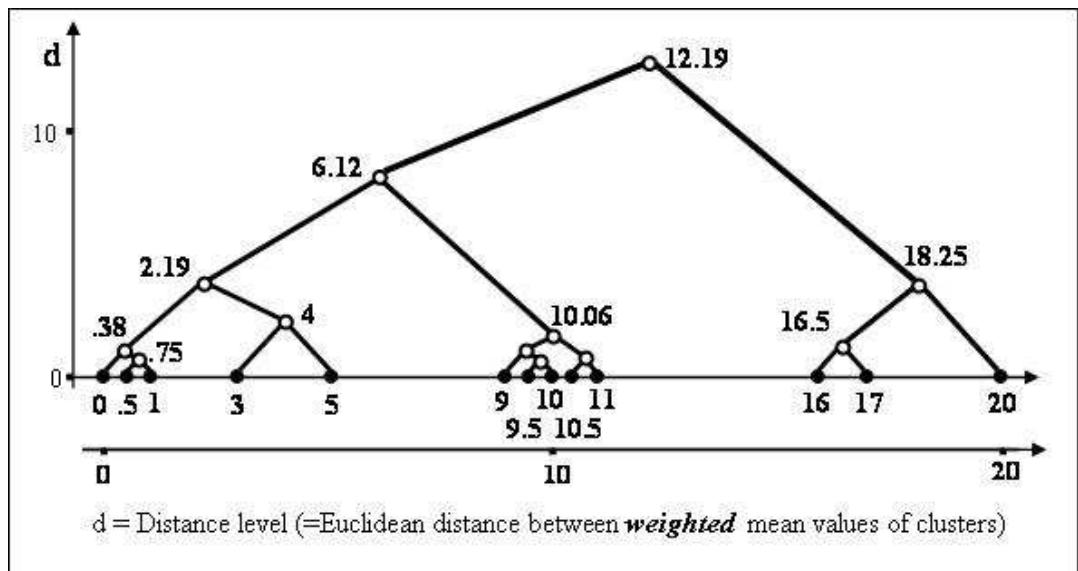


Figure 17: A non-equidistant dendrogram of 13 points located on the real line.

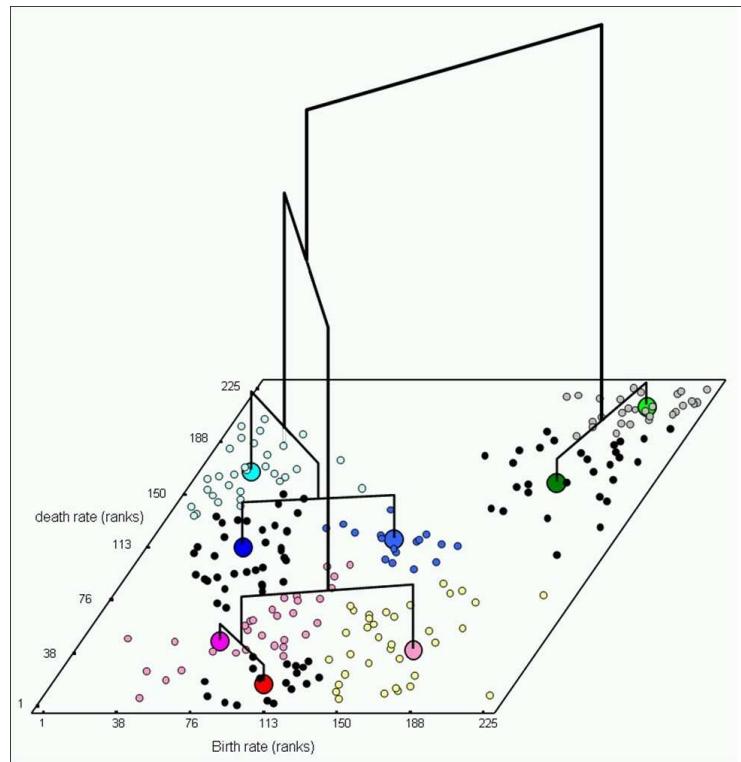


Figure 18: A so-called plot-dendrogram based on demographic data of 227 countries.

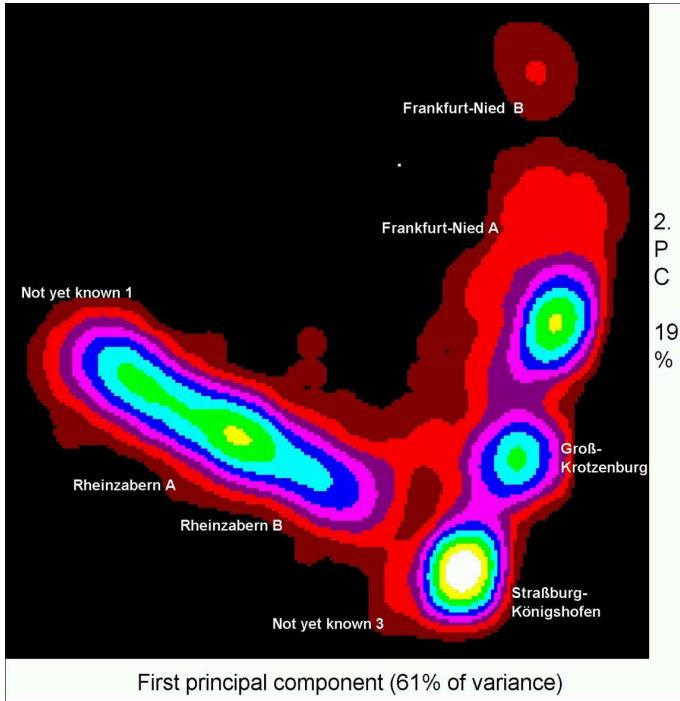


Figure 19: Cuts at several levels of the bivariate nonparametric density estimate.

decision making about the appropriate number of clusters. This decision is based on such well-known measures of correspondence between partitions like the *Rand's* index ([20]), the *adjusted Rand's* index of Hubert and Arabie [8], and the index of Fowlkes and Mallows [4]. Second, the stability of each individual cluster is assessed based on measures of similarity between sets, e.g., the asymmetric measure of cluster agreement or the symmetric *Jaccard* measure. It should be mentioned that it makes sense to investigate the (often quite different) specific stability of clusters of the same clustering on the same data. Often one can observe that the clusters have a quite different stability. Some of them are very stable. Thus, they can be reproduced and confirmed to a high degree, for instance, by bootstrap simulations. They are both homogeneous inside and well separated from each other. Moreover, sometimes they are located far away from the main body of the data like outliers. On the other side, hidden and tight neighboring clusters are more difficult to detect and they cannot be reproduced to a high degree. In the third and most detailed level of validation, the reliability of the cluster membership of each individual object will be assessed.

Here we don't consider special properties like compactness and isolation as it is done in [9]. A general purpose technology for validation is recommended that works well especially in highdimensional settings. In low dimensional cases and in cases where projection methods result in good approximations into R^2 or R^3 , graphical methods are often the better and more efficient choice for validation. What are stable clusters from a general statistical point of view? These clusters can be confirmed and reproduced to a high degree. To define stability with respect to the individual

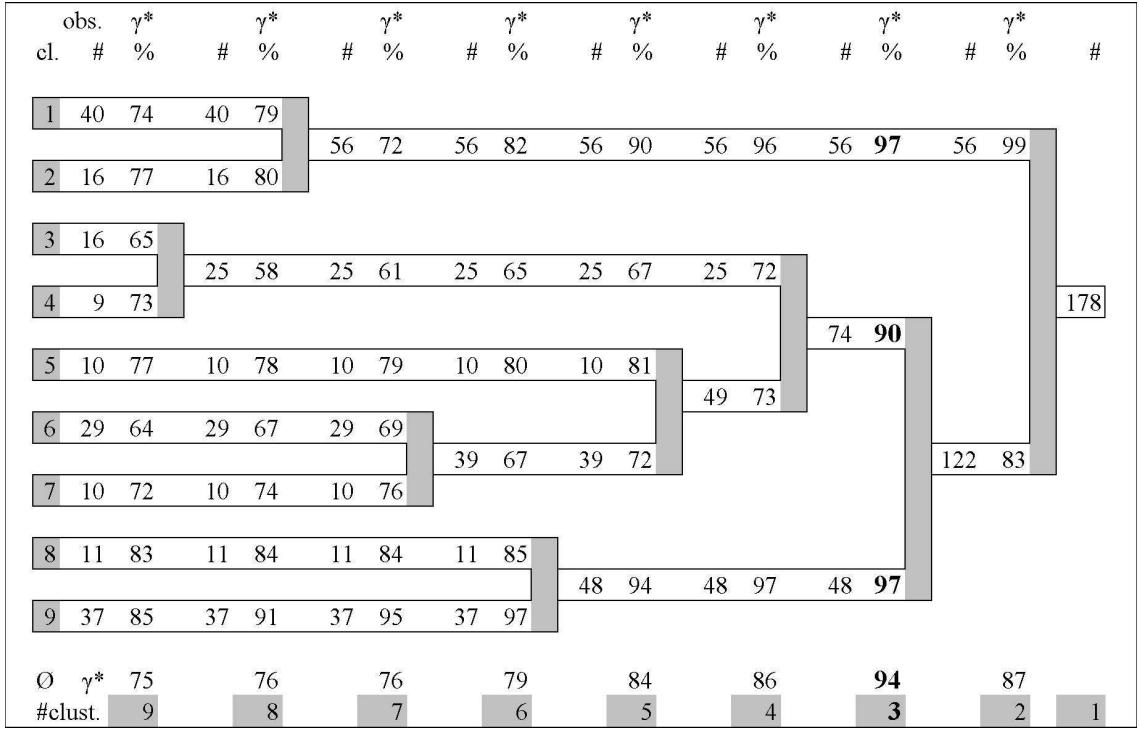


Figure 20: Dendrogram (extract) of the wine dataset with assessment of stability of nodes based on measure (13).

clusters, measures of correspondence between a cluster \mathcal{E} and a cluster \mathcal{H} such as

$$\tau(\mathcal{E}, \mathcal{H}) = \frac{|\mathcal{E} \cap \mathcal{H}|}{|\mathcal{E} \cup \mathcal{H}|} \quad (11)$$

or

$$\gamma(\mathcal{E}, \mathcal{H}) = \frac{|\mathcal{E} \cap \mathcal{H}|}{|\mathcal{E}|} \quad (12)$$

have to be defined. (\mathcal{E} and \mathcal{H} are nonempty subsets of some finite set.) Hennig [7] suggests the *Jaccard* coefficient τ (11). This measure is symmetric and it attains its minimum 0 only for disjoint sets and its maximum 1 only for equal ones. The asymmetric measure γ assesses the rate of recovery of subset \mathcal{E} by the subset \mathcal{H} . It attains its minimum 0 only for disjoint sets and its maximum 1 only if $\mathcal{E} \subseteq \mathcal{H}$ holds. We obviously have $\tau \leq \gamma$.

Now suppose, a clustering of a set of entities $\mathcal{C} = \{1, \dots, i, \dots, I\}$ into a collection of K subsets $\{\mathcal{C}_1, \dots, \mathcal{C}_k, \dots, \mathcal{C}_K\}$ of \mathcal{C} has to be investigated. Let \mathcal{C}_k be one individual cluster whose stability has to be assessed. To investigate the stability, validation techniques based on random resampling are recommended. Let us consider one simulation step: Clustering of a randomly drawn sample of the set of entities \mathcal{C} into a collection of K clusters $\{\mathcal{H}_1, \dots, \mathcal{H}_K\}$ in the same way as clustering the whole set \mathcal{C} . The definition of stability of cluster \mathcal{C}_k using measure γ (12) is based on the most similar cluster

$$\gamma_k^* = \max_{\mathcal{H}_i \in \{\mathcal{H}_1, \dots, \mathcal{H}_K\}} \gamma(\mathcal{C}_k, \mathcal{H}_i) . \quad (13)$$

By repeating resampling and clustering many times, the stability of the cluster \mathcal{C}_k can be assessed, for instance, by computing the median or the average of the corresponding values of γ_k^* . Let us denote such an estimate $\hat{\gamma}_k^*$.

Illustrating this let us have a look at the hierarchical clustering of a real data set: the wine recognition data² (for details see [15]). Altogether there are 178 Italian wines that are described by 13 constituents (variables). Here we worked with ranks instead of the original values that come from scales that are not comparable one with each other. Fig. 20 shows the schematic dendrogram of Ward's clustering for up to 9 clusters. Each node (cluster) of the binary tree is denoted by both the corresponding number of objects (symbol #) and the average rate of recovery (13) in %. The three-cluster solution is emphasized in bold type. While looking for stable clusters and for an outstanding number of clusters you should keep in mind that a hierarchy is a set of nested partitions. Therefore it is recommended to walk step by step through the binary tree (dendrogram) from the right hand side (that corresponds to the root of the tree) to the left. At each step $K - 1$ clusters remain unchanged and one cluster is divided only into two parts. Usually, the higher the number of clusters K becomes during the trip through the dendrogram the smaller amount of changes of the averaged measures of stability can be expected that are given at the bottom of the figure. Some of the clusters remain unchanged during many steps such as the cluster of 56 observations at the top of Fig. 20. However, the value of stability of this cluster decreases from 99% for the partition into 2 clusters to 72% only for the partition into 7 clusters because of the altering clusters in its neighborhood.

It is difficult to fix an appropriate threshold to consider a cluster as stable. To support the decision about stable regions, the clusters can often be visualized in low dimensional projections by applying methods like discriminant analysis (DA), PCA, and multidimensional scaling (MDS). The simulation itself is computationally expensive.

Now forget that the classes are known beforehand in the case of the three-class data that was presented above (for instance, see Fig. 6 or Fig. 7). Is it possible to confirm by simulations that there are three clusters? The simulation results concerning the determination of the number of clusters are given in Fig. 21. $D_{ih}Ex$ cluster analysis applied (pairwise clustering by the exchange method, see the result at the right hand side of Fig. 13). The simulation results are based purely on clustering of data by resampling techniques. Hubert and Arabie [8] recommended the adjusted *Rand* index R based under the assumption of the generalized hypergeometric model:

$$R = \frac{\sum_{k=1}^K \sum_{m=1}^M \binom{n_{km}}{2} - [\sum_{k=1}^K \binom{n_{k\cdot}}{2} \sum_{m=1}^M \binom{n_{\cdot m}}{2}] / \binom{n_{\cdot \cdot}}{2}}{\frac{1}{2} [\sum_{k=1}^K \binom{n_{k\cdot}}{2} + \sum_{m=1}^M \binom{n_{\cdot m}}{2}] - [\sum_{k=1}^K \binom{n_{k\cdot}}{2} \sum_{m=1}^M \binom{n_{\cdot m}}{2}] / \binom{n_{\cdot \cdot}}{2}}. \quad (14)$$

For the notations concerning \mathbf{N} see above. This measure is appropriate for the decision about the number of clusters K because it takes the value 0 when the Rand index equals its expected value for each k , $k = 2, 3, \dots, K$. The median of the *adjusted*

²<http://www.ics.uci.edu/~mlearn/MLSummary.html>

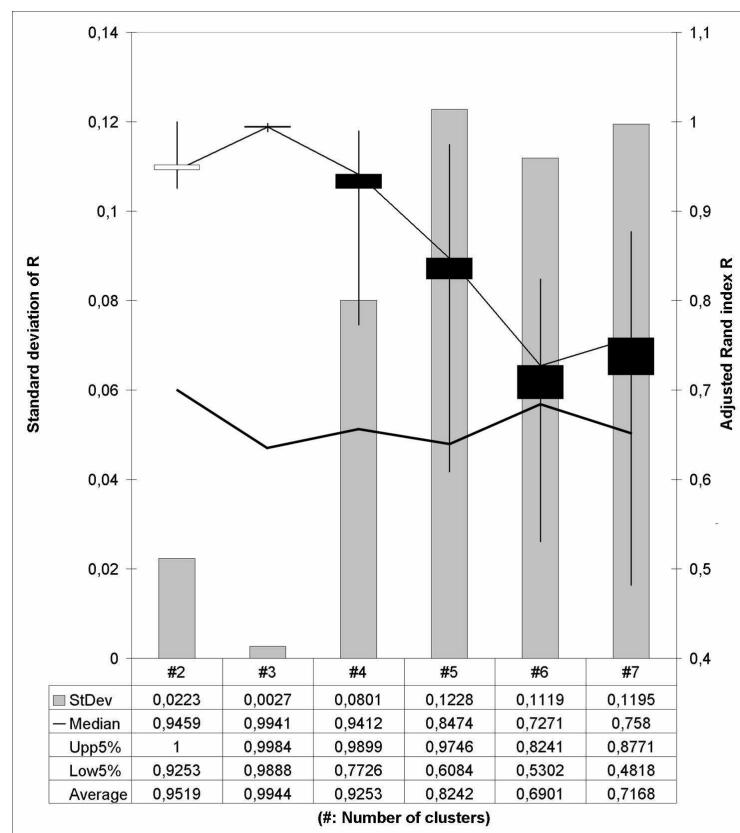


Figure 21: Statistics of the *adjusted Rand's* index versus number of clusters.

Rand's values (the scale is at the right hand side of the plot) achieved its maximum value at three clusters. Moreover, the standard deviation of the 250 *adjusted Rand's* values for each partition into $K = 2, 3, \dots$ cluster has its minimum value also at three clusters. This supports the decision for the solution into three clusters. More than three clusters are less likely because the clusters can not be confirmed to a high degree and their stability decreases rapidly. Further statistics like the average over 250 *adjusted Rand's* values are given at the bottom of the table.

Additionally, for reasons of comparison, the thick line in Fig 21 represents a so-called reference curve for the median of *adjusted Rand's* values that are obtained from randomly generated datasets without a class structure like the one shown in Fig. 14. The reference curve depends on the dimensionality J . It tends to zero if J increases. In R^{20} , for instance, the reference values are nearly equal to 0.1 for $K = 2, 3, \dots$. It should be kept in mind that a stable cluster solution in K classes, say $K = 3$ in our case, affects at least the stability of cluster analysis into $K - 1$ and $K + 1$ clusters to some degree. Or to a high degree as documented in Fig 21, where both the two-cluster and four-cluster solution have *adjusted Rand's* values that are far from the reference curve. Obviously, as also indicated in Fig 21, the influence of the true solution should become less important by going to solutions of $K + 2, K + 3, \dots$ clusters. In hierarchical cluster analysis, the influence of stable clusters can be much higher usually because they can remain unchanged during many steps of amalgamation (see Fig. 20).

Concerning adaptive weighting of the variables, for example, the aim is to estimate in automatic mode what counts and what doesn't count for finding clusters. Often the performance and stability of these methods can be improved by using them in a local fashion [14]. The improvement of stability can be measured by simulation studies such as described above.

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2 Resolving ambiguity in segmentation problems by the method of variants

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Abstract

Often feature extraction from objects in pattern recognition, such as images or acoustic signals, is ambiguous. Ambiguity occurs, in particular, in segmentation problems. In order to resolve ambiguities, the statistical method of variants has been developed in the last decade. The method is applied here to the segmentation of random, cyclic processes.

Keywords: segmentation problems, ambiguity, variant analysis, parameter estimation, sun spots

2.1 Segmentation and ambiguity

Segmentation is the decomposition of complex objects such as images or acoustic signals in simpler components. The components are subsequently analyzed and classified. Well-known examples are speech processing, see Rabiner (1989), optical character recognition, see Casey and Lecolinet (1996), gene finding in functional genetics, see Majoros (2007), www.geneprediction.org, and Fig. 22, and the chromosome classification problem, see Ritter and Gao (2008) and Fig. 23.

One encounters substantial ambiguity during the segmentation process when the object allows more than one interpretation so that it is not immediately clear where the object should be cut. In such situations it is beneficial to offer more than one solution and to postpone the resolution of the ambiguity to a later statistical analysis. The data extracted from various possible solutions for the same object are called *variants* of the object under study, see Ritter (2000), Ritter and Gallegos (2000), Ritter and Gallegos (2002). The variants make up an *ambiguous data set*. Whereas, in a classical data set, each object is represented by a single line, it may occupy several lines in an ambiguous data set, see. Fig. 24. It is there where the method of variants catches the ambiguity. Each line labelled with the same object corresponds to some interpretation, the one that comes from the correct interpretation is the (unknown) *regular variant*. It may happen that the correct interpretation is not available or has not been found. Then there is no regular variant and the object must be considered an outlier.

AGCTTTCATTCTGA^TGCAACGGCAATATG^TTCTCTGTGTGGATTAAA
 AAAGAGTGTCTGA^TAGCAGCTCTGA^TACTGGTTACCTGCCGTGA^TGTAAAT
 TAAAATTTATGA^TCTTAGGTCACTAATACTTAACCAATATAGGCATAG
 CGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGA^TAACGCATTA
 GCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGC^TGGCT
 GACCGTACAGGAAACACAGAAAAAGCCCGCACCTGA^TCAGTGC^TGGGCT
 TTTTTTCGACCAAAGGTAACGAGGTAACAAACCATGCGAGTGTGA^TAGT

Figure 22: The initial section of the genome of E. coli. Possible start and stop codons of genes, ATG and TGA, are indicated. Not every ATG initiates and not every TGA terminates a gene which gives rise to ambiguity.



Figure 23: A human metaphase (left) and the associated karyogram. Automatic segmentation of the metaphase in its 46 chromosomes displayed in the karyogram is not an easy task since the touchings and overlappings may allow several interpretations of the image thus giving rise to ambiguities.

obj1	1.23	2.34	obj1	1.23	2.34
obj2	4.26	3.00	obj1	4.26	3.00
obj3	7.28	7.42	obj2	7.28	7.42
obj4	1.91	2.84	obj2	1.91	2.84
obj5	4.02	3.04	obj2	4.02	3.04
obj6	1.02	2.04	obj3	1.02	2.04

Figure 24: Classical (left) and ambiguous data set

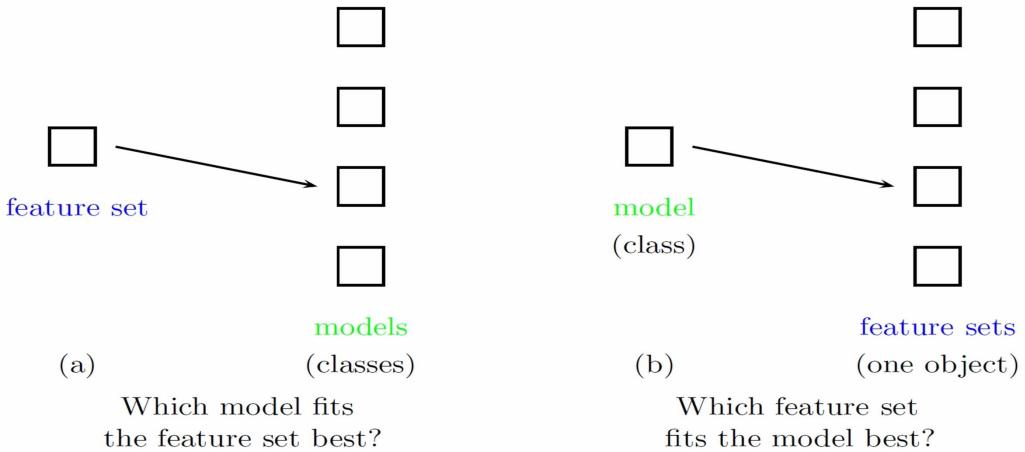


Figure 25: Comparison of classification (left) and variant selection

Of course, ambiguity occurs also in domains other than segmentation. The Fall meeting was in part dedicated to the study of a data set consisting of ancient Roman tiles, see these proceedings. The features of the data set are the contents of nineteen minerals and metals determined by a chemical analysis of probes taken from the tiles. However, the tiles are inhomogeneous so that the probes of some tiles might not be typical, see Dolata and Werr (1998/99). Since this causes errors it would be beneficial to analyze probes taken from several sites on the same tile thus creating variants. The ambiguity can be resolved in the subsequent analysis.

The simplest question about an ambiguous data set is this: given variants of one object, find its regular variant, i.e., discover the correct interpretation given some information on it. It was the subject matter of Ritter and Gallegos (2000). This question is in some sense dual to discriminant analysis, see Fig. 25. All statistical questions that arise in the study of classical data sets can also be asked for ambiguous data sets – parameter estimation, discriminant analysis, clustering, Parameter estimation in ambiguous data sets was treated in Ritter and Gallegos (2006), discriminant analysis in Ritter and Gallegos (2000) and in Ritter and Pesch (2001). Variant analysis was applied in several contexts to image analysis, in particular to the problem of chromosome classification, see Ritter and Schreib (2000, 2001), Ritter and Pesch (2001), and Ritter and Gao (2008).

2.2 Parameter estimation in ambiguous data sets

The application studied in Sect 2.3 needs parameter estimation in ambiguous data sets, the subject matter of Gallegos and Ritter (2006). In this section, I review some of the results referring the interested reader to the paper for more details and for proofs.

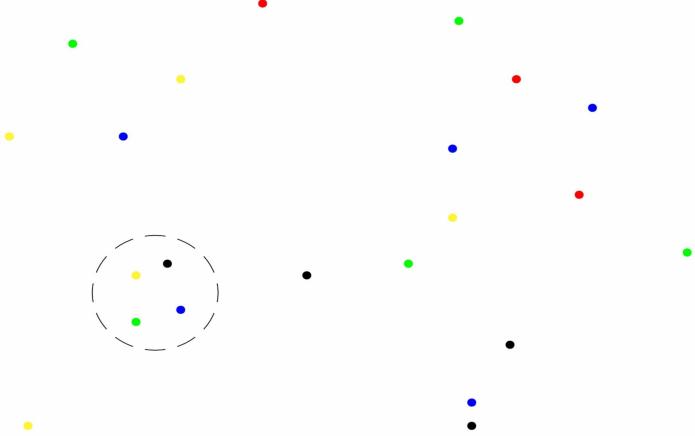


Figure 26: Scatter plot of an ambiguous data set of five objects including an outlier. Each color stands for an object, the regular variants are encircled, and the outlier is plotted in red.

