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Bachelor thesis Computer Science

Dynamic Event Detection in Data Streams

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Abstract

How can events be recognized in a data stream? And what is the definition of an event? Current event recognition procedures define possible events (or event types) statically when the system starts. However, in data streams, the definition should develop dynamically over time as the data and their focus changes over time.

The first goal of this bachelor thesis is to define what an event is and how events can be recognized from static data. Depending on the definition, a suitable data set has to be found and chosen in order to create a system which is capable of recognizing events. In the second part, the events should be recognized from a data stream and therefore support dynamic event recognition.

This work uses news API's as data streams and tries to assign the received news articles to different events. An event is defined as a list of different news articles writing about the same story. A possible event could be "Brexit" or an upcoming election. It's important to keep in mind that new events can and should be created over time.

Assigning news articles to an event can be done by clustering the news articles. In order to achieve best possible results, a comparison between different clustering techniques has been completed. It was revealed that HDBSCAN is a promising candidate for our use case as it delivered the best results.

Unfortunately HDBSCAN was not made for data coming from data streams but this thesis will show one possible solution on how to deal with this. This work was able to process up to 20'000 news articles with HDBSCAN. A possible continuation of this work could try to extend this number to process more data at once.

Preface

The following bachelor thesis *Dynamic Event Detection in Data Streams* was written as part of our computer science studies at the ZHAW Zurich University of Applied Sciences.

After our lectures on artificial intelligence, we realized that we wanted to deepen our knowledge in this area. This thesis was the perfect opportunity to increase our expertise on topics such as natural language processing and cluster analysis.

Special thanks go to our two supervisors, Dr. Andreas Weiler and Prof. Dr. Kurt Stockinger, for their ongoing and effective support during the writing of this thesis.

We would also like to thank our two lecturers Prof. Dr. Thilo Stadelmann and Prof. Dr. Mark Cieliebak for their lectures on artificial intelligence.

At last but not least, we would like to thank our fellow students and the entire ZHAW staff for our great time at ZHAW.

Daniel Milenkovic and David Pacassi Torrico

Contents

1 Introduction

1.1 Problem formulation

How can events be recognized in a data stream? While searching for events in a data stream, the definition of an event is not always clear. Providing static definitions, as most approaches do, does not suffice for the application in dynamic data streams, which change over time. Additionally the behaviour of the data stream is an important factor in itself, since blockages of overflows in the system have to be prevented.

An example for a dynamic data stream can be found in a stream of news articles, which are published in irregular time intervals and different quantities over time. Thus detecting events based on an incoming stream of news articles is a challenging task.

The goal is to develop and evaluate a methodology to detect events in a dynamic stream of news articles.

1.2 Motivation

Todo.

2 Related Work

Text based event detection is a diverse field and with increasingly large amounts of available information online a compelling topic for research. With the popularity of social media a lot of research around event detection has been done on micro blogs[1] such as Twitter[2][3]. However this thesis focuses on news articles as the primary data source. Text based clustering as a technique for event detection has already been explored with different approaches such as using custom methods based on neural networks[4] or by using a modified version of DBSCAN to account for its sensitivity for differences in cluster densities[5]. Based on the promising results with DBSCAN we want to further explore text clustering using its successor HDBSCAN[6] and apply it in an online setting. Regarding the clustering validation there has already been research into recognising biases of different scoring functions [7] and developing custom scoring functions as a result[8].

3 Theoretical basics

In order to fully understand our work, it is important to ensure a few basics in the area of natural language processing (NLP). In this chapter we'll explain how the most important techniques used in our thesis work.

3.1 Text preprocessing

When working with text data, many algorithms and processes will need to distinguish words from another. In most cases this is done by creating a dictionary of all known words and/or by *vectorizing* text data in order to make them comparable. While this works in theory, in reality we deal with a tremendous amount of data. This results in huge directories or many vectors and does not only take up more disk space but also text processing (computation and comparison) will take more time to process.

What does that mean? Let's have a look at the following words:

- switzerland
- Switzerland
- SWITZERLAND

Anyone of us will be able to extract the same meaning out of these three words: The country *Switzerland*. However, for machines the terms are different because they're written differently. That's why in most cases it makes sense to lowercase all text before processing them. That way we can ensure that the above words also share the same meaning for a machine and thus reduce the dictionary size.

Lowercasing text can just be the beginning though. Depending on the size of a document, it might make sense to not use all text inside a document. A good example for this would be books. Vectorising books would take too much computational power and time to process. In such cases, the text size would have to be reduced. This could be accomplished by processing a summary of the book instead of the book itself or by extracting the most relevant words from the whole book. Later could be done with *Keyterm extraction* or with *Entity extraction*.

If we're not dealing with books but with articles or papers, there are also other alternatives to Keyterm and Entity extraction. Using *Text Stemming* or *Text Lemmatisation* we can simplify terms and group them together to reduce the dictionary size. More about this in the sub sections below.

Exceptions There are a few use cases where lowercasing a text isn't desired. For example when trying to detect the writer's sentiment. Someone who would write a few or all words of a sentence in uppercase might be angrier than someone who doesn't.

3.1.1 Keyterm extraction

Todo.

3.1.2 Named Entity Recognition

Todo.

3.1.3 Text Stemming

Text Stemming is a form of Text Normalization which aims to simplify words by reducing the inflectional forms of each word into their word stems. For example, the words *connected*, *connecting*, *connection* share a similar meaning and could therefor be simplified to the base term **connect**.

The first paper describing a stemming algorithm was written by Julie Beth Lovins[9] as early as in 1968. In her algorithm she used an ordered list of 294 suffixes to strip them out and then applies one of 29 associated application rules followed by a set of 35 rules to check if the remaining stem has to be modified furtherly.

Lovins' stemming algorithm was very successful but got mostly replaced by M.F. Porters stemming algorithm[10] published in 1980. In his paper, M.F. Porter was able to process his suffix stripping algorithm in 6'370 out of 10'000 words and thereby reducing the vocabulary size by **one third**. The algorithm simply follows 5 steps with replacement and/or removal rules and is therefor very easy and efficient.

M.F. Porter improved his stemming algorithm even further by publishing the Porter2 stemming algorithm[11] in 2002 which is widely known as the *Snowball stemming algorithm*.

There are even more stemming algoriths, very well known are the Lancester stemming algorithm[12] and the WordNet stemming algorithm[13]. Since M.F. Porter's snowball stemming algorithm is the most widely used one, we decided to go with his algorithm.

3.1.4 Text Lemmatisation

Similar to *Text Stemming*, Text Lemmatisation has the same goal to group together the inflected forms of a word but follows a different approach to do so. Instead of processing terms with fixed steps and defined rules, Text Lemmatisation normally includes a dictionary lookup for the words and also takes in consideration to which part of a sentence a term belongs to. This results in more accurate root terms but also asks for more computational power than Text Stemming. See following table for a comparison:

#	**Original word**	**Stemmed**	**Lemmatised**
1	written	written	write
2	greatest	greatest	great
3	best	best	best
4	fastest	fastest	fastest
5	highest	highest	high
6	compute	comput	compute
7	computer	comput	computer
8	computed	comput	compute
9	computing	comput	compute
10	studies	studi	study
11	studying	studi	study
12	university	univers	university
13	universities	univers	university
14	universe	univers	universe
15	universal	univers	universal

Table 1: Comparison of Text Stemming and Text Lemmatisation.

3.2 Data Representation

Todo.

3.2.1 Word Frequency

Todo.

3.2.2 tf-idf

Todo.

3.3 Clustering

Clustering finds similarities in different news articles based on their content and groups them together, while unrelated news are regarded as noise. The challenge now arises to find an appropriate clustering method, which is able to work with data of varying densities and of high dimensionality.

3.3.1 *k*-means clustering

k-means clustering is an iterative clustering method which assigns all data points in a given data set into k clusters, where k is a predefined number of clusters in the data set.

