Soft-Subspace Clustering on a High-Dimensional Musical Dataset

EMIL JUZOVITSKI

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Supervisor: Johan Gustavsson Examiner: Pawel Herman

School of Electrical Engineering and Computer Science

Host company: Soundtrack Your Brand AB

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Abstract

Clustering analysis techniques can be used to solve various tasks. In this thesis we look at the possibility of using clustering techniques to help generate novel music playlists by clustering a high dimensional dataset of songs. We compare how a new sort of clustering methods called *Soft-subspace* clustering (SSC), which weights features independently for each cluster, performs compared to the popular *K-means* algorithm. The SSC algorithms of *EWKM* (*Entropy Weighted K-means*), *FSC* (*Fuzzy Subspace-Clustering*), and *LEKM* (*Log-Transformed Entropy Weighting K-means*), were tested on the dataset. Parameters were tuned based on an external validation index. The best performing SSC algorithm, which ended up being *LEKM*, was then compared to the results of *K-means* through a committee of judges. The results show that both *LEKM* and *K-means* are capable to cluster the dataset, and generate novel clusters. Both algorithms create clusters of high general quality, but there is no shown benefit of using *LEKM* over *K-means* on the given dataset. For a more conclusive result, a larger sample dataset would be needed.

Sammanfattning

Metoder av Klusteranalys kan användas för att lösa mångfaldiga problem. I denna avhandling granskar vi möjligheten att använda klusteringstekniker för att hjälpa att skapa spellistor med nya musikaliska teman genom att klustra en hög-dimensionell datamängd av låtar. Vi jämför hur en ny sort a klustringsmetoder så kallade Soft-subspace clustering (SSC), som viktar attributen separat för varje kluster, presterar gentemot den välkända K-means algoritmen. Tre SSCalgoritmer var testade på datamängden: EWKM (Entropy Weighted K-means), FSC (Fuzzy Subspace-Clustering), och LEKM (Log-Transformed Entropy Weighting K-means). Deras parametrar justerades genom att använda ett externt validerings-index. Den bäst presterande SSC algoritmen, vilket var LEKM, var sedan jämförd med K-means av en kommitté av sakkunniga individer. Resultaten visar att både *LEKM* och *K-means* är kapabla att klustra datamängden, och generera kluster med nya musikteman. Båda algoritmerna skapar kluster av hög generell kvalité, men resultaten visar ingen fördel att använda LEKM över K-means på den givna datamängden. För ett mer slutfattande resultat, skulle bland annat ett större dataset behövas.

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Chapter 1

Introduction

Clustering analysis is the exploratory art of finding *clusters* (groups) in a dataset [1]. Data objects are grouped by their similarity, with the most similar objects being categorized into the same group, a cluster. There are many applications for clustering. Two examples are: deciding what items to put in the same aisle in a shop — in order to increase revenue — and, categorizing insurance holders into risk groups — to provide the best price to each customer.

Various types of clustering methods exist, they differ in how similarity between points are measured, and how a cluster is defined. The properties of the dataset to be clustered, is what decides the suitability of a method. The data-types (categorical, numerical or mixed), the size (the number of data objects), and the feature-dimensionality (the number of attributes describing an object) of a dataset are critical factors when choosing a method. Picking the right method can be the difference between inadequate- and stellar-clustering performance.

1.1 Problem Description

The stakeholder of this thesis is a music streaming platform tailored for the retail industry. It tries to solve the unique needs the industry has in regard to music. For example, songs with special retail licenses are provided on the platform. Beyond licensing, the platform works on providing the right company, the right music, often in the form of a playlist.

Substantial effort and employee hours (money) are spent by the retail industry, on the creation (and navigation) of musical *playlists* (compositions of songs)

that fit the company.

To provide a cheaper and faster alternative, a service has been created by the stakeholder where pre-curated playlists, that fit many types of businesses and occasions, are offered through the music streaming platform. All the retail customer has to do is to pick a playlist based on playlist recommendations given by the platform.

Playlists are created by professional music composers employed by the stakeholder. The process of creating distinct playlists with high quality is extensive for the professional composers. A time-consuming part of the process is to search for candidate songs. Currently, expert knowledge is used to find candidate artists and songs.

Here, we explore the possibility of generating candidate songs for novel playlists, by grouping songs through clustering analysis, in order to simplify the process for playlist composers.

The given dataset is a real-world, high-dimensional and, mixed dataset. It is a set of *song objects* extracted from an internal music database. Each song is a vector of features — where different features describe the song through different song properties. The vector consists of two types of features, general metadata — such as *Duration* and *Artists* — and audio-based features — that describe songs through an extraction of audio features of the song.

In this thesis we focus on clustering the audio-based features, which include 160 features (high-dimensional) that are numerical by nature.

1.2 Problem Statement

Clustering high-dimensional data suffers from the *Curse of dimensionality* [2, 3, 4] i.e. any two points with the same cluster membership are bound to have features in which there are large distances between the points [5]. As such, it is hard to assess which points are actually similar as the distance is dominated by dissimilar features which are often irrelevant features.

A popular choice for clustering *K-means*, does not take into account the dimensionality of a dataset, which can result in the complications mentioned above. Feature reduction techniques that try to reduce the amount of features needed in a dataset, can be used in order to avoid dimensionality problems. The drawback is that common methods such as PCA (Principal Component Analysis),

lead to a loss of information [6], and disregard the fact that different clusters can depend on different features.

Soft-subspace clustering (SSC) [6, 7, 8] is a new clustering method type. It is designed specifically to tackle the problems of high-dimensionality, by embedding cluster-specific weights to features. Like many new types of algorithms, the number of algorithms of this type is increasing.

In this thesis we study how the traditional *K-means* algorithm compares to *Soft-subspace* clustering(SSC) algorithms on the given musical dataset. There are two problem statements of the thesis.

In order to answer how K-means compares to SSC algorithms, an SSC algorithm has to be chosen. Thus, the first problem statement is:

With an expanding set of soft-subspace algorithms, what is a suitable softsubspace algorithm for the given high-dimensional dataset, based on genre purity?

Given a selected SSC algorithm, the second and main problem statement becomes:

How does the performance of a soft-subspace clustering algorithm compare to K-means on the given high-dimensional dataset, from the perspective of novelty and general quality, when validated through a committee of judges?

1.3 Objective

The objective is to determine whether clustering algorithms (*K-means* or *SSC*-algorithms) can be used for the generation of thematically playlists. More specifically, there should exist clusters generated by the algorithms that have a *novel* musical theme and a high musical quality in accordance to professional playlist composers.

1.4 Ethics, Sustainability and Societal Aspects

Ethical concerns are commonplace in automatic categorization. In the context of the song dataset, songs from a specific cluster could be used to generate a

playlist for a popular streaming platform. That cluster might have it pivotal that an artist's country of origin is a specific country. Artists outside of that country that otherwise fit the cluster, are disregarded due to a seemingly, artificial wall. As such, artists from less established markets can become invincible for that playlist resulting in loss of revenue. Ethically, it is questionable whether county of origin, should have merit or not. From a cluster quality standpoint excluding some songs, for a better precision is a worthy trade-off. In this thesis only audio data is processed for clustering, which forces the algorithm to only compare songs based on audio.

High-dimensional datasets are frequent in the real-world. The comparison between the lesser known SSC-algorithms and K-means on the given dataset are beneficial for researchers and data-scientists looking for the possibility to cluster high-dimensional data. This thesis provides results on a new real-world dataset, without any bias towards a self-published algorithm. Additionally, obstacles of the algorithms are discussed for the algorithms on the given dataset that can occur in other datasets with the chosen algorithms.

1.5 Scope

This thesis focuses on the problem of clustering high-dimensional data. Other properties such as mixed data are mentioned, but not addressed. Algorithms chosen for evaluation were numerical in nature, and the features of the dataset was preprocessed to only include numerical data.

The dataset is given as is, the only feature manipulation done to the dataset are preprocessing techniques common for cluster analysis such as: sampling a subset of the dataset and normalizing features. The process of picking and sampling audio features before the pre-processing is not within the scope of the project.

Chapter 2

Background

The fundamentals of clustering are introduced in this chapter. Distance measurements of varying data-types are shown. Hierarchical, partition and, density-clustering are all described. The chapter details how the popular *K-means* algorithm functions and continues by mentioning different feature-weighted clustering algorithms including *Soft Subspace Clustering* (SSC) that are based on *K-means*. The chapter ends with a method justification for the research design.

2.1 Objective of Clustering

Given a dataset $\mathcal{D} = \{X_1, X_2, ..., X_n\}$ — where $X_i = [x_{i1}, x_{i2}, ..., x_{im}]$ is a single data point with m attributes (features) – and the input parameter k (a positive integer), the objective of partition clustering is to divide objects into k disjoint clusters $C = \{C_1, C_2, ..., C_k\}$, where similar data points are partitioned into the same cluster [9].

The objective varies between clustering types, the above objective is as stated just for (hard-membership) partition-based clustering (See section 2.3.2), but the general idea of partitioning similar points to the same cluster, is shared by all clustering methods. Another type of clustering methods is e.g. *density*-based clustering where the objective is to separate local dense areas (with high similarity) from noise (See section 2.3.3 for more details) [10].

2.2 Similarity and Distance Measures

The similarity between points has to be quantified numerically in order to be used in an algorithm. The relative closeness between two points X_i and X_j is quantified numerically through a *similarity measurement* $s(X_i, X_j)$ [11]. A high value indicates that the points are close, while a low measure indicates that the points are dissimilar. Values of $s(X_i, X_j)$ go between 0 and 1. Another solution is to quantify the dissimilarity of two points instead. The dissimilarity is described through a *distance measurement* $d(X_i, X_j)$ — where $d(X_i, X_j) \geq 0$.

Distance measures are often used with quantitative data, i.e. numerical data. Similarity measures are frequently used when data is qualitative, i.e. categorical and mixed data [12]. Both measurements are symmetric, i.e. $d(X_i, X_j) = d(X_j, X_i)$. An exception is subspace clustering methods - check section 2.4 for more details.

Distances (and similarities) can be measured in many ways and are often explicitly created for a dataset with attributes of one specific data type. The sections below introduce some popular distance and similarity approaches for different data types, starting with the most common numerical data, continuing with categorical data, and ending with approaches that combine the two in *mixed* data.