Let E be a sample space. We are given an ambiguous data set $(x_i)_{i=1}^n$ of n objects, object i being observed by b_i variants $x_{i,h} \in E$, $1 \leq h \leq b_i$, i.e., $x_i = (x_{i,1}, \dots, x_{i,b_i})$. The data set may contain (gross) outliers. Fig. 26 visualizes an ambiguous data set with an outlier. The task is to estimate the positions of the regular variants in the data set and the outliers. If this has been successfully performed then it is a classical task to estimate the parameters of the regular variants. However, it is not possible to estimate these positions without knowing the model and vice versa. As a way out of this deadlock we estimate both simultaneously. To this end, we establish a statistical model of the ambiguous data set with outliers. We assume that the number of regular elements is at least r ($\leq n$). There are several models, the simplest is the *spurious variants model* which we use here. It postulates that the irregular variants of an object contain no information on its regular variant. Denoting the (unknown) set of regular objects by $R \subseteq 1..n$, we assume here for simplicity $\#R = r$ and start with the basic *ordered* model of an object $i \in R$ with (observed) number b_i of variants,

$$Z_i = (Z_{i,1}, \dots, Z_{i,b_i}) : \Omega \rightarrow E^{b_i}.$$

Here, $Z_{i,1}$ stands for the regular variant of the regular object i . It is distributed according to some probability with density function f_γ on E , $\gamma \in \Gamma$, and the family $(Z_{i,1})_{i \in R}$ of regular variants is assumed to be statistically independent. A simple way of dealing with spuriousness is to assume that the $(b_i - 1)$ -tuple of irregular variants is “flat” given the regular. Moreover, a spurious *outlier* $i \in 1..n \setminus R$ is an object that lacks a regular variant and we assume that Z_i is altogether “flat.”

Since we do not know the position of the regular variant of object i , we observe Z_i only in disorder, i.e., we observe $X_{i,k} = Z_{i,T_i(k)}$ for some random permutation T_i in

\mathcal{S}_{b_i} . The items to be estimated from these observations are the parameter $\gamma \in \Gamma$ of the regular population, the set of regular elements R , and the *variant selection* $\mathbf{h} = (h_i)_{i \in R}$, i.e., the regular variant h_i of all $i \in R$. The variant selection \mathbf{h} is a partial function on $1..n$ with support $\text{supp } \mathbf{h}$. It is shown in Gallegos and Ritter (2006) that, under some natural conditions of independence, the logarithm of the *trimmed likelihood function* of the present model is

$$\log f_{\mathbf{h}, \gamma}(x_1, \dots, x_n) = \sum_{i \in R} \log f_\gamma(x_{i, h_i}). \quad (15)$$

The likelihood function is the criterion to be optimized w.r.t. all $\gamma \in \Gamma$, all r -element subsets $R \subseteq 1..n$, and all r -tuples $(h_i)_{i \in R}$. This looks like a formidable task, but there is the following proposition which justifies an efficient, alternating algorithm. The proposition detects an improvement of the criterion before the new parameters are computed.

Proposition. Let \mathbf{h} and \mathbf{h}_{new} be two variant selections s. th.

$$\sum_{i \in \text{supp}(\mathbf{h}_{\text{new}})} \log f_{\gamma(\mathbf{h})}(x_{i, h_{\text{new}, i}}) > \sum_{i \in \text{supp}(\mathbf{h})} \log f_{\gamma(\mathbf{h})}(x_{i, h_i}). \quad (16)$$

Then the parameters computed from the “new” variant selection strictly increase the Criterion (15).

The proposition suggests the following

Reduction step.

Input: a selection \mathbf{h} ;

Output: a selection with larger Criterion (15) or the signal “stop.”

- (i) Compute the ML-estimate $\gamma(\mathbf{h})$ for the \mathbf{h} -regular observations;
- (ii) compute the log-density of each variant (i, k) , $i \in 1..n$, $k \in 1..b_i$, w.r.t. $\gamma(\mathbf{h})$;
- (iii) for each object i , determine the variant with the maximum value;
- (iv) the r largest maxima determine R_{new} and the selection \mathbf{h}_{new} ;
- (v) if \mathbf{h}_{new} satisfies (16), return \mathbf{h}_{new} ; else “stop.”

There is the following theorem.

Theorem. If the reduction step does not output the “stop” signal then it improves the Criterion (15).

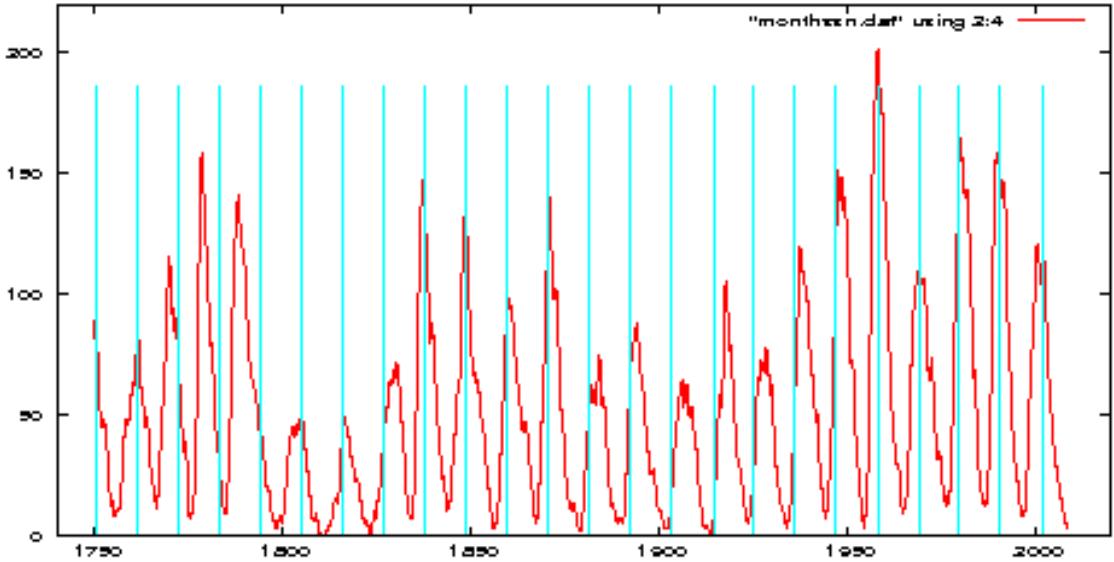


Figure 27: The time series of the smoothed numbers of sunspots. The equidistant bars show its non-periodicity.

The reduction step alternates parameter estimation, variant selection, and trimming thereby improving the criterion. In an overall algorithm one iterates reduction steps. Since there are only finitely many variant selections \mathbf{h} , the iteration must come to a standstill with the “stop”–signal at a selection–parameter pair that fit each other. The selection may be called a *minimum–distance selection* (MDS). The minimum of the criterion is an MDS but there are many others so that the algorithm has to be replicated, possibly many times, with random or purposefully chosen initial selections in order to attain a high value of the criterion.

All universal optimization paradigms, such as local ascent, the Metropolis algorithm, Gibbs–sampling, and genetic algorithms, too, may be applied to the present problem of optimizing Criterion (15).

Of course, classical data sets (with or without gross outliers) are contained in the present set-up by way of $b_i = 1$ for all i . In the normal case, Criterion (15) extends Rousseeuw’s (1985) minimum covariance determinant estimator (MCD) for robust estimation of the covariance matrix in classical data sets. Still in this case, the reduction step extends Rousseeuw and Van Driessens’s (1999) for robust parameter estimation.

2.3 Application: segmentation of a random cyclic process

The foregoing theory may be applied to the segmentation of a random cyclic process: the smoothed, monthly values of the numbers of sunspots observed since the year 1749. They are found under the URL www.sidc.be/. The time series is cyclic

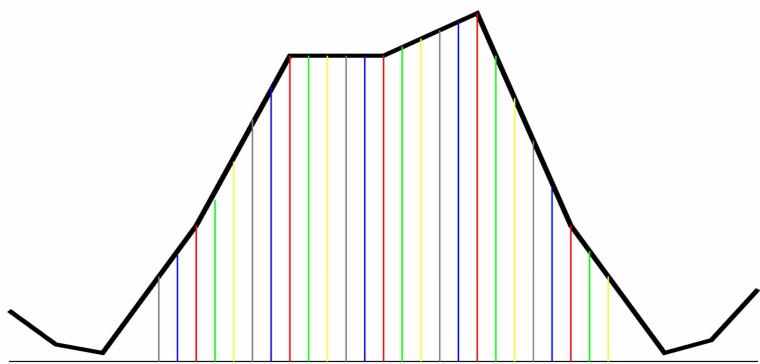


Figure 28: Variant extraction. In this graphic, a sunspot cycle is sampled equidistantly in five ways at the locations shown in different colors. Each color corresponds to a variant.

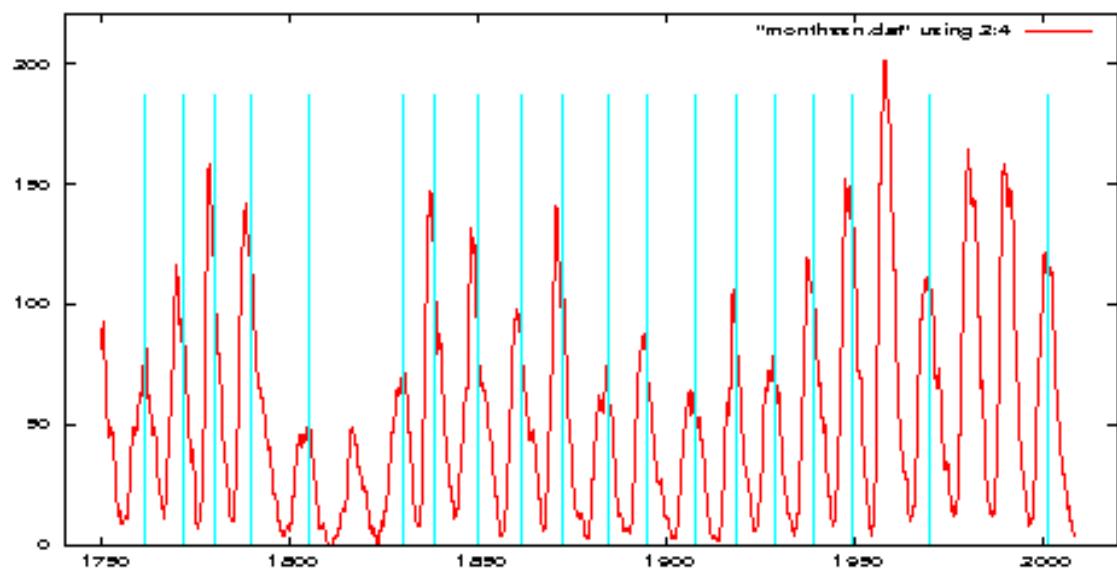


Figure 29: The sunspot cycles determined by variant analysis with four outliers.

with a cycle time of about eleven years but not quite periodic as is seen from the positions of the equidistant bars in Fig. 27. Some of them hit the peaks, others are right in between. The aim is to synchronize the 23 full cycles. To this end, we consider them the objects of our analysis. We sample each cycle at all points of the time pattern -48 -36 -24 -15 15 24 36 48 months around each peak to obtain an 8D-observation. This pattern is shifted by $-35, -30, -25, \dots, 35$ months in order to generate fifteen variants of each cycle, see a different pattern with shifts indicated by different colorings in Fig. 28. In this way each spike is represented by fifteen 8-dimensional variants and the ambiguity about the cycle phases is caught in this ambiguous data set. Variant selection and parameter estimation as described in Sect. 2.2 matches the most typical cycle phases thereby synchronizing the cycles. The algorithm was run with four discarded objects and the result is presented in Fig. 29. Interestingly, three high, good-looking cycles are discarded – although they look complete they are atypical. It is rather broken spikes that are the rule. Also a small cycle with a thin peak is discarded.

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3 Archäometrische Daten römischer Ziegel aus *Germania Superior*

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Abstract

Roman stamped bricks and tiles are under investigation coming from different findspots in *Germania Superior*. Their chemical composition was measured by X-ray fluorescence analysis. Here we describe both the archaeological background and the research aims. A data set on the chemical composition of 613 bricks and tiles was carried out using methods of cluster analysis, and the results obtained were interpreted archaeologically.

Keywords: archaeometry, X-ray fluorescence analysis, cluster analysis

3.1 Zum Inhalt der Wissenschaftsdisziplin Archäometrie

Es ist bei der Besprechung archäometrischer Daten sicher nicht ohne Wert, einleitend den Inhalt und das Anliegen der Archäometrie darzulegen. Der Name selbst – obwohl von den altgriechischen Wörtern *archaios* (alt, altehrwürdig) und *metréō* (messen) ableitbar – ist nicht antik, vielmehr geht er auf das erste Organ dieses Wissenschaftszweiges zurück: die Oxfordzeitschrift »*Archaeometry*«, die im März 1958 erstmals erschien und sich – und damit zugleich den durch sie repräsentierten Wissenschaftszweig – heute mit “*Archaeometry is an international research journal covering the application of the physical and biological sciences to archaeology and the history of art. The topics covered include dating methods, artifact studies, mathematical methods, remote sensing techniques, conservation science, environmental reconstruction, biological anthropology and archaeological theory.*” [13] definiert. Hierbei müssen unter den *physical sciences* neben der Physik auch die Chemie, Mineralogie, Geologie, Astronomie und andere, von den biologischen und medizinischen Richtungen verschiedene Naturwissenschaften verstanden werden. Weiterhin kommen in der Archäometrie viele Technikwissenschaften zur Anwendung, und auf der Seite der Geisteswissenschaften ist in dieser Hinsicht außer der Mathematik zumindest noch die Philologie zu erwähnen. Fig. 30 zeigt vereinfacht die „Stützen“ der Archäometrie, die sich in naturwissenschaftliche (einschließlich technische), geisteswissenschaftliche und zwischen diesen beiden einzuordnende unterscheiden lassen.

Die Archäometrie im modernen, derzeitigen Sinne hat sich erst in den 1950er Jahren herausgebildet und etabliert, ihre Anfänge gehen aber bereits auf das letzte Jahrzehnt

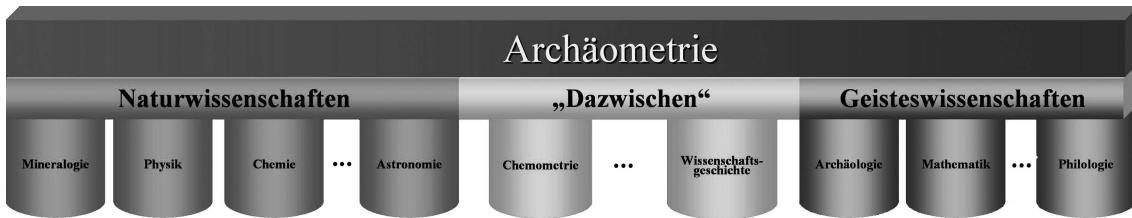


Figure 30: Die „Stützen“ der Archäometrie

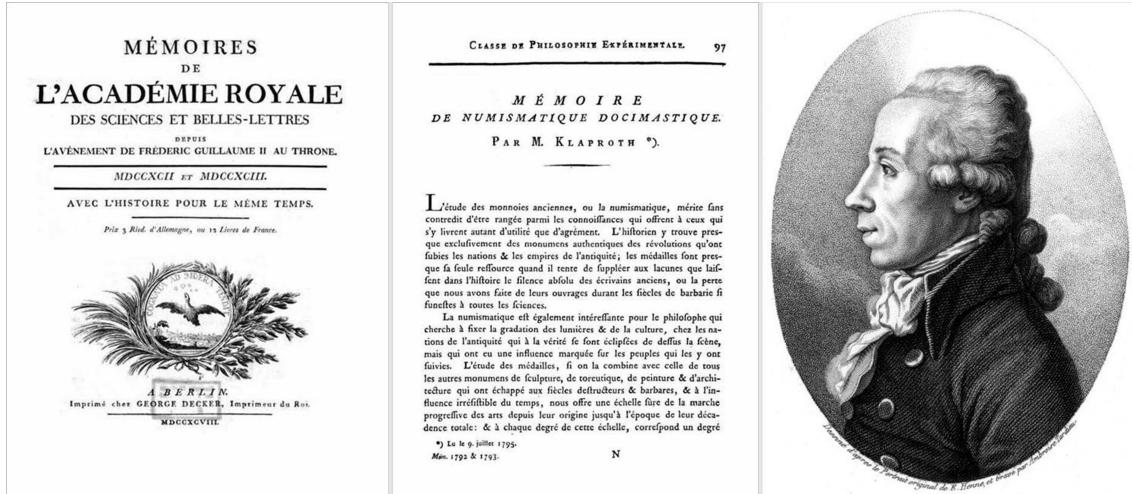


Figure 31: Martin Heinrich Klaproth und die erste Publikation archäometrischen Inhalts

des 18. Jahrhunderts zurück. Es handelt sich dabei um chemisch-analytische Untersuchungen von griechischen und römischen Münzen, welche der Chemiker und Apotheker Martin Heinrich Klaproth (1743–1817) (Fig. 31) in seinem Berliner Privatlaboratorium vorgenommen hatte. An der Königlich Preußischen Akademie der Wissenschaften zu Berlin, deren ordentliches Mitglied Klaproth seit 1788 war, stellte er 1795 seine diesbezüglichen Ergebnisse vor. Dieser erste Vortrag archäometrischen Inhalts, «*lu le 9. juillet 1795*», ist 1798 in französischer [3] (Fig. 31) und ein Jahr später in deutscher Sprache [4] publiziert worden.

Von den zitierten, in [13] genannten “topics” der Archäometrie muss Klaproths erste und nachfolgende Arbeiten sowie eine Anzahl weiterer anderer Forscher im 19. Jahrhundert zu den “artifact studies” gerechnet werden, die man erweiternd als Gebiet der archäometrischen Materialuntersuchungen verallgemeinern kann. Diese Richtung wird für die hier zu schildernden Untersuchungen von Bedeutung sein. Von spezielleren Arbeitsrichtungen wie der Archäoastronomie abgesehen, lässt sich die Archäometrie neben den Materialuntersuchungen in zwei weitere Hauptrichtungen untergliedern, die hier nur genannt, in den weiteren Ausführungen aber keine Rolle spielen werden. Hierher gehören die naturwissenschaftliche Datierung bzw.

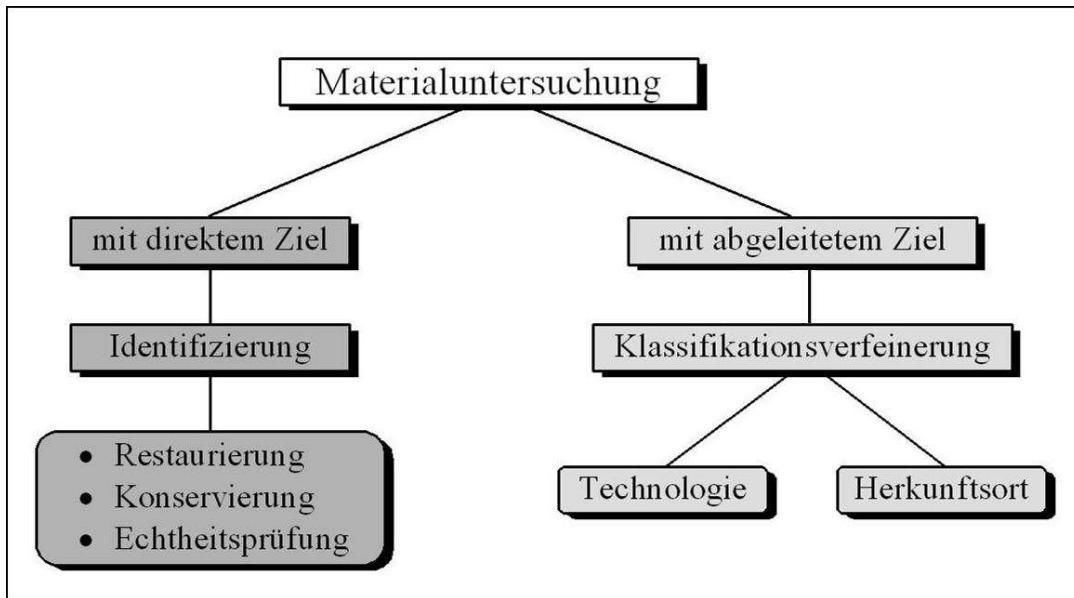


Figure 32: Ziele der archäometrischen Materialuntersuchung

Altersbestimmung – etwa vermittels ^{14}C -, Thermolumineszenz-Methode u.a. – und die Prospektion (lat. *prospicio* = voraussehen, ausschauen – also die Erkundung und Erfassung archäologischer Stätten eines Gebietes), wobei neben anderen an die Bio- und geophysikalische Prospektion (Sondierung von Unbekanntem unter der Erdoberfläche) zu denken ist.

3.2 Ziele archäometrischer Materialuntersuchungen

„Das Gebiet der Materialuntersuchungen ist das am weitesten verzweigte und aufgefächerte Teilgebiet der Archäometrie.“ stellte Hans Mommsen fest ([6], S. 65). Fig. 32, in der die beiden wesentlichen Ziele dieser Richtung aufgezeigt werden, stellt gewissermaßen graphisch verdichtete Aussagen Mommsens dar ([6], S. 12–14, 66).

Materialuntersuchungen mit der direkten Zielsetzung der Identifizierung sind im Zusammenhang mit dem hier Darzustellenden ohne Interesse. Die zu beschreibenden Untersuchungen von Ziegeln auf der Grundlage ihrer Materialanalyse und deren mathematisch-statistische Auswertung verfolgt das abgeleitete Ziel einer verfeinerten Klassifizierung. Dabei sollte die Verfeinerung darin bestehen, die bekannten Klassifikationsmerkmale der betrachteten Ziegel wie beispielsweise ‘grobe Tonkeramik’, ‘römisch’ oder ‘geziegelt von Legion Nr. ...’ durch die Angabe ihrer Provenienz, d.h. ihres Herstellungsortes zu präzisieren. Die Frage nach der Herstellungsart bzw. der Technologie der Ziegelproduktion spielte hier keine Rolle.

Rohstoff	Ein <i>anorganisch-nichtmetallisches pulvriges</i> Material
Prozess I (Formung)	wird <i>plastisch</i> geformt
Prozess II (Brennen)	und anschließend durch <i>Wärmeeinwirkung (Hitze)</i>
Produkt	in einen <i>irreversibel verfestigten</i> Werkstoff umgewandelt.

Figure 33: Definition des Werkstoffs Keramik

3.3 Zum Werkstoff Keramik

Da die zugrunde liegende Materialart die Auswahl und Anwendung der heranzuhziehenden Untersuchungs- oder Analysemethode bzw. -methoden und in gewissem Umfang auch der benutzten mathematisch-statistischen Verfahren der Auswertung beeinflusst, sei eine kurze Betrachtung des Materials Keramik, aus dem (gebrannte) Ziegel bestehen, vorgenommen. Die Definition eines Keramikwerkstückes lässt sich durch Charakterisierung des Ausgangsstoffes, der beiden grundsätzlichen Prozess-Schritte bei der Herstellung und des Endproduktes vornehmen, wie es in der Übersicht (Fig. 33) entnommen werden kann. Dabei sind die wesentlichen Aussagen kursiv gesetzt.

Bildet das Lockergestein Ton (plastische Bestandteile: verschiedene Tonminerale, nichtplastische Bestandteile: Quarz, Feldspäte, Calcit, Dolomit, Glimmer u.a.) den wichtigen Bestandteil des anorganischen Rohstoffpulvers, so heißt der erzeugte Werkstoff Tonkeramik oder auch einfach nur Keramik. Gebrannte Ziegel, gefertigt aus Ton, Lehm, Löß oder Letten, gehören also zu dieser Werkstoffklasse. Andere Keramikarten, wie etwa die Oxidkeramiken, zu welchen die bereits in der Antike gefertigte Quarzkeramik zählt, brauchen hier folglich nicht betrachtet zu werden.

Das Material der Tonkeramik, der Scherben, ist inhomogen aus verschiedenen kristallinen und amorphen (glasigen) Bestandteilen zusammengesetzt. Sind alle Inhomogenitäten mit bloßem Auge nicht erkennbar (Korngrößen < 0,2 mm), so spricht man von Feinkeramik, anderenfalls von Grobkeramik. Die nach [2] gestaltete Übersicht (Fig. 34) zur Einteilung der tonkeramischen Werkstoffe verdeutlicht, dass es sich bei gebrannten Ziegeln um einen porösen grobkeramischen Werkstoff handelt.

Diese Tatsache muss beispielsweise bei den Probenahmen beachtet werden, da ein zu kleiner Bereich, aus welchem Material entnommen wird bzw. welcher einer analytischen Untersuchung unterzogen wird, nicht repräsentativ für die interessierende mittlere chemische Zusammensetzung oder andere Eigenschaften des Werkstücks zu sein braucht.

Dieser Inhomogenität der Ziegel ist eine Arbeit von J. Dolata und U. Werr [1] gewidmet, in welcher auf einem einzigen *later* an zehn verschiedenen Stellen relativ große Probemengen entnommen (Fig. 35) und analysiert wurden. Zu dieser Publikation [1] siehe auch den Beitrag von Gunter Ritter in diesem Report (Sect. 2).