How does k-means clustering work At the very beginning, k-means creates k centroids at random locations. It then repeats following instructions until reaching convergence:

- For each data point: Find the nearest centroid
- Assign the data point to the nearest centroid (cluster)
- For each cluster: Compute a new cluster centroid with all assigned data points

Advantages

- Very simple and easy to understand algorithm

Disadvantages

- Initial (random) centroids have a strong impact on the results
- The number of clusters (k) has to be known beforehand
- Unable to handle noise (all data points will be assigned to a cluster)

3.3.2 DBSCAN

DBSCAN stands for *Density-Based Spatial Clustering of Applications with Noise* and is a density based clustering algorithm.

A big advantage of DBSCAN is that it is able to sort data into clusters of different shapes.

How does DBSCAN work DBSCAN requires two parameters in order to work:

1. epsilon - The maximum distance between two data points for them to be considered as in the same cluster.
2. minPoints - The number of data points a neighbourhood has to contain in order to be considered as a cluster.

Having these two parameters defined, DBSCAN will iterate through the data points and try to assign them to clusters if the provided parameters match. If a data point can't be assigned to a cluster, it will be marked as noise point.

Data points that belong to a cluster but don't dense themselves are known as **border points**. Some border points could theoretically belong to two or more clusters if the distance from the point to the clusters don't differ.

Advantages

- Does not need to know the number of clusters beforehand.
- Is able to find shaped clusters.
- Is able to handle noise points.

Disadvantages

- DBSCAN is not entirely deterministic.
- Defining the right epsilon value can be difficult.
- Unable to cluster data sets with large differences in densities.

3.3.3 HDBSCAN

HDBSCAN is a hierarchical density-based clustering algorithm [6], based on DBSCAN and improves its sensitivity for clusters of varying densities. Therefore defining an epsilon parameter, which acts as a threshold for finding clusters, is no longer necessary. This makes the algorithm more stable and flexible for different applications.

How HDBSCAN works Since HDBSCAN is the focus for this thesis, we want to give a more detailed explanation of its inner workings, than for k-means or DBSCAN.

HDBSCAN only requires one parameter to be set beforehand:

1. minPoints - The number of data points a neighbourhood has to contain in order to be considered as a cluster.

The algorithm consist of five steps, which are as follows:

1. Transforming the space At its core HDBSCAN is a single linkage clustering, which are typically rather sensitive to noise. A single noise point between clusters could act a bridge, which would result in both clusters to be seen as one. To reduce this issue, the first step is to increase the distances of lower density points. This is achieved by to comparing the core distances between two points with the original distance to get the the mutual reachability distance. The core distance $core_k(x)$ is defined as the radius of a circle around point x, so that k neighbours are contained within this circle. TODO describe example in Figure 1.

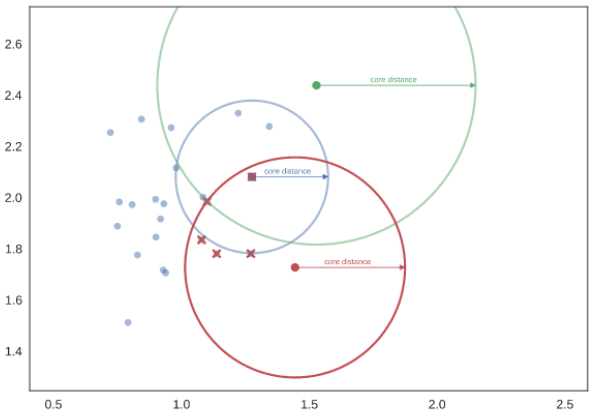


Figure 1: The core distances. TODO give more detailed explanation.

Once the core distances are known, the mutual reachability distance between two points is defined as follows:

$$d_{mreach}(a,b) = max\{core_k(a), core_k(b), d(a,b)\}$$

where $d(a,b)$ is the original distance between a and b. Therefore if two points are close together, but the density around one point is rather low, the core distance will be greater than the original distance and thus the two points appear to be less close together when considering the mutual reachability distance.

2. Build the minimum spanning tree Based on the mutual reachability distances, the next step is to find points close to each other. This is done by creating a minimum spanning tree, where edges are weighted according to the mutual reachability distance and a point is represented by a vertex. The minimum spanning tree is created one edge at a time, always choosing the lowest distance to a vertex not yet in the tree. This is done until each vertex is connected, which results in the minimal set of edges, such that dropping any edge will cause the disconnect of one or more vertices from the tree.

3. Build the cluster hierarchy Once the minimum spanning tree is complete, it is converted into a hierarchy of connected clusters, by sorting edges of the tree by distance and iterate through, creating a new merged cluster for each edge. The dendogram in Figure 2 shows a possible cluster hierarchy.

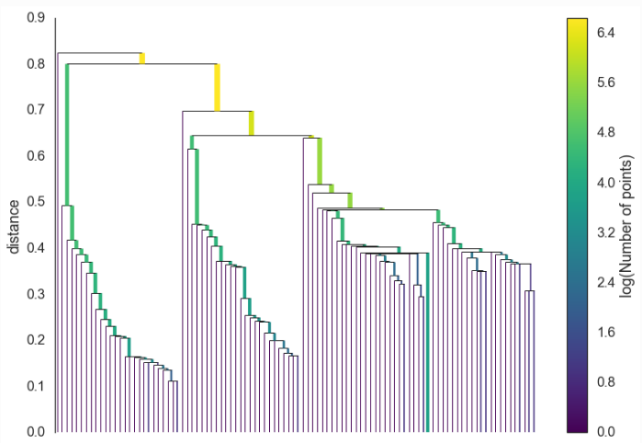


Figure 2: The cluster hierarchy shown as a dendogram

At this stage we have to flatten the hierarchy to get the final clusters, which provide the best representation of the current data set. DBSCAN simply cuts through the hierarchy using a fixed parameter, usually called epsilon, to get the final clusters. This approach does not work well with clusters of varying densities and the epsilon parameter itself is unintuitive, requiring further exploration to find optimal values. This is were HDBSCAN improves upon DBSCAN, by taking additional steps for finding relevant clusters.

4. Condense the cluster tree The fourth step consists of condensing the previously built cluster hierarchy into a smaller tree. The process starts at the top where all vertices still belong to the same cluster. Iterating through the hierarchy, for each split the two resulting clusters are compared against a predefined minimum cluster size. If the size of a cluster is below the minimum, its points will be discarded, while the other cluster remains in the parent cluster. If both cluster sizes are above or equal the minimum, the clusters are considered as true clusters. This is repeated until no more splits can be made.

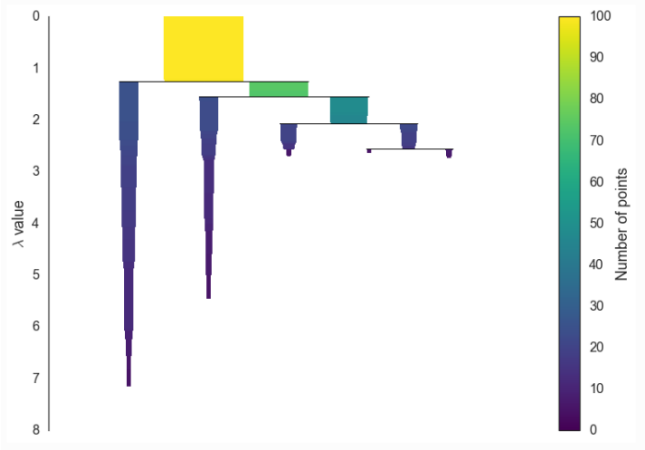


Figure 3: Condensed cluster hierarchy

5. Extract the clusters The extraction of the final clusters from the condensed tree is based on the stability per cluster and once it is selected, none of its subclusters can be chosen. The stability is based on the persistence of a cluster, which is measured by $\lambda = \frac{1}{distance}$. The stability for a cluster C is defined as

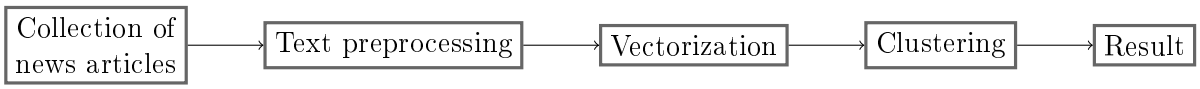
$$\sum_{p \in \mathrm{C}}^{|C|} (\lambda_p - \lambda_{birth}) \tag{1}$$

where λ_p describes when point p fell out of the cluster and λ_{birth} describes when the cluster was created. Now calculating the stability for each cluster starts at the leaf nodes and ends when the root is reached. A cluster is selected if its stability is larger the sum of stabilities of its children. If the sum child stabilities is larger than that of its parent, the parent stability will be set to the value of the sum of its children, but no selection will be done. Based on this approach the final clusters will be selected, with regards to varying densities and noise.