2.2.1 Numerical Similarity Measures

The Euclidean distance is a common measurement for the distance between two vectors, the measurement is shown in eq. (2.1). A frequent choice for distance measurement in clustering analysis is the squared Euclidean [2, 13, 14], shown in eq. (2.2).

$$d(X_i, C_l) = \sqrt{\sum_{j=1}^{m} (x_{ij} - c_{lj})^2}$$
 (2.1)

$$d(X_i, C_l) = \sum_{j=1}^{m} (x_{ij} - c_{lj})^2$$
(2.2)

The Euclidean distance is a special case of the Minkowski distance (eq. 2.3) where q=2. The Euclidean and other Minkowski distances often involve a preprocessing step of normalizing the dataset features [2]. Features with higher variance will otherwise have a higher contribution in deciding the clusters. Similar to many other measurements, the *curse of dimensionality* diminishes the ability to differentiate distances between points in high-dimensional data [3].

$$d(X_i, C_l) = \sum_{j=1}^{m} |x_{ij} - c_{lj}|^{q^{\frac{1}{q}}}$$
(2.3)

The mentioned distances can be converted to a similarity measurement — with values between 0 and 1 — by using the Gaussian kernel as shown in eq. (2.4) [15].

$$s(X_i, C_l) = \frac{\exp(-0.5 \cdot d(X_i, C_l))}{\sum_{t=1}^k \exp(-0.5 \cdot d(X_i, C_t))}$$
(2.4)

2.2.2 Categorical Similarity Measures

Categorical data is not commonly referred as a single datatype. It is instead a group of datatypes consisting of nominal and ordinal data. Unique properties separate the types from each other.

Nominal data — e.g. chemical elements in a periodic table — are either identical or different. Ordinal data — e.g. shirt sizes — can be more or less similar. Additionally, nominal data does not have to be information balanced either — some values are more important than others — e.g. if two songs share the same artist it is more information than if they do not [1].

Most clustering algorithms that cluster categorical data do not take into account the differences between the data types mentioned above. There are distance measures that do (see *daisy function* in [1]) but implementing them in a clustering algorithm would increase the complexity of the algorithms. The rest of the similarity measures below considers ordinal data nominal. From this point onward, both nominal and ordinal will be referred as categorical data, and treated as nominal data.

In its purest form a categorical similarity is simply *yes* or *no*, as shown in eq. (2.5), i.e. are two attribute values the same? [1, 16]

$$\delta(x_{ij}, x_{kj}) = \begin{cases} 1 & \text{if } x_{ij} \neq x_{kj} \\ 0 & \text{otherwise} \end{cases}$$
 (2.5)

To define the similarity between a point and a cluster representation, the number of mismatches can be used as shown in eq. (2.6) [9, 17]. A cluster representation in this case, is defined by the most frequent attribute values of the points in the cluster. This method is used in *K-modes* and the cluster representation is referred as a *mode* [17] (see section 2.3.2.1).

$$d(X_i, C_l) = \sum_{i=1}^{m} \delta(x_{ij}, C_{lj})$$
(2.6)

Another way to define the similarity is to compare the values of X_i and the values of all data points $\forall X_k \in C_l$ for each attribute as shown in eqs. (2.8) and (2.9) [15, 16]. In this method a cluster representation is not necessary. To allow fast computations of distances between points and clusters the frequency of each value of each cluster is stored in a frequency matrix. The weight w_j is an attribute weight defining how important an attribute is. The weights of each attribute is based on the Shannon entropy, how to calculate the entropy is mentioned in section 2.4.

$$s(x_{ij}, x_{kj}) = 1 - \delta(x_{ij}, x_{kj})$$
 (2.7)

$$s(x_{ij}, C_{lj}) = \frac{\sum_{X_k \in C_l} s(x_{ij}, x_{kj})}{\sum_{X_k \in C_l} [x_{kj} \neq null]}$$
(2.8)

$$s(X_i, C_l) = \sum_{j=1}^{m} w_j s(x_{ij}, C_{lj})$$
(2.9)

2.2.3 Mixed Similarity Measures

Mixed data measures are simply a combination of numerical and categorical measures. That is, categorical attributes are measured with a categorical measurement, and numerical features are measured with a numerical measurement. The important question is how to weigh the different measures to create

a single similarity measure between X_i and, X_j or C_l . Weighing specifics is mentioned in section 2.4.

Huang proposes the similarity measure shown in eq. (2.10) [9], w_l determines how important categorical data (denoted with c) is compared to its numerical counterpart (denoted with r) for cluster l. In a popular partition-based algorithm K-Protoypes, a simplification is made, local weights w_l for each cluster l is replaced with a single global weight w. The weight w is a user-defined input.

$$d(X_i, C_l) = \sum_{j=1}^{m_r} (x_{ij}^r - c_{lj}^r)^2 + w_l \sum_{j=1}^{m_c} \delta(x_{ij}^c, c_{lj}^c)$$
 (2.10)

Cheung and Jia [15] propose representing numerical data as an vector X_i^r —where numerical data is denoted by r—while letting each categorical attribute (denoted by c) have its own weight. The amount of categorical attributes is denoted by m_c , and the total amount of attributes is denoted by $m_f = m_c + 1$ as all numerical values share one weight. The similarity measure is seen in eq. (2.11). The categorical weights are automatically weighed through information gain, as such the algorithm is a *feature weighting* algorithm. See section 2.4 for more details.

$$s(X_i, C_l) = \frac{1}{m_f} s(X_i^r, C_l^r) + \frac{m_c}{m_f} \sum_{j=1}^{m_c} w_j s(x_{ij}^c, c_{lj}^c)$$
 (2.11)

2.3 Clustering Algorithms

Clustering algorithms are often divided into categories. Hierarchical, partition and density-based clustering are the largest categories [18]. Each of the given types are introduced in the sections below.

2.3.1 Hierarchical Clustering

A hierarchical algorithm generates a set of nested clusters, also known as a dendogram [2, 18]. There are two approaches for hierarchical clustering, *Agglomerative* and *divisive* hierarchical clustering.

In agglomerative clustering, each point starts being its own cluster. In the next step it merges with the most similar cluster. This repeats until all points are in one cluster.

Divisive clustering does instead the opposite: every point starts in the same cluster. In the next step the cluster gets split up into two clusters. This repeats until every point is in its own cluster.

CURE [2], BIRCH [19] and, ROCK (categorical) [16] are popular algorithms of hierarchical clustering. The creation of a dendogram in these clustering algorithms results in a high time complexity $(O(n^2 \cdot log(n)))$ that make the algorithms less suitable for larger datasets however, by running the algorithms on a sample representation of the dataset, as used in CURE and ROCK bigger datasets can be managed [2, 18]. In addition to creating a dendogram, the type includes methods which are able to partition clusters with an arbitrary shape.

2.3.2 Partition Clustering

In partition clustering a partition of clusters U is found by iteratively optimizing a cost function [2, 14, 18]. The algorithms include two iterative steps of assigning each point to the most similar cluster center representation, and, updating a cluster center representation — which is a mean in K-means and the most central point in K-medoids see(section 2.3.2.1).

The algorithms converge when no data points switch cluster association or on a user-defined convergence delta for the cost function. The time complexity is dependent on the amount of iterations. The number of iterations is not known beforehand and could vary depending on the chosen initial cluster centers — a usual approach is to randomly choose K clusters from the dataset as initial clusters centers. Partitioning algorithms handle larger datasets better than most hierarchical approaches.

2.3.2.1 K-means Family

K-means is arguably the most common clustering algorithm. The cost function (also known as objective function) of which K-means is optimized on is shown in eqs. (2.12) and (2.13), n refers to the amount of objects, m to the amount of attributes (features) and k is the amount of clusters. The cost function is either minimized eq. (2.12) or maximized eq. (2.13) [14].

$$P(U,C) = \sum_{l=1}^{k} \sum_{i=1}^{n} \sum_{j=1}^{m} u_{il} d(x_{ij}, c_{lj})$$
 (2.12)

$$P(U,C) = \sum_{l=1}^{k} \sum_{i=1}^{n} \sum_{j=1}^{m} u_{il} s(x_{ij}, c_{lj})$$
 (2.13)

U is a partition matrix of size $N \times K$. The partition matrix shows in which clusters point X_i is in. In hard clustering one point can only exist in a single cluster C_l . Thus, $u_{il} = [0,1]$ and $(\sum_{l=1}^k u_{il}) = 1$. Otherwise, points can be members of multiple clusters with different probabilities that sum up to 1. This can be referred to as Fuzzy-memberships and often includes a fuzziness index, a variable deciding the importance of the generated weights [7].

There are many algorithms based on K-means, they can be referred to as the K-means family of clustering [13]. Different similarity functions determine what K-means family algorithm the optimization represents [14]. Euclidean distance would result in *K-means*. The categorical similarity shown in eq. (2.6) results in *K-modes* [17]. If the similarity is the mixed type shown in eq. (2.10) the optimization represents *K-Prototypes* [9]. Additional algorithms in the class (*Weighted-K-means*, *EWKM*, *FSC* etc.) [6, 8, 14] tweak the distance function (measurement) to include some sort of weighting (see section 2.4 for more).

Optimizing the cost function P(U,C) is done by iteratively optimizing the function on one variable and treating the other one as a constant. Our sub-optimization problems (**P1**, **P2**) becomes:

P1. Assign each point to the most similar cluster.

Fix
$$C = \hat{C}$$
, optimize $P(U, \hat{C})$

P2. Update the mean for each cluster.

Fix U =
$$\hat{U}$$
 optimize $P(\hat{U}, C)$

For **P1.** we update U by eq. (2.14).

$$u_{il} = \begin{cases} 1 & d(X_i, C_l) \le d(X_i, C_t) & \text{for } 1 \le t \le k \\ 0 & \text{for } t \ne l \end{cases}$$
 (2.14)

For **P2.** we update C — updating each center representation — through the equations below:

• For numeric values solved by obtaining the average:

$$c_{lj} = \frac{\sum_{i=1}^{n} u_{il} x_{ij}}{\sum_{i=1}^{n} u_{il}}$$
 (2.15)

• For categorical values, one option is defining the center as mode [17], which is solved by:

$$c_{lj} = a_j \tag{2.16}$$

where a_j is the most frequent value of attribute j in C_l .