Tonkeramische Werkstoffe	grob	porös (WAF > 6%)	Ziegel (gebrannt), ...
		dicht (WAF ≤ 6%)	Klinker, ...
	fein	porös (WAF > 2%): Tongut	Irdengut Steingut
		dicht (WAF ≤ 2%): Tonzeug	Steinzeug Porzellan

Figure 34: Einteilung der keramischen Werkstoffe (WAF: Wasseraufnahmefähigkeit)

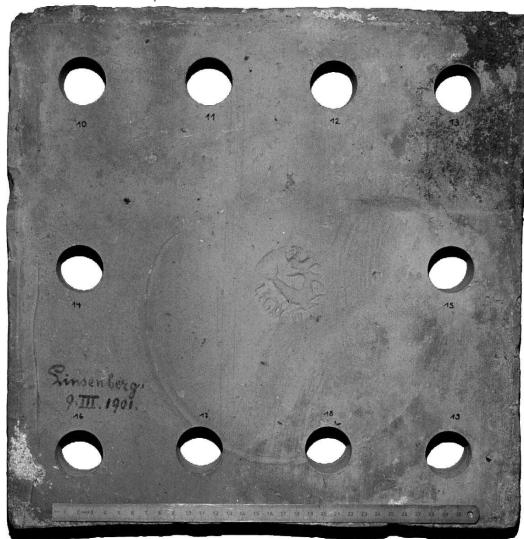


Figure 35: Auf Homogenität bzw. Inhomogenität beprobter Ziegel [1] (*later der LEG(egionis) XXII P(rimigeniae) P(iae) F(idelis)*, hadrianisch, Herstellungs-Provenienz: Frankfurt-Nied, 38 x 38 x (4,5-5) cm)

3.4 Archäologische Fragestellung und Bestimmung der archäometrischen Daten

Die untersuchten römischen Ziegel (*tegulae, lateres, imbrices, tubuli* etc.) stammen aus Fundorten, die auf dem Gebiet der römischen Provinz *Germania Superior* (Obergermanien) liegen. Wie es in den Provinzen üblich war, wurden die Ziegel in Heeresziegeleien produziert. Die damit beauftragten militärischen Einheiten (Legionen, Kohorten) versahen eine größere Anzahl ihrer Erzeugnisse mit ihrem Stempel. Die hier in Betracht gezogenen Ziegel trugen eine solche Kennzeichnung der jeweiligen Militäreinheit, aus der sich mehrere archäologische Informationen ablesen lassen.

Da der Fundort eines Ziegels im Allgemeinen nicht mit seinem Herstellungsort übereinstimmt, bestand die an die Archäometrie gestellte Frage darin, mit naturwissenschaftlichen und mathematischen Methoden Aussagen zur Lokalisierung von Heeresziegeleien in Obergermanien zu erarbeiten. Aus der Kenntnis dieser Provenienzen und der ihnen zugeordneten Ziegel bzw. Stempeltypen etc. sind weitere archäologische und historische Feststellungen zu erwarten.

Zur Lösung dieser Aufgabe wurden 613 Ziegel beprobt und deren chemische Zusammensetzung ermittelt. Da man davon ausgehen kann, dass eine Tonlagerstätte ein typisches chemisches Zusammensetzungsmuster (CZM) besitzt, das sich von dem anderer unterscheidet und dass diese Lagerstätte die Rohstoffquelle einer gesuchten, in ihrer Nähe liegenden Heeresziegelei ist, sollte es möglich sein mit Hilfe von Referenzmaterial und durch Einsatz von Verfahren der automatischen Klassifikation Gruppierungen der Ziegel zu erhalten, die einer in ihrer Lokalität bekannten oder auch unbekannten Ziegelei zugeordnet werden können. Mit anderen Worten: Es gilt die Annahme, dass eine Rohstoffquelle/Tongrube mit typischem, durch den Produktionsprozess unverändertem CZM mit einem Ziegeleiorb korrespondiert.

Als Methode für die chemische Analyse wurde die wellenlängendiffusive Röntgenfluoreszenzanalyse (WD-RFA) ([6], S. 99–107) benutzt. Hier wird die Erscheinung der Fluoreszenz ausgenutzt, deren Zustandekommen in einem nach dem polnischen Physiker Alexander Jablonski (1898–1980) benannten Diagramm sehr schematisch erklärt wird (Fig. 36): Die Absorption von elektromagnetischer Strahlung $h\nu_A$ (h : Plancksches Wirkungsquantum, ν : Frequenz) – im Falle der RFA Röntgenlicht – bewirkt eine Anregung von Elektronen aus Niveaus niedrigere Energie in solche höherer Energie. Die Rückkehr in den energetisch bevorzugten Zustand geschieht bei der Fluoreszenz in zwei Schritten, einem strahlunglosen Übergang in ein Niveau niedrigerer Energie und der nachfolgenden Rückkehr in den Ausgangszustand unter Emission der Fluoreszenzstrahlung $h\nu_F$ mit $\nu_F < \nu_A$.

Da eine bestimmte Atomsorte durch eine typische Menge von Energieniveaus $E_i = h\nu_i = \frac{hc}{\lambda_i}$ (c : Lichtgeschwindigkeit, λ : Wellenlänge) charakterisiert ist, lässt sich beim Auftreten bestimmter Frequenzen bzw. Wellenlängen bei der Fluoreszenz (charakteristische Röntgenlinien) auf das Vorhandensein entsprechender Atomsorten bzw. chemischer Elemente schließen (qualitative Analyse). Die Intensität der jeweilig

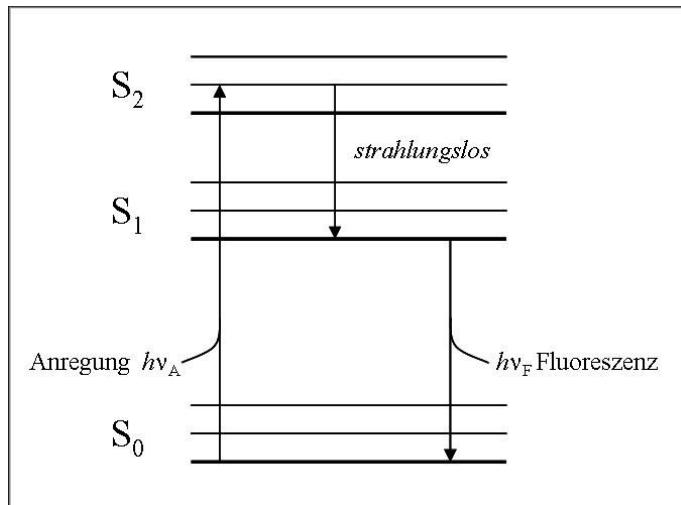


Figure 36: Schematisches Jablonski-Diagramm zur Erläuterung der Fluoreszenz

zugehörigen Strahlung ist der Anzahl der Atome des Elements proportional (quantitative Analyse). In einem Röntgen-Fluoresenzspektrum (Abszisse/Qualität: Energie, Frequenz, Wellenlänge; Ordinate/Quantität: Intensität) somit die Informationen über die in einer untersuchten Probe vorhandenen chemischen Elemente und deren Menge (Gehalt) enthalten.

Das Schema einer WD-RFA-Messanordnung, mit der solche Spektren aufgenommen werden können, wobei die Empfindlichkeit und Selektivität größer ist als der alternativen energiedispersiven RFA, zeigt Fig. 37. Die Wirkung des Analysator- oder Bragg-Kristalls beruht auf der Anwendung der nach William Henry Bragg (1862–1942) und William Lawrence Bragg (1890–1971) benannten Gleichung $n\lambda = 2d \sin \theta$, wobei d der Abstand der Gitterebenen des Kristalls und n die (ganzzahlige) Interferenzordnung sind. Damit ist die Wellenlängen λ und somit die Energie mit dem durch Drehung des Bragg-Kristalls einstellbaren Glanzwinkel θ in direkte Verbindung gebracht. Der gemäß dem Reflexionsgesetz nachzustellende Detektor misst die auftreffende Menge der Röntgenstrahlung.

Die Vermessung der 613 Ziegel-Proben mit der WD-RFA wurde im Laboratorium von Gerwulf Schneider an der Freien Universität Berlin durchgeführt.

Entsprechend der im vorhergehenden Absatz erwähnten Inhomogenität wurden den untersuchten Ziegeln verhältnismäßig große zylindrische Proben entnommen (vgl. Fig. 35). Um eine gewisse Homogenisierung des Materials zu erhalten, wurden diese anschließend pulverisiert. Unter Verwendung von Lithiumborat wurden aus dem Pulver die zu vermessenden Schmelztabletten hergestellt. (Die im Lithiumborat enthaltenen Elemente Lithium, Bor und Sauerstoff werden von der RFA nicht erfasst.)

Die ermittelten Masse-Anteile von 19 chemischen Elementen wurden für diese Auswertung benutzt. Dabei handelt es sich um

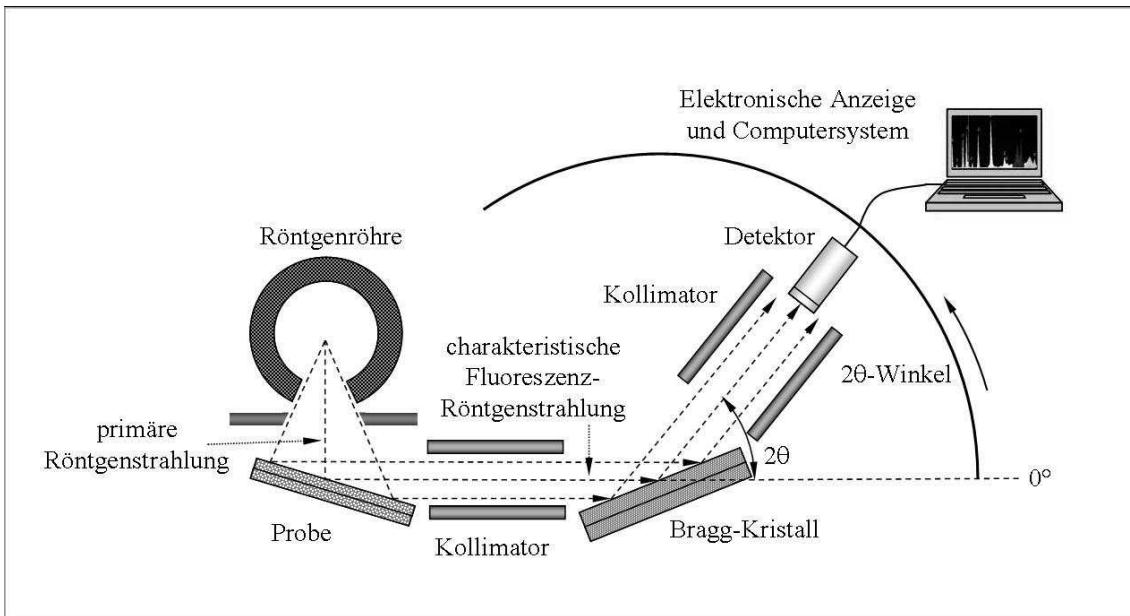


Figure 37: Schema einer Messanordnung der wellenlängendiffusiven Röntgenfluoreszenzanalyse

- neun Hauptelemente (Angabe als Oxid, Maßangabe: %): Natrium (Na_2O), Magnesium (MgO), Aluminium (Al_2O_3), Silizium (SiO_2), Kalium (K_2O), Calcium (CaO), Titan (TiO_2), Mangan (MnO), Eisen (Fe_2O_3) sowie
- zehn Spurenelemente (Angabe als Element, Maßangabe: ppm): Vanadium (V), Chrom (Cr), Nickel (Ni), Zink (Zn), Rubidium (Rb), Strontium (Sr), Yttrium (Y), Zirkonium (Zr), Niob (Nb), Barium (Ba).

Einige weitere ebenfalls bestimmte Gehalte wie beispielsweise diejenigen von Phosphor (P_2O_5), Chlor (Cl), Kupfer (Cu) und Zinn (Sn) wurden im Weiteren nicht berücksichtigt, da entweder die Messwerte apparativ bedingt zu ungenau sind oder – wie beim Phosphor – eine Kontamination von phosphorhaltigen Substanzen (z.B. Phosphaten) während der Bodenlagerung der Ziegel nicht auszuschließen ist.

Das Ergebnis der archäometrischen Messungen bestand somit in einer 613×19 -Datenmatrix $\mathbf{X}^{(0)} = (x_{ij}^{(0)})$, die unter Anwendung von Verfahren der multivariaten Statistik, insbesondere der Clusteranalyse ausgewertet werden musste.

3.5 Datenaufbereitung und -auswertung – Clusteranalyse

Beim Betrachten der folgenden Übersicht der (gerundeten) Minimal-, Maximal- und Mittelwerte der 19 Variablen (Fig. 38) stellt man fest, dass der Wertebereich zahlenmäßig, d.h. ohne Berücksichtigung der Maßangabe fast fünf Zehnerpotenzen von 10^{-2} (Minimum MnO) bis $9,14 \cdot 10^2$ (Maximum Ba) umfasst. Ähnlich verhält

Variable	SiO ₂	TiO ₂	Al ₂ O ₃	Fe ₂ O ₃	MnO	MgO	CaO	Na ₂ O	K ₂ O
Maßangabe	%								
Minimum	51,14	0,43	9,00	2,58	0,01	0,49	0,18	0,11	1,14
Maximum	81,10	2,52	25,10	9,97	0,14	4,14	21,50	1,30	6,07
Mittelwert	68,05	0,90	15,28	4,61	0,06	1,74	5,85	0,61	2,74

Variable	V	Cr	Ni	Zn	Rb	Sr	Y	Zr	Nb	Ba
Maßangabe	<i>ppm</i>									
Minimum	44	47	3	13	69	67	17	103	1	256
Maximum	147	323	123	361	193	474	52	421	65	914
Mittelwert	82	109	49	73	132	201	30	215	21	477

Figure 38: Übersicht über den Wertebereich und die Mittelwerte der 19 Variablen

es sich mit den Mittelwerten: $6 \cdot 10^{-2}$ (MnO) bis $4,77 \cdot 10^2$ (Ba). Eine Umrechnung der Angaben von Prozent in *ppm* ($1\% = 10^4\text{ ppm}$) oder umgekehrt würde den Zahenumfang noch erweitern: 1 *ppm* (Minimum Nb) bis $8,11 \cdot 10^5\text{ ppm}$ (Maximum SiO₂).

Die Werte der einzelnen Variablen mussten also hinsichtlich ihrer Größenordnungen für die Clusteranalyse vergleichbar gemacht werden. Als besonders geeignet hat sich dafür erwiesen, die Werte $x_{ij}^{(0)}$ jeder der 19 Variablen jeweils durch deren Mittelwert $\bar{x}_j^{(0)}$ zu dividieren, d.h., die folgende Transformation

$$\mathbf{X}^{(0)} = (x_{ij}^{(0)}) \longrightarrow \mathbf{X}^{(v)} = (x_{ij}^{(v)})$$

mit

$$x_{ij}^{(0)} \longrightarrow x_{ij}^{(v)} = \frac{x_{ij}^{(0)}}{\bar{x}_j^{(0)}}$$

und

$$\bar{x}_j^{(0)} = n^{-1} \sum_{q=1}^n x_{qj}^{(0)} \quad (j = 1, 2, \dots, 19)$$

durchzuführen. Dabei ist n die Anzahl der betrachteten Objekte (Proben), für den gesamten Datensatz beträgt also $n = 613$.

Bei dieser Transformation ist die Standardabweichung der transformierten Variablen gleich dem Variationskoeffizienten der ursprünglichen, d.h. gemessenen. Alle transformierten Variablen haben denselben Mittelwert $\bar{x}_j^{(v)} = 1$.

Zur Lösung der archäologischen Fragestellung nach der Provenienz der Heeresziegel wurde der Datensatz $\mathbf{X}^{(v)} = (x_{ij}^{(v)})$ mit $n \leq 613$ Objekten mittels hierarchischer und partitionierender Verfahren der Clusteranalyse in Klassen zerlegt. Hinsichtlich der jeweils zugrunde liegenden Theorie siehe beispielsweise [5], [7–10]

und [12]. Eine beschreibende Übersicht über die mit den Ziegeluntersuchungen herangezogenen Verfahren ist in [A5] zu finden.

Im Einzelnen wurden hauptsächlich benutzt:

- (a) das hierarchische Verfahren nach J.H. Ward [12], basierend auf dem Varianzkriterium

$$V_k = \text{tr}\left(\sum_{\alpha=1}^k \mathbf{W}_\alpha\right) \longrightarrow \text{Minimum}$$

$$(\mathbf{W}_\alpha = \sum_{i \in C_\alpha} (\mathbf{x}_i - \bar{\mathbf{x}}_\alpha)(\mathbf{x}_i - \bar{\mathbf{x}}_\alpha)^T: \text{Produktsummenmatrix für die } \alpha\text{-te Klasse } C_\alpha).$$

Das Ward-Verfahren wurde für die Datenanalyse im Rahmen der archäometrischen Ziegeluntersuchungen ausgewählt, da es zu den wenigen hierarchischen Verfahren gehört, die sich aus einem statistischen, auf Verteilungsannahmen über die Daten basierenden Modell ableiten lässt.

- (b) das modifizierte Ward-Verfahren mit dem Zielkriterium

$$V_k^{\log} = \sum_{\alpha=1}^k n_\alpha \log \text{tr}\left(\frac{\mathbf{W}_\alpha}{n_\alpha}\right) \longrightarrow \text{Minimum}$$

(logarithmiertes gemitteltes Varianzkriterium), wobei n_α die Masse der Klasse C_α bedeutet.

Dieses Verfahren ist geeignet, wenn in einigen Klassen bei großer Variablenanzahl nur geringe Objektanzahl vorhanden ist. Das ist bei den römischen Ziegelproben tatsächlich der Fall.

- (c) das auf John B. MacQueen [5] zurückgehende partitionierende k -Means-Verfahren

Dieses Verfahren sucht nach lokalen Minima des unter (a) genannten Varianzkriterium V_k , das die Fehlerterme zu den Klassenmitteln (Zentren) summiert.

- (d) die zentrenfreie Variante zum k -Means-Verfahren

Hier werden die unter (a) bzw. (b) genannten Varianzkriteria zentrenfrei formuliert:

$$V_k = \text{tr}\left(\sum_{\alpha=1}^k \mathbf{W}_\alpha\right) = \sum_{\alpha=1}^k \frac{1}{n_\alpha} \sum_{x_i \in C_\alpha} \sum_{x_h \in C_\alpha, h > i} d_{ih}^{E^2}$$

bzw.

$$V_k^{\log} = \sum_{\alpha=1}^k n_\alpha \log \text{tr}\left(\frac{\mathbf{W}_\alpha}{n_\alpha}\right) = \sum_{\alpha=1}^k n_\alpha \log\left(\sum_{x_i \in C_\alpha} \sum_{x_h \in C_\alpha, h > i} \frac{1}{n_\alpha^2} d_{ih}^{E^2}\right),$$

wobei

$$d_{ih}^{E^2} = \|\mathbf{x}_i - \mathbf{x}_h\|^2 = \sum_{j=1}^l (x_{ij} - x_{hj})^2$$

die quadrierte euklidische Distanz zwischen den Beobachtungen \mathbf{x}_i und \mathbf{x}_h und l die Variablenanzahl sind.

(e) die adaptive Variante des k -Means-Verfahrens

Statt der quadrierten euklidischen Distanz $d_{ih}^{E^2}$ wird die gewichtete quadrierte euklidische Distanz

$$d_{\mathbf{Q}}^2 = \|\mathbf{x}_i - \mathbf{x}_h\|_{\mathbf{Q}}^2 = \sum_{j=1}^l q_j |x_{ij} - x_{hj}|^2$$

zwischen den Beobachtungen \mathbf{x}_i und \mathbf{x}_h benutzt, wobei die q_j nichtnegative Gewichte sind, die im Iterationsprozess adaptiv bestimmt werden.

3.6 Auswertung und archäologische Interpretation

In einem Anhang (s.u.) wurden diejenigen Publikationen aufgelistet, die sich mit der Anwendung mathematisch-statistischer Methoden bei Untersuchungen obergermanisch-römischer Ziegel beschäftigen. Bei den letzteren handelt es sich in der Mehrzahl der Fälle um solche, deren archäometrische Daten in der oben beschriebenen Matrix erfasst sind.

In diesem Abschnitt sollen einige der wichtigsten Aussagen und Resultate dargestellt werden, welche aus der multivariaten statischen Analyse dieses Datensatzes ablesbar sind.

Die Clusteranalyse mit dem ursprünglichen Verfahren nach Ward ließ insbesondere zwei Gesichtspunkte deutlich werden: (A) Die gewonnene optimale Zerlegung in acht Klassen entspricht in großen Zügen der archäologischen Erfahrung. (B) Die ermittelten Klassen sind in ihrer Stärke sehr unterschiedlich, so dass es – wie im vorhergehenden Abschnitt erwähnt – sinnvoll ist, das modifizierte Ward-Verfahren zur Anwendung zu bringen. Obwohl das erhaltene Klassifikationsergebnis als eine positive Hypothesenstütze zu werten ist, wurde es im Hinblick auf die Komplexität der archäologischen Fragestellung als „*nur eine Vor-Interpretation von Daten*“ aufgefasst und berücksichtigt, dass in diesem Sinne Verfahren der automatischen Klassifikation „*den Charakter von numerischen Experimenten haben, die Korrelationen aufzeigen können aber nicht Kausalitäten.*“ [11]. Daher wurde das Resultat durch die archäologische Erfahrung leicht ‘überformt’ [A5], [A9], [A23], wie es der nicht einheitlich durchgehende („schiefe“) Schnitt im Dendrogramm zeigt (Fig. 39).

Auf diese Weise ließen sich insgesamt sieben Orte von Heeresziegeleien erkennen,

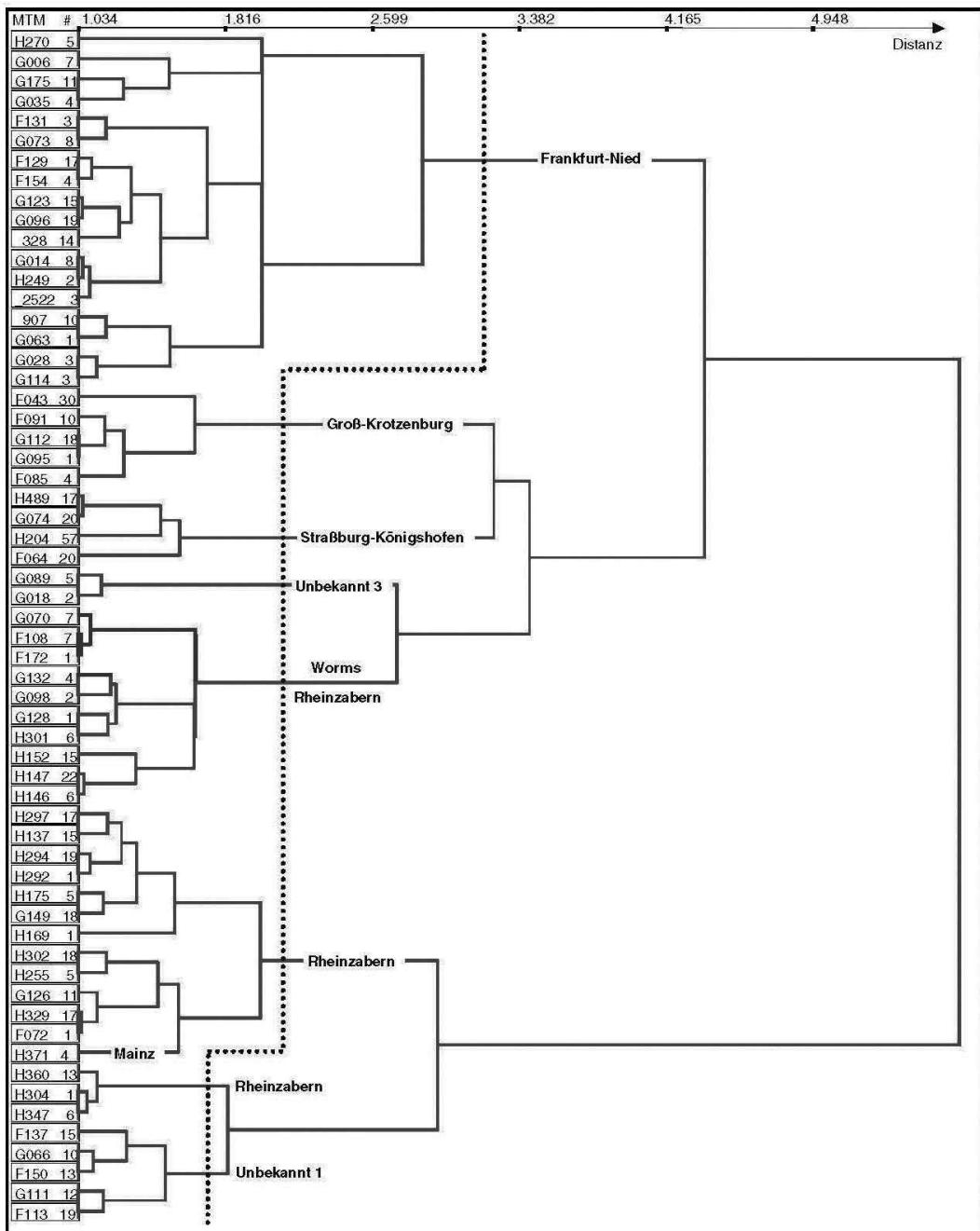


Figure 39: Rechter Teil des Dendrogramms (Ward-Verfahren) mit schiefem Schnitt unter Einbeziehung archäologischen Erkenntnisstandes (MTM: *Most Typical Member*)

Heeresziegelei-Ort	Lateinischer Name	Heutiges Land	Abkürzung	Objektanzahl
Rheinzabern	<i>Taberna</i>	Rheinland-Pfalz	Rh	192
(Frankfurt-)Nied	<i>Nidda</i>	Hessen	FN	137
Straßburg-Könighofen	<i>Argentorate</i>	Elsass (Frankreich)	SK	113
Unbekannt 1			U1	67
Groß-Krotzenburg		Hessen	GK	63
Worms (ehemals 'Unbekannt 2')	<i>Borbetomagnus</i>	Rheinland-Pfalz	Wo	19
Unbekannt 3			U3	7

Figure 40: Zur Lokalisierung von Heeresziegeleien

von denen fünf benennbar und zwei hinsichtlich ihrer Provenienz bisher noch nicht festlegbar sind. Die Übersicht (Fig. 40) präzisiert diese Aussage.