4 Design and Implementation

The methodology consist of three parts, where each part builds upon the results from the previous one. Initially the test data is created, which will be used for all evaluations. Once the data is available, we evaluate HDBSCAN and determine the settings, which lead to optimal results regarding our specific use case. The final part applies the results obtained from the previous evaluation in an online setting.

4.1 Data flow



TODO describe

4.2 Data set

Before any clustering method can be implemented or evaluated, it is important to rely on the right data set for training and evaluation.

4.2.1 Data set candidates

As our goal is to detect events in data streams, we've evaluated different data sets and their possibilities to extract events from their data themselves.

Data set	Number of rows	Description
GDELT 2.0	575'000'000+	Print and web news from around the world.
ChallengeNetwork	4'449'294	Network packages including anomalies.
One Million Posts Corpus	1'011'773	User comments to news articles.
Online Retail Data Set	541'909	Customer retail purchases of one year.
News Aggregator Dataset	422'937	Clustered news articles.
Dodgers Loop Sensor Data Set	50'400	Number of cars driven through a ramp.
10k German News Articles	10'273	German news articles.

Table 2: Evaluated data set candidates ordered by data set size.

We could extract events from all data sets mentioned in Table 2.
The extracted events could be as follows:

- Network packages
  - Cyber attacks depending on suspicious packets.
- User comments
  - Change of public opinion during time.
- Retail purchases
  - Change of purchasing behavior based on product choices.
- Traffic
  - Traffic changes due to baseball games.
- News articles
  - Development of a certain news story.

However, from above data sets only two contained prelabeled events:

1. Dodgers Loop Sensor Data Set
   - 81 labeled events.
2. News Aggregator Dataset
   - 422'937 labeled events.

As we didn't want to lose too much time in manually clustering data, we've decided to go with one of these two. Regarding our two options, our choice was simple:
We went for the **The News Aggregator Dataset** since it not only provided more data, but our work built on the news articles use case could later be continued with real live data. The **GDELT 2.0** data set for example, provides around 1'000 to 2'000 new news articles every 15 minutes.

4.2.2 Data retrieval

Unfortunately the data set did not contain the news articles themselves but rather only the URL's to the news articles. This was done so due to copyright restrictions on the content. Fortunately there are web scraping tools designed to retrieve the content from news articles specifically. We decided to use Newspaper3k[14], a Python3 library that allows us to retrieve the text from news articles easily.

The library only requires an URL to download and extract the news article from a website, see following example:

```
from newspaper import Article

url = 'http://fox13now.com/2013/12/30/new-year-new-laws-obamacare-pot-guns-and-drones/'
article = Article(url)
article.download()
article.text # Contains the article's text.
```

Listing 1: Retrieve the news article from an URL.

All we had to do now is to run this code for all news articles. To speed this process up, we've loaded the data set into a database and run 8 concurrent processes which retrieved the news articles content from the web in different batches.

4.2.3 Data cleansing

The data set contains news articles collected from March 10th to August 10th of 2014. Five years later, many resources are not online anymore or are not accessible from Europe due to GDPR. We've used following SQL query to filter out news articles that were most likely corrupt:

```
SELECT *
FROM news_article
WHERE
    newspaper_text IS NOT NULL
    AND TRIM(COALESCE(newspaper_text, '')) != ''
    AND hostname NOT IN ('newsledge.com', 'www.newsledge.com')
    AND newspaper_text NOT LIKE '%GDPR%'
    AND newspaper_text NOT LIKE '%javascript%'
    AND newspaper_text NOT LIKE '%404%'
    AND newspaper_text NOT LIKE '%cookie%'
```

```
        AND newspaper_keywords NOT LIKE '%GDPR%'
        AND newspaper_keywords NOT LIKE '%javascript%'
        AND newspaper_keywords NOT LIKE '%404%'
        AND newspaper_keywords NOT LIKE '%cookie%'
        AND title_keywords_intersection = 1
```

Listing 2: Retrieve valid news articles.

4.3 Clustering Evaluation

4.3.1 Design

The goal of the clustering evaluation is to find the optimal parameters and preprocessing methods for applying HDBSCAN in an online setting. Therefore the clustering evaluation is designed to run HDBSCAN on our test data, using a combination of different text processing methods, vectorizers and parameters. Additionally each evaluation includes k-means as well, to provide a benchmark to compare HDBSCAN to. Once a clustering has been performed, the result is measured based on the ground truth and stored in a database for later analysis.

Another important consideration is the variety of samples to use for a clustering run. Using only a single set of samples might bias the score against this specific set of samples, and some methods might perform better or worse depending on the samples. To introduce variability, while still retaining repeatability, an evaluation run will be repeated a certain number of times and each repetition will load a new sample set. New sets of samples are chosen linearly instead of randomly. For example if we define the number of repetitions as two with a sample size of 1000, the evaluation will first be done on the first 1000 samples with all possible settings and the second run will load the next 1000 samples, thus containing sample with indices ranging from 1001 to 2000. The reason we do not load random sets of samples is repeatability. If we make any changes in the implementation or the scoring function, we want to be able to compare the new results with the previous ones in a deterministic manner.

4.3.2 Scoring Function

The scoring function is essential for measuring the result of a clustering method. The score should reflect the quality of the individual clusters and of the clustering as a whole. The number of existing measures for clustering is vast and can be split into two main categories. Internal measures determine the score based on criteria derived from the data itself and external measures depend on criteria non-existent in the data itself such as class labels. Since the ground truth is known in our test data, we are going to apply an external measure.

Initially we used Normalized Mutual Information (NMI) as our primary scoring function. The NMI is an entropy-based measure and tries to quantify the amount shared information between the clusterings. The score proved to work well for our initial evaluations, but upon closer inspection certain anomalies were found. An example is given in table 3, where K-means achieved a rather high score, regardless of the significant difference between the true amount of clusters and the approximation using $\sqrt{n}$. One explanation for this result is the bias of NMI for higher numbers of clusters[15].

Algorithm	**Sample Size**	**NMI**	$\mathbf{n_{true}}$	$\mid \mathbf{n_{true}} - \mathbf{n_{predicted}} \mid$
k-means	19255	0.754	600	457
HDBSCAN	19255	0.742	600	2

Table 3: K-Means has a higher NMI score than HDBSCAN, while having a much larger difference in number of clusters.

Other scoring functions such as V-Measure or the Adjusted Rand Index showed similar unexpected results with different clusterings. Therefore we decided to develop our own scoring function based on

the ideas of Maximum Matching[16] and the Jaccard Index, which we call MP-Score.

Calculating the score The scoring function first calculates the similarity between pairs of clusters, where each cluster belongs to a different clustering. We use the Jaccard Index to measure the similarity, which is defined as

$$\frac{|A \cap B|}{|A \cup B|} \tag{2}$$

To illustrate the process we start with an example. We use T and C as our clusterings, where T is the ground truth and C is the predicted clustering. The clusterings are defined as follows:

$$T = \{\{1,2,3\},\{4,5,6,7\},\{8,9\}\}$$
$$C = \{\{1,2\},\{3,4,5,6\},\{7\},\{8,9\}\}$$

We calculate the similarity as defined in Equation (2), for each possible pair between T and C starting with $t_1 = \{1,2,3\}$ and $c_1 = \{1,2\}$:

$$similarity(t_1, c_1) = \frac{|t_1 \cap c_1|}{|t_1 \cup c_1|} = \frac{|\{1,2\}|}{|\{1,2,3\}|} = \frac{2}{3} = 0.667$$

After doing this for each possible pair we get the similarity matrix A:

$$A = \begin{pmatrix} similarity(t_1,c_1) & \dots & \dots & similarity(t_1,c_4) \\ \vdots & \vdots & \vdots & \vdots \\ similarity(t_3,c_3) & \dots & \dots & similarity(t_3,c_4) \end{pmatrix} = \begin{pmatrix} 0.667 & 0.167 & 0 & 0 \\ 0 & 0.6 & 0.25 & 0.4 \\ 0 & 0 & 0 & 1.0 \end{pmatrix}$$

As a next step we have to select the most relevant similarity values from each row of the similarity matrix.