• For mixed values, one option is representing the cluster as a Prototype[9, 13]. The solution is simply to use eq. (2.15) for numerical attributes and eq. (2.16) for categorical.

The steps of clustering k-means family algorithms, thus becomes:

- 1. Choose initial cluster representatives C^0
- 2. Fix C^t = \hat{C} , optimize $P(U^t, \hat{C})$, Obtain $P(U^{t+1}, \hat{C})$ if $P(U^t, \hat{C}) = P(U^{t+1}, \hat{C})$

return $P(U^t, \hat{C})$ (Convergence)

- 3. Fix $U^{t+1} = \hat{U}$, optimize $P(\hat{U}, C^t)$ Obtain $P(\hat{U}, C^{t+1})$ if $P(\hat{U}, C^t) = P(\hat{U}, C^{t+1})$ return $P(\hat{U}, C^t)$ (Convergence)
- 4. Repeat steps 2. and 3.

2.3.2.2 K-medoid Family

In *K-medoids* a cluster is represented by the most central object in a center — a medoid. The cost function looks at the total deviation between points in the cluster and the medoid [20]. Compared to eq. (2.12) the difference is that the distance function compares a point X_i with the medoids C_l^m of that cluster. Using medoids instead of a mean results in a more robust clustering performance. The tradeoff is *K-medioids* runtime. *K-medioids* is usually

implemented through the *PAM* algorithm (an efficient implementation of *K-medioids*) which has a time complexity of $O(tk(n-k)^2)$ per iteration, whereas the basic *K-means* (LLoyd's implementation) has an iteration complexity of O(tnkm) [20].

Extensions of *PAM*, such as *CLARA* and *CLARANS* are approaches to improve the scalability of the clustering type by clustering on a sample representation which improves the run time [20]. *CLARANS* improves the simple sampling procedure in *CLARA*. It defines a sample of cluster medoids as a node in a graph which is the whole dataset. Neighbouring nodes differ by one medoid. *PAM* traverses all neighbours for each node it traverses to find the node with minimum distance between points. CLARA can be seen as only finding the minimum of a sub-graph containing only the sample points. *CLARANS* samples dynamically neighbours while traversing the graph not restricting the traversal to a subgraph.

2.3.2.3 Determining k and k-initialization

One aspect of using a clustering algorithm that often gets overlooked, is the parameters chosen as inputs for the algorithm. When using hierarchical- and partition-based clustering the value of k has to be decided.

A way to determine the k is by running the algorithm with different values of k and then through an internal or external criterion measure (see section 2.5.1) decide the best K for the dataset [9, 21]. Running an algorithm multiple times makes the process of clustering multiple times slower, and should be avoided for larger datasets.

Sampling is used in CLARA, CLARANS [20] to find medoids for the whole dataset. The idea is that a small randomly uniform sample of the dataset (40+2k points) can represent the whole dataset, in terms of clustering tendencies. The same sampling process can be used to find k and so, finding a k for a sample would be finding an approximation of k for the whole dataset. The algorithm still has to be ran on the sample multiple times and evaluated against the inner criterion, but the time to compute the clusters for a sample rather than the whole dataset is significantly less.

Cheung and Jia propose another approach [15, 22]. Here, competitive learning is used — giving every cluster a weight that together with the distance function determines the chance of a datapoint becoming a member of the cluster. When a datapoint is asssigned to the cluster, that cluster's weight and its neighbour's

weight increase, and the rest of the clusters' weights decrease. Eventually, some clusters disappear. The positive aspect of this approach is determining the amount of clusters occurs during the clustering process removing the need to cluster the dataset multiple times. Note: A user input of maximum number of clusters k^* is required.

In addition to choosing k, picking good initial points is also a problem that should be considered. Good initial clusters allow for a faster convergence while bad ones can result in convergence on a suboptimal result [22, 23], forcing multiple clusterings to obtain a result of confidence. While random uniform sampling is a way to initialize k centers there are more robust solutions, that can exclude picking e.g. outliers allowing the result to be less random.

For numerical data, *K-means*++ [23] proposes replacing uniformly at random sampling with the steps seen in section 2.3.2.3. It is also possible to add an initialization step for categorical and mixed data as mentioned in [22].

- 1. Pick one center C_l uniformly at randomly
- 2. Pick a new center C_i , choosing point $X_i \in \mathcal{D}$ with probability $\frac{d(X_i,C_q)^2}{\sum_{t=1}^k d(X_t,C_q)}$, where C_q is the already chosen point with the minimum distance to X_i,X_t .
- 3. Repeat 1. and 2. until *K* points have been picked.

2.3.3 Density-Based Clustering

Density-based clustering algorithms define clusters to be higher-density areas — a local area with a relative high number of data points, i.e. higher density than noise [2, 10, 14, 18]. DBSCAN [10] is the most well known clustering algorithm where each data point in a cluster must have a user defined MinPts in its \mathcal{E} -neighborhood, where $d(X_i, X_j) < \mathcal{E}$ and \mathcal{E} is user-defined. The shape of the created clusters is defined by the chosen distance measure.

The algorithms of this type perform well on larger low-dimensional datasets especially on spatial data [10].

2.4 Feature-Weighted Clustering

K-means assumes that all attributes/features are of the same importance [1]. If one were to scale the range of one attribute by two, it would become twice as important for the clustering result. To allow attributes of naturally smaller value ranges the same importance as attributes with larger value ranges, attributes are often normalized.

After normalizing the attributes, a weighting step can be added, where attributes are given a weight based on its perceived importance in relation to other attributes. It helps remove the importance of features that are irrelevant, which is necessary for good performance on most dataset as using irrelevant attributes damages the clustering performance [1]. Using irrelevant features is in fact worse than not using the attribute at all. Moreover, increasing the importance of a relevant attribute allows them to be regarded more in the clustering and can thus, result in better performance.

Deciding on how to weight attributes is hard. A simple solution is using technical expertise to assign attribute weights. In e.g. data-mining, a dataset is often of high-dimensionality as it may be generated from a database with hundreds of tables and columns [8]. The high degree of dimensions makes it almost impossible to manually determine the weights of the attributes.

A fairly popular way to handle high-dimensional data is through the use dimensionality-reduction techniques e.g. PCA [24, 25]. This is a possible first step in clustering analysis, occurring before the actual clustering. In short, dimensionality-reduction techniques try to find the minimum set of representative attributes that account for the properties of the dataset. It can be hard to interpret the results from PCA. PCA also assumes that all clusters care about the same features [4]. An assumption that often is false in high-dimensional datasets.

Another possibility which is introduced in the next section, is to add steps to the clustering algorithm to automate the process of weighting features.

2.4.1 Automated Feature-Weighting

Feature-weighting can also be done automatically. Automatic feature-weighting is commonly referred as *feature weighting* and is often achieved by extending a *k-means* like algorithm. An additional *attribute weight* variable is added

to the cost function given in eq. (2.12). How the cost function changes from eq. (2.12) depends on what concepts we use to automate the weighting.

One algorithm of this class is *w-k-means*, which extends *k-means* by adding a weight to each attribute [14]. *W-k-means* uses the cost function in eq. (2.17). The cost function introduces two new variables: W — a weight vector containing the weights for each attribute — and β — a hyper-parameter defining the importance of the weight vector. The below **P3.** is the new subproblem of updating W.

P3. Update the weights of all attributes.

Fix
$$C^{t+1} = \hat{C}$$
 and $U^{t+1} = \hat{U}$, optimize $P(\hat{U}^t, \hat{C}^t, W^{t+1})$

An additional step corresponding to the optimization of **P3.** extends the steps (in-between 3. and 4.) of k-means. Attribute weights are updated based on the intra-cluster variance through eq. (2.19), where less variance corresponds to a larger weight.

4. Let
$$\hat{U} = U^{t+1}$$
, $\hat{C} = C^{t+1}$, optimize $P(\hat{U}^t, \hat{C}^t, W^{t+1})$
Obtain $P(\hat{U}, \hat{C}, W^{t+1})$
if $P(\hat{U}, \hat{C}, W^t) = P(\hat{U}, \hat{C}, W^{t+1})$.
return $P(U^{\hat{t}+1}, C^{\hat{t}+1}, W^t)$ (Convergence)

$$P(U, C, W) = \sum_{l=1}^{k} \sum_{i=1}^{n} \sum_{j=1}^{m} u_{il} w_{j}^{\beta} d(x_{ij}, c_{lj})$$
 (2.17)

$$D_{j} = \sum_{l}^{k} \sum_{1}^{n} \hat{u}_{il} d(x_{ij}, c_{lj})$$
 (2.18)

$$\hat{w}_{j} = \begin{cases} 0 & D_{j} = 0\\ \frac{1}{\sum_{t=1}^{m} \left[\frac{D_{j}}{D_{t}}\right]^{\frac{1}{\beta-1}}} & D_{j} \neq 0 \end{cases}$$
 (2.19)

The function can be modified to allow clustering on mixed data by using a suitable distance measurement [22].

Instead of using a fuzzy weighting i.e. having a input variable deciding the importance of the weight vector (β) , another option is to decide the intra-cluster distance through information gain, in other words: Shannon entropy. Entropy can be said to be the amount of "disorder" in a system. Entropy is used in [8, 15]. Using the entropy works for both numerical and categorical data. In [15] the importance of an categorical attribute is defined as the average entropy of each value of the attribute. This is shown in eq. (2.20). To allow weights in the range of $\{0,1\}$ the importance is divided by the total importance of all attributes in the dataset as shown in eq. (2.21).

$$H_j^c = -\frac{1}{m_r} \sum_{t=1}^{m_r} p(a_{tj}) log(p(a_{tj}))$$
 (2.20)

$$w_j = \frac{H_j^c}{\sum_{t=1}^{d_c} H_t^c}$$
 (2.21)

Where: m_r is the number of different values of attribute j, and a_{tj} is the t:th value of attribute j and d_c is the number of categorical attributes.