Weiterhin gibt es eine kleine Referenzgruppe mit vier Proben von neuzeitlichen Ziegeln aus Mainz und eine Sonderklasse von elf nicht referenzfähigen Objekten.

Das archäologisch überformte Ergebnis der Clusteranalyse nach Ward ist in Form eines Hauptkomponentenplots in Fig. 41 dargestellt.

Bei der Anwendung des modifizierten Ward-Verfahrens konnten wiederum acht Klassen ('Cluster Nr. 1' bis 'Cluster Nr. 8') als optimale Zerlegung des Datensatzes abgeleitet werden (Ellenbogentest). Fig. 42 verdeutlicht dieses Ergebnis.

In der Pivot-Tabelle (Fig. 43) sind die beiden Clusteranalysen-Resultate gegenübergestellt worden.

Aus dieser Übersicht ist ersichtlich, dass die Klassen 'Straßburg-Könighofen', 'Groß-Krotzenburg' und 'Unbekannt 3' als stabil bezeichnet werden können. Die der Provenienz Frankfurt-Nied zugeordneten Proben lassen sich in zwei Klassen aufspalten. Ähnlich verhält es sich mit der Provenienz Rheinzabern. Allerdings enthält 'Rheinzabern A' die ursprünglich 'Unbekannt 1' zugeordneten Ziegel und 'Rheinzabern B' diejenigen einer Wormser Heeresziegelei. Es konnte aber in einigen Arbeiten, die jeweils den relevanten Teildatensatz analysierten, gezeigt werden, dass die Frankfurt-Nied zugeordneten Ziegel signifikant in zwei Klassen aufgeteilt werden können ([A6], [A17]) und dass sich ebenso sowohl 'Worms' [A10] als auch 'Unbekannt 1' [A12] von den Rheinzabern-Klassen unterscheiden lassen. Schließlich erwies sich die Aufteilung der Ziegel mit der Provenienz Rheinzabern auf zwei Klassen als annehmbar. Diese Aussagen sind auch mit der in Fig. 44 wiedergegebenen zweidimensionalen Dichteschätzung vereinbar.

Um das Ergebnis der Klassifikation mit dem modifizierten Ward-Verfahren zu demonstrieren, wurde die Distanzmatrix $\mathbf{D} = (d_{ij})$ in der Weise graphisch dargestellt, dass bestimmte Intervalle der Distanzwerte durch eine Grauwertstufe wiedergegeben werden. Hier wurde die Festlegung getroffen, steigende Unähnlichkeit in zehn Stufen von Schwarz bis Weiß zu unterscheiden. In Fig. 45 ist die Distanzmatrix auf diese Weise in einem repräsentativen Auszug (251 Objekte) dargestellt, wobei Zeilen und Spalten nach der 1. Hauptachse (Fig. 42) sortiert wurden.

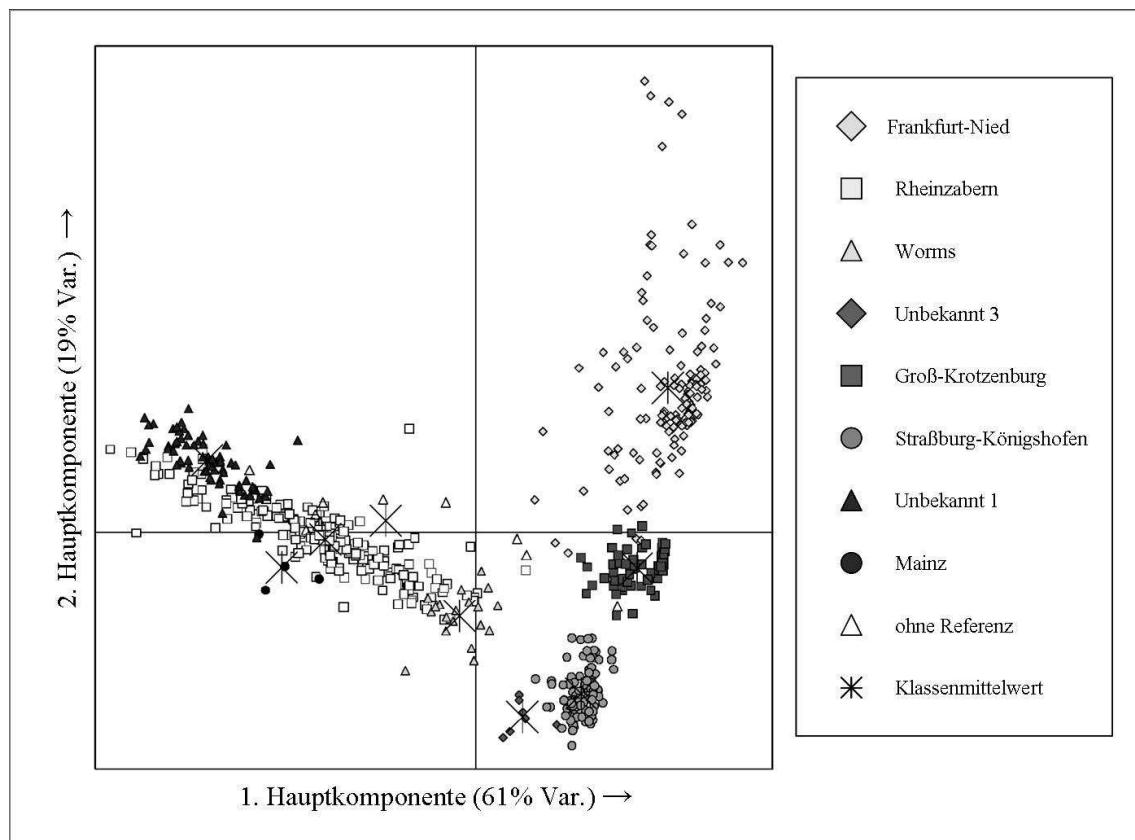


Figure 41: Auftragung der 1. und 2. Hauptkomponente mit Einfärbung der Objekte nach dem archäologisch überformten Klassifikationsergebnis der Clusteranalyse nach Ward (s. Fig. 39)

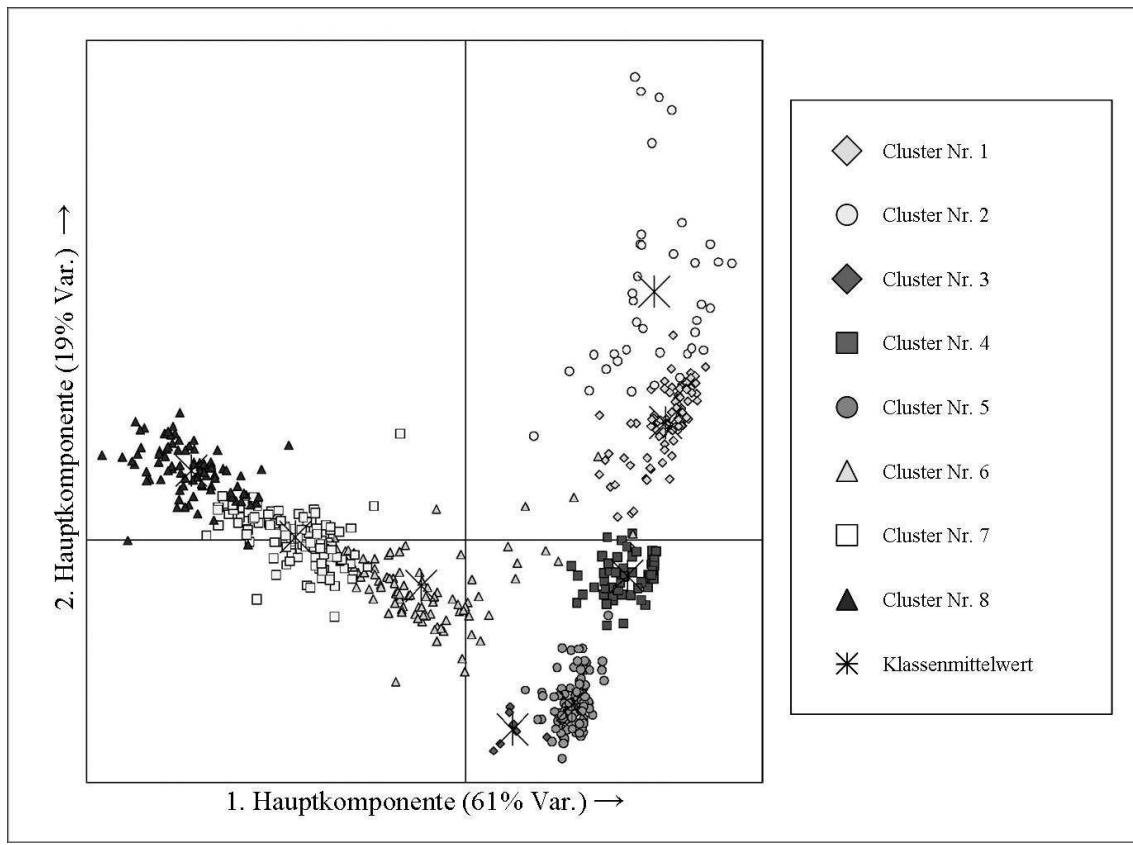


Figure 42: Auftragung der 1. und 2. Hauptkomponente mit Einfärbung der Objekte nach dem mit dem modifizierten Ward-Verfahren erhaltenen Klassifikationsergebnis

		Ward-Verfahren & archäologische Überformung									Total
		FN	Rh	Wo	U3	GK	SK	Mainz	U1	o. Ref.	
modifiziertes Ward-Verfahren	Frankfurt-Nied A	Cluster 1	92								92
	Frankfurt-Nied B	Cluster 2	38								38
	Unbekannt 3	Cluster 3				7					7
	Groß-Krotzenburg	Cluster 4	1				63				64
	Straßburg-Königshofen	Cluster 5						113		1	114
	Rheinzabern B	Cluster 6	6	66	19					3	94
	Rheinzabern A	Cluster 7		106					4	5	115
		Cluster 8		20					67	2	89
		Total	137	192	19	7	63	113	4	67	613

Figure 43: Vergleich zweier Klassifikationsresultate

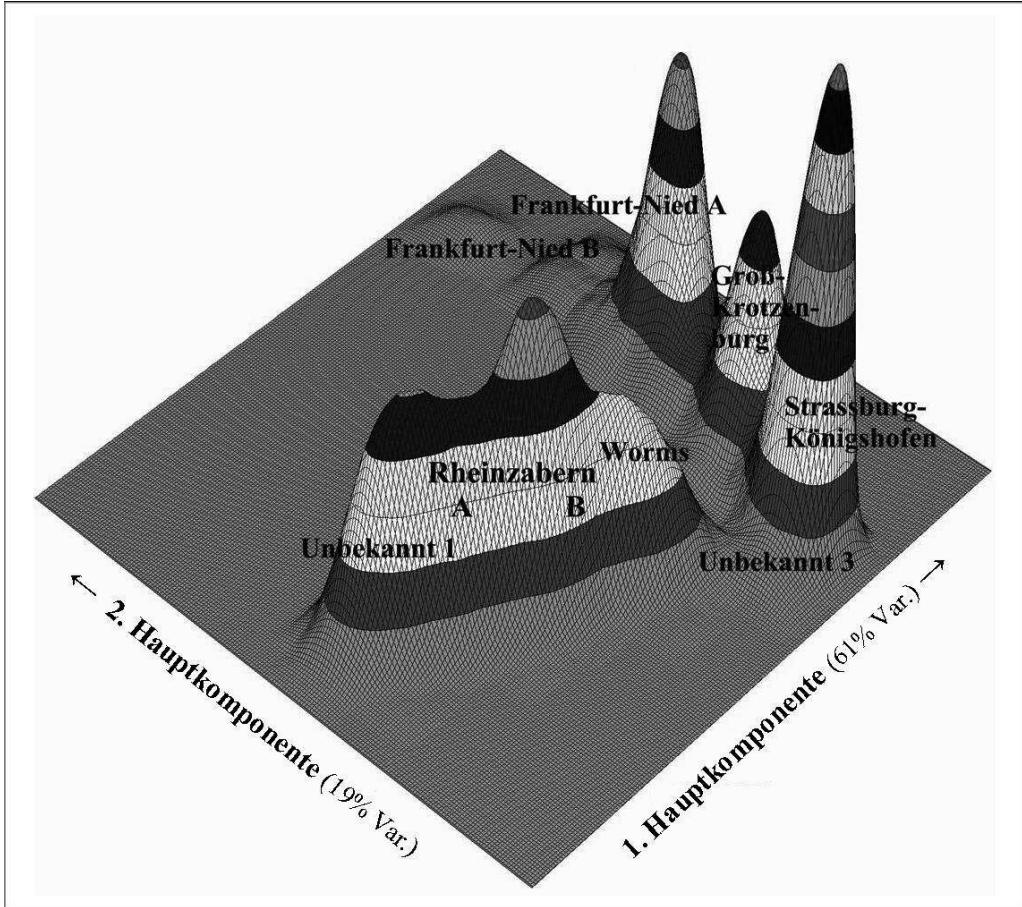


Figure 44: Zweidimensionale Dichteschätzung über der von der 1. und 2. Hauptachse aufgespannten Ebene

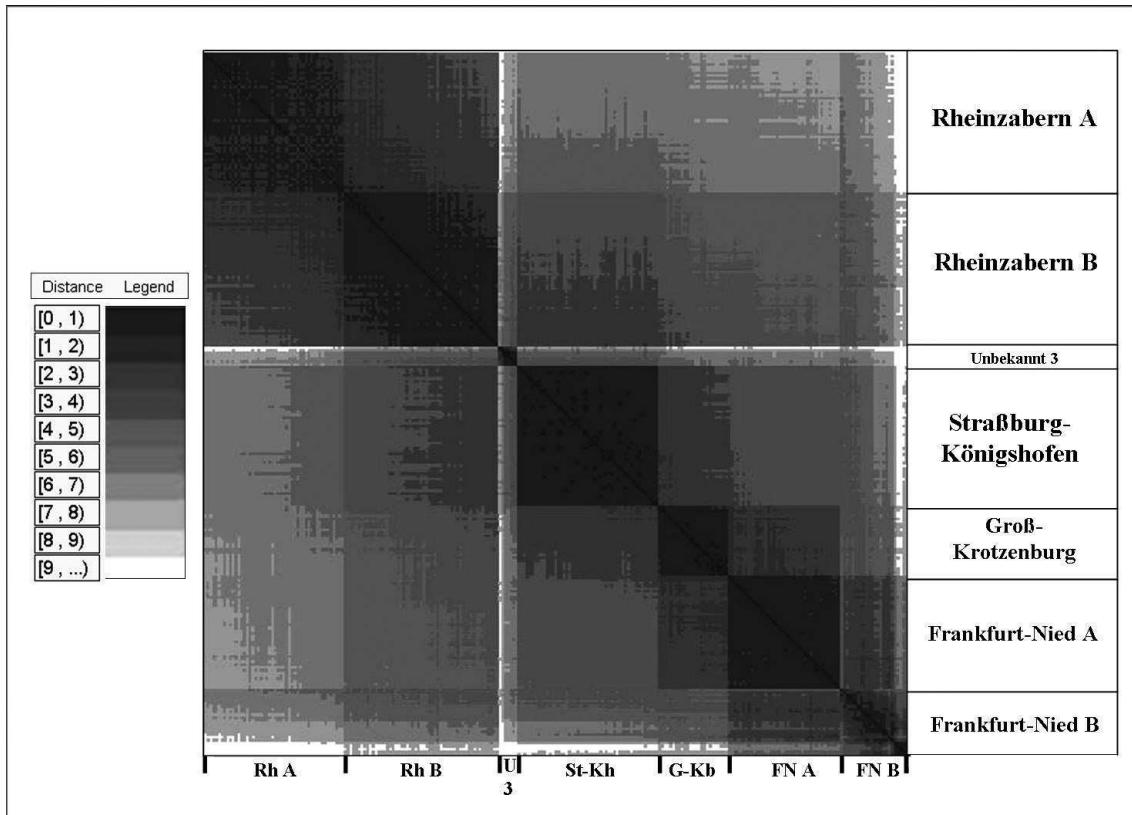


Figure 45: Darstellung der Distanzmatrix mit nach der 1. Hauptachse (Fig. 42) sortierten Zeilen und Spalten

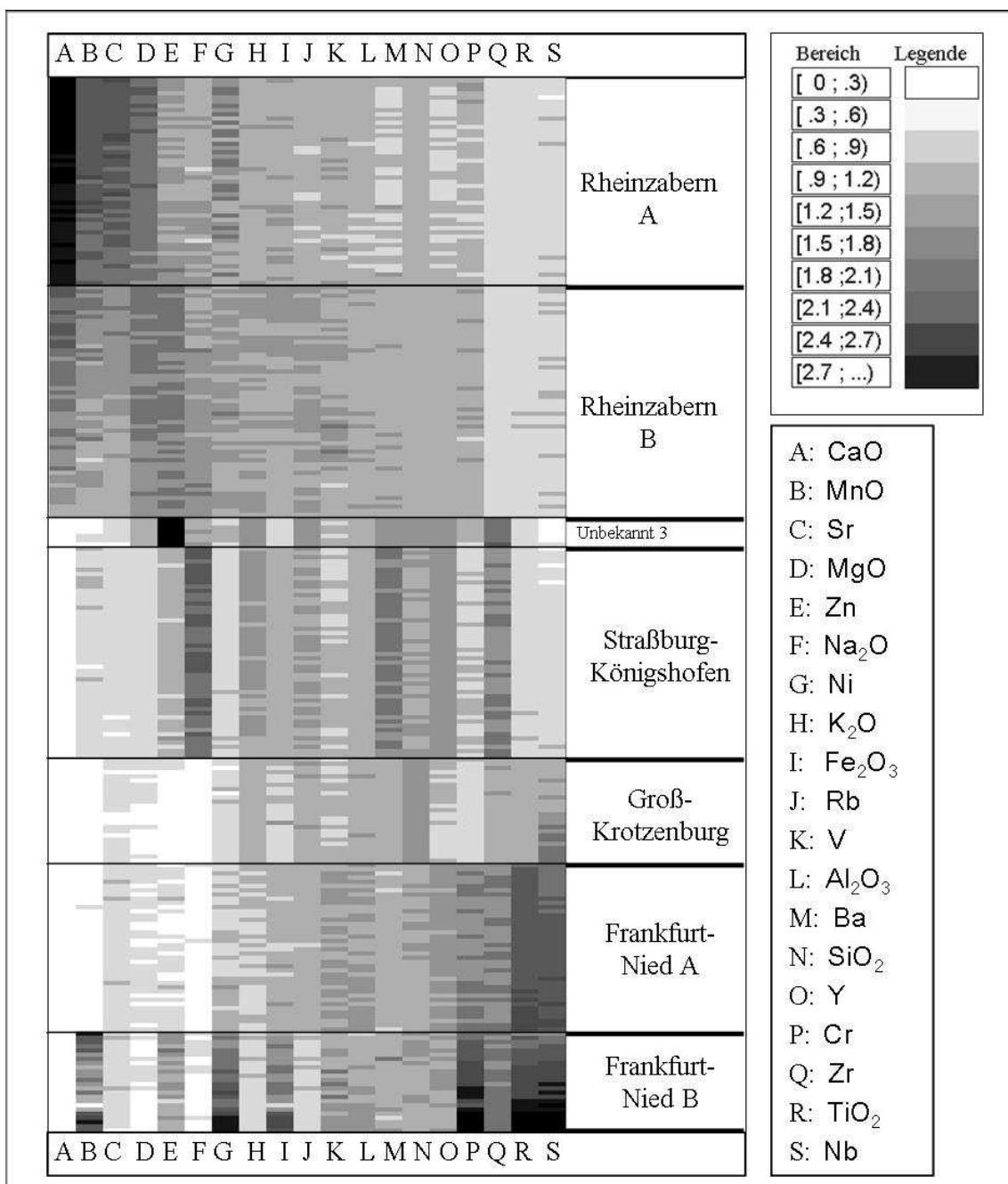


Figure 46: Sortieren der Oxid- und Spurenelementkonzentrationen (transformierte Werte) nach der 1. Hauptachse

In Fig. 45 werden die Klassen ebenso wie ihre interne Differenzierung gut erkennbar. Offenbar ist ‘Rheinzabern A’ nicht so einheitlich wie ‘Rheinzabern B’. Analoges kann beim Vergleich der Klassen ‘Frankfurt-Nied A’ und ‘Frankfurt-Nied B’ festgestellt werden, wobei hier die letztere die geringere Einheitlichkeit zeigt.

Zur Charakterisierung der Klassen hinsichtlich ihrer chemischen Zusammensetzung kann die Darstellung der Fig. 46 dienen. Dabei wurden die Muster $\mathbf{x}_j^{(v)}$ ($j = 1, \dots, 19$) der transformierten Variablen für eine repräsentative Teilmenge von 251 Objekten nach der 1. Hauptachse sortiert. Die einzelnen Werte der Variablen werden in zehn Graustufen von Weiß bis Schwarz verdeutlicht, wobei ein Wert umso größer ist, je dunkler er dargestellt wird.

Aus Fig. 46 lassen sich somit bestimmte Besonderheiten der aufgeführten Klassen bzw. Provenienzen von Heeresziegeleien erkennen. So unterscheiden sich die beiden Rheinzabern-Klassen durch ihre extrem hohen (Gruppe A) und sehr hohen (Gruppe B) CaO-Gehalte von allen anderen Klassen. Die Proben von ‘Unbekannt 3’ besitzen die größten Zn-Gehalte, die für große Distanzen zu den anderen Klassen bzw. Objekten verantwortlich sind und auf diese Weise für die Stabilität dieser recht kleinen und heterogenen Klasse sorgen. ‘Straßburg-Königshofen’ ist charakterisiert durch hohe Gehalte an Na₂O, Ba sowie Zr und ‘Frankfurt-Nied’ (besonders die Gruppe B) durch große bis größte Gehalte an TiO₂, Nb und Cr, während die Groß-Krotzenburg zugeordneten Ziegel ein relativ ausgeglichenes Elementmuster aufweisen, etc.

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Anhang

Publikationen aus den Jahren 2000 – 2009
 (in chronologischer Reihenfolge nach dem Jahr des Erscheinens)

zur Anwendung mathematischer Methoden bei der Untersuchung obergermanisch-römischer Ziegel aus dem Weierstraß-Institut für Angewandte Analysis und Stochastik, Berlin (Hans-Joachim Mucha), dem Institut für Chemie der Humboldt-Universität zu Berlin (Hans-Georg Bartel) und der Generaldirektion Kulturelles Erbe Rheinland-Pfalz, Mainz (Jens Dolata)

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4 Fuzzy Spectral Clustering by PCCA+

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Abstract

Given pairwise similarities between data points, spectral clustering makes use of the eigenvectors of the corresponding similarity matrix to perform dimensionality reduction for clustering in fewer dimensions. One example from this class of algorithms is the Robust Perron Cluster Analysis (PCCA+). In contrast to other algorithms, PCCA+ does not assign each object to exactly one cluster but it results in a fuzzy clustering where every object belongs to all clusters with certain membership values. The present article explains the main ideas of PCCA+ and presents the results of clustering the data sets provided by the organizers of the 30th Fall Meeting 2008 of the AG-DANK.

Keywords: spectral clustering, graph Laplacian, Perron cluster, PCCA+

4.1 Introduction

Clustering deals with the problem of separating data objects in different clusters according to their similarities. A partition of n objects o_1, \dots, o_n into k clusters C_1, \dots, C_k can be represented by an indicator matrix $\chi \in IR^{n \times k}$ with

$$\chi(i, j) = \begin{cases} 1, & \text{if } o_i \in C_j \\ 0, & \text{else} \end{cases} .$$

The idea of fuzzy clustering is to perform a relaxation by discarding the condition on the discrete values for χ and instead allow χ to take values in the interval $[0, 1]$ such that

$$0 \leq \chi(i, j) \leq 1, \quad \sum_{j=1}^k \chi(i, j) = 1 \quad \forall i = 1, \dots, n.$$

The entry $\chi(i, j)$ can be interpreted as membership value of object i with respect to cluster j . The matrix χ is therefore denoted as *membership matrix*.

The method we apply to obtain the membership matrix χ is called *Robust Perron Cluster Analysis* (PCCA+) [1, 7]. This method belongs to the class of *spectral clustering* algorithms. In recent years, a number of articles shed light on spectral clustering. We especially recommend [4], which also contains an extensive list of references to this topic.

The article is organized as follows. First, we summarize the basics of spectral clustering in Sect. 4.2, before we give a short introduction to PCCA+ in Sect. 4.3. In Sect. 4.4, we briefly discuss the choice of an appropriate similarity measure.

4.2 Spectral Clustering

The starting point for spectral clustering are objects o_1, \dots, o_n with pairwise similarities $s_{ij} > 0$, $i, j = 1, \dots, n$. The data can be represented in form of an undirected *similarity graph* $G = (V, E)$, where the vertices $V = \{v_1, \dots, v_n\}$ represent the objects o_i . Each edge between two vertices v_i and v_j carries a weight $w_{ij} \geq 0$, which enters the *adjacency matrix* $W = (w_{ij})_{i,j=1,\dots,n}$. The *degree matrix* D is defined as the diagonal matrix with entries

$$d_i = \sum_{j=1}^n w_{ij}$$

on the diagonal.