Finding relevant values in the similarity matrix non-trivial, since clusters do not share labels across different clusterings. To solve this, we make two assumptions:

1. The higher the similarity between two clusters, the more likely it is, that both clusters are describing the same group of documents.
2. Each cluster can be associated with a cluster from another clustering only once.

Based on those assumptions we select the highest similarity value per row, whose column is not already associated with another row. Applying this selection function f to our previously calculated similarity matrix A results in the set containing the most relevant similarity values.

$$f(A) = \begin{pmatrix} \mathbf{0.667} & 0.167 & 0 & 0 \\ 0 & \mathbf{0.6} & 0.25 & 0.4 \\ 0 & 0 & 0 & \mathbf{1.0} \end{pmatrix} = \{0.667, 0.6, 1\}$$

As we can see, there were no collisions between columns and we simply get the highest value per row. Consider the following example with an similarity matrix B, which does contain a collision:

$$f(B) = \begin{pmatrix} \mathbf{0.75} & 0.375 & 0.427 & 0.375 \\ 0.4 & \mathbf{0.667} & 0.571 & 0.8 \\ 0.333 & 0.25 & 0.4 & \mathbf{1.0} \end{pmatrix} = \{0.75, 0.667, 1\}$$

The selected similarity for the second row is 0.667 instead of 0.8. This is because the fourth column is already associated with the third row, while having an similarity greater than 0.8. Therefore based on our assumption that clusters cannot be associated twice, the second highest similarity is used for the second column. In case no association could be found, the value would be set to zero.

As a third step we have to calculate the weights to be used for the final The weight is based on the number of elements inside the cluster and necessary to represent differences in predicted and true number of clusters in the final score. It is defined as follows

$$w_{ij} = \frac{|t_i| + |c_j|}{|T| + |C|} \tag{3}$$

where T is the ground truth with $t_i \in T$ and C the predicted clustering with $c_j \in C$. Therefore the weight for a pairing $t_i c_j$ includes both the size of the true cluster and the size of the predicted cluster. The reason both sizes are used, is that we want to reflect if the overall number of predicted clusters is different from the ground truth. Using only the true number of elements as the weight, would affect the score if $|C| < |T|$, but not $|C| > |T|$. Therefore the number of predicted elements has to be included as well.

In the fourth and final step we calculate the weighted average

$$\text{MP-Score} = \sum_{i=0}^{|S|} w_i s_i \{w_i \in W \wedge s_i \in S\} \tag{4}$$

where S is the similarity matrix with $s_i \in S$ and w_i the corresponding weight in W. Using our previously selected similarity values $S = f(A) = \{0.667, 0.6, 1\}$ and the corresponding weights $W = \{0.278, 0.444, 0.222\}$, the calculation for the final average would be done as follows:

$$\text{MP-Score} = (0.278 * 0.667) + (0.444 * 0.6) + (0.222 * 1) = \mathbf{0.674}$$

The final score for the evaluation of the predicted cluster C with the true cluster is 0.674.

Comparison against other measures The test scenarios in table 4 show the resulting scores of our similarity score, NMI and completeness. It is important to note that NMI and completeness work with cluster labels assigned to each document, instead of considering elements inside a single cluster. This means the clustering will be flattened into one dimension, where each document is assigned the label of the cluster it appears in. The array containing the labels for the first scenario would look as follows: $C = [1, 1, 1, 2, 2, 2, 2, 3, 3]$.

As a final note, repeating the evaluation shown in table 3 a second time using the MP-Score, the score (Table 5) for K-means is much lower than HDBSCAN. This reflects what we would expect based on the big difference in the amount of predicted clusters.

The full implementation of the scoring function can be found in the appendix as Listing 6.

Test scenarios with ground truth $T = \{\{1,2,3\},\{4,5,6,7\},\{8,9\}\}$				
Nr.	Predicted Clustering C	NMI	ARI	MP-Score
1	$C = \{\{1,2,3\},\{4,5,6,7\},\{8,9\}\}$	1.0	1.0	1.0
2	$C = \{\{1,2\},\{3,4,5,6\},\{7,8,9\}\}$	0.564	0.308	0.637
3	$C = \{\{1,2,3\},\{4,5,6\},\{7\},\{8,9\}\}$	0.895	0.771	0.847
4	$C = \{\{1,2,3\},\{4,5\},\{6,7\},\{8\},\{9\}\}$	0.821	0.591	0.583
5	$C = \{\{1\},\{2\},\{3\},\{4\},\{5\},\{6\},\{7\},\{8\},\{9\}\}$	0.651	0	0.227
6	$C = \{\{1,2,3,4,5\},\{6,7,8,9\}\}$	0.434	0.182	0.433
7	$C = \{\{1,2,3,4,5,6,7,8,9\}\}$	0.0	0	0.321
8	$C = \{\{7,2,4\},\{8,9,6,3\},\{1,5\}\}$	0.219	-0.108	0.392

Table 4: Direct comparison of different scoring functions

Algorithm	**Sample Size**	**Similarity**	$\mathbf{n_{true}}$	$\mid \mathbf{n_{true}} - \mathbf{n_{predicted}} \mid$
k-means	19255	0.137	600	457
HDBSCAN	19255	0.605	600	2

Table 5: The similarity score reflects the difference in number of predicted clusters.

4.3.3 Implementation

The evaluation process is done with our own evaluation framework. The framework allows for automated and repeatable evaluation runs. Results are stored in a database for later analysis. The main features include:

- Defining the number of stories to run the evaluation with and load all news articles from those stories.
- Repeating evaluation runs with different sets of data.
- Providing different vectorizers for converting the textual data into a vector space model.
- Defining a range for each parameter of a clustering method and running it with each possible combination of those parameters.
- Storing the result the result in a database and creating relations between news articles, clusters and evaluation runs. This allows for manual inspection and analysis of individual articles inside a predicted cluster.

The implementation is done with Python. Clustering methods and vectorizers are provided by the scikit-learn library[17]. We decided to use Scikit-learn because of its rich documentation, the wide range of tools and algorithms it provides for clustering and our previous experience with it. Additionally the framework runs in a fully dockerized environment, which includes the database. This allows the framework to run independently from the underlying host, as long as the host supports docker. This principle was useful for developing and testing the framework in a local environment and deploying it on a remote server for long running evaluations, without worrying about setting up and installing all dependencies again.

Defining cluster parameters The parameters for each available clustering method are defined beforehand in a dictionary as can be seen in Listing 3. Parameters are defined as a list of possible variations. For example if we want to run HDBSCAN with two different metrics *cosine* and *euclidean*, we define the metric parameter as `"metric": ["cosine", "euclidean"]`. When running a clustering method, it will be executed with each possible combination of parameters. This means a single evaluation of HDBSCAN, will include 16 different runs, since there are two different metrics and eight different

options for *min_cluster_size*. This is important to consider for running clustering methods with long processing times or running evaluations on large sample sizes.

```
parameters_by_method = {
    self.kmeans: {
        "n_cluster": ["n_square", "n_true"]
    },
    self.hdbscan: {
        "min_cluster_size": range(2, 10),
        "metric": ["cosine", "euclidean"]
    },
    self.meanshift: {"cluster_all": [True, False]},
    self.birch: {
        "branching_factor": range(10, 100, 10),
        "threshold": range(2, 6),
    },
    self.affinity_propagation: {
        "affinity": ["euclidean"],
        "convergence_iter": [15],
        "damping": np.arange(0.5, 0.9, 0.1),
        "max_iter": [50, 100, 200, 500],
    },
    self.spectral_clustering: {
        "affinity": ["rbf"],
        "assign_labels": ["kmeans", "discretize"],
    },
}
```