2.4.2 Soft-subspace Clustering

The previous mentioned methods make an assumption the same reduced features are of interest for all clusters. This is not inherently true, clusters usually have their unique subspaces. In an example where clusters represent medical patient groups and patients (the objects of the dataset) are represented by patient information (age, gender, traveling history etc.), the patient information (features) characteristics of each group is different i.e. there are differences to why a patient is hospitalized between patient groups. One patient group could represent malaria patients, and in that case *traveling history* is important, i.e. it doesn't vary much within the cluster. In a patient group which represents e.g. Parkinsons' decease the traveling history is less important as it varies throughout the cluster, instead what is important is the age of the patient, with less variance being shown for that feature. The above example shows that, subspaces are often different between clusters.

Subspace-clustering allows clusters to have their own feature subspace [8, 22, 26, 27], hence the name. It is a cluster analysis-specific way to deal with high-dimensionality. Irrelevant features can be discarded per cluster resulting in reduce of dimensionality while losing less information than other techniques.

There are two types of subspace-clustering techniques. The fist type is *Hard-subspace clustering*. Hard-subspace clustering tries to find the exact subspaces [8, 22, 26, 27]. PROCLUS and CLIQUE are two algorithms of the category. The second type is *Soft-subspace clustering* (SSC). SSC-algorithms find the approximate subspaces of all clusters. Each cluster is given a weight attribute vector, the vector determines the association probability of each feature for that given cluster [6]. Finding exact subspaces is computationally heavy, as such soft-subspace clustering is in general faster than its counterpart, with an often linear time complexity.

Automated-Weighting Algorithm (AWA) [28] is a soft-subspace approach similar to w-k-means, the difference is that for the cost function of AWA: w_j^β is replaced with w_{lj}^β — a weight for an attribute in a cluster C_l . The algorithm does not work when the variance of an attribute in a cluster is zero as the learning rules denominator becomes zero [29]. FWKM (Feature weighted K-means) [29] and FSC (Fuzzy-subspace clustering) are two alternatives to AWA which solve the problem by adding a small value to the distance function, forcing the variance to not be zero. In FWKM that value is based on a formula and recalculated during each iteration, in FSC the small value is a constant ϵ determined beforehand. Otherwise the algorithms are equivalent. All three algorithms only look at the intra-cluster distance. The three algorithms are often referred as being Fuzzy-weighting-algorithms due to features having different degrees of association in different clusters, and a fuzziness index is used to decide the importance of the weight [7]. Below is the cost function of FSC, where β is the fuzziness index.

$$P(U, C, W) = \sum_{l=1}^{k} \left[\sum_{i=1}^{n} \sum_{j=1}^{m} u_{il} w_{lj}^{\beta} d(x_{ij}, c_{lj}) + \epsilon \sum_{j=1}^{m} w_{lj}^{\beta} \right]$$
(2.22)

where:
$$\beta \ge 1$$
 (2.23)

$$w_{lj} = \frac{1}{\sum_{t=1}^{m} \left[\frac{D_{lj} + \epsilon}{D_{lt} + \epsilon}\right]^{\frac{1}{\beta - 1}}}$$
(2.24)

where:
$$D_{lj} = \sum_{X_i \in C_l} d(x_{ij}, c_{lj})$$
 (2.25)

$$P(U,C,W) = \sum_{l=1}^{k} \left[\sum_{i=1}^{n} \sum_{j=1}^{m} u_{il} w_{lj} d(x_{ij}, c_{lj}) + \gamma \sum_{j=1}^{m} w_{lj} log(w_{lj}) \right]$$
(2.26)

where:
$$\gamma \ge 0$$
 (2.27)

$$c_{lj} = \frac{\sum_{X_i \in C_l} x_{ij}}{\operatorname{Count}_{X_i \in C_l}} \tag{2.28}$$

$$u_{lj} = \min_{1 \le l \le k} \left(\sum_{j=1}^{d} w_{lj} d(x_{ij}, c_{lj}) \right)$$
 (2.29)

$$w_{lj} = \frac{\exp(\frac{-D_{lj}}{\gamma})}{\sum_{t=1}^{m} \exp(\frac{-D_{lt}}{\gamma})}$$
(2.30)

where:
$$D_{lj} = \sum_{X_i \in C_l} d(x_{ij}, c_{lj})$$
 (2.31)

A recent paper introducing the *LEKM* algorithm (log-transformed entropy weighting K-means), has modified EWKM [6]. Two problems of EWKM are addressed: EWKM is very sensitive to γ , and noisy data. To solve the problems EWKM was modified to use log-transformed distances. The modification allows intra-cluster variances of different features to become smaller and more similar, decreasing the chance of one dominant feature of a cluster. Additionally, centers are set in such fashion that noisy data are less impactful. LEKM is shown below.

$$P(U, C, W) = \sum_{l=1}^{k} \sum_{i=1}^{n} u_{il} \left[\sum_{j=1}^{m} w_{lj} \ln \left[1 + d(x_{ij}, c_{lj}) \right] + \gamma \sum_{j=1}^{m} w_{lj} \ln(w_{lj}) \right]$$
(2.32)

where:
$$\gamma \ge 0$$
 (2.33)

$$c_{lj} = \frac{\sum_{X_i \in C_l} \left[1 + d(x_{ij}, c_{lj}) \right]^{-1} x_{ij}}{\sum_{X_i \in C_l} \left[1 + d(x_{ij}, c_{lj}) \right]^{-1}}$$
(2.34)

$$u_{lj} = \min_{1 \le l \le k} \left(\sum_{j=1}^{d} w_{lj} \ln \left[1 + d(x_{ij}, c_{lj}) \right] + \gamma \sum_{j=1}^{d} w_{lj} \ln w_{lj} \right)$$
(2.35)

$$w_{lj} = \frac{\exp(\frac{-D_{lj}}{\gamma})}{\sum_{t=1}^{m} \exp(\frac{-D_{lt}}{\gamma})}$$
(2.36)

where:
$$D_{lj} = \frac{\sum_{X_i \in C_l} \ln \left[1 + d(x_{ij}, c_{lj}) \right]}{\text{Count}_{X_i \in C_l}}$$
 (2.37)

2.5 Evaluation

There are two main ways of which clustering are evaluated: internal and external criterion.[31]. The types are sometimes referred to as cluster validation indices [32].

2.5.1 Inner Criteria

Internal criterion is an unsupervised validation approach and can be described as evaluating the results without respect to external information [32]. An internal criterion tries to verify the objective of the clustering algorithm on the dataset. For example: making sure that points assigned to the same cluster are in general more similar than points outside of the cluster.

2.5.1.1 Average Silhouette Coefficient

The average silhouette coefficient upon all data points shown in eq. (2.42), is one way to evaluate the internal criteria [33]. A single silhouette coefficient

shown in eq. (2.41), looks at a data point's intra-cluster similarity — similarity to points within the same cluster, and, inter-cluster similarity — similarity with points outside of the cluster. \bar{s}_{co} goes between -1 and 1 where a high value (close to 1) indicates a natural clustered dataset.

When $s_{co}(X_i)$ is a high value (close to 1) a point is well clustered, i.e. the intracluster similarity is high relative to the inter-cluster similarity [33]. The same reasoning is extended to $\overline{s}_{co}(\mathcal{D})$ where a high value is a well clustered dataset. The measure is common to use when tuning the parameters of traditional partitioning algorithms. There is limited information on how to implement and use the measurement or any other internal index for subspace clustering methods. Unlike, k-means soft-subspace clustering have asymmetric distances between two points of different clusters.

$$d_{avg}(X_i, C_l) = \frac{\sum_{X_k \in C_l} d(X_i, X_k)}{Count(X_k \in C_l)}$$
(2.38)

$$a(X_i) = d_{avg}(X_i, C_a)$$
, where $(X_i \in C_a)$ (2.39)

$$b(X_i) = \min_{C \neq C_a} (d_{avg}(X_i, C))$$
(2.40)

$$s_{co}(X_i) = \frac{b(X_i) - a(X_i)}{\max(a(X_i), b(X_i))}$$
(2.41)

$$\overline{s}_{co}(\mathcal{D}) = \frac{\sum_{i=1}^{N} s_{co}(X_i)}{N}$$
(2.42)

2.5.2 External Criteria

External criterion is a supervised validation approach and can be described by the following sentence: Validation of the results by imposing a pre-defined structure on the dataset, i.e. data not used for generating the clustering results [32].

The external criterion requires validation data in addition to an external measurement. Validation data could be a sample of the dataset that is labeled with a class, i.e. a ground truth. If the dataset is already labeled by a feature and that feature is not used for clustering, then that dataset can be easily evaluated based on that feature through a external measurement.

In many cases, the clustered data is not labeled — often the reason to why an unsupervised approach was used in the first place. Even if a label exists it

might not be a goal for the research to exclusively produce results that evaluate well to the validation data. There could be a hope to find *new* classes. The validation data can in these cases be replaced by expertise — a panel of judges with knowledge of the data [31]. A sample of clusters can then be given to the judges to assess. Combining the judges with a measurement tool allows the dataset to be given a score that corresponds to the external validity of the dataset.

2.5.2.1 External Measurements

Purity is one measurement for the external criterion. It measures the mean ratio of the most dominant class in each cluster. The data-points are labeled with a class beforehand [31]. Equation (2.43) defines the measurement, $C = \{c_1, c_2, ..., c_k\}$ is the set of clusters, and $\Psi = \{\Psi_1, \Psi_2, ..., \Psi_t\}$ is the set of *truth*-classes. The measurement is easy to compute. A downside is that the equation does not penalize small clusters as such small clusters produces a high score.

$$P(C, \Psi) = \frac{1}{n} \sum_{l=1}^{k} \max_{1 \le j \le t} |C_l \cap \Psi_j|$$
 (2.43)

F-measure is another measurement for the evaluation of the external criteria. The measurement is shown in eq. (2.46)[31]. The resulting clusters of an algorithm are seen as a series of decisions on each pair of data-points in the set.

An ideal clustering in this reasoning would mean all similar points are within the same cluster, i.e. only *True Positives* and no *False Positives*. In reality, some non-similar pairs are clustered together leading to *False Positives*. Similarly, *True Negatives* and *False Negatives* can exist.

The terms can be combined to create the *precision* and *recall*. The precision defines the ratio of *True Positives* on all positives — pairs in the same cluster. The precision is shown in eq. (2.44). The recall on the other hand measures the ratio of how many similar pairs have been clustered together given all possible similar pairs.