There are several possibilities to construct the similarity graph, for example the ε -neighborhood graph or k -nearest neighbor graphs, which are sparse representations of the data. As long as the number n of objects is of moderate size (about ≤ 2000), we prefer the *fully connected graph* with $w_{ij} = s_{ij}$.

Given a set o_1, \dots, o_n of objects, it is mostly more intuitive to compute *pairwise distances* d_{ij} instead of similarities. A popular way to transform these distances into similarities is the *Gaussian similarity function*

$$s_{ij} = \exp(-\beta d_{ij}^2), \quad \beta = \frac{1}{2\sigma^2}. \quad (17)$$

The parameter σ controls the width of the neighborhoods.

Clustering is now equivalent to finding a partition of the graph such that edges between different clusters have a low weight and edges within a cluster have high weight. The most common spectral clustering algorithms have the following form:

1. Construct a similarity graph with weighted adjacency matrix W .
2. Compute a graph Laplacian L .
3. Compute the first k eigenvectors $X = [x_1, \dots, x_k]$ of L .
4. For $i = 1, \dots, n$ let $y_i \in IR^k$ be the i th row of X . Cluster the points $(y_i)_{i=1,\dots,n}$ into clusters C_1, \dots, C_k .

Spectral clustering requires only the computation of a few eigenvectors, which is quite easy with standard numerical software like MATLAB.

The different algorithms differ in the computation of the graph Laplacian and the clustering of the rows of X . For properties of graph Laplacians, the reader is referred to [4]. For example, in normalized spectral clustering according to [5], the Laplacian is computed by

$$L = I - D^{-1}W.$$

There are several reasons why this Laplacian should be favored over other constructions, see [4].

The matrix $P = D^{-1}W$ is a row-stochastic matrix and can be interpreted as transition matrix of a random walk which jumps from vertex to vertex. The transition probability of jumping in one step from vertex i to vertex j is given by $p_{ij} = w_{ij}/d_i$. If the graph is connected and non-bipartite, then the random walk possesses a unique stationary distribution $\pi = [\pi_1, \dots, \pi_n]^\top$ given by $\pi_i = d_i / \sum_j d_j$. Spectral clustering corresponds to finding a partition of the graph such that the random walk stays long within the same cluster and seldom jumps between clusters. Since P and $L = I - P$ have the same eigenvectors, spectral clustering on L is equivalent to spectral clustering on P .

The clustering of points $(y_i)_{i=1,\dots,n}$ in step 4 is usually done by the k -means algorithm, but any other method could be used instead. One possible choice is PCCA+, which will be explained in the following Section.

4.3 Robust Perron Cluster Analysis (PCCA+)

The transition probability matrix $P = D^{-1}W$ represents a Markov chain on the state space $S = \{o_1, \dots, o_n\}$. In case of a decomposable Markov chain or, equivalently, a disconnected similarity graph, an appropriate permutation of objects according to their connectedness results in a block-diagonal matrix P with k blocks. This matrix has a k -fold eigenvalue $\lambda = 1$. The corresponding eigenvectors $X = [x_1, \dots, x_k]$ are piecewise constant on the blocks and can thus be used to identify the clusters. In fact, the rows of X can be considered as vertices of a $(k - 1)$ -dimensional simplex. Every object can be assigned to one of the k vertices and thus to one of the k clusters.

Generally, the matrix P constructed from practical data is not decomposable. However, if there are k hidden clusters, P has a cluster of eigenvalues $1 = \lambda_1 > \lambda_2 > \dots > \lambda_k > 1 - \varepsilon$ near the Perron eigenvalue $\lambda_1 = 1$. The rows y_i of the corresponding eigenvectors still nearly form a simplex. the first eigenvector is always constant, the rows can be considered

The goal of PCCA+ is to identify the vertices of a simplex σ_{k-1} such that all points y_i are located within the simplex. Then every point y_i can be assigned to one of the k vertices and thus to one of the k clusters by a certain membership vector $\chi(i, :) = [\chi(i, 1), \dots, \chi(i, k)]$.

The identification of such a simplex is equivalent to finding a non-singular transfor-

mation matrix \mathcal{A} such that

$$\chi = X\mathcal{A}$$

and

$$(1a) \quad \chi(i, j) \geq 0 \quad \forall i \in \{1, \dots, n\}, j \in \{1, \dots, k\} \quad (\text{positivity}),$$

$$(1b) \quad \sum_{j=1}^k \chi(i, j) = 1 \quad \forall i \in \{1, \dots, n\} \quad (\text{partition of unity}).$$

Among the feasible transformation matrices we search for a matrix \mathcal{A} such that the resulting membership vectors $\chi(i, :)$ are as crisp as possible, i.e. the columns $\chi(:, j)_{j=1, \dots, n}$ should be as close to indicator vectors as possible. This can be achieved by maximizing the objective function [10]

$$I(\mathcal{A}; X, \pi) = \sum_{i=1}^k \frac{\langle \chi_i, \chi_i \rangle_\pi}{\langle \chi_i, e \rangle_\pi} \leq k, \quad (18)$$

where e denotes the vector with all entries equal to 1. To summarize, PCCA+ aims at

$$\text{maximizing} \quad I(\mathcal{A}; X, \pi)$$

subject to

$$(1) \quad \chi(i, j) \in \sigma_{k-1} \quad \forall i \in \{1, \dots, n\} \quad (\text{simplex}),$$

$$(2) \quad \chi = X\mathcal{A}, \mathcal{A} \text{ non-singular} \quad (\text{invariance}).$$

Constraint (1) is just a compact formulation of conditions (1a) and (1b).

One has to maximize a convex function with linear constraints, which is not a trivial task. However, the optimization problem can be solved by the Nelder-Mead algorithm provided that a good initial guess for \mathcal{A} is available. This starting guess is obtained by the *inner simplex algorithm* as described in [8].

Finally, in order to obtain a partition of data points into clusters, the real-valued solution matrix χ needs to be re-transformed into a discrete indicator matrix by

$$o_i \in C_k \quad \text{if} \quad \chi(i, k) = \max_j \chi(i, j).$$

Number of clusters

Since the number of clusters k is unknown in advance, it is recommended to run the cluster algorithm several times with different input values for k and to choose the “best” solution. In order to evaluate the quality of the solution, several criteria can be used:

- The spectral gap. If there are k well-separated clusters, there will be a significant gap between the eigenvalues λ_k and λ_{k+1} .

- The condition of the invariant subspace X [6]. In case of k well-separated clusters, the corresponding invariant subspace X spanned by the first k eigenvectors of P or L is well-conditioned. In case of a reversible Markov chain or a symmetric similarity matrix S , respectively, this criterion is equivalent to the spectral-gap criterion.
- The *minChi*-criterion [9]. In general, the initial guess for \mathcal{A} is infeasible, i.e. it leads to a membership matrix χ with negative entries. However, if there exist well separated clusters, the value

$$\text{minChi} = \min_i \min_j \chi(i, j)$$

will be close to zero. Thus, one can decide for the number k that maximizes the minChi-value.

- Optimality of the solution. Since $I(\mathcal{A}; X, \pi) \leq k$, one could choose the number k for which $I(\mathcal{A}; X, \pi)/k$ is maximal.

In general, if there are k well-separated clusters, all proposed criteria will favor this number.

4.4 Similarity Graph

We compute pairwise similarities s_{ij} by the Gaussian similarity function (17). However, the results of spectral clustering are quite sensitive to the choice of the distance function $d(o_i, o_j)$. Although the Euclidean distance

$$d_{ij} = \|o_i - o_j\|_2$$

is a natural choice, it is not always appropriate, as illustrated in Fig. 47. Clustering based on the Euclidean distance assumes that the data points are grouped to “compact” clusters where the objects within one cluster are either mutually similar to each other or they are similar with respect to a common representative or centroid. If a cluster is larger than different clusters, spectral clustering distance will fail. Whenever data subsets occupy elongated regions like spiral arms or circles, an alternative distance function based on connectedness of data points is required. Such a distance function has been introduced in [2, 3] in conjunction with path based clustering. Path based clustering assigns two objects to the same cluster if they are connected by a path with high similarity between adjacent objects on the path. The *effective distance* between two objects is calculated as the minimum over all path distances,

$$d_{ij}^{\text{eff}} = \min_{p \in \mathcal{P}_{ij}(E)} \left\{ \max_{1 \leq k < |p|} d_{p[k]p[k+1]} \right\}.$$

Here, $\mathcal{P}_{ij}(E)$ denotes the set of all paths from object i to object j and $d_{p[k]p[k+1]}$ denotes the Euclidean distance between the k th and $(k+1)$ th object on the path. The

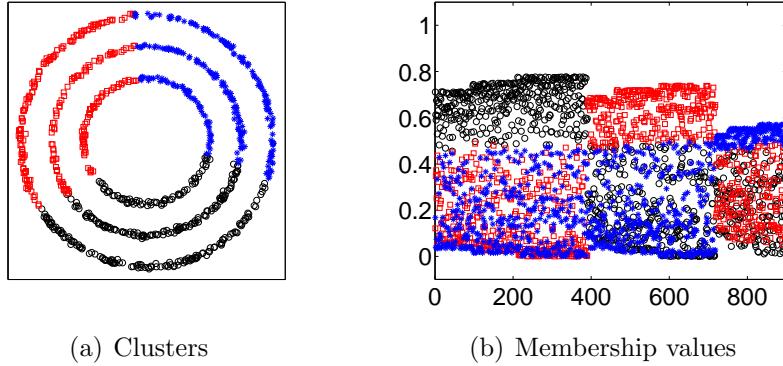


Figure 47: Example for a point set where the Euclidean distance is inappropriate to identify clusters. The separation between the clusters is quite weak, which is illustrated by the small membership values of the data points.

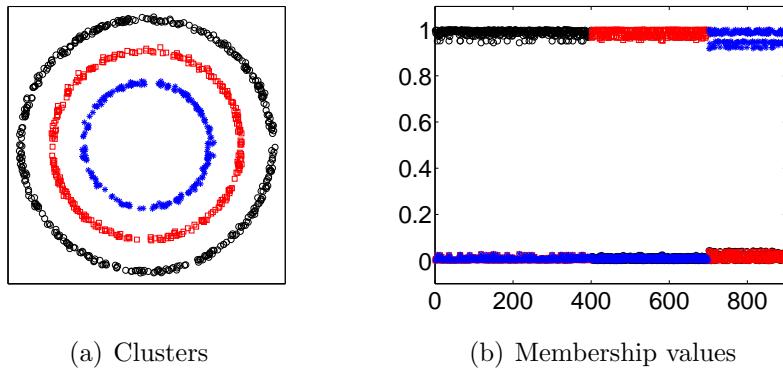


Figure 48: Example for a point set where the use of effective distances results in the desired clustering. The separation between clusters is strong, illustrated by the fact that the membership vectors are nearly indicator vectors.

matrix D^{eff} can be computed recursively by a variant of Kruskal's minimum spanning tree algorithm [2]. Again, the corresponding similarity matrix S is computed by the Gaussian function (17). Fig. 48 illustrates the result of fuzzy spectral clustering based on the effective distance matrix.

4.5 Examples

The clustering results for the data provided for the 30th Fall Meeting of the working group AG–DANK at <http://www.fim.uni-passau.de/de/fim/fakultaet/lehrstuehle/ritter/ag-dank.html> are presented separately in Sect. 7.3 and Sect. 8.3.

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5 Merging Gaussian mixture components - an overview

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Abstract

The problem of merging Gaussian mixture components is discussed in a situation where a Gaussian mixture is fitted but the mixture components are not separated enough from each other to interpret them as “clusters”. The problem of merging Gaussian mixtures is not statistically identifiable, therefore merging algorithms have to be based on subjective cluster concepts. Several different methods are proposed.

Keywords: model-based cluster analysis, multilayer mixture, unimodality, prediction strength, ridgeline, dip test

Introduction

The Gaussian mixture model is often used for cluster analysis (for an overview and references see Fraley and Raftery, 2002, and McLachlan and Peel, 2000). This approach is based on the assumption that \mathbb{R}^p -valued observations $\mathbf{x}_1, \dots, \mathbf{x}_n$ are distributed i.i.d. according to the density

$$f(\mathbf{x}) = \sum_{j=1}^s \pi_j \varphi_{\mathbf{a}_j, \Sigma_j}(\mathbf{x}), \quad (19)$$

where $\pi_j > 0 \forall j$, $\sum_{j=1}^s \pi_j = 1$, $\varphi_{\mathbf{a}, \Sigma}$ is the density of the p -dimensional Gaussian distribution with mean vector \mathbf{a} and covariance matrix Σ . Given a fixed s , the parameters can be estimated by Maximum Likelihood using the EM-algorithm. The data points can then be classified to the mixture components by maximizing the estimated a posteriori probability that \mathbf{x}_i was generated by mixture component j ,

$$\hat{P}(\gamma_i = j | \mathbf{x}_i = \mathbf{x}) = \frac{\hat{\pi}_j \varphi_{\hat{\mathbf{a}}_j, \hat{\Sigma}_j}(\mathbf{x})}{\sum_{i=1}^s \hat{\pi}_i \varphi_{\hat{\mathbf{a}}_i, \hat{\Sigma}_i}(\mathbf{x})}, \quad (20)$$

where γ_i is defined by the two-step version of the mixture model where

$$P(\gamma_i = j) = \pi_j, \quad \mathbf{x}_i | (\gamma_i = j) \sim \varphi_{\mathbf{a}_j, \Sigma_j}, \quad i = 1, \dots, n \text{ i.i.d..} \quad (21)$$

A standard method (though not the only one) to estimate the number of components s is the Bayesian Information Criterion (BIC, Schwarz, 1978), see Fraley and Raftery (2002) for details. The outcome is called EM/BIC.

In cluster analysis usually every mixture component is interpreted as a cluster, and pointwise maximization of (20) defines the clustering. The idea is that a mixture formalizes that the underlying distribution is heterogeneous with several different populations, all of which are modelled by homogeneous Gaussian distributions. Keeping in mind that there is no unique definition of a “true cluster”, and not necessarily assuming that the Gaussian mixture model assumption holds precisely, it could be said that this method employs the Gaussian distribution as the prototype shape of clusters to look for.

From a practical point of view, perhaps the most important problem with this approach is that for most applications Gaussian distributions are too restricted to formalize the cluster shapes one is interested in. For example, mixtures of two (or more) Gaussian distributions can be unimodal, and in such distributions there is no gap (and in this sense no separation) between the different Gaussian subpopulations. In many applications in which the number of clusters is not known, the EM algorithm together with the BIC yield a larger optimal number of mixture components than what seems to be a reasonable number of clusters when looking at the data.

The hierarchical principle for merging Gaussian components, which is used in the present paper, works as follows:

1. Start with all components of the initially estimated Gaussian mixture as current clusters.
2. Find the pair of current clusters most promising to merge.
3. Apply a stopping criterion to decide whether to merge them to form a new current cluster, or to use the current clustering as the final one.
4. If merged, go to 2.

Two criteria are needed, namely in step 2 a rule to find the pair of clusters best to merge and the stopping rule in step 3.

5.1 The Nature of the Problem

The merging problem looks as follows. Given a Gaussian mixture with s components as below, find $k \leq s$ and mixtures f_1^*, \dots, f_k^* of components of the original mixture so that each original Gaussian component appears in exactly one out of f_1^*, \dots, f_k^* , and

$$f(\mathbf{x}) = \sum_{i=1}^s \pi_i \varphi_{\mathbf{a}_i, \Sigma_i}(\mathbf{x}) = \sum_{j=1}^k \pi_j^* f_j^*(\mathbf{x}), \quad (22)$$

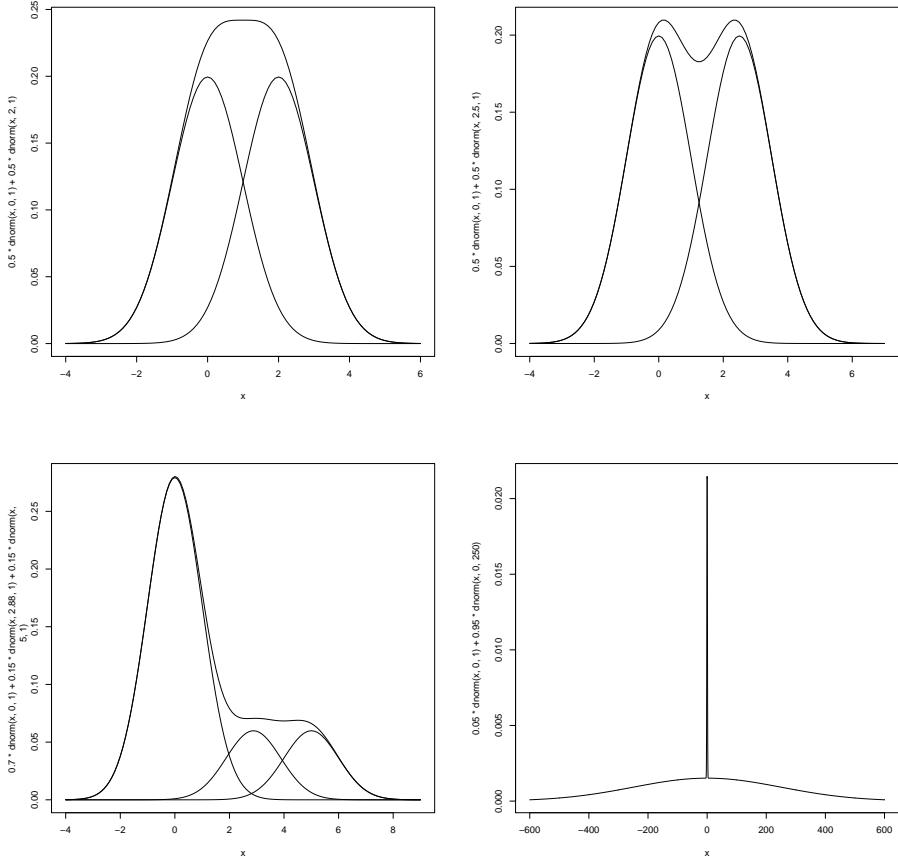


Figure 49: Four one-dimensional Gaussian mixtures.

where π_j^* is the sum of the π_i of the Gaussian components assigned to f_j^* . For datasets, clustering can be done by maximizing estimated posterior probabilities

$$\hat{P}(\gamma_i^* = j | \mathbf{x}_i = \mathbf{x}) = \frac{\hat{\pi}_j^* \hat{f}_j^*(\mathbf{x})}{\sum_{i=1}^s \hat{\pi}_i^* \hat{f}_i^*(\mathbf{x})}, \quad (23)$$

by analogy to (20) with $\gamma_1^*, \dots, \gamma_n^*$ defined by analogy to (21).

From (22), however, f_1^*, \dots, f_k^* are not identifiable. Imagine $s = 3$ and $k \leq 3$. In terms of the density and therefore the likelihood, it does not make a difference whether f_1^* is a mixture of the first two Gaussian components and f_2^* equals the third one, or f_1^* mixes the first and the third Gaussian component and f_2^* equals the second one, or any other admissible combination.

It is well known that there is no objective unique definition of what a “true cluster” is, so there is necessarily a subjective component in the decision how to merge components.

The situations in Figure 49 illustrate that essentially different cluster concepts may be of interest. Particularly the role of unimodality may be controversial. Some

researchers may find it intuitive to identify a cluster with a set of points surrounding a density mode, and in most situations the unimodal mixture at the top left of Figure 49 may be regarded as generating a single cluster (except if there are strong reasons to believe that “true clusters” should at least be approximately Gaussian, be mixtures unimodal or not, i.e., not demanding any “separation” between clusters). However, in some applications the unimodal mixtures at the bottom of Figure 49 may not be regarded as a single cluster, because the modes in these examples are surrounded by dense “patterns” of the data that seem to be separated from what goes on in the tails, which is caused by other Gaussian components. But it is not clear that these mixtures in any case should not be merged into a single cluster, because there is no separating “gap” between them, which may be required to speak of “clusters”.

On the other hand, multimodal mixtures may also be accepted as single clusters if the modes are not properly separated as in the upper right plot in Figure 49. Note also that ML-estimation of Gaussian mixtures applied to data generated from uniform distributions tends to come up with multimodal Gaussian mixtures.

Therefore, in order to define a suitable method for merging normals, the statistician has to decide

- whether only gaps in the density are accepted as separation between different clusters (“modality based cluster concept”) or whether a dense data subset around a mode should be separated from clearly less dense data subsets even if the latter cannot be assigned to another mode (“pattern based cluster concept”),
- how strong the separation between different clusters should at least be (regardless of which of the two concepts is chosen, though the meaning of “separation” differs between them to some extent),
- what the role of the number of points in a cluster is, i.e., how strongly “cluster-shaped” small data subsets should be in order to constitute an own cluster.

The present paper offers a range of methods to deal with various decisions in these respects (for the last one, one may consider the inclusion of a “uniform noise component” in the mixture, as mentioned in the Introduction).

5.2 Methods Based on Modality

The ridgeline unimodal method

Under a strong version of the modality based cluster concept, the “strong modality merging problem” is to find a partition of the mixture components so that all resulting clusters are unimodal but any further merging would result in a cluster that is no longer unimodal. This requires an analysis of the modality of Gaussian

mixtures. The most advanced paper on this topic, to my knowledge, is Ray and Lindsay (2005). They showed that for any mixture f of s Gaussian distributions on \mathbb{R}^p there is an $s - 1$ -dimensional manifold of \mathbb{R}^p so that all extremal points of f lie on this manifold.

For $s = 2$, this manifold is defined by the so-called “ridgeline”,

$$\mathbf{x}^*(\alpha) = [(1 - \alpha)\Sigma_1^{-1} + \alpha\Sigma_2^{-1}]^{-1}[(1 - \alpha)\Sigma_1^{-1}\mathbf{a}_1 + \alpha\Sigma_2^{-1}\mathbf{a}_2], \quad (24)$$

and all density extrema (and therefore all modes which may be more than 2 in some situations) can be found for $\alpha \in [0, 1]$.

Unfortunately, for $s > 2$, Ray and Lindsay’s result does not yield a straightforward method to find all nor even the number of modes. Therefore, their results can in general only be used to solve the strong modality merging problem approximately. The **unimodal ridgeline method** is defined by the hierarchical principle as follows.

1. Start with all components of the initially estimated Gaussian mixture as current clusters.
2. Using the mean vectors and covariance matrices of the current clusters (initially the Gaussian components), use the 2-component Gaussian mixture derived from these parameters on the ridgeline (24) to check whether it is unimodal for any pair of two current clusters.
3. If none of these is unimodal, use the current clustering as the final one.
4. Otherwise,
 - (a) merge all of the pairs leading to unimodal mixtures.
 - (b) go to step 2.

In order to apply this principle to data, means and covariance matrices are replaced by their ML-estimators for Gaussian mixture components. For mixtures of two or more Gaussians appearing as current clusters in the hierarchy, mean vectors and covariance matrices can be computed using the weights of points in the current cluster computed by summing up the weights (20) for all involved mixture components.

The ridgeline ratio method

Even if the cluster concept is modality based, in some situations the statistician may want to allow clusters that deviate from unimodality as long as the gap between the modes is not strong enough to interpret them as belonging to two separated clusters. One reason for this is that clusters may be required to be strongly separated. Another reason is that, as a result of too small sample size or particular instances of non-normality, data from unimodal underlying distributions may be approximated by EM/BIC by a multimodal Gaussian mixture.

A straightforward method to deal with this is to replace the demand of unimodality in the previous session by a cutoff value r^* for the ratio r between the minimum of the mixture density f and the second largest mode in case that there is more than one.

The dip test method

Tantrum, Murua and Stuetzle (2003) defined a hierarchical merging algorithm for the modality based cluster concept, the stopping rule of which is a sufficiently small p -value of Hartigan and Hartigan's (1985) dip test for unimodality. To use a significance test for unimodality is intuitively appealing if the statistician wants to merge components if the resulting mixture cannot be statistically distinguished from a unimodal distribution. As a modification of Tantrum, Murua and Stuetzle's method, I suggest to replace the log-likelihood difference by the ridgeline ratio r defined in Section 5.2. Here is the proposed **dip test method** in more detail:

1. Choose a tuning constant $p^* < 1$.
2. Start with all components of the initially estimated Gaussian mixture as current clusters.
3. Using the mean vectors and covariance matrices of the current clusters, use the 2-component Gaussian mixture derived from these parameters on the ridgeline (24) to compute r for any pair of current clusters.
4. Consider the data subset \mathbf{x}^* of points classified to the union of the pair of current clusters maximizing r by maximizing (23).
5. Let \mathbf{x}^{*1} be the projection of \mathbf{x}^* onto the discriminant coordinate based on the pooled covariance matrix of the two involved current clusters, separating the two current cluster means (this is necessary because the dip test operates on one-dimensional data).
6. If the p -value of the dip test applied to \mathbf{x}^{*1} is $\leq p^*$, use the current clustering as the final one.
7. Otherwise merge this pair of current clusters and go to step 3.

5.3 Methods Based on Misclassification Probabilities

The methods introduced in this Section formalize versions of the pattern based cluster concept as opposed to the modality based one. Misclassification probabilities provide an intuitive possibility to formalize separation between different clusters in a different way than density gaps. For example the two components of the scale mixture on the lower right side of Figure 49 are not separated in the sense that there are no gaps between them, but nevertheless the misclassification probability

between them is low. Obviously, the misclassification probability would be low as well in case of a strong density gap between components, so that in many clear cut situations both concepts arrive at the same clustering.