Listing 3: Predefined parameters for different clustering methods

CLI The evaluation framework provides a command line interface to start evaluation runs and specify a number of settings. Listing 4 shows the full interface.

```
usage: cluster_evaluation_framework.py [-h] [--rows ROWS] [--stories STORIES]
                                       [--methods METHODS]
                                       [--vectorizers VECTORIZERS]
                                       [--tokenizers TOKENIZERS] [--runs RUNS]

Run different clustering methods, with a variety of different settings.
data_mining
optional arguments:
  -h, --help            show this help message and exit
  --rows ROWS           number of samples to use for clustering
                        default: 1000
  --stories STORIES     number of stories to load samples from. This parameter
    overrides the rows parameter if set.
  --methods METHODS     options: kmeans, hdbscan, meanshift, birch,
    affinity_propagation, spectral_clustering
                        default: all available options
  --vectorizers VECTORIZERS
                        options: CountVectorizer, TfidfVectorizer
                        default: all available options
  --tokenizers TOKENIZERS
                        options: newspaper_text, text_keyterms, text_entities,
    text_keyterms_and_entities, text_lemmatized_without_stopwords,
    text_stemmed_without_stopwords
                        default: all available options
  --runs RUNS           number of runs per clustering method
```

```
22                    default: 1
```

Listing 4: Command line interface for the evaluation framework

4.4 Online Clustering

4.4.1 Design

Detecting events in a stream of news articles will be achieved by using an online clustering approach. An event is described by the occurrence of multiple news articles to the same subject. The events of interest for this application are the discovery of new stories and the extension of existing stories. Thus we define our two types events as follows:

- New event: A new cluster of news articles appears in the data stream, which describe the same story.
- Event extended: An existing story is extended by additional news articles.

HDBSCAN will be applied as the clustering method, using the optimal settings as discovered in the previous evaluation. Additional preprocessing of news articles before clustering is going to be explored as part of evaluation as well and will be implemented accordingly for the online clustering.

Since HDBSCAN only supports static data sets, the clustering will be done in batches using a time based sliding window approach. Events are detected by comparing the resulting clusters with the previous ones.

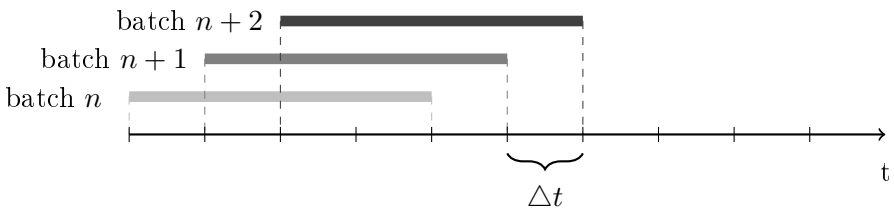


Figure 4: Timeline showing the sliding window approach

Finding pairs clusters Thus we define our two events as follows: To be able to compare clusters of different batches with each other, we have to find pairs of clusters between batches, which describe the same story. This is done by applying the same assumptions as for the scoring function used in the evaluation. Therefore clusters are paired based on their similarity calculated with the Jaccard index as shown in equation 2. If the similarity is above a certain threshold, both clusters are seen as describing the same story.

Sliding window An important consideration for determining existing or new clusters is the overlap of samples between batches. If the overlap is too small, similar clusters will no longer be detected as such, which would result in an increasingly high error rate. Finding optimal values for the step size between batches and the number of samples for each batch is therefore essential for our online clustering approach.

4.4.2 Implementation

The online clustering implemented for this thesis does not operate in a true online setting, but rather it takes our existing test data and simulates a data stream over time. The simulated approach allows us to directly compare the resulting events with the ground truth and thus evaluate different settings. The implementation is done with Python and runs in a similar dockerized environment as the evaluation framework.

Comparing clusters To detect events between batches of clusterings, we have find pairs of clusters describing the same story. This problem is solved in the evaluation framework as part of the scoring function, by calculating the similarity for each possible cluster pair. The resulting time complexity is $O(n^2)$, which we deemed acceptable for the static evaluation. However in a dynamic setting such as the online clustering, performance is an important factor, since it restricts the lengths of the time delta between batches and the overall batch size. Thus we decided to use Locality-Sensitive Hashing (LSH)[18] to find similar clusters. This reduces the time complexity to $O(log(n))$. The implementation for LSH is provided by the datasketch library[19].

Detecting Events Once we have found pairs of clusters, which represent the same story, detecting events becomes trivial. For each pair we look for news articles, which are only present in the new cluster. These articles are then summarized in as an extension of an existing event. Clusters from the new batch without a matching cluster from the previous batch are seen as new events.

Measuring the quality of events Since events are themselves clusters of news articles, we apply the MP-Score to measure detected events against events taken from the ground truth. This gives an indication if the detected events contain the same news articles as true events and thus the rate of false positives and false negatives. Calculating the score is $O(n^2)$, but since the application runs on a simulated timeline, time complexity is only a minor concern.

CLI The application provides a command line interface to run the simulation with different parameters such as the start date, number of days to run and the batch size.

```
usage: online_clustering.py [-h] [--full-cluster] [--verbose] [--rows ROWS]
                            [--full_rows FULL_ROWS] --date DATE
                            [--run_n_days RUN_N_DAYS] [--threshold THRESHOLD]

Run the batchwise clustering over a simulated stream of news articles.

required arguments:
  --date DATE

optional arguments:
  -h, --help            show this help message and exit
  --full-cluster        run a full clustering once a day
                        default: False
  --verbose
                        default: False
  --rows ROWS           number of samples to process per batch
                        default: 1000
  --full_rows FULL_ROWS
                        number of samples to process for the full clustering
  --run_n_days RUN_N_DAYS
                        number of days to run the batchwise clustering
                        default: 1
  --threshold THRESHOLD
                        similarity threshold for cluster matching
                        default: 0.75
```

Listing 5: Command line interface for the online clustering

5 Results

5.1 Clustering Evaluation

The goal of this evaluation is to measure the accuracy of HDBSCAN, with different parameters and preprocessing methods. The most suitable approach will then be used for the online clustering to detect changes in a news stream.

5.1.1 Setup

Text Preprocessing The first step in working with text is to apply Natural Language Processing techniques for improving the quality of the data before clustering it. We look the five different preprocessing methods as described in section **??** and evaluate each. The methods are:

- Full text with stop word removal
- Key terms
- Named Entities
- Text Lemmatisation
- Text Stemming

Text Vectorization Before the text can be clustered, it has to be transformed into a vector space model. We look at two different models:

- Word Frequency
- tf-idf

Parameters HDBSCAN has a range of parameters, which can be tuned to fit our data set. We focus on the two primary ones:

- Min cluster size: The minimum size of a cluster. We run the evaluation with a range from two to nine as the $min\_cluster\_size$.
- Metric: The distance measure between points. We apply the metrics "cosine" and "euclidean".

The primary parameter for K-Means is the number of clusters. Since K-Means is used as a baseline to evaluate HDBSCAN, we provide the true number of clusters for each run. Therefore K-Means runs with an optimal starting point.

Running the evaluation The evaluation is done with different sets of news articles per run. This means if we define a run to use 30 stories and set it to repeat five times, each repeat will load 30 different stories from the data set. This is done to get a more diverse set of samples. Each run will be repeated at least three times. Lower numbers of stories allow for more repetitions due to lower processing times.

5.1.2 Evaluation

The first run is done with 60 stories, which results in approximately 2000 news articles, over five repetitions. Table 6 shows the resulting accuracy for each parameter in combination with each preprocessing method and vector space model. The highest score per parameter is highlighted as bold. The first insight we get is the variety in accuracy scores for different min cluster sizes. The lowest min cluster size results in the lowest accuracy, while increasing this parameter leads to an increasingly

better score. The highest accuracy is reached with a min cluster size of six, while increasing it further reduces the score again. The large difference in accuracy between different min cluster sizes, shows the importance this parameters has on the quality of the clustering and requires some knowledge of the data beforehand. In our case we have a wide range of different cluster sizes as shown in Figure 5, with clusters containing as little as two news articles. Based on this distribution we expected the min size cluster size to be low. The distribution also explains the drop in accuracy after a min cluster size of 6, since an increasingly number of clusters are being ignored.