 β in eq. (2.46) determines in what ratio *precision* and *recall* should be taken account to. $\beta < 1$ results in precision being more important and $\beta > 1$ results

in more importance to the recall. The balanced F-measure is called the F_1 measure and is defined in eq. (2.47). It weighs the impact of precision and recall the same. The F-measure is common in information retrieval. It is, however more complex *Purity* and requires more effort to implement.

$$P = \frac{TP}{TP + FP}$$

$$R = \frac{TP}{TP + FN}$$
(2.44)

$$R = \frac{TP}{TP + FN} \tag{2.45}$$

$$F_{\beta} = \frac{(\beta^2 + 1) \cdot P \cdot R}{\beta^2 \cdot P + R} \tag{2.46}$$

$$F_{\beta=1} = \frac{2 \cdot P \cdot R}{P + R} \tag{2.47}$$

Where:

TP are true positives, FP false positives, FN false negatives, and, β is a weight between P and R, a $\beta > 1$ emphasizes the R.

 $\approx O(tnkm)$

Mixed

Yes

Type Algorithm **Properties** Time Complexity Data Type Weighted $O(n^2log(n))^*$ Hierarchical **CURE** Numerical **BIRCH** $O(n)^*$ Numerical $O(n^2 \cdot log(n))^*$ **ROCK** Categorical $O(n^2)^*$ Density **DBSCAN** Numeric Partition K-means (Lloyd) O(tnkm)Numerical **PAM** $O(tk(n-k)^2)^*$ Numerical $O(t(k(40+k)^2+k(n-k)))^*$ **CLARA** Numerical $O(n^2)^*$ **CLARANS** Numerical K-modes O(tnkm)Categorical O(tnkm)K-Prototypes Mixed Yes^a **OCIL** Yes^a O(tnkm)Mixed WKM Numerical^b O(tnk + tkm + tm) Yes^c O(tnk + tk + tkm)Numerical^b **FSC** Yes^d O(tnk + 2tkd)Numerical^b Yes^e **EWKM** LEKM $\approx O(tnkm)**$ Numerical^b Yes^e

Table 2.1: Properties of algorithms discussed in this chapter [6, 8, 12, 22, 26]

WOCIL

^a Not all features have independent weights.

^b Has been modified to allow mixed data.

^c Only Feature weighting.

^d Fuzzy-Weighting, Within-distance

^e Entropy-Weighting, Within-distance

^{*} Dimensionality disregarded in complexity notation

^{**} Exact complexity is not given, but mentioned to be slower than EWKM due to how cluster centers are updated.

2.6 Summary and Method Justification

Table table 2.1 summarizes the properties of all the mentioned algorithms in this chapter.

The findings of the pre-study suggest that feature-weighted clustering can be used to attack the challenging problem of clustering high-dimensional data by reducing the weight of irrelevant features. Algorithms such as *Weighted K-means*, *FSC*, *EWKM* and *LEKM* have all been introduced. The mentioned algorithms manage high-dimensional data clustering in different ways. The last three, are examples of soft subspace clustering — an extension of *feature weighting*, which allows each cluster an individual subspace. The soft-subspace methods have been shown to deal with high-dimensional data better than traditional algorithms while still allowing a time complexity (linear) similar to traditional partitioning algorithms.

Due to the previous mentioned benefits of SSC algorithms, three types of SSC methods will be tested for this thesis. They are *EWKM*, *FSC* and *LEKM*. *EWKM* is chosen as it takes into account the information gain in the cost function. FSC is chosen for the purpose of having an algorithm with different properties, i.e. being a *Fuzzy* SSC algorithm that does not take into account information gain. *LEKM* is added for its use of logarithmic distances that could possibly help resolve problems with noisy data. To evaluate the performance, the algorithms will be compared to the traditional *K-means* algorithm.

The evaluation will consist of a supervised external index due to the difficulty of implementing a correct internal validation for *SSC* algorithms. Results were to be tested against a ground truth label through the measurement of purity and a panel of judges respectively.

The chosen methods are possible to implement for mixed data, but are not originally implemented for the purpose. From a thesis standpoint, tackling the high-dimensionality of a dataset is the main priority. Therefore, only numerical features of the dataset are used — See *Dataset* in section 3.2 for more details.

Chapter 3

Method

This method chapter subjects the reader to the framework used to qualitatively compare the different algorithms on the given dataset.

3.1 Method Design Overview

In order to generate results and compare the three different algorithms, a method design was planned and executed. The overall design is shown in fig. 3.1, it includes the step of *Preprocessing*, *Implementation*, *Parameter Selection* and *External Evaluation*.

3.2 Dataset

The given dataset is a real-world, high-dimensional and, mixed- dataset. It is a set of *song objects* extracted from an internal music database. There are in total $5 \cdot 10^7$ songs in the dataset. Each song is a vector of features where different features describe the song through different song properties. The vector consists of two types of features, general metadata and audio-based features.

The general metadata includes attributes that predominantly identify the song independent of audio analysis. Features of the type includes *Album* (string), *Artist* (string), *Title* (string) and *Year of Origin* (ordinal). The type also includes *BPM* (numerical, zero to around 200) and *Energy-feel* (ordinal, one to

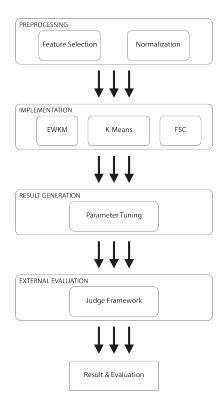


Figure 3.1: Method Design

ten). These features include both numerical and categorical features — features stored as strings can be converted to categorical data.

The core features are the audio-based features, and are derived from a supervised neural network. They are a sample of the neuron weights in a network trained to determine the genre of a song. Each song consists of an audio embedding — devised from an audio spectrogram — and a *genre* label — used to train the network.

Our dataset includes the *genre* feature. There are 33 possible genres for the songs in the dataset.

3.3 Pre-processing

The amount of dataset objects and features were reduced in the preprocessing stage for various reasons.

For the ease of testing — reducing computation time — the original dataset

of songs was randomly sampled and reduced to a size of $5 \cdot 10^4$.

With a focus on tackling the problem of high-dimensionality, the choice was to use the numerical methods *EWKM*, *LEKM*, *FSC*, and, *K-means*. That left a restriction to only select numerical features as input. Given that the audio vector was used to categorize songs in the neural network, the hypothesis was that clustering analysis could also be done exclusively on that feature-space. The dataset was therefore preprocessed to only include the subspace of audiofeatures.

As a next step in preprocessing, all features were normalized to the same variance, a way to make sure that all features have the same impact on the algorithm. For normalization Z-score was used, see eq. (3.1). X_j is the vector of all datapoints for feature j, μ_j is the mean values for datapoints in feature j, σ_j is the standard deviation of feature j and Z_j is the normalized vector.

$$Z_j = \frac{X_j - \mu_j}{\sigma_j} \tag{3.1}$$

3.4 Implementation

3.4.1 **EWKM**

An implementation of the EWKM algorithm is available in R and CSRAN through the wskm package [34]. The code is written in C and wrapped for R. All of the source code is obtainable from Github¹.

There are modifications made in the implementation that differ from the original research paper [8]. Additional normalization steps have been added when calculating w_{lj} . Equation (3.4) shows how w_{lj} , the feature weight, is updated in the given implementation. Occurrences of empty clusters during partitioning are managed by re-sampling cluster centers, i.e. restarting the algorithm; in the original algorithm empty clusters were not treated. Finally, a convergence delta can be set by the user which decides the percentage of change needed between two iterations for convergence.

¹https://github.com/SimonYansenZhao/wskm/

$$\lambda_{lj} = \exp\left(\left(\frac{-D_{lj}}{\gamma}\right) - \max_{\forall t \in C_l} \left(\frac{-D_{lt}}{\gamma}\right)\right)$$
(3.2)

$$\lambda_{lj} = \max\left(\frac{\lambda_{lj}}{\sum_{t=1}^{m} \lambda_{lt}}, \frac{0.0001}{m}\right)$$

$$w_{lj} = \frac{\lambda_{lj}}{\sum_{t=1}^{m} \lambda_{lt}}$$
(3.3)

$$w_{lj} = \frac{\lambda_{lj}}{\sum_{t=1}^{m} \lambda_{lt}} \tag{3.4}$$

Per request of the stakeholder along with the author's familiarity with Python and Pandas DataFrame, the code was re-wrapped for Python using numpy-C-API [35] — allowing for the dataset to be sent in to the algorithm as a numpy array. The C-code was tweaked to not be dependent on R's unif_rand() function.

FSC 3.4.2

The FSC implementation was created by the thesis author and is based on the C-code of EWKM. The methods of calculating cost, updating weights and updating cluster memberships were modified to correspond to the FSC algorithm as shown in eq. (2.22), and eq. (2.24). γ is replaced by β , and the small value of ϵ was set to 0.001 as proposed in [7].

3.4.3 LEKM

LEKM like FSC was created by the author, and was also based on the source code of EWKM [34]. The same steps are necessary for this algorithm as EWKM, both are based on negative entropy, the difference was how the costs, weights, and partitions were updated. How they were updated corresponds to the equations of LEKM shown in eqs. (2.33) to (2.37). A slight modification is that the right-hand side, i.e. the negative entropy is dropped from when updating partitions.

The modification is based on a discussion with one of the authors of the original LEKM paper. The gist of the discussion was that the entropy should not be used for updating clusters, and could result in negative distances.

3.4.4 K-means

EWKM is equivalent to K-means when $\lim_{\gamma \to 0}$, although simply setting $\gamma = 0$ forces division by zero. As such it was simpler to use another package for K-means. As a popular clustering algorithm, K-means is widely available for Python. The PyClustering implementation of K-means was used for this report [36]. The implementation was created in C++ and wrapped for Python.

All algorithm specific parameters are ran with all k candidates. The best performing combination of parameters are deemed the best candidates for the algorithm.

3.5 Parameter Selection

Algorithms were tested with multiple candidate parameters on the dataset in order to find the most suitable parameters. The results of the different parameters were compared based on an external validation index, a *purity* score. The best parameters in accordance to the index were deemed the most suitable, and chosen as the parameters for the algorithm for further tests.

For generating results, convergence was set to occur if the cost delta between previous iteration and current was less than 0.5%.