The Bhattacharyya distance method

The Bhattacharyya distance is a general distance between two distributions related to the overall Bayes misclassification probability for the 2-class problem with arbitrary class probabilities. This is bounded from above by $\exp(-d)$, where d is the Bhattacharyya distance (**reference**). For two Gaussian distributions with mean vectors and covariance matrices $\mathbf{a}_j, \Sigma_j, j = 1, 2,$, the Bhattacharyya distance is (Fukunaga, 1990)

$$d = \frac{(\mathbf{a}_1 - \mathbf{a}_2)^t \bar{\Sigma}^{-1} (\mathbf{a}_1 - \mathbf{a}_2)}{8} + \frac{1}{2} \log \left(\frac{|\bar{\Sigma}|}{\sqrt{|\Sigma_1| |\Sigma_2|}} \right), \quad (25)$$

where $\bar{\Sigma} = \frac{1}{2}(\Sigma_1 + \Sigma_2)$. For data, the parameters can of course be replaced by their estimators.

The Bhattacharyya distance between two mixtures of Gaussians cannot be computed in a straightforward way. Therefore, for hierarchical merging, I again suggest to represent mixtures of Gaussians by their overall mean vector and covariance matrix and in this sense to treat them as single Gaussians. The **Bhattacharyya distance method** looks as follows:

1. Choose a tuning constant $d^* < 1$.
2. Start with all components of the initially estimated Gaussian mixture as current clusters.
3. Compute the (in case of mixtures with more than one component approximately) estimated Bhattacharyya distances d between all pairs of current clusters from their mean vectors and covariance matrices.
4. If $d < d^*$ for all pairs of current clusters, use the current clustering as the final one.
5. Otherwise, merge the pair of current clusters with maximum d and go to step 3.

Here d^* formalizes the degree of separation between clusters. By analogy to r^* above, d^* could be chosen by subject matter considerations or by simulations from borderline distributions.

Directly estimated misclassification probabilities

Instead of estimating the Bhattacharyya distance, misclassification probabilities $p_{ij} = P(\tilde{\gamma}_1^* = i | \gamma_1^* = j) = \frac{P(\tilde{\gamma}_1^* = i, \gamma_1^* = j)}{\pi_j^*}$ between components of a mixture distribution can also be estimated directly from the results of the EM algorithm. Here γ_1^* denotes the mixture component number that generated the first data point (or any other point according to the i.i.d. assumption, as long as only probabilities are of interest), and $\tilde{\gamma}_1^*$ is the mixture component to which the point is classified by maximizing the population version of (23), i.e., by the Bayes rule with true parameters.

π_j^* can be estimated by $\hat{\pi}_j^*$. Note that

$$\hat{P}(\tilde{\gamma}_1^* = i, \gamma_1^* = j) = \sum_{h=1}^n \hat{P}(\gamma_h^* = j | x_h) 1(\hat{\gamma}_h^* = i) \quad (26)$$

is a consistent estimator of $P(\tilde{\gamma}_1^* = i, \gamma_1^* = j)$, where $\hat{\gamma}_h^*$ denotes the data based classification of data point \mathbf{x}_h , estimating $\tilde{\gamma}_h^*$, by maximizing (23), which also defines $\hat{P}(\gamma_h^* = j | x_h)$. $1(\bullet)$ denotes the indicator function.

Therefore,

$$\hat{p}_{ij} = \frac{\hat{P}(\tilde{\gamma}_1^* = i, \gamma_1^* = j)}{\hat{\pi}_j^*}$$

is a consistent estimator of p_{ij} . This works regardless of whether the mixture components are Gaussian distributions or mixtures of Gaussians. Therefore it is not needed to represent mixtures by their mean vectors and covariance matrices in order to compute \hat{p}_{ij} . The method of directly estimated misclassification probabilities (**DEMP method**) below therefore does not treat mixtures of Gaussians as single Gaussians in any way.

1. Choose a tuning constant $q^* < 1$.
2. Start with all components of the initially estimated Gaussian mixture as current clusters.
3. Compute $q = \max(\hat{p}_{ij}, \hat{p}_{ji})$ for all pairs of current clusters.
4. If $q < q^*$ for all pairs of current clusters, use the current clustering as the final one.
5. Otherwise, merge the pair of current clusters with maximum q and go to step 3.

5.4 The predictive strength method

Tibshirani and Walther's (2005) predictive strength approach to estimate the number of clusters is based on a different concept of misclassification. Instead of assessing

the classification of the data points to the clusters, it assesses how well it can be predicted whether pairs of points belong to the same cluster. Furthermore, instead of estimating the misclassification passively, by recomputing the clustering on subsamples, the approach does not only take into account the separation of the estimated clusters, but also the stability of the clustering solution.

For the merging problem, a special version of the predictive strength method is required. This leads to the following **predictive strength method** for the merging problem (assuming that s is the number of Gaussian mixture components estimated by EM/BIC):

1. Choose a tuning constant $c^* < 1$. For $k = 2, \dots, s$, repeat m times:
 2. Split the dataset in two halves.
 3. Cluster both halves as follows:
 - (a) Apply EM, fixing s .
 - (b) Apply the DEMP method to the solution, stopping at k clusters.
 4. Use the clustering \mathcal{C}_1 of the first half of the data to predict the cluster memberships (of clusters in \mathcal{C}_1) of the points of the second half of the data by maximizing (23) for every point of the second half with respect to the mixture components in \mathcal{C}_1 .
 5. For every cluster in the clustering \mathcal{C}_2 of the second half of the data, compute the proportion of correctly predicted co-memberships of pairs of points by the membership predictions of \mathcal{C}_1 . Record the minimum over clusters \tilde{c} of these proportions.
 6. Repeat steps 3 and 4 exchanging the roles of the two halves.
 7. Let c be the average of the $2m$ recorded values of \tilde{c} . Use the largest k with $c \geq c^*$ as the estimated number of clusters.

Conclusion

Several different hierarchical methods to merge Gaussian mixture components have been proposed. They correspond to different cluster concepts. The problem of merging Gaussian mixture components is not identifiable without subjective decisions about the cluster concept. Simulations, discussion, choice of the tuning constants and further details will be published elsewhere.

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6 Classification of workers with different exposure levels to fumes of bitumen

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Abstract

Bitumen is a widely used construction material. Emissions from hot bitumen applications are of long-standing health-concern. The objective of the German Human Bitumen Study is to investigate potential irritative and genotoxic effects in mastic-asphalt workers. Here discriminant analysis was used to classify mastic-asphalt and construction workers into exposure related classes using irritative biomarkers. Additionally, the workers are classified by smoking status using the same irritative biomarkers to prove whether the selected irritative variables measured in induced sputum (interleukin-8, neutrophil granulocytes, leukotriene B₄, interleukin-1 β , nitrate and nitrite, and total protein) are capable of distinguishing between workers with different health effects. Linear discriminant analysis, quadratic discriminant analysis and the k -nearest neighbour method were applied. Current smokers and non-smokers could be distinguished best by 3-nearest neighbour (estimated error rate 0.14). None of the applied methods discriminated between the different exposure groups with acceptable error rates, especially highly exposed workers with a shift-exposure above 14.7 mg/m³ fumes of bitumen were not correctly classified. Possible explanations are the small sample size of the highly exposed workers, the artificial cut-off at 14.7 mg/m³, and the daily changing exposure levels of the workers.

Keywords: Bitumen, irritative effects, discriminant analysis

Introduction

Asphalt is a mixture of the binder bitumen with inorganic material (sand, gravel) (note: bitumen is referred to as asphalt in North America). It is used mainly for road paving. In the 1970s, bitumen replaced coal tar as a binder in Germany after tar was assessed as human carcinogen. Bitumen is the fraction of the crude oil remaining after distillation of the evaporated components and contains about 5 mg/kg benzo[*a*]pyrene, whereas coal tar contains approximately 5000 mg/kg benzo[*a*]pyrene

(IARC (1987)). The International Agency for Research on Cancer (IARC) classified extracts of steam-refined and air-refined bitumen as possible human carcinogens in Group 2B (IARC (1985, 1987)). In 2001, the German Committee for Hazardous Substances (AGS) lowered the occupational threshold limit for fumes of bitumen to 14.7 mg/m³ (bitumen condensate standard), respectively 10 mg/m³ (mineral oil standard) (Rühl (2001)). For mastic-asphalt workers the threshold limit was deferred, because it was assumed that a reduction of the exposure level below that threshold was not possible by technical measures. The objective of the German Human Bitumen Study was to investigate the exposure levels and potential irritative and genotoxic effects in mastic-asphalt workers. First analyses with data of this study pointed towards irritative effects of fumes of bitumen on the airways (Raulf-Heimsoth et al. (2007a), Raulf-Heimsoth et al. (2007b)).

A broad set of variables characterizes irritative effects. In order to implement this complex information in assessing health effects by exposure, discriminant analysis can be used to classify the workers into exposure-related classes regarding their health effects.

The traditional way of conducting discriminant analysis was introduced by R. A. Fisher, known as linear discriminant analysis (LDA) (Johnson and Wichern (2002)). The linearity of this method comes from the assumption of a common covariance matrix. Here, hyperplanes separate the classes. When the assumption of a common covariance matrix is not satisfied, one uses an individual covariance matrix for each group. This leads to a quadratic surface of the boundaries between discrimination regions and so this discrimination method is called quadratic discriminant analysis (QDA) (Henery (1994)). The k -nearest neighbour method classifies an observation by assigning the class label most frequently represented among the k nearest observations. Ties are broken at random. The k -nearest neighbour method is a non-parametric technique that is computationally complex. It is often successful when the decision boundary is irregular. Asymptotically the error rate of the 1-nearest neighbour method is never more than twice the Bayes rate (Duda et al. (2001)).

Here, three classification methods were applied to distinguish groups with different exposure levels of fumes of bitumen: workers with no exposure to fumes of bitumen serving as reference group, low-exposed workers with bitumen exposure lower than 14.7 mg/m³, and highly exposed workers with a shift concentration above 14.7 mg/m³.

6.1 Methods

The German Human Bitumen Study was conducted as a cross-sectional cross-shift study. The study group consisted of 280 bitumen-exposed men at 42 construction sites and 74 non-exposed male workers at 14 outdoor construction sites as reference group. A structured questionnaire was applied in a face-to-face interview to assess lifestyle habits, medical history, and other factors. All workers were examined after shift. Blood and urinary samples and induced sputum were collected to deter-

mine biomarkers of exposure, irritative or other health effects. Induced sputum was generated by inhalation of hypertonic saline solution and considered a non-invasive technique to collect biological material from the deeper airways. In induced sputum, cytokines were determined using commercial monoclonal “sandwich” enzyme immunoassays. During shift, personal air sampling in the workers’ breathing zone was carried out to measure exposure to fumes of bitumen. The measurement was done with a German GGP sampler. Here, concentration of fumes of bitumen is given by bitumen condensate standard, which is about 1.47 times the concentration of fumes of bitumen given by mineral oil standard used in Germany until 2007 (BGIA (2008)). Further details about the study are given in Raulf-Heimsoth et al. (2007b). All study subjects provided written informed consent prior to examination. The study was approved by the Ethics Committee of the Ruhr-University Bochum and was conducted in accordance with the Helsinki Declaration.

Median and interquartile range were presented to describe the data. Linear discriminant analysis, quadratic discriminant analysis, and k -nearest neighbour were applied to classify the different groups by exposure or smoking status. The prior probabilities were set proportional to sample size. Additionally, results of LDA and QDA with equal prior probabilities were presented. Using the k -nearest neighbour method, the data was analyzed with different values of k . In the binary classification problem ties are avoided by selecting k odd. In the three group classification problem ties are broken at random. The predictive validity of the classification rules was assessed by the leave-one-out approach of Lachenbruch and Mickey (1968). The continuous variables were log-transformed because of their skewed distributions. Subjects with any missing values were excluded from the discriminant analysis. Values below limit of quantitation (LOQ) were set to 2/3 LOQ. The calculations were performed with the statistical software SAS/STAT, version 9.2 (SAS Institute Inc., Cary, NC, USA) (PROC DISCRIM). For the k -nearest neighbour method the leave-one-out method was programmed without using the CROSSVALIDATE option in SAS/STAT.

6.2 Results

Table 1: Characteristics of the study population of the Human Bitumen Study

	Reference group N = 74	Low-exposed workers $\leq 14.7 \text{ mg/m}^3$ N = 251	High-exposed workers $> 14.7 \text{ mg/m}^3$ N = 29
Age (years)	38	40	40
(median; interquartile range)	(32 - 46)	(33 - 47)	(35 - 46)
Current smokers N (%)	37 (50 %)	161 (64 %)	19 (66 %)
Fumes of bitumen (mg/m^3)	-	4.3	22.6
(median; interquartile range)		(2.2 - 7.3)	(18.1 - 34.5)

Table 1 depicts the characteristics of the study groups. 61 % of all workers were current smokers, with slightly less current smokers in the reference group (reference 50 %, low-exposed 64 %, high-exposed 66 %). Median shift concentration of fumes of bitumen in exposed workers (total) was 4.99 mg/m³ with an interquartile range of 2.50 - 8.67 mg/m³. 251 exposed workers had a shift concentration lower than 14.7 mg/m³ of fumes of bitumen and 29 men had a concentration higher than 14.7 mg/m³.

Table 2: Distribution of irritative biomarkers measured in induced sputum in German workers

	N _{miss} ^a	LOQ ^b	N < LOQ	Reference group N = 74 Median (Q1 - Q3) ^c	Low-exposed workers N = 251 Median (Q1 - Q3) ^c	High-exposed workers N = 29 Median (Q1 - Q3) ^c
Inter-leukin-8	5	3 pg/ml	1	1207 (522 - 3278)	3714 (1837 - 9196)	3145 (929 - 13402)
Neutrophil ^d	13	- [$\times 10^4$]	-	5.6 (1.3 - 33.2)	4.2 (0.2 - 21.8)	15.6 (1.5 - 90.0)
Leukotriene B ₄	35	11.7 pg/ml	0	1662 (1147 - 2501)	1735 (1085 - 2485)	2236 (915 - 2594)
Inter-leukin-1 β	35	0.4 pg/ml	1	19.0 (8.7 - 34.7)	24.3 (14.3 - 50.4)	26.1 (10.9 - 36.3)
Nitrate/nitrite	6	5 μ M	38	7.5 (5.3 - 12.2)	16.2 (9.6 - 25.6)	13.5 (8.6 - 19.4)
Total protein	11	10 μ g/ml	0	339 (210 - 638)	714 (430 - 1110)	411 (244 - 1165)
Inter-leukin-5	5	2 pg/ml	88	1.3 (1.3 - 12.4)	10.4 (5.5 - 22.2)	4.6 (1.3 - 15.0)
Inter-leukin-6	36	3 pg/ml	111	7.5 (2.0 - 31.0)	16.0 (2.0 - 64.0)	64.3 (2.0 - 134.6)

^a N_{miss}: number of missing observations

^b LOQ: limit of quantitation

^c Q1 - Q3: interquartile range

^d Neutrophil granulocytes

Table 2 shows the distribution of biomarkers of irritative effects in induced sputum that were candidates for the discriminant analyses. Interleukin-5 and interleukin-6 were below LOQ for 88 respectively 111 workers and, therefore, excluded from analysis. All other variables served as discriminant variables.

In order to prove whether the selected irritative parameters are capable of distinguishing between workers with different health effects, a discriminant analysis was performed for smoking status because smoking is known to induce irritative effects.

Table 3: Results of discriminant analyses with smoking status as class variable and age and irritative biomarkers^a measured in induced sputum as discriminant variables using leave-one-out cross-validation

	Error rate	Correct classification (%)	
		Non-smoker N = 115	Current smoker N = 182
Proportional prior			
Linear discriminant analysis	0.29	62 (54%)	150 (82%)
Quadratic discriminant analysis	0.30	60 (52%)	148 (81%)
Equal prior			
Linear discriminant analysis	0.27	83 (72%)	136 (75%)
Quadratic discriminant analysis	0.31	79 (69%)	125 (69%)
3-Nearest neighbour	0.14	92 (80%)	164 (90%)

^a interleukin-8, neutrophil granulocytes, leukotriene B₄, interleukin-1 β , nitrate and nitrite, and total protein

Table 3 presents the classification results for LDA, QDA and 3-nearest neighbour to categorize non-smokers and current smokers. The 3-nearest neighbour method distinguished smokers from non-smokers better than LDA and QDA with an estimated error rate of 0.14 using leave-one-out cross-validation. Figure 50 shows the error rate as a function of the numbers of neighbours. To avoid tied votes k is selected odd. To categorize the smoking status $k = 3$ yields the smallest error rate.

In the next step, the discriminant analysis was applied to classify workers according to the different exposure levels (none, low and high exposure). The analysis was stratified by smoking status, because smoking was a strong irritative factor. The presented results in Figure 50 and Table 4 show the combined classification results for non-smokers and current smokers. Applying 2-nearest neighbour, the estimated error rate for non-smokers was 0.18 and for current smokers 0.24 using leave-one-out cross-validation. Combining the classification results of non-smokers and current smokers yields an estimated misclassification error of 0.22. Estimated error rates of k -nearest neighbour of different values of k are shown in Figure 1. The smallest estimated error rate has 2-nearest neighbour but this classification rule produces many tied votes. Five-nearest neighbour has the advantage that less ties occur. Both results together with LDA and QDA are presented in Table 4. Highly exposed workers were poorly classified by all methods except 2-nearest neighbour. Using equal priors instead of proportional priors by LDA and QDA improved the

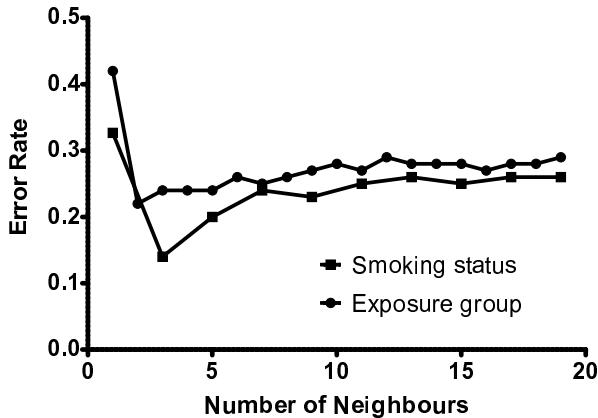


Figure 50: Estimated error rate of k -nearest neighbour with different values of k using leave-one-out cross-validation classifying smoking status and exposure group

classification of highly exposed workers and workers of the reference group, whereas the large group of low-exposed workers were classified worse.

6.3 Discussion

The 3-nearest neighbour method performed better than LDA and QDA to differentiate between non-smokers and current smokers. The two smoking groups could be well distinguished. Therefore, the selected biomarkers seem to be capable of detecting irritative effects. The classification of the three exposure groups was more difficult and none of the methods discriminated with acceptable error rates. Especially the group of the highly exposed workers could not be distinguished from the other groups. There are various possible explanations for this poor result. First, the group of the high-exposed workers was small and, therefore, likely not informative to develop a decision rule. Two-nearest neighbour was the only method that correctly classified a highly exposed worker with a higher probability than classifying at random. This method uses very few observations to classify a new subject that supports this theory. Second, the cut-off to separate highly exposed workers from low-exposed workers is artificial, and there is no clear cut point between these two groups. Third, a worker exposed during the observed shift at a high level could be exposed to lower levels in the preceding shifts and vice versa. Other analyses revealed that the observed biomarkers indicate chronic effects as well and do not clearly show short-time effects during a single working shift (data not shown). Overall, it was possible to differentiate unexposed workers from exposed workers. The differences between reference workers and exposed workers to fumes of bitumen might be caused by bitumen exposure, but also different working conditions might have contributed to the effects. In the final analysis of this study, further discriminant analysis methods shall be applied to improve the classification. One emphasis will be set on statistical methods that can deal with categorical variables as for

Table 4: Results of discriminant analyses with exposure group as class variable and age and irritative biomarkers^a measured in induced sputum as discriminant variables stratified by smoking status using leave-one-out cross-validation

	Error rate	Correct classification (%)		
		Reference	Low-exposed workers	High-exposed workers
		N = 71	N = 204	N = 22
Proportional prior				
Linear discriminant analysis	0.25	28 (39%)	193 (95%)	1 (5%)
Quadratic discriminant analysis	0.30	25 (35%)	181 (89%)	2 (9%)
Equal prior				
Linear discriminant analysis	0.48	39 (55%)	108 (53%)	6 (27%)
Quadratic discriminant analysis	0.39	47 (66%)	132 (65%)	3 (14%)
2-Nearest neighbour	0.22	41 (58%)	179 (88%)	13 (59%)
5-Nearest neighbour	0.24	35 (49%)	189 (93%)	2 (9%)

^a interleukin-8, neutrophil granulocytes, leukotriene B₄, interleukin-1 β , nitrate and nitrite, and total protein

example CART in order to include variables with a fair amount of measurements below LOQ in the analysis. Besides classification techniques, regression models will be applied to analyze the influence of fumes of bitumen on different biomarkers as shown in the analyses presented by Raulf-Heimsoth et al. (2007b).

Acknowledgment

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Part II

Data Analyses

As in the past years, the participants of the meeting were invited to take part in a data analysis experiment. There is a plethora of existing data analysis methods and the idea is to apply them to various data sets with different characteristics in order to learn about their strengths and weaknesses. For this purpose, three data sets were issued about two months before the event. One of them, the Tiles Data Set, is of archaeological origin made available by the working group J. Dolata/H.-G. Bartel/H.-J. Mucha. The two others are synthetic and designed by G. Ritter. Three working groups took part in the experiment, Gerhard Pöppel and Reinhard Schachtner from Infineon Regensburg, Gunter Ritter from the University of Passau, and Susanna Röblitz and Marcus Weber from the Zuse Institute Berlin. The methods employed were Projection Pursuit, Spectral Clustering, MCLUST, and the Trimmed Determinant Criterion. We now present the results ordered by data sets.

7 Roman Tiles Data Set

An introduction to the Roman tiles data set was presented in Hans-Georg Bartel's contribution, Sect. 3.

7.1 Gerhard Pöppel and Reinhard Schachtner: Analysis I by Projection Pursuit

Meanwhile it is an established tradition that for the Fall Meeting of the AG-DANK given data sets should be analyzed by the participants. This kind of contest affords an opportunity to get an impression which kind of data can be treated with which kind of method to fulfill the given task. Because different participants usually use different approaches one can learn a lot about appropriate methods.

We tried to analyze the three data sets within limited time of half a day all in all. Fifty percent of our restricted time is spent on the data set "Archaeometric data of Roman bricks and tiles from the Rhine area of Germany". The rest of the time goes in equal parts to the artificial data sets "Berlin08_synth1" and "Berlin08_synth2" which are also very interesting.

We mainly used Projection Pursuit and Mixture Models for our three analyses. We tried to analyze the data without additional background information which can be found in the corresponding papers: Dolata (2000), Mucha et al. (2005), Mucha et al. (2003).

Group	Run 10 Projection 688	SiO ₂	TiO ₂	Al ₂ O ₃	Fe ₂ O ₃	MnO	MgO	CaO	Na ₂ O	K ₂ O	V	Cr	Ni	Zn	Rb	Sr	Y	Zr	Nb	Ba	Counts
not_further_classified	0.00	Mean 68.81	1.10	16.25	5.02	0.05	1.63	3.56	0.58	2.80	67.64	138.19	55.76	97.57	131.33	165.79	33.87	258.96	25.36	491.21	75.00
A	1.00	Mean 74.14	0.66	14.82	4.23	0.03	1.14	0.83	1.00	3.05	68.21	82.44	35.17	63.73	143.73	112.87	36.35	295.55	14.24	661.56	107.00
B	2.00	Mean 72.86	1.73	16.84	4.53	0.03	0.90	0.62	0.22	2.18	95.27	158.63	46.60	45.94	118.72	137.63	33.88	288.87	39.90	422.07	100.00
C	3.00	Mean 76.06	0.88	15.11	3.68	0.02	0.86	0.56	0.25	2.47	69.74	75.37	32.58	34.73	130.21	110.03	24.56	221.11	25.55	466.40	62.00
D	5.00	Mean 61.42	0.63	14.57	4.89	0.08	2.53	12.12	0.67	2.85	84.35	99.85	56.76	90.58	130.76	299.56	26.22	135.10	14.72	416.73	253.00
E	8.00	Mean 67.48	0.65	15.03	4.77	0.06	2.33	5.47	0.83	3.18	81.02	99.29	48.16	83.02	148.02	169.33	36.63	268.13	15.44	544.89	63.00
																				660.00	

Figure 51: Cluster characterization via the mean values of the archaeometric original variables

On one hand this is a possibly unnecessary restriction and a loss of available information, on the other hand this additional information would be not available if you did the analysis from beginning. Let us see what is the outcome if one has only the data and the task to cluster the data. In any case before we select any method we always have a view on the original variables and do some univariate statistics on that. So one gets an impression about their distributions, about univariate outliers etc. From that we decided to use Projection Pursuit (Friedman and Tukey (1974), Posse (1995)) for exploratory data analysis in order to find the "best" 2-dimensional

views to the dataset. These “best” views are defined by the highest projection index.