Clustering	**Word Frequency**					**tf-idf**				
HDBSCAN	Full Text	Key terms	Entities	Lemmatised	Stemmed	Full Text	Key terms	Entities	Lemmatised	Stemmed
min_size: 2, metric: cosine	0.289	0.265	0.223	**0.305**	0.297	0.286	0.268	0.26	0.296	0.3
min_size: 2, metric: euclidean	0.101	0.093	0.110	0.101	0.106	0.301	0.170	0.241	**0.306**	0.301
min_size: 3, metric: cosine	0.488	0.456	0.465	0.48	0.487	0.472	0.446	0.457	**0.493**	0.478
min_size: 3, metric: euclidean	0.172	0.129	0.176	0.174	0.182	0.472	0.306	0.464	**0.500**	0.478
min_size: 4, metric: cosine	0.630	0.555	0.625	0.552	0.577	0.577	0.586	**0.646**	0.589	0.581
min_size: 4, metric: euclidean	0.320	0.182	0.214	0.315	0.332	0.611	0.416	0.559	0.613	**0.615**
min_size: 5, metric: cosine	0.716	0.652	0.656	**0.718**	0.718	0.688	0.664	0.632	0.686	0.692
min_size: 5, metric: euclidean	0.355	0.217	0.266	0.41	0.389	**0.703**	0.512	0.607	0.686	0.692
min_size: 6, metric: cosine	0.693	0.715	0.608	0.701	0.708	0.738	0.729	0.613	**0.751**	0.747
min_size: 6, metric: euclidean	0.179	0.280	0.292	0.202	0.164	0.738	0.408	0.622	**0.778**	0.763
min_size: 7, metric: cosine	0.631	0.611	0.552	0.643	0.634	0.689	0.685	0.553	0.718	**0.722**
min_size: 7, metric: euclidean	0.122	0.392	0.307	0.073	0.099	0.689	0.336	0.539	0.718	**0.722**
min_size: 8, metric: cosine	0.571	0.603	0.514	0.592	0.574	0.685	0.647	0.531	**0.711**	0.695
min_size: 8, metric: euclidean	0.056	0.339	0.338	0.025	0.057	0.685	0.286	0.522	**0.711**	0.695
min_size: 9, metric: cosine	0.542	0.569	0.476	0.544	0.541	0.602	0.614	0.499	0.637	**0.640**
min_size: 9, metric: euclidean	0.065	0.236	0.310	0.025	0.033	0.602	0.216	0.475	0.637	**0.640**
K-Means										
n_cluster: n_true	0.531	0.588	0.514	0.536	0.536	**0.713**	0.653	0.584	0.672	0.693

Table 6: Accuracy for combinations of parameter and preprocessing with a sample size of 60 stories (approx. 2000 articles)

Comparing the two vector models, shows the majority of best scores per parameter achieved by tf-idf. Additionally the different metrics show a significant difference when using the vector model based on word count. With tf-idf the difference between both metrics is often negligible.

As for the optimal preprocessing, text lemmatisation appears to provide the highest accuracy in general or at least being fairly close to the highest score. This is to be expected, since text lemmatisation reduces the dimensions by grouping words into their base form, while still retaining most of the text. In contrast to key term and entity extraction, which both result in a drastic reduction of the dimensions, and therefore less detail. It is important to note, that we used pretrained models for key term and entity extraction. Specifically training on a news corpus might improve the performance of both methods, but it was decided as to be out of scope for this thesis.

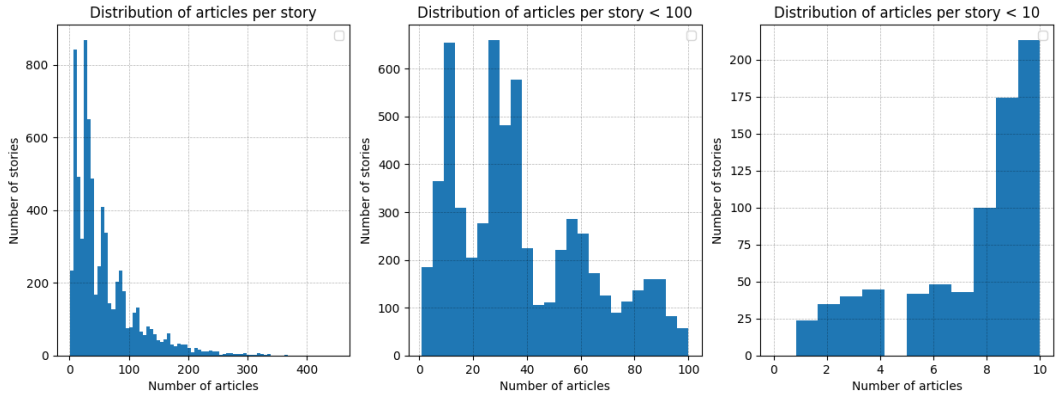


Figure 5: Distribution of cluster sizes.

After determining the optimal settings for text preprocessing and vectorization, we increase the sample

sizes for our evaluation runs, to get a deeper insight into the behaviour of HDBSCAN with larger data sets. Figure 6 shows the scores achieved with different parameters over an increasingly large set of samples. Based on this Figure we see the metric *cosine* to be generally better than *euclidean*, even if *euclidean* is occasionally more accurate.

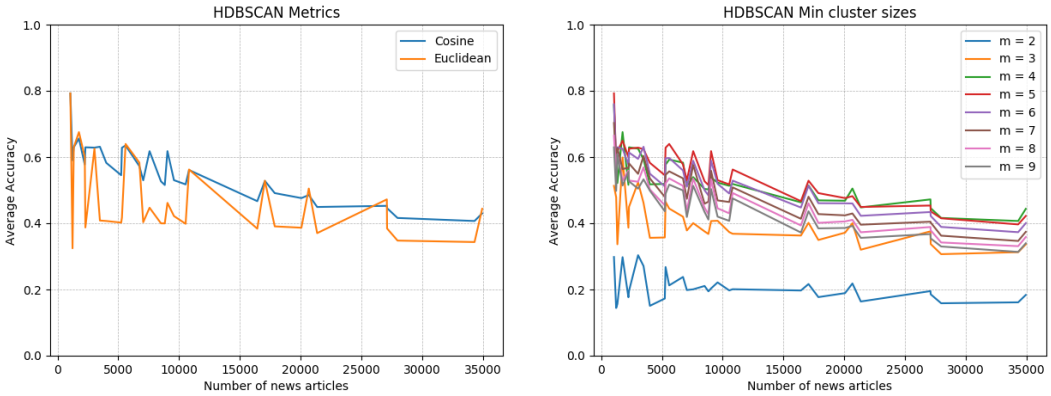


Figure 6: Accuracy for different parameters

One of the advantages HDBSCAN has over other clustering algorithms, is the ability to work with noise, since we intent on applying it in an online setting, where noisy data is to be expected. At the same time, the number of articles classified as noise should be kept to a minimum. However the noise ratio shown in Figure 7 is higher, than we would expect it to be based on our test data. A variety of factors play into the high noise ratio. One major influence is due to the used *min_cluster_size*. Each news article belonging to a cluster ignored due to a size too small, will be counted as noise. In addition to the false positives due to the min cluster size, the test data does still contain noisy data, even after our efforts in cleaning up the data as good as possible. Nonetheless the expected noise ratio based on the test data is less than 10%, nowhere close to the 20% of the current evaluation. Decreasing the noise ratio is certainly an important part in future improvements.

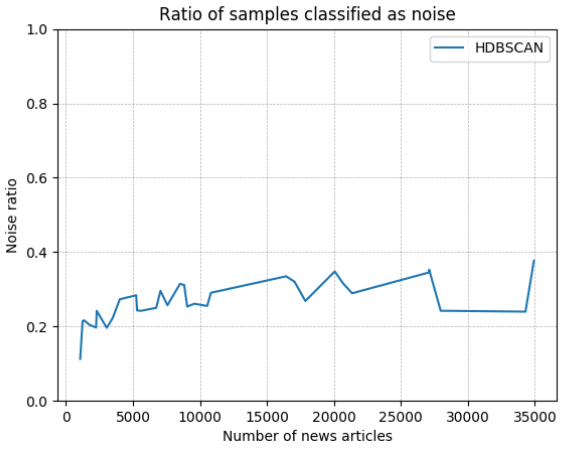


Figure 7: Number of news articles classified as noise.