3.5.1 **Purity**

An external validation index was created using the *genre* feature as a ground truth in combination with the measurement of *purity*. To create the purity score, the most dominant genre of each cluster was aggregated and divided by the total amount of songs in the dataset.

3.5.2 Amount of Clusters

The problem of deciding the amount of clusters (k) is global as all the clustering algorithms chosen are partition based. This section describes how k was chosen for all of the chosen algorithms.

For the choice of k, it was decided to not use a competitive learning strategy. The strategy would add another layer of complexity on the algorithms and a

possible point of error. k was instead based on the *purity* results of the whole sample.

Candidate values of k were restricted to 50, 100, and, 500 in order to reduce the time needed to generate results. The values were chosen to give an approximation on how large k should be. The minimum of 50 clusters was based on that the number of genres in the dataset was 33, and generated clusters should at least be as specific as a genre label. 500 was decided as the maximum amount for k to keep the average cluster size to be above 100.

3.5.3 **EWKM**

EWKM introduces the γ parameter. The recommended range of $\gamma \approx (0.5,3)$ which was mentioned in Jing, Ng, and Huang [8] and Williams et al. [34], was extended with smaller values $(0.0005,\,0.001,\,0.005,\,0.01,\,0.05,\,0.1)$ as candidate values. The smaller values were added to avoid possible problems with the objective function being negative due to a large negative entropy.

Results of gamma values with immediate convergence were discarded as the behaviour was deemed unwanted, and not what was expected from the algorithms.

3.5.4 FSC

The unique parameters of FSC, β — the fuzzyness variable, and ϵ — a small constant, were set to 2.1 and 0.00001, respectively, in [7]. In our tests β was varied between 1.5 and 30 while ϵ was kept to the value mentioned in the report Gan, Wu, and Yang [7].

3.5.5 LEKM

In Gan and Chen [6] values of β were varied between 1 and 16 with a decreasing score after a value of 2.0. Our candidate values ranged between 0.5 and 10. Similarly to EWKM, results of immediate convergence were disregarded.

3.5.6 K-means

K-means does not have any hyper-parameter that needs to be tweaked. The only thing that was necessary for the result generation was to run K-means on all values of k.

3.5.7 Ranking songs and clusters

Songs were sorted in ascending order based on their distance to their respective cluster center. The distance is equivalent to the distance used for assigning a partition to an object. For *k-means* that was the regular euclidean distance. For SSC algorithms the distance included the feature weights of the cluster. The distances differ from SSC algorithm to another as e.g. *LEKM* uses log-transformed distances.

Clusters were similarly sorted in ascending order. The distance for a cluster was set as the average distance of songs with a membership in the cluster.

The sorting was used as a ranking, based on the idea that "better" clusters would have smaller distances than "worse" clusters. The reason for not using a genre accuracy for the ranking was to allow clusters that have novel themes that are not genre-specific a chance to be high ranked.

The ranking allowed for a cutoff in songs and clusters, i.e. the top five clusters could be chosen. To not have the same genre type of clusters again and again in the top 5, each genre could only appear as dominant in one cluster (except for pop and rock, as they were regarded as larger genres with more diversity). As such, after sorting the top five clusters were picked from small to large distance with the condition stated above.

3.6 Expert Evaluation

To answer how performance varied between traditional and SSC algorithms in terms of novelty and cohesion (similarity), a test was created. In this test professional composers were used as evaluation judges.

The platform of the evaluation was a webpage created by the author. In here, different clusters could be browsed. Each cluster was represented by 10 30-second song previews. The chosen songs were sampled based on a half-normal

distribution, i.e. songs with a relative small distance had a higher chance to be picked than those with a high distance. A picture of the webpage is shown in fig. 3.2. Django ² and Bootstrap 4³ were used to build the page.

The top five ranked clusters of each algorithm were chosen for the test. In addition to the 10 clusters sourced from the algorithms, five more clusters were added that were sourced from existing playlists on the stakeholder platform.

The test was conducted as a blind test to remove any bias playlist clusters might have. The composers did not know that the clusters had different sources. In their minds they were all from the same machine learning algorithm.

Initially, the idea was that composers would rate a cluster on *similarity* and *novelty* (from a scale of 1-10). After showing a mock test and discussing it with the head of product experience, head of machine learning, and a number of composers at the stakeholder, it was conducted that the parameters had to be modified. There were two reasons: the terms were unclear for the composers, and, a general quality was hard to transcribe from the scores.

To adhere to the problems, *similarity* was divided into *audio similarity*, and *cultural similarity*. *Novelty* was changed to a term more familiar to the composers — *playlist uniqueness*, i.e. how unique the cluster would be as a playlist compared to already existing playlists on the platform. Additionally, a *general quality* field was added to solve the second problem of scores not translating to a general quality. A text box was also added where the composers could add any description they thought summarized the cluster.

The composers and author were situated in the same room. All composers evaluated the clusters together, as they had mentioned in earlier discussions that they believed they can give a more accurate score together if they were allowed to discuss the clusters in as a team. Discussions the composers had during the evaluation were recorded. The author also answered questions the composers had on how to navigate the webpage.

²https://www.djangoproject.com/

³https://getbootstrap.com/

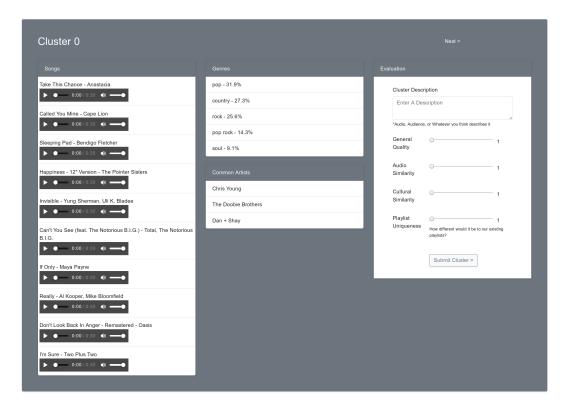


Figure 3.2: Screenshot of the evaluation website.

From the left-hand-side song samples are shown and played, In the middle statistics about genres and common artists. On the right-hand-side the evaluation is situated with a general description text area, and sliders for the rest of the evaluation categories.

Chapter 4

Results

The results of this chapter has been divided into two sections: *General Results* and *Evaluation Results*. *General Results* shows how different algorithms performed in terms of *purity*, *convergence speed* and *feature weight distribution*. The section ends with a summary showing the best parameters and purity scores for each algorithm. *Evaluation Results* presents the expert evaluation scores of *K-means*, the best performing *SSC-algorithm*, and playlists in table 4.2.

4.1 General Results

Below sections describe the results of K-means, EWKM, LEKM, and FSC with different parameters on the dataset. The section is summarized by table 4.1, which shows the *purity* of the best performing parameters for each algorithm.

To avoid repetitiveness algorithm-specific figures are shown only for k = 500. The choice of k = 500 is justified as it is the best performing k for algorithms in regards to purity (see section 4.1.5).

4.1.1 **EWKM**

Figure 4.1 presents the purity given different values of γ for EWKM. From the figure we see a trend of the purity slowly decreasing until a value of $\gamma = 2$,

where a steep increase occurs to a score of 0.44.

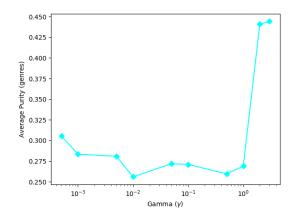
Figure 4.2 shows the corresponding amount of iterations until convergence. The amount of iterations needed to converge is decreasing with the value of γ . Here, we see the immediate convergence of values of 0.05 and higher.

Figure 4.3 shows the amount of restarts needed to generate non-empty cluster partitions. Most value selections needed zero or one restarts. The outlier was the choice of 0.01, which required 10 restarts. Selections larger than 2.0 resulted in zero restarts.

Immediate convergence (with no restarts) — as shown in the figures to be 2.0 and higher, were caused by the Shannon entropy being more negative than the total dispersion within clusters, making the objective function negative.

Figure 4.4 represents the feature weights of each cluster as colored grids (often referred to as a meshgrid) for various choices of γ . The grids in fig. 4.4 show the weight of a specific feature for a cluster as a colored rectangle. Yellow denotes a high feature weight, while purple denotes a low value. A cluster's feature weight vector is a horizontal line in the grid. For all the tested values of γ that did not result in immediate convergence, the weight distribution of the clusters were similar. One feature was often dominant, i.e. had a high weight (around 1) while the rest had feature weights near zero. The grids do however, show a trend of less dominant features being produced with larger values of γ .

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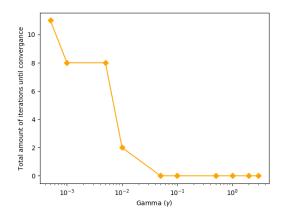


Figure 4.1: Purity accuracy of EWKM given various values of γ (k=500).

Figure 4.2: Iterations until convergence of EWKM given various values of γ (k=500).

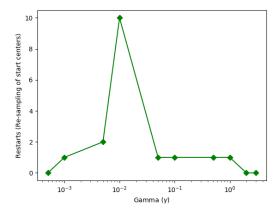


Figure 4.3: Restarts of EWKM given various values of γ (k=500).

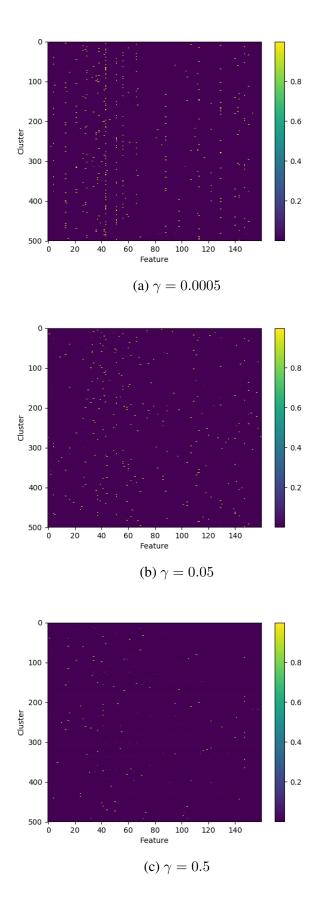


Figure 4.4: Feature-weight meshgrid of EWKM (k = 500).