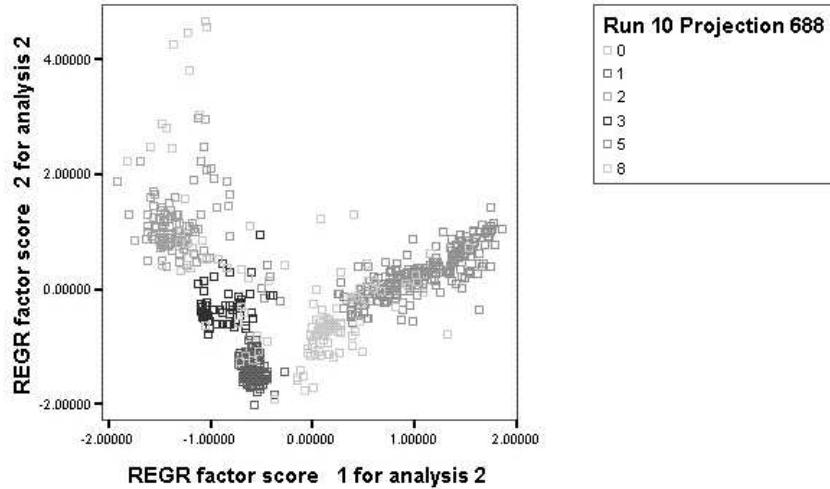


Figure 52: Scatterplot of the first two principal components of the archaeometric data

We use a Chi-Square-Index with 9 cells as described in Rohatsch et al. (2006). Instead of spheroid data we use z-standardized variables with an anti-index to avoid trivial views of linear correlations. It turns out that Projection Pursuit does a good job on that dataset. One can easily mark different clusters from different views and we stopped investigating after the finding of 6 regions (5 selected clusters and one rest-cluster which includes some further substructure). To characterize the clusters, the mean values of the original variables can be considered (see Fig. 51).

Typical accumulations of oxides and trace elements characterize the clusters. In many cases also simple scatterplots after PCA of the original variables show some of the underlying structure found by Projection Pursuit, as can be seen in Fig. 52:

There are many different views of Projection Pursuit which allows the recognition of substructures in already found clusters. So it seems that Projection Pursuit can detect a lot of further details which may be of interest for the specialists.

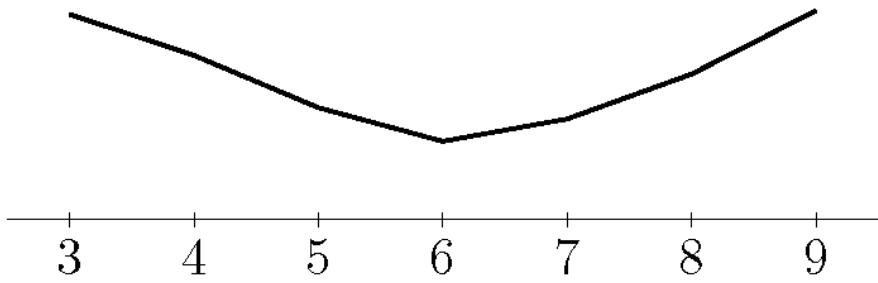


Figure 53: Tiles data: the BIC curve of the favorite solutions with three to nine clusters suggested by the posterior-density-HDBT-ratio plot.

7.2 Gunter Ritter: Analysis II by Model Based Clustering

I clustered the data set with a statistical criterion based on a heterogeneous classification model with unknown cluster sizes for normal data with full covariance matrices and allowing gross outliers, the TDC (Trimmed Determinant Criterion) according to Gallegos and Ritter (2009), see also Gallegos and Ritter (2005). Visual inspection of the 2D scatter plots suggests that the data set contains outliers. I assumed an amount of ten percent. Visual inspection also shows that some of the features are noticeably correlated. For this reason and in order to diminish sample space dimension, I deleted SiO_2 , TiO_2 , CaO , and K_2O from the feature list so that sample space dimension is fifteen. The number of clusters was determined with the BIC model selection criterion.

The BIC curve, see Fig. 53, clearly pleads for six clusters. However, there may be one or a few small clusters, in particular of size ≤ 15 , hidden in the set of 66 discarded elements (outliers) which I did not further analyze. Cluster sizes of the favorite partition with six clusters are 145, 111, 111, 105, 61, and 61. Visual inspection of the clusters obtained suggests that there are more outliers than the assumed 66. The MnO-Y-plot of the partition is presented in Fig. 54.

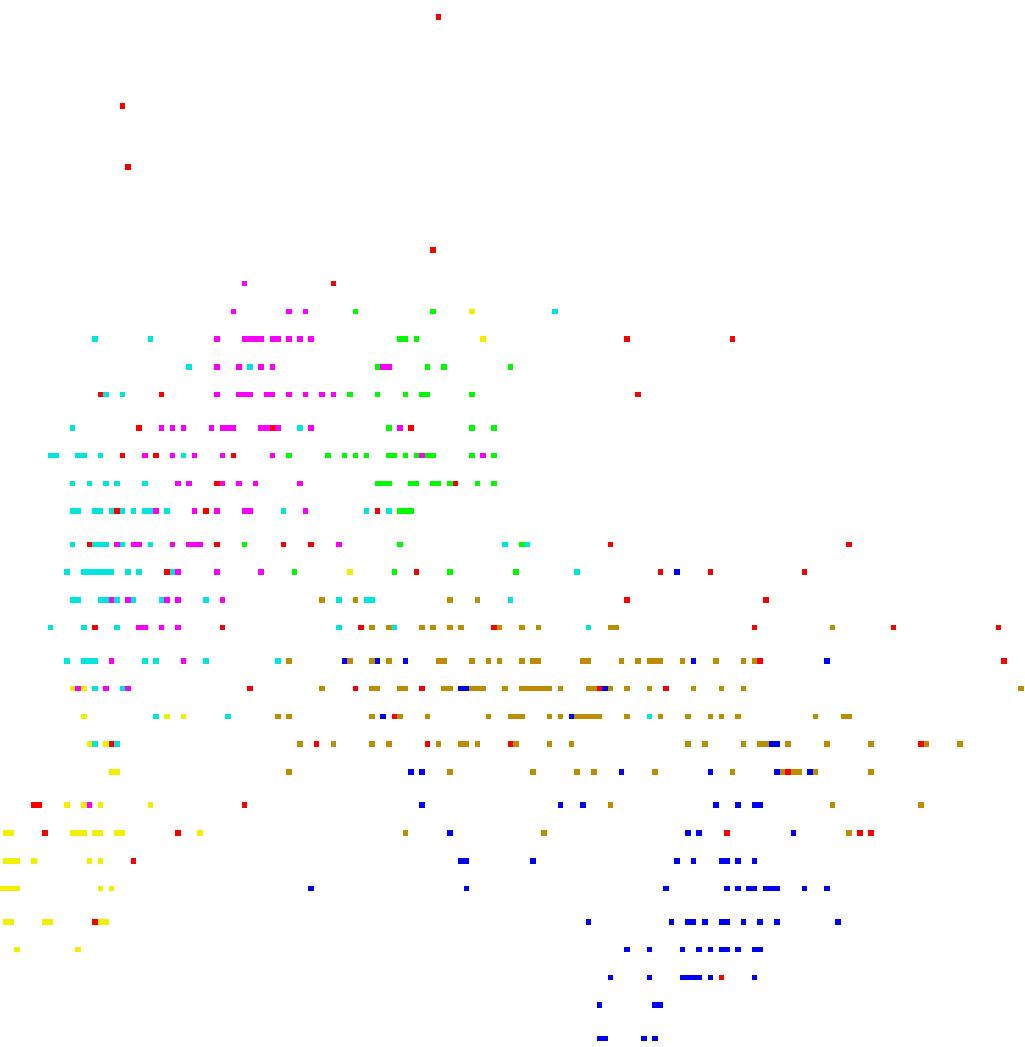


Figure 54: MnO-Y plot of the favorite partition obtained from the heteroscedastic TDC with model selection criterion BIC. Outliers are plotted in red.

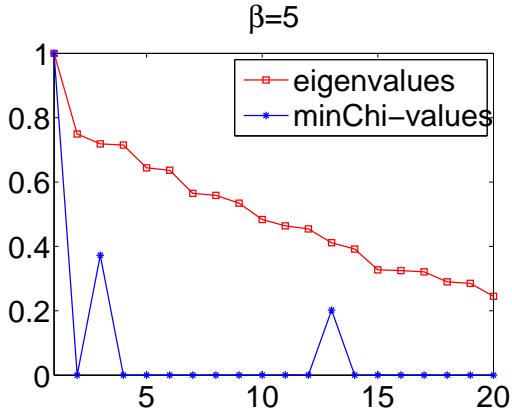


Figure 55: Tiles from Dolata: minChi-values and eigenvalues for different numbers of clusters.

7.3 Susanna Röblitz and Marcus Weber: Analysis III by Spectral Clustering

The method applied here is described by the authors at full length in Sec. 4. Because spectral clustering is scale dependent, a preprocessing step before distance computation is recommended. Since the different features have different ranges of values, we first normalized the data column-wise by dividing every column by its mean value. Afterwards, we computed the matrix D^{eff} of all pair-wise effective distances (fully connected graph). At this point, we figured out that there are two objects with the same effective distance to all other objects, namely H169 and H301. That means, the effective distances between all other objects are smaller than the effective distances between H169 or H310 and the other objects. In other words, these two objects represent outliers. The cluster algorithm will always put them into two single-object clusters. Therefore, we removed them from the data before we started the algorithm.

In the computation of the Gaussian similarity function (17), we set the parameter $\beta = 5$. However, the results turned out to be quite insensitive with respect to the choice of β in the interval $[0.5, 10]$. Fig. 55 illustrates the eigenvalues and the minChi-values of the initial guess for different numbers of clusters $k = 1, \dots, 20$. Based on this information, we decided to consider the choices $k = \{4, 6, 8, 9\}$ in detail.

The resulting membership values for $k = 4$ are illustrated in Fig. 56. In fact, the separation between the four clusters is clearly visible on the $(\text{Na}_2\text{O}, \text{CaO}, \text{Sr})$ sub-manifold. Re-transformation of membership values to indicator vectors gives the assignment of objects to the clusters as listed in Tab. 5.

If we choose $k = 6$, the partition of objects into clusters is the same as for $k = 4$, accept the two objects H880 and H857, which are isolated from cluster 2 and put into single clusters.

Table 5: Tiles from Dolata: Partition into $k = 4$ clusters. The objects have been numbered according to their position in the original data file.

k	objects
1	5 6 7 8 9 10 11 12 13 14 16 47 48 49 50 51 52 53 54 55 56 57 58 60 61 63 64 65 66 67 68 69 70 71 72 73 74 80 88 90 102 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 153 154 155 156 157 158 159 160 161 162 163 164 165 167 168 169 174 181 185 187 195 199 200 201 203 204 220 226 227 228 231 232 233 235 236 237 240 241 242 249 262 264 267 270 275 276 277 280 282 283 286 287 288 290 293 294 295 296 297 299 300 301 302 303 304 305 306 307 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 346 347 350 353 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 381 382 383 384 385 386 387 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 416 417 469 472 492 493 496 506 508 509 510 511 512 513 514 515 516 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 574 575 576 577 578 579 580 581 582 583 584 585 586 587 603 604 605 606 607 613 614 615 616 617 618 619 620 621 623 624 625 626 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660
2	1 2 3 4 15 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 62 75 94 100 101 103 104 105 106 107 108 109 110 111 112 113 114 115 116 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 166 170 171 172 173 175 176 177 178 179 182 183 184 186 188 189 190 191 192 193 194 196 202 205 206 207 208 209 210 211 212 213 214 215 216 217 219 221 223 224 225 229 230 234 238 239 244 248 252 253 254 255 259 261 265 266 268 269 271 272 273 274 281 284 285 289 291 292 298 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 345 351 352 355 380 415 466 467 468 470 471 473 474 475 476 486 487 488 489 490 491 494 495 497 498 499 500 501 502 503 504 505 507 608 609 610 611 612 622 627
3	59 76 77 78 79 81 82 83 84 85 86 87 89 91 92 93 95 96 97 98 99 180 218 222 243 245 246 247 251 260 263 278 279 308 343 344 348 349 354 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 477 478 479 480 481 482 483 484 485 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602
4	197 198 250 256 257 258 573

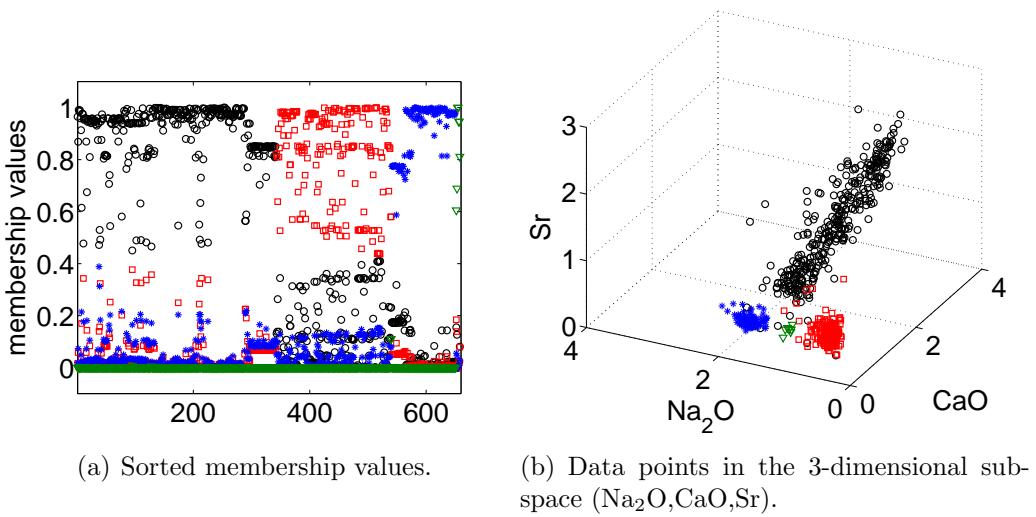


Figure 56: Tiles from Dolata: Partition into $k = 4$ clusters.

For $k = 8$, we obtain three isolated objects (H888, H857, G017) and cluster 2 is split into two clusters, compare Tabs. 5 and 6. The membership values are illustrated in Fig. 57. The two views in Fig. 58 show that the clusters are indeed separated from each other.

$k = 9$ results in the same clustering as $k = 8$, accept object G018 (no. 198), which is isolated from cluster 5 and put into a single cluster.

A further increase of the number of clusters leads to a splitting of clusters and separation of outliers. Tab. 7 contains the values of the objective function $I(\mathcal{A}; X, \pi)$ from (18). The values I/k are quite similar such that it is difficult to determine the “best” number of clusters.

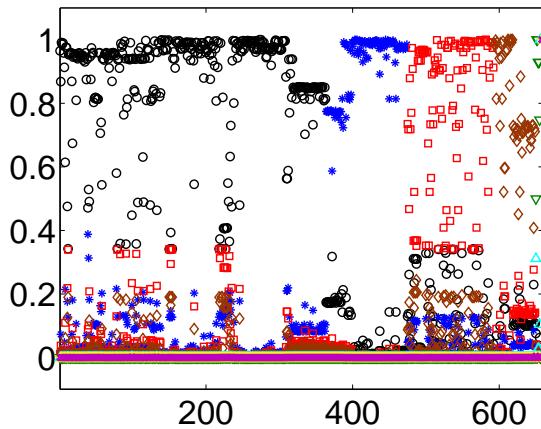


Figure 57: Tiles from Dolata: Sorted membership values for the partition into $k = 8$ clusters. Three clusters contain only one object, such that only five clusters are shown here.

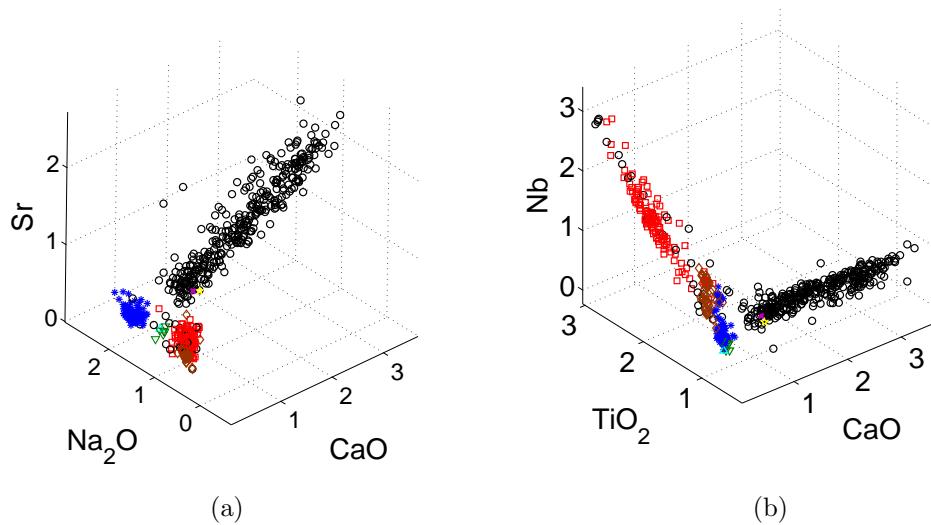


Figure 58: Tiles from Dolata: Data points in different sub-spaces.

Table 6: Tiles from Dolata: Partition into $k = 8$ clusters. The objects have been numbered according to their position in the original data file.

k	objects
1	5 6 7 8 9 10 11 12 13 14 16 18 47 48 49 50 51 52 53 54 55 56 57 58 60 61 63 64 65 66 67 68 69 70 71 72 73 74 80 88 90 102 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 153 154 155 156 157 158 159 160 161 162 163 164 165 167 168 169 174 179 181 185 187 189 195 199 200 201 203 204 220 223 226 227 228 231 232 233 235 236 237 240 241 242 249 253 262 264 267 270 275 276 277 280 282 283 286 287 288 290 293 294 295 296 297 299 300 301 302 303 304 305 306 307 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 328 331 334 336 346 347 350 353 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 381 382 383 384 385 386 387 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 416 417 466 467 469 470 471 472 486 487 488 489 490 491 492 493 495 496 506 508 509 510 511 512 513 514 515 516 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 574 575 576 577 578 579 580 581 582 583 584 585 586 587 603 604 605 606 607 613 614 615 616 617 618 619 620 621 623 624 625 626 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660
2	59 76 77 78 79 81 82 83 84 85 86 87 89 91 92 93 95 96 97 98 99 180 218 222 243 245 246 247 251 260 263 278 279 308 343 344 348 349 354 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 477 478 479 480 481 482 483 484 485 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602
3	1 2 3 4 15 17 19 20 39 94 103 104 108 113 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 166 170 171 172 173 175 177 178 182 183 184 186 188 190 191 192 193 194 196 202 205 206 207 208 209 210 211 212 213 214 215 216 217 219 221 224 225 229 230 234 238 244 248 252 254 255 261 265 266 268 269 284 285 289 291 292 298 326 327 329 330 332 333 335 337 338 339 340 341 342 345 351 468 473 474 475 476 497 498 499 500 501 502 503 504 505 507
4	21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 40 41 42 43 44 45 46 62 75 100 101 105 106 107 109 110 111 112 114 115 116 176 239 259 271 272 273 274 281 352 355 380 415 494 608 609 610 611 612
5	198 250 256 257 258 573
6	197
7	627
8	622

Table 7: Tiles from Dolata: Values of the objective function I in the computed (local) optimum for different cluster numbers k .

k	4	6	8	9
I	3.34	4.91	6.21	7.07
I/k	0.84	0.82	0.78	0.79

7.4 Hans-Joachim Mucha, Hans-Georg Bartel, Jens Dolata: Vergleich der Klassifikationsergebnisse zum “*Roman Tiles Data Set*”

Als Vergleichspartition für die vorhergehenden drei hier präsentierten Klassifikationsergebnisse wird die mit dem (gewöhnlichen) hierarchischen Ward-Verfahren ([10]) berechnete Partition P8DANK in acht Cluster benutzt. (P8DANK steht für die Partition in acht Cluster für den auf der DANK-Tagung verfügbar gemachten “*Roman Tiles Data Set*”.) Diese ist das Ergebnis auf Basis des quadrierten euklidischen Distanzmaßes, angewandt auf die Datenmatrix, deren Elemente (Messwerte) zuvor gemäß Wert/Mittelwert transformiert wurden (siehe Sec. 3). Die Zerlegung in acht Klassen wird durch den Ellbogentest nahe gelegt (Fig. 59). Die 8-Klassen-Partition P8DANK ist hinsichtlich der sinngebenden archäologischen Interpretation ähnlich zu den Analysen der 613×19 -Matrix (siehe unten und Sec. 3). Der Ellbogentest zeigt, dass auch eine 5-Klassen-Partition statistisch auffällig ist.

Die Festlegung einer Vergleichspartition ist notwendig, weil es sich hier um eine reale, durch physikalische Messungen an Fundobjekten erhaltene Datenmatrix handelt, deren wahre Klassenzerlegung *a priori* unbekannt ist.

Die Partition P8DANK kann mit üblicher Standardsoftware unter Benutzung der hier erstmalig in Fig. 63 bis Fig. 74 angegebenen kompletten 660×19 -Datenmatrix erhalten werden. Hierbei liegen die ersten 613 Objekte (Proben) den Ausführungen in Sec. 3 zugrunde, während die weiteren 47 Proben mit dem Fundort Boppard am Rhein den Datensatz “*Roman Tiles*” vervollständigen. Die Werte der Variablen 1 bis 9 (Oxide) in der 660×19 -Datenmatrix sind gerundet angegeben (siehe die entsprechenden Skalenfaktoren). Die genauen Werte findet man in [1], [6] sowie auf der Internetseite der Arbeitsgruppe AG-DANK unter <http://www.fim.uni-passau.de/fileadmin/files/lehrstuhl/ritter/agdank/TilesFromDolata.txt>.

Im Folgenden wird die Partition P8DANK jeweils den oben präsentierten Klassifikationsergebnissen P5PP+rest von Gerhard Pöppel und Reinhard Schachtner (Sec. 7.1), P6MB+outliers von Gunter Ritter (Sec. 7.2) sowie P4SC und P8SC von Susanna Röblitz und Marcus Weber (Sec. 7.3) gegenübergestellt. Die von den obigen Autoren dokumentierten Mini-Cluster sind der besseren Lesbarkeit wegen hierbei nicht berücksichtigt. Aus dem gleichen Grunde sind die Zeilen und Spalten der Kreuztabelle (Kontingenztafeln) umgeordnet worden und zwar so, dass die größten Zahlen

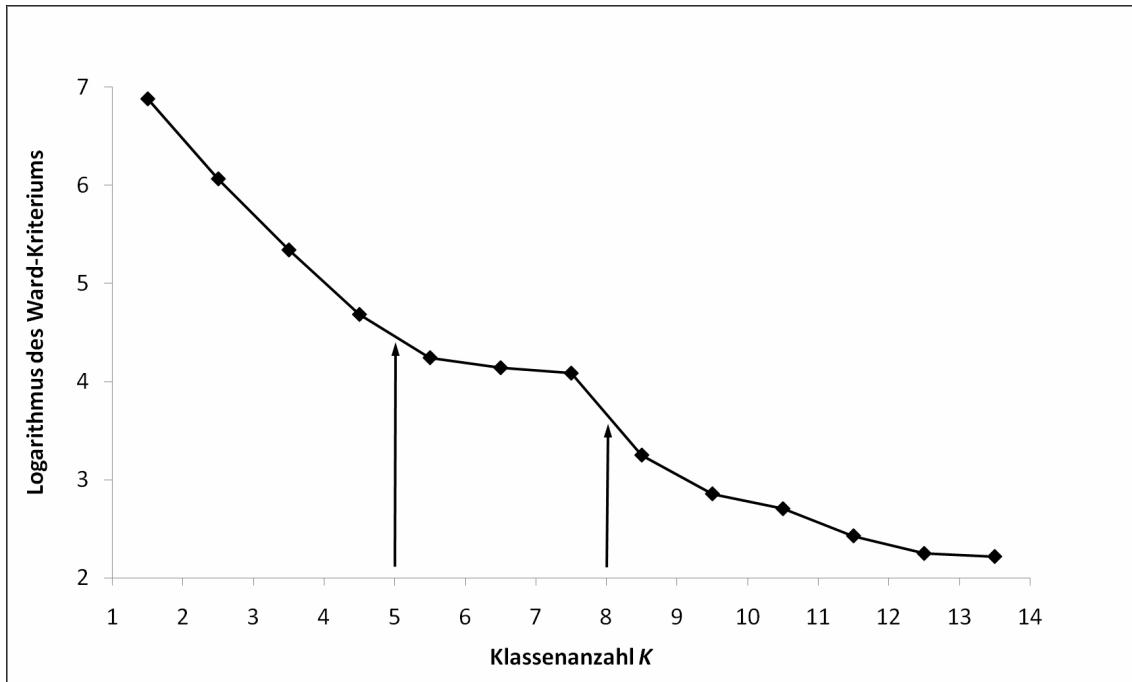


Figure 59: Auswahl einer optimalen Clusteranzahl des Ward-Verfahrens mit dem Ellbogentest

P8ModWARD $\cup C_{\text{Boppard}}$	P8DANK								Total
	Cluster Nr.								
1	2	3	4	5	6	7	8	Total	
Frankfurt-Nied A	92								92
Frankfurt-Nied B	14	24							38
Unbekannt 3				7					7
Großkrotzenburg	1				63				64
Straßburg-Königshofen						114			114
Rheinzabern B, inkl. Worms	6		88						94
Rheinzabern A.1			5				110		115
Rheinzabern A.2, inkl. Unbekannt 1								89	89
C_{Boppard}			45	2					47
Total	113	24	138	9	63	114	110	89	660

Figure 60: Vergleich der Klassenzerlegungen P8ModWARD $\cup C_{\text{Boppard}}$ und P8DANK

in den ‘Hauptdiagonalen’ positioniert sind. Von allen hier eingesetzten Verfahren werden die Ziegel aus der Provenienz ‘Straßburg-Könighofen’ mit hoher Trefferquote als ein Cluster identifiziert. Dieses stabilste Cluster ist in den folgenden Kreuztabelle in fetter Schrift hervorgehoben. Weitere stabile und in hohem Grade reproduzierbare Herstellungsorte sind ‘Großkrotzenburg’ und ‘Frankfurt-Nied A’. Das Auffinden des kleinen Clusters ‘Unbekannt 3’ (siehe Sec. 3 und Fig. 60) gelingt nur mit “spectral clustering” (letzte Spalte der Kreuztabellen P8DANK-P8SC und P8DANK-P4SC).