Having found the optimal settings to run HDBSCAN with, we can start comparing the overall performance with K-Means. Figure 8 shows a similar behaviour for both clustering methods in value and variance of the accuracy. Although HDBSCAN is generally more accurate than K-Means, the difference gets smaller with an increase in the sample size.

Increasing the sample size results for both HDBSCAN and K-means in a small loss regarding the

accuracy as can be seen in Figure 8. However the accuracy seems to stabilize around the 0.7 mark.

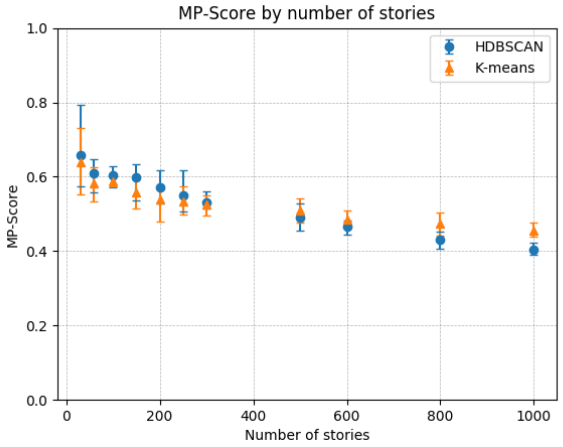


Figure 8: Comparison of the average accuracy between K-means and HDBSCAN

While HDBSCAN and K-means provide a similar accuracy, the biggest difference can be noted in the processing time in relation to the number of samples. K-means has a time complexity of $O(n^2)$ in contrast to HDBSCAN with a time complexity of $O(nlog(n))$, which is demonstrated by Figure 9. Although running the evaluation has also shown the space complexity for HDBSCAN to be substantially higher for larger amounts of samples than with K-means. Trying to run HDBSCAN with 100'000 news articles caused in a memory error, even with 64GB of RAM, while K-means was able to complete the clustering.

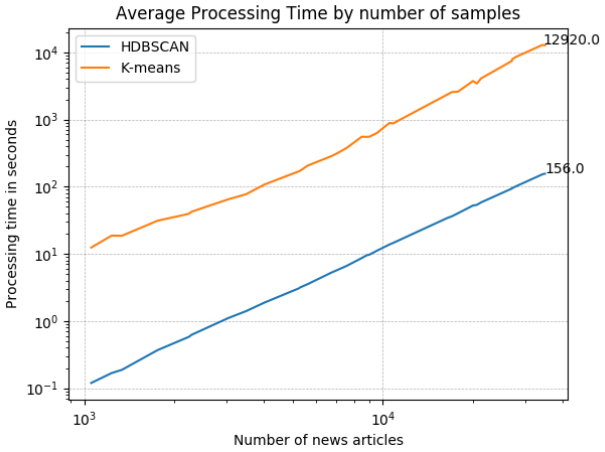


Figure 9: Processing time in seconds

Figure 10 shows, that the difference between predicted over the true number of clusters is fairly low and appears to be roughly linear with the overall number of clusters.

As a final note, we compare HDBSCAN with six different clustering methods taken from scikit-learn. Each method is run with a variety of parameters and the best scores are shown in Figure 11. HDBSCAN provides the highest accuracy, while being still being one of the fastest algorithms. Based on this data, we can assume HDBSCAN to be a good candidate for our use case.

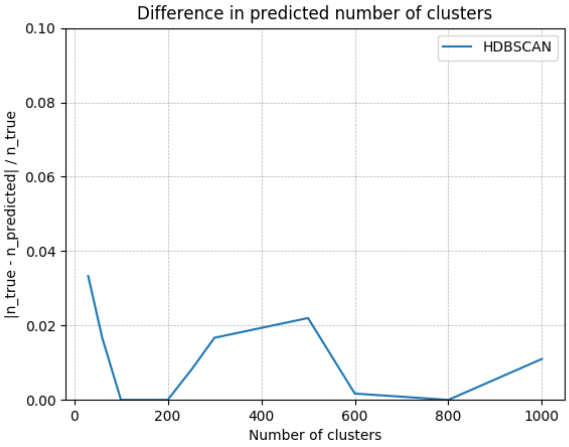


Figure 10: Ratio of difference over predicted with true number of clusters

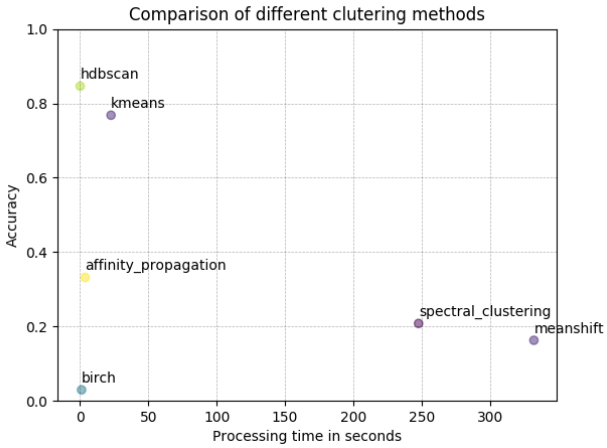


Figure 11: Comparison of different clustering methods with a sample size of approximately 1000 news articles

5.1.3 Conclusion

The evaluation has shown HDBSCAN to be a good candidate to use for news clustering. It provides an better accuracy than K-means, while being significantly faster to process. The predicted number of clusters is consistent with an increasing number of samples and fairly close the truth. Additionally we have shown the required preprocessing and vectorization steps with the ideal parameters to achieve the most accurate results for our data set. On the flip side the noise ratio is quite high and the space complexity is problematic with larger data sets. Overall HDBSCAN provides an acceptable accuracy, while still leaving room for further improvements.

5.2 Online clustering

5.2.1 Setup

The online clustering is done on a simulated stream of news articles based on the same data set as used in the clustering evaluation. This allows for direct comparison between the detected events and the ground truth. The settings to run the clustering are as follows:

- Text Lemmatisation
- Vectorizer: tf-idf

- Clustering method: HDBSCAN
- Min cluster size: 5
- Distance metric: cosine

The clustering is run over 30 days with a total of 42'916 news articles. The distribution of news articles this time period is illustrated in Figure 12. The time delta, which is the amount of time between two batches, is set to one hour.

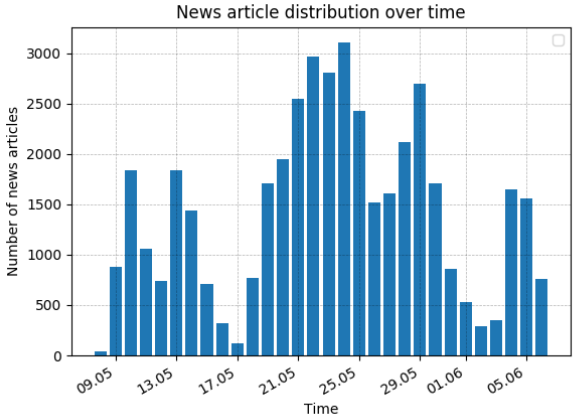


Figure 12: Incoming news articles over 30 days

5.2.2 Evaluation

The goal of the online clustering is to detect new events in an incoming stream of news articles and changes in existing events. This evaluation analyses the results of our simulated test runs with different batch sizes.

Figure 13 shows the differences between the number of detected events and the number of true events for both new and existing topics. Based on this data we see the impact of different batch sizes for the accuracy in detected events. The difference with a batch size of 5000 news articles is significantly lower than the batch size of 1000. The difference is especially noticeable in the time period between the 21.05 and 25.05. The reason for this spike can be found in the distribution of incoming news articles as shown in Figure 12. During this period we receive up to 3000 news articles in a single day. This means by using a lower batch size such as 1000, the overlap between batches gets too small to reliably detect changes between batches, which causes too many new topics to be detected.

Although a larger batch size does not simply equal a better difference, as can be seen in Figure 13 by comparing the differences using a batch size of 3000 with a batch size of 5000. The batch size n=3000 shows a generally lower difference in the detection of new events than with n=5000. The differences between both batch sizes are less significant when detecting changes in existing events.