4.1.2 **LEKM**

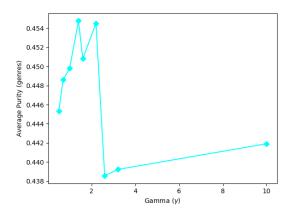
The purity scores of LEKM are shown in fig. 4.5. With higher values of gamma the purity is increasing until a peak purity is reached at $\gamma=1.4$ with a score of 45.5%. For values ≥ 2.6 the purity decreases steeply to values of 43.8%, these values correspond to values of immediate convergence.

The amount of iterations until convergence is shown in fig. 4.6. Higher values resulted in increasingly more iterations needed, with the peak reached at 20 iterations with $\gamma=2.2$, until a drop to zero — immediate convergence — occurs at values of 2.6 and larger. Compared to EWKM, the γ 's of LEKM are larger when immediate convergence occurs.

The feature weight grids of LEKM is shown in fig. 4.7, note that colors represent different values for each grid. We see that there are multiple features representing the cluster through the figures. Certain features are dominant in very few clusters (visible as a purple-dominant vertical line in the grid) while others are dominant in most clusters (visible as a yellow-dominant vertical line in the grid). The highest weights are also small compared to EWKM, but are still, larger than the least important features of the cluster. The dispersion between small and large weight values decrease with a higher γ .

Another perspective of how the weights differ given various γ is shown in fig. 4.8. The plots of the figure show the values of all feature weights in all clusters, summarized into a histogram. The resulting histograms show a distribution with properties of a normal distribution, similar to what is mentioned in [8]. From smaller to larger values of γ , we see the deviation of the distribution decrease, leading to a more and more uniform distribution.

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Figure 4.5: Purity accuracy of LEKM given various values of γ (k=500).

Figure 4.6: Iterations until convergence of LEKM given various values of γ (k=500).

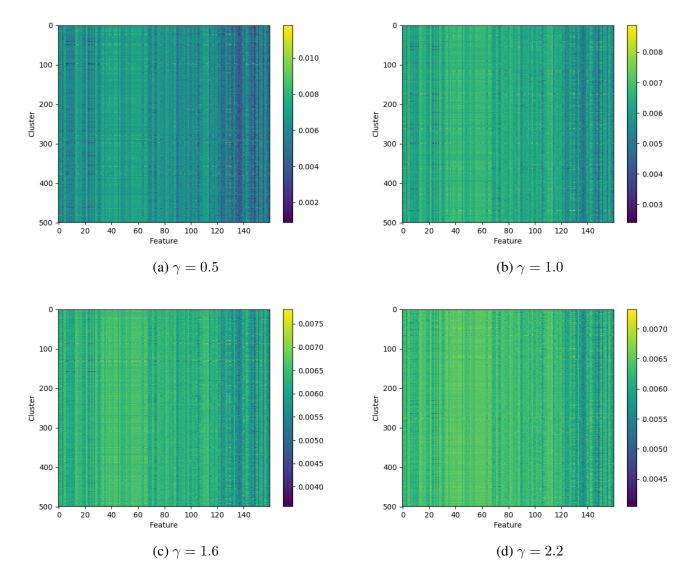


Figure 4.7: Feature-weight meshgrid of LEKM (k=500)

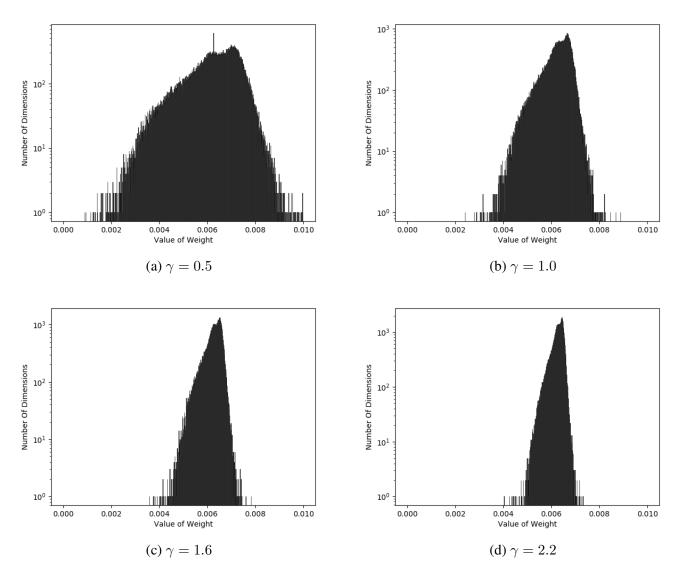


Figure 4.8: Distribution of feature weights values upon all clusters (k=500)

4.1.3 FSC

Figure 4.9 shows how the algorithm performs in terms of purity on the dataset. From the figure we can see that the purity scores keep increasing and that the best score is found where $\lim_{\beta\to\infty}$, for our test a limit was set to $\beta=30$ and was therefore the best performing value. The most significant increase occurs between $\beta=1.8$ and $\beta=2.02$ with an increase from 0.29 to 0.40.

The amount of iterations, as shown in fig. 4.10, are high for smaller values of β and equal two for larger β .

Figure 4.11 shows how feature weights are distributed along clusters. A selection of a lower β ($\beta=1.5$) results in a single dominant feature weight for most clusters, similar to EWKM. As γ increased, more and more features were given importance in clusters. Again, note the scale of the meshgrids, some small amount of clusters had larger differences between feature weight values than other clusters, resulting in a more "blue" than "yellow" picture. A choice of $\beta=1.5$ is shown to have feature weights that led to a single dominant weight per feature. Higher values resulted in uniform more dominant features. Similar to LEKM, certain features appeared dominant feature in many clusters, while other features were deemed unimportant for multiple clusters.

In terms of distribution as shown in fig. 4.12, the resulting distribution are positively skewed, but like LEKM the distribution ended up being more sharp for larger values of β .

4.1.4 K-means

K-means converged after seven iterations given k = 500. The purity score was 45.4% as shown in table 4.1.

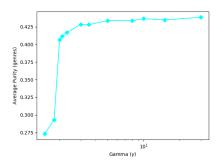


Figure 4.9: Purity accuracy of FSC given various values of γ (k=500).

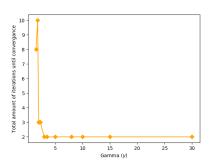


Figure 4.10: Iterations until convergence of FSC given various values of γ (k=500).

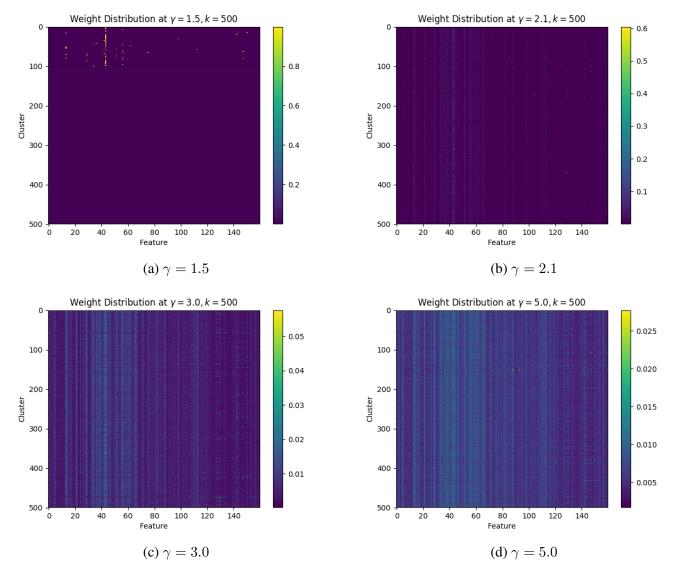


Figure 4.11: Feature-weight meshgrid of FSC (k = 500)

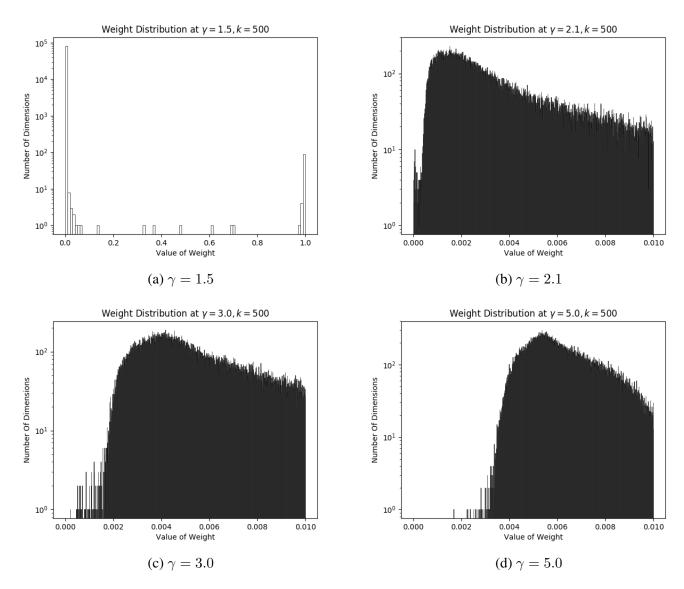


Figure 4.12: Distribution of feature weights values upon all clusters

4.1.5 Summary

The best parameters, together with their *purity* scores are shown for k = 50, 100, 500 in table 4.1 for each algorithm. The table shows that k = 500 achieves the best purity scores for all algorithms except EWKM (where k = 100 results in the greatest purity). For k = 50 and k = 100, *K-means* is the best performing algorithm, but only marginally. For k = 500 *LEKM* performs

marginally better than K-means with the best overall score of (45.5%). For all values of k, EWKM is the worst performing algorithm.

	K-means EWKM		LEKM		FSC		
k	Purity	γ	Purity	γ	Purity	β	Purity
50	39.0%	0.005	28.2%	0.0	38.8%	30.0	38.0
100	40.8%	0.005	28.9%	2.1	40.6%	15	39.6
500	45.4%	0.001	28.6%	1.4	45.5%	30.0	43.8%

Table 4.1: Best parameter- and purity-score (γ, β) given k, where scores represent the mean purity of three runs.

4.2 External Evaluation

The results of the blind test can be found in table 4.2. The table shows how five of the clusters of each source were rated on average. The clusters sourced from playlists were rated better than K-means and LEKM on all parameters except novelty. For *General Quality*, there was a score difference between playlists (7.7) and the algorithms (K-means - 6.6, and LEKM - 6.4). Both algorithms were rated better in comparison to playlists, on *Audio Similarity* than *Cultural Similarity*. Regarding K-means vs LEKM, K-means performed marginally better than LEKM in all categories, where the biggest difference is in novelty.