P8DANK - P5PP+rest (siehe “Analysis I”):

106	0	0	0	0	(8)
0	99	0	0	0	(11)
0	0	87	0	7	(19)
0	61	0	63	0	(14)
0	5	0	0	54	(4)
0	88	0	0	0	(1)
0	0	13	0	1	(10)
1	0	0	0	0	(8)

Die letzte Spalte stellt hier kein Cluster dar (die entsprechenden Zahlen sind deshalb eingeklammert), sondern laut dem Text von Pöppel und Schachtner in Sec. 7.1 einen Rest, der nicht weiter untersucht wurde. Auf die gleiche Weise ist die Menge der Ausreißer (“outliers”) in der letzten Spalte der folgenden Tabelle markiert.

P8DANK - P6MB+outliers (siehe “Analysis II”):

111	0	0	0	0	0	(3)
0	96	0	0	0	4	(13)
0	0	76	24	0	0	(10)
0	0	19	65	0	0	(5)
0	0	50	16	61	0	(11)
0	0	0	0	0	57	(6)
0	15	0	0	0	0	(9)
0	0	0	0	0	0	(9)

P8DANK - P8SC (siehe “Analysis III”):

137	0	0	0	0	0
3	111	0	0	0	0
9	0	104	0	0	0
1	0	5	57	0	0
0	0	0	0	6	0
109	0	0	0	0	0
89	0	0	0	0	0
15	0	9	0	0	0

P8DANK - P4SC (siehe ‘‘Analysis III’’):

$$\begin{bmatrix} 137 & 0 & 0 & 0 \\ 3 & \mathbf{111} & 0 & 0 \\ 3 & 0 & 110 & 0 \\ 0 & 0 & 24 & 0 \\ 0 & 0 & 2 & 7 \\ 1 & 0 & 62 & 0 \\ 109 & 0 & 0 & 0 \\ 89 & 0 & 0 & 0 \end{bmatrix}$$

Bislang wurde als Vergleichspartition jeweils P8DANK benutzt. Vergleicht man hingegen das Ergebnis von Gerhard Pöppel und Reinhart Schachtner (P5PP+rest) mit demjenigen von Gunter Ritter (P6MB+outliers), so erhält man vier sehr gut übereinstimmende Cluster, wie die zuhöhere Kontingenztafel verdeutlicht.

P5PP+rest - P6MB+outliers:

$$\begin{bmatrix} 134 & 0 & 0 & 0 & 4 & 103 & (12) \\ 0 & \mathbf{104} & 0 & 0 & 0 & 0 & (3) \\ 0 & 0 & 96 & 0 & 0 & 0 & (4) \\ 2 & 0 & 0 & 57 & 0 & 1 & (3) \\ 0 & 0 & 4 & 0 & 51 & 0 & (7) \\ (9) & (7) & (11) & (4) & (6) & (1) & (37) \end{bmatrix}$$

Dies scheint die beste Übereinstimmung zu geben, und sie ist fast perfekt, wenn man bedenkt, dass Pöppel und Schachtner ein Cluster weniger haben. Wie weiter oben erwähnt, stellen die in Klammern angegebenen Zahlen (hier in der letzten Zeile) kein Cluster dar. Wie weiter aus der obigen Tafel erkennbar ist, besteht dieser Rest zum großen Teil aus Beobachtungen, die das Verfahren von Gunter Ritter als Ausreißer qualifiziert ($n = 37$).

Im Folgenden soll die hier benutzte Vergleichspartition P8DANK mit den in Sec. 3 skizzierten archäometrischen Ergebnissen in Beziehung gebracht werden. Es seien die in Fig. 43 der Sec. 3 charakterisierte 8-Klassen-Partition, die bei der Clusteranalyse der 613 x 19-Datenmatrix unter Verwendung des modifizierten Ward-Verfahrens erhalten wurde, mit P8ModWARD und die Menge der 47 in Sect. 3 nicht besprochenen, in Boppard gefundenen Objekte mit C_{Boppard} bezeichnet. Die in Fig. 60 wiedergegebene Gegenüberstellung der Vergleichspartition P8DANK mit $P8\text{ModWARD} \cup C_{\text{Boppard}}$ zeigt, dass beide Klassenzerlegungen im Wesentlichen übereinstimmen.

Die Objekte (Proben) der Menge C_{Boppard} werden zwei Klassen von P8DANK zugeordnet: die überwiegende Mehrheit von 45 Objekten (d.h. 95,7 %) zu der Klasse, die weitgehend mit ‘Rheinzabern B’ übereinstimmt, und der kleine Rest von nur zwei Objekten (d.h. 4,3 %) einer sonst mit ‘Unbekannt 3’ identischen Klasse. Diese Verhältnisse illustriert Fig. 61.

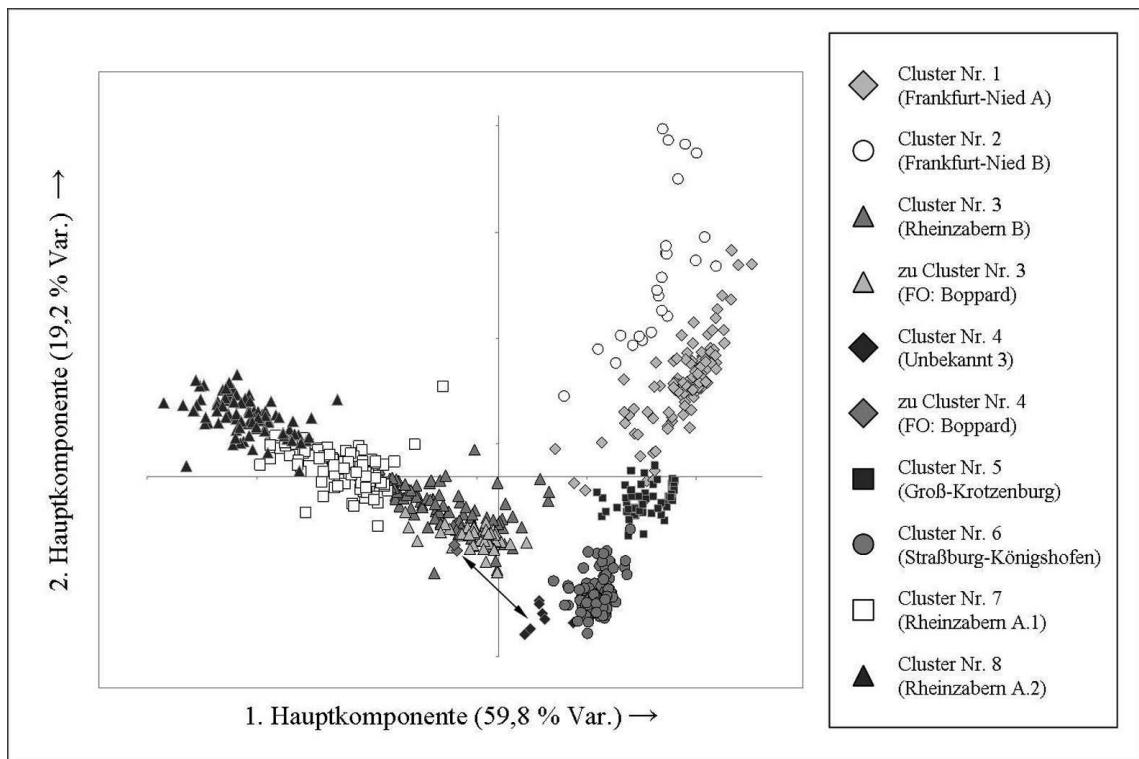


Figure 61: Auftragung der 1. und 2. Hauptkomponente mit Einfärbung der Objekte nach der Klassenzerlegung P8DANK (FO: Fundort)

P8DANK				
Cluster Nr.	Zuordnung zu Provenienz	Objektanzahl	davon	Abweichung gegenüber P8ModWARD
1	Frankfurt-Nied A	113		+ 21
2	Frankfurt-Nied B	24		- 14
3	Rheinzabern B, inkl. Worms	138	45 aus $C_{Boppard}$	- 6 + 5 = - 1
4	Unbekannt 3	9	2 aus $C_{Boppard}$	± 0
5	Großkrotzenburg	63		- 1
6	Straßburg-Königshofen	114		± 0
7	Rheinzabern A.1	110		- 5
8	Rheinzabern A.2, inkl. Unbekannt 1	89		± 0

Figure 62: Zur archäologischen Charakterisierung der Klassenzerlegung P8DANK

In der in Fig. 62 gegebenen Tabelle wird die Partition P8DANK hinsichtlich der Zuordnung ihrer Klassen zu den gemäß den Ausführungen in Section 3 erkannten Provenienzen von obergermanischen Heeresziegeleien charakterisiert. Das Klassifikationsresultat P8DANK rechtfertigt somit die Annahme von Produktionsstätten römischer Ziegel in Großkrotzenburg, Straßburg-Königshofen sowie in den noch nicht bestimmten Lokalitäten ‘Unbekannt 1’ und ‘Unbekannt 3’ in vollem Maße. Hier ist anzumerken, dass die eigenständige Existenz eines Ziegeleiortes ‘Unbekannt 1’ durch lokal-adaptive Clusteranalyse [2] sehr wahrscheinlich gemacht werden konnte, so dass 67 (d.h. 75,3 %) der 89 Objekte der Klasse ‘Rheinzabern A.2’ dieser Herstellungs-Provenienz zugeordnet werden können.

Auf analoge Weise ist in [6] das Bestehen von Heeresziegeleien in Worms bzw. deren Unterscheidbarkeit von solchen in Rheinzabern mathematisch-statistisch durch modellbasierte Clusteranalyse glaubhaft gemacht worden. So stammen aus der Gruppe ‘Rheinzabern B’ offensichtlich neben 19 weiteren die 45 erwähnten Ziegel der Menge $C_{Boppard}$ aus Ziegeleien in Worms.

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8 Synthetic Data Set 1

8.1 Gunter Ritter: Structure of the synthetic data set Berlin08_synth1

Sampling

Berlin08_synth1 is a five-dimensional numerical data set consisting of four spherical, non-normal clusters of sizes 500, 300, 300, and 200, respectively. The four cluster centers are the extreme points of a regular tetrahedron, namely,

```
0.8 0.8 0.8 0.8 0.0  
-0.8 -0.8 0.8 0.8 0.0  
0.8 -0.8 0.8 -0.8 0.0  
-0.8 0.8 0.8 -0.8 0.0
```

Each cluster is sampled in the following way: (1) Data points are sampled from the 5D standard normal; (2) each data point is multiplied by its norm; (3) the data points are shifted by the cluster center.

Comment

Cluster centers are at the mutual distance $\sqrt{2 \cdot 1.6^2} \approx 2.26$. This means that, without the multiplication (2), the data set would consist of moderately separated, spherical normal clusters of equal (unit) variance. It could be clustered by classical k -means since cluster sizes are not too unbalanced. Of course, there would be a good number of errors since separation is not perfect. The point is the multiplication which attracts small data points to the center and drives away points of size > 1 creating a heavy tail. Nevertheless, 332 out of the 500 data points sampled for class 1 are closer to their center than to any of the other three centers. However, even a method that manages to understand the structure of the data set will probably misclassify at least 1/3 of the data (unless it is clairvoyant).

8.2 Gerhard Pöppel and Reinhard Schachtner: Analysis A by MCLUST

The Projection Pursuit approach did not reveal a clear cluster structure on the Berlin08_synth1 dataset. Therefore we utilized a “VVV-Mixture Model” approach (Fraley and Raftery (1999), Fraley and Raftery (2006), Stritt et al. (2007)). The result of the Mixture Model analysis indicates that the subgroups of the data interfuse a lot (see Fig. 75).

Group	Class		feat0	feat1	feat2	feat3	feat4		Counts
A	0.00	Mean	-0.36	-0.37	0.79	0.02	-0.08		220.00
B	1.00	Mean	0.67	0.88	1.85	0.98	-0.36		62.00
C	2.00	Mean	0.20	0.14	0.47	0.19	-0.05		362.00
D	3.00	Mean	0.13	0.19	0.85	0.29	0.14		366.00
E	4.00	Mean	0.53	0.09	0.73	0.00	-0.03		290.00
									1300.00

Figure 75: Cluster results for the Berlin08_synth1 data gained by Mixture Models

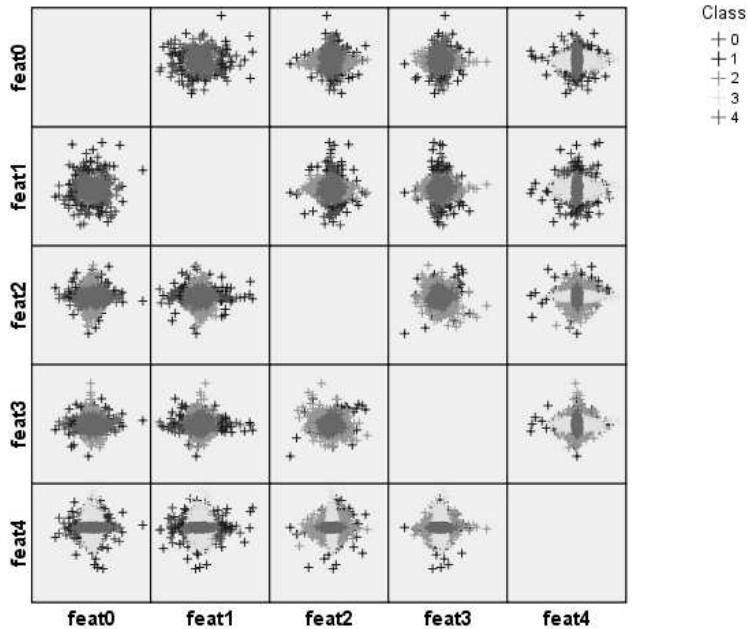


Figure 76: Scatterplots of the original variables of the Berlin08_synth1 data

Consideration of the scatterplots of the original data as shown in Fig. 76 indicates that the projection onto variable $\text{feat}1$ and $\text{feat}2$ shows an orthogonal orientation of group A (class = 0) versus group C (class = 2), whereas the projection onto variable

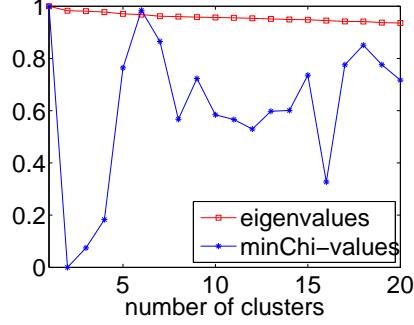


Figure 77: Synthetic data set 1: minChi-values and eigenvalues for different numbers of clusters.

feat2 and feat4 shows an orthogonal orientation of group C (class = 3) versus D (class = 4).

8.3 Susanna Röblitz and Marcus Weber: Analysis B by Spectral Clustering

This is another application of the method that is described by the authors at full length in Sec. 4. A first look at the data set did not reveal any elongated regions of data points, so we decided to use the Euclidean distance. From the distance matrix we computed a k -nearest neighbor graph with $k = 10$ and weighted the edges by

$$w_{ijk} = \frac{1}{2^{j_k}}, \quad j_k = 1, \dots, 10,$$

where j_k denotes the k th nearest neighbor. Afterwards, W was symmetrized by

$$w_{ij}^* = \max(w_{ij}, w_{ji}).$$

Then the matrix $P = D^{-1}W^*$ was used for spectral clustering. The minChi-criterion indicates that there are at most four clusters (see Fig. 77), but the resulting clusters are not well separated, see Fig. 78. The partition can be visualized best in the two-dimensional space spanned by features 1 and 4, where the clusters are more or less separated by the coordinate axes. The contingency table presented in Sec. 8.4 summarizes the assignment of objects to the clusters after re-transformation of the membership matrix χ to an indicator matrix.

In sum, we suggest that there are in fact four clusters which are not well-separated but overlap each other. Some characteristic properties are listed in Tab. 8.

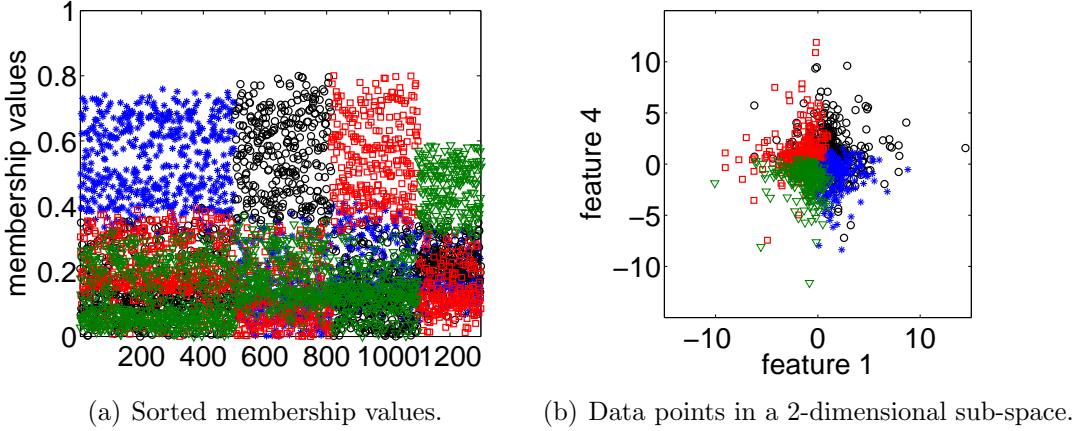


Figure 78: Synthetic data set 1: Partition into $k = 4$ clusters.

Table 8: Synthetic data set 1: Some characteristics of the identified clusters.

k weight	objects	χ -weighted mean	χ -weighted standard dev.
1404.50	502	(0.81, 0.79, 0.67, 0.81 – 0.10)	(1.94, 1.99, 2.00, 2.09, 1.99)
2326.57	312	(–0.82, –0.53, 0.72, 0.69, 0.08)	(1.92, 2.03, 2.04, 2.12, 1.86)
3322.00	282	(0.98, –0.46, 0.91, –0.51, 0.06)	(1.89, 2.08, 2.01, 1.99, 1.97)
4246.94	204	(–0.57, 0.50, 0.72, –0.60, –0.08)	(1.96, 2.13, 2.00, 2.00, 1.87)

8.4 Gunter Ritter and Hans-Joachim Mucha: Comparison of Results

Here, we are in a better situation for an assessment of the performance of clustering techniques than before. This is because the true classification is known and we may establish contingency tables w.r.t. the true classification.

Model-based methods of clustering depend on a statistical model. In particular, Fraley and Raftery's MCLUST is based on normal models. Although the clusters of this data set are sampled from spherical populations the "VVV-Mixture Model" is not well adapted to the data set because of its heavy tails. Therefore, MCLUST produces a good number of errors on this data set. This is seen from the contingency table below. It compares the partition obtained by Pöppel/Schachtner in "Analysis A" for the "VVV-Mixture Model" with the true partition.

$$\begin{bmatrix} 153 & 137 & 113 & 71 & 26 \\ 63 & 92 & 69 & 61 & 15 \\ 93 & 73 & 65 & 54 & 15 \\ 57 & 60 & 43 & 34 & 6 \end{bmatrix}$$

On the other hand, sphericity of the clusters offers good conditions for a distance based method such as Spectral Clustering. In fact, Röblitz/Weber approach with this method the optimal error rate predicted in Sect. 8.1. The following contin-

gency table which compares their partition obtained in “Analysis B” for Spectral Clustering with the true partition.

$$\begin{bmatrix} 366 & 52 & 57 & 25 \\ 54 & 186 & 29 & 31 \\ 45 & 49 & 183 & 23 \\ 37 & 25 & 13 & 125 \end{bmatrix}$$

Obviously, spectral clustering outperforms normal, model-based cluster analysis on this data set.

As Pöppel and Schachtner mention, *Projection Pursuit* encounters problems with this data set. The reason is the heavy overlapping. Sphericity and equal spread of all clusters is a condition for the functioning of *k-means*. However, k-means yields an unsatisfactory result on this data set due to the overlapping caused by the heavy tails.

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9 Synthetic Data Set 2

9.1 Gunter Ritter: Structure of the synthetic data set Berlin08_synth2

Sampling

The construction of the numerical data set Berlin08_synth2 starts with 300 data points sampled from NV_{0,V_1} , 500 from NV_{0,V_2} , and 500 from NV_{0,V_3} , where the V_j 's are the diagonal matrices with diagonals $(1, 10^{-6}, 1, 1, 1)$, $(0.25, 10^{-6}, 0.25, 1, 1)$, and $(1, 10^{-6}, 0.25, 0.25, 1)$, respectively. The whole data set is subsequently rotated by the orthogonal matrix

$$\begin{pmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1/2 & 1/2 & 1/2 & -1/2 \\ 0 & -1/2 & 1/2 & 1/2 & 1/2 \\ 0 & 1/2 & -1/2 & 1/2 & 1/2 \\ 0 & -1/2 & -1/2 & 1/2 & -1/2 \end{pmatrix},$$

and multiplied by 2. Finally, the third group is shifted by the vector $1.5 e_3$, e_3 = the third unit vector.

Comment

The second group lies within the first since it has the same mean and a smaller covariance matrix. It is, therefore, legitimate to speak of two clusters, one of them not normal. These two clusters are completely separated since, after rotation, the variance in the direction of the shift is small. Viewed from an appropriate direction the data set looks like two parallel needles.

9.2 Gerhard Pöppel and Reinhard Schachtner: Analysis by Projection Pursuit

Using kurtosis indices for Projection Pursuit leads to a clear structure of two disjunct clusters, which are separated along the hyperplane $0.5\text{feat1} - 0.5\text{feat2} + 0.5\text{feat3} - 0.5\text{feat4}$. Since Projection Pursuit did not detect further disjunct substructures we stopped analyzing this dataset at that point. We neither did characterize in detail the clusters found.

Group	Run 1 Projection 97		feat0	feat1	feat2	feat3	feat4	Counts
A	0.00	Mean	-0.02	-0.06	1.46	0.02	0.01	500.00
B	1.00	Mean	0.02	0.04	-0.04	-0.05	0.03	800.00
								1300.00

Figure 79: Cluster Separation of the Berlin08_synth2 data found by Projection Pursuit

Note that this cluster structure can be seen in the scores of the lowest eigenvalue, consulting the scatterplots of the PCA tranformed data (see Fig. 80).

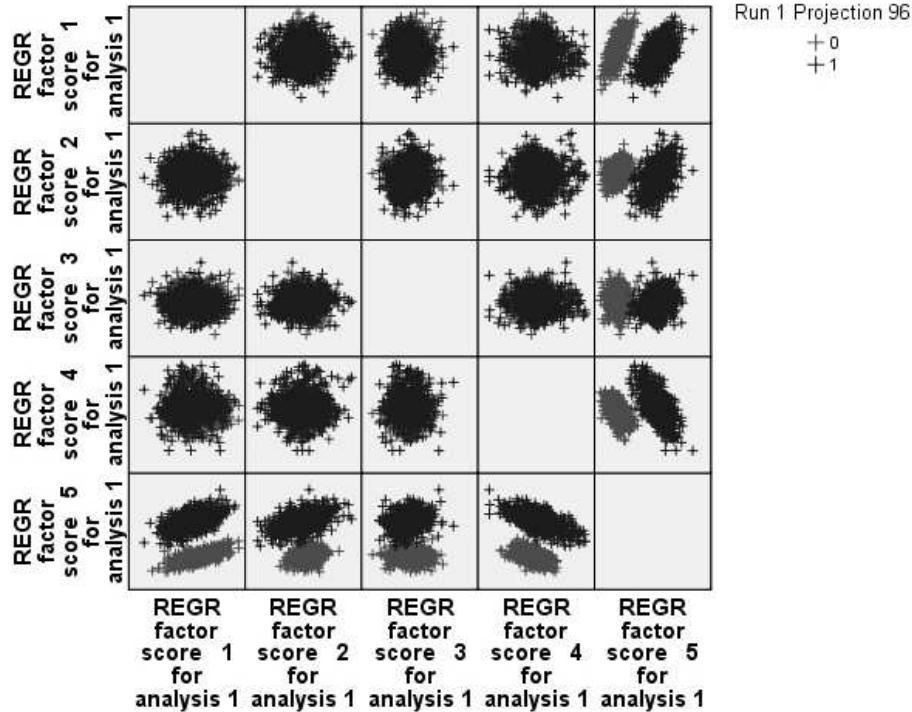


Figure 80: Scatterplots of the PCA transformed Berlin08_synth2 data

9.3 Gunter Ritter and Hans-Joachim Mucha: Comparison of Results

This data set can be interpreted as consisting of two well-separated, elliptical clusters. It is, therefore, well suited for clustering with Projection Pursuit or model-based methods. In fact, Pöppel and Schachtner present a perfect partition in two clusters obtained with Projection Pursuit. This is plain from the following contingency table which crosses their partition with the correct one.

$$\begin{bmatrix} 500 & 0 \\ 0 & 500 \\ 0 & 300 \end{bmatrix}$$

A distance-based method such as Spectral Clustering does not seem to be a method well-suited for this data set. The reason are the oblong clusters. Susanna Röblitz and Marcus Weber write: “We did not succeed in clustering this data set [by spectral clustering]. That means, from a distance-based point of view there is only one cluster. Maybe model-based clustering methods could be appropriate here.”

Indeed, we applied a heteroscedastic cluster criterion based on full normal assumptions with the BIC model selection criterion. The latter was uncertain whether there were two or three clusters but both solutions that we obtained were reasonable.

Part III

List of participants

List of participants of the 30th DANK Fall Meeting, Nov. 14th to 15th 2008, Berlin

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