There were also results obtained from the discussions of the blind test. Clusters from the algorithms were mentioned to have a core of songs that had an "obvious" theme. In addition to the core, there were an additional two-three songs in the shown sample of the songs, that were *culturally* different according to the composers. The songs' artists had a different audience than the core songs. For well performing clusters that difference added depth to the playlist in a positive fashion, e.g. adding reggae to a hip-hop cluster. For bad performing clusters the mixins were off-putting for the theme of the cluster, and made the cluster worse in terms of general quality but also in terms of *Playlist Uniqueness*, e.g. adding country songs to an indie rock core.

	Evaluation						
Source	General Quality	Audio Similarity	Cultural Similarity	Playlist Uniqueness			
Playlist	7.7 (1.2)	7.8 (1.5)	7.7 (0.6)	4.5 (3.5)			
K-means LEKM	6.6 (2.5) 6.4 (3.4)	7.0 (2.3) 6.4 (2.4)	6.2 (2.9) 6.0 (2.5)	5.4 (3.2) 3.8 (2.6)			

Table 4.2: Mean rating and standard deviation (in brackets) of five clusters given source type

Chapter 5

Discussion

The objective of this thesis was to answer the dataset specific objective, of whether clustering algorithms can be used to find high-quality novel musical themes. The problem statement asked if there was a performance difference between *K-means* and *SSC-algorithms* on the given high-dimensional dataset, and what SSC-algorithm is suitable for the given dataset.

In this paper, *K-means* and SSC algorithms have been compared for a given high-dimensional dataset. Three SSC algorithms (EWKM, FSC, LEKM) were selected for the comparison with K-means. The given dataset was preprocessed to only include numerical audio features — based on neuron weights of a trained supervised neural network — and normalized using the *z-score*. The dataset was sampled to a size of 50k. Two external evaluation indices were set up, a *purity* measurement based on a genre feature of the dataset, and a blind test involving a panel of expert judges. The purity measurement was used to find suitable input parameters — algorithm specific ones, e.g. β and k (given a choice of 50, 100, 500). Additionally, the algorithm with the best purity score (LEKM) was used as the SSC-algorithm for comparison with K-means in the blind test. The blind-test was composed of clusters of different sources: Playlist, K-means, and LEKM. The expert judges — playlist composers — had to evaluate the clusters based on multiple criteria.

The rest of the discussion is divided into *General Results* and *Evaluation Results*. *General Results* refers to the discussion around how algorithms behaved for different parameter selections, both in terms of feature weight distribution and purity. *Evaluation Results* refers to the discussion of the blind-test results. The sections also critiques the method selection of generating the given

results.

5.1 General results

Based on previous papers [7, 8], a high-dimensional dataset such as this one, should see SSC-algorithms improving clustering performance by lessening the weight of irrelevant features through automatic feature weighting. The *General Results* showed negligible difference between K-means and the best performing SSC algorithm. This can be seen as a surprising result, after all, SSC algorithms are made for high-dimensional datasets.

Properties of the dataset could have made it less suitable for SSC algorithms, a reason for the difference between the results obtained and what was shown in [8]. One possibility is that the dataset had in a sense already had its features selected beforehand: the 160 neuron weights selected as features were already picked from a larger quantity of neurons based in the neural network. SSC algorithms could theoretically had boosted the performance even with the feature sampling, by finding the unique subspaces of each cluster, but it did not. There was no significant improvement of purity performance with LEKM, and a downgrade in performance occurred with the usage of EWKM. It can be concluded that SSC-algorithms are not beneficiary for the given dataset. On the other-hand, it can be questioned whether the dataset as it was pre-sampled is a good representation of a high-dimensional dataset. The results could have been more representative if another publicly available dataset was used. As it stands now, there is a limitation on how the results can be extended to other datasets.

The fairly popular soft subspace clustering algorithm of EWKM performed poorly on the dataset. The possible choices of γ was restricted to lower values in order to avoid immediate convergence. For values that did not immediately converge, the algorithm suffered from single feature-weight dominance in clusters, making it hard to represent the clusters in an impactful manner. The algorithm had clearly failed the task of feature reduction, which in turn had resulted in worse purity scores. This shows that the algorithm should not be used for just any numerical high-dimensional dataset.

The problem of dominant weights was not mentioned in the paper introducing the algorithm [8], in the paper the weights were supposed to be of a normal distribution, with some features more and less important per cluster. FSC had the accuracy scores increase in comparison to EWKM. The best scores were found with with an increasingly large β . A larger β resulted in feature weights becoming more uniform in each cluster. What essentially FSC offered in feature weighting, was disregarded when selecting larger values, i.e. $\beta=15,30$. From this standpoint the best (and largest) β was not true to subspace clustering, there was no significant feature weight dispersion, but for this dataset it was not necessary according to the purity scores. A reason could be that the algorithm failed to determine the important-from the unimportant-features, and clusters were given subspaces of actually unimportant features. For this case, it would be better to allow all features the same weight. This would also mean that the algorithm failed in terms of feature reduction.

LEKM, which created feature weights that were normally distributed on each cluster, performed similarly to K-means. It had one advantage to K-means. A smaller fraction of features had an impact when calculating the distance between data-object and cluster center, when using the best γ . Unlike EWKM, features were normally distributed, which shows the benefit of using log-transformed distances. Clusters could be dimensionally reduced to a smaller subspace without impacting the accuracy negatively unlike *FSC*. The algorithm is based on this, suitable for this dataset and other datasets of high-dimensionality.

The chosen external validation index — Purity with *Genres* as a ground truth — promotes the choice of values based on *genre* homogeneity. It is probable, that more homogeneous *genre* clusters are in general of better quality than those with more *genre* dispersion. What it failed to do is to promote genre novelty — new types of genres based on unique properties. A better choice of parameters could have been found if the index would have taken the novelty into account, however, *genre* was the only label provided for the dataset.

That the highest value of k (500), would have the highest purity value was not unexpected — smaller clusters tend to allow for higher purity accuracy. The F_1 score could have avoided such bias, but as mentioned in the background, would involve more complex computations. The choice of candidate k's, which were decided by the author to be 50, 100, and 500, could have been extended with more options for the higher probability of finding the optimal k. This suggested extension would have exponentially increased the result generation process, as each k requires an array of algorithm-specific parameter values to be tested.

5.2 Evaluation results

The evaluation scores of the blind-test indicate that the clusters generated by the algorithms could be used to create playlists. This is reflected by the general quality scores of the algorithms. The audio similarity was through discussions and metrics fairly high along all clusters. While as mentioned, some songs do not fit the general theme of the cluster due to cultural differences such occurrences could be tuned out by a composer generating a playlist through the use of filters.

It can therefore be stated that the audio features selected in the preprocessing were indeed enough to cluster the songs, and the algorithms were indeed capable of clustering the dataset. However, to improve the cultural similarity score one should consider adding features such as origin year, and, country of origin.

Generated K-means clusters performed better than playlists on *Playlist Uniqueness*, while *LEKM* clusters performed worse. K-means can therefore be seen as meeting the criteria for novel clusters. LEKM on the other hand, can not be confirmed to create novel clusters, and would require additional testing on more clusters. Based on discussions with playlist composers and how they rated clusters, *Playlist Uniqueness* in a cluster was rated lower, if the *General Quality* was deemed bad. The explanation of the criteria could skewed the results, and could have been explained better by the author before the blind-test.

To summarize the *Evaluation Results*, K-means performed slightly better than LEKM in every category. The results indicate that K-means perform at least as good as LEKM, which for the most part corresponds to the results of purity. For statistical confidence that K-means performs better on the dataset than LEKM, a larger cluster sample size would have been needed.

5.3 Future Work

Adding additional features to the feature-space of the given dataset could have seen the results of the algorithms improve. The cultural similarity — where the algorithms struggled compared to the playlists — could have been helped by metadata such as origin year. To use more of the metadata e.g. *artist* (represents songs with the same artist), categorical features would have been needed to be used. There are two main ways to tackle the problem of mixed data with

soft-subspace clustering. Modify the given algorithm's distance measurement to adhere to mixed data or use a mixed data clustering algorithm. The former is not a trivial task, and so the latter could be a better choice. The WOCIL algorithm mentioned in [22] would then be a suitable choice the for mixed data clustering on the dataset.

All the given results are based on the 50k sample of the larger dataset. Scaling the clustering process to the larger 50-million set should impact k-means negatively. Feature reduction could at that point become more essential for the clustering process, and so, SSC algorithms could become more useful.

Moving to a larger dataset requires more processing. Using a single thread on a single core is not efficient. An idea would instead be to scale the algorithms across multiple computer nodes using a distributed framework. The distributed implementation of the algorithms would require the code to be rewritten to fit the capabilities of the framework.

Algorithms based on k-means are non-deterministic due to the sampling of initial centers. Finding and using suitable sampling techniques as mentioned in [6] specifically made for subspace-clustering could improve the results of the soft-subspace clustering methods.

Many of the internal validation indices that exist for clustering analysis take both intra-cluster distance and inter-cluster distance into account — an ideal clustering should have clusters far between. The chosen SSC algorithms were all based on intra-cluster distance. No account was taken on the distance between clusters. A natural step to improve performance would be to find an algorithm which takes both conditions into account.

Chapter 6

Conclusions

The given high-dimensional musical dataset — sampled to a size of 50k, and processed to only hold numerical features — had LEKM as the best performing SSC-algorithm. The comparisons done between K-means and LEKM show that there is no significant performance difference between the algorithms, i.e. feature-weighting did not improve the performance. Similar Purity scores were found for both algorithms. Based on a panel of judges, any of the two algorithms could be used to produce clusters of high general quality and audio similarity, although K-means performed better in terms of novelty. The results indicate that the generated clusters could be used as a tool when composing new playlists based on the dataset. Future work should see a comparison between K-means and LEKM on a larger sample of the dataset, to see if there is a benefit for feature weighting on a larger scale. A larger sample would need the code of LEKM to be rewritten for a distributed network. From a broader perspective on how SSC-algorithms performs on high-dimensional datasets, another dataset comparison is needed.

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