Based on the overall differences, we do not know the accuracy of those predictions. If the difference between newly detected events and true events is zero, there is still the possibility, that the events itself are different from the ground truth, and thus contain false positives. To measure the quality of events, we can look at the collection of events in a single batch as a subset of clusters, where each event is represented by a cluster containing all relevant news articles. Since we now have two clusterings, one containing detected events and the other with events taken from the ground truth, we can apply our MP-Score as a metric to get an insight into the quality of the detected events over the ground truth. Figure 14 shows the MP-Scores for an online clustering using a batch size of 1000. Since there

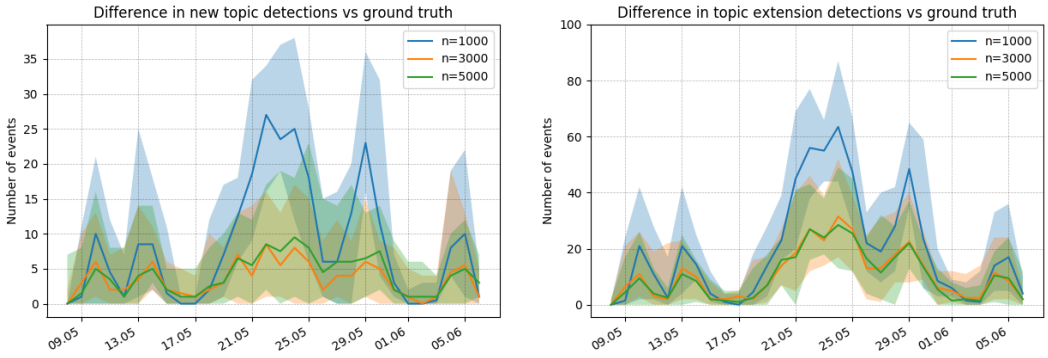


Figure 13: Comparison between the difference in detected and true events. The line represents the median, while the area shows the range from the minimum to the maximum value

is quite a large variance, the score is shown as a boxplot, where a single box represents a full day. The large variance is already the first indication, that the quality is rather low. Meaning that there are still many false positives and false negatives.

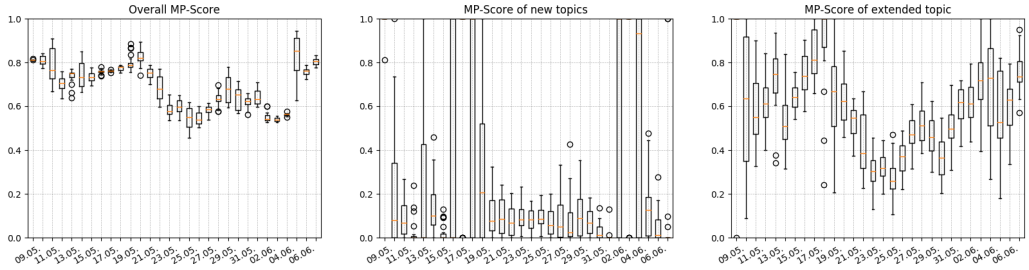


Figure 14: MP-Scores for clusterings using batch size of 1000

Looking at an increased batch size of 5000 in Figure 15, we note that there is less variance in the overall MP-Score, which compares the full clustering with the ground truth. Although the variance for new and existing event detections is still fairly high. Additionally while the variance is high, the median for new topics is mostly around 0.1. This tells us that most of the newly detected events do not correspond with new events according to the ground truth. The detection of extensions of existing events is generally more accurate with a median between 0.5 and 0.8 using n=5000, but there is still are wide variance noticeable.

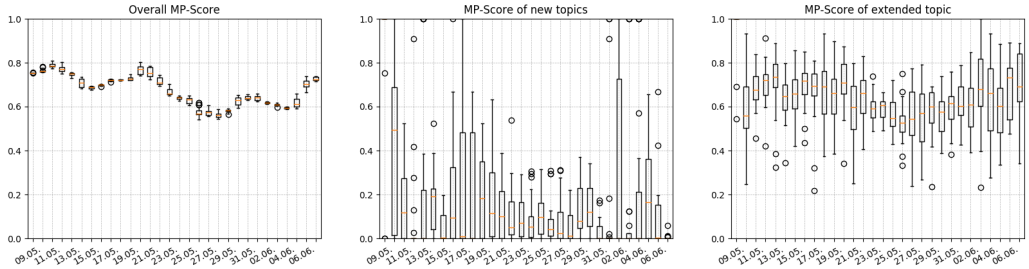


Figure 15: MP-Scores for clusterings using batch size of 5000

One of the reasons for the difference in the accuracy of the detection of new events and the extension

of events might be explained by the *min_cluster_size*. In the current setting the *min_cluster_size* is set to 5, which means if an event occurs in batch one containing only four news articles, it will be discarded as noise. If the second batch contains additional news articles for the same event, it will be detected as a new occurrences, but the ground truth treats it as an existing event. To see how this affects the result we run the same simulation with a batch size of n=3000 a second time, but only considering new events from the ground truth if the number of news articles is greater or equal to the *min_cluster_size*.

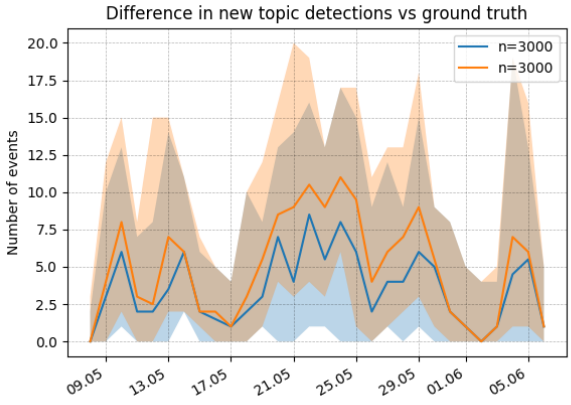


Figure 16: Differences in predictions vs ground truth using batch size of 3000.

Limiting new events in the ground truth based on the *min_cluster_size* gives the opposite result as initially expected. Figure 16 clearly shows an increase in the difference between predicted events and the adjusted ground truth. This means we already detected more new events than there were present in the ground truth and limiting it based on the *min_cluster_size* only lowered the true number of events, thus leading to an increase in the difference. A look at the raw data from an initial simulation run in Figure 17 validates this assumption.

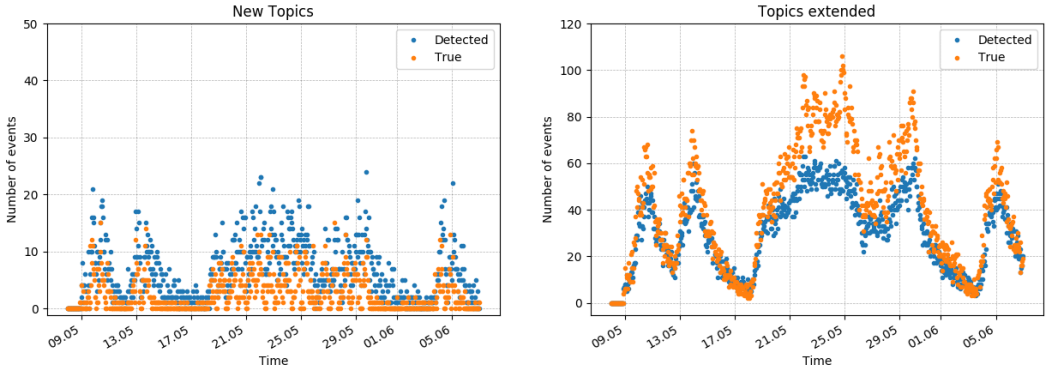


Figure 17: Number of events with a batch size of 3000

The raw data in Figure 17 also shows a direct correlation between the number of detected new events and the number of detected changes in events. The more changes we missed, the more new events are detected. This is to be expected, since the detection of changes depends upon finding similar pairs of clusters in two different batches. If a cluster in the current batch could not be matched to a cluster from the previous batch, the cluster from the current batch will be seen as a new event. Therefore the accuracy in finding pairs of clusters in crucial to a better performance. The online clustering makes use

of Locality Sensitive Hashing as explained in section 4.4.2. The current threshold value for determining the similarity is set to 0.75. To see the impact on the similarity threshold, we run the online clustering again with a batch size of n=3000 and different threshold values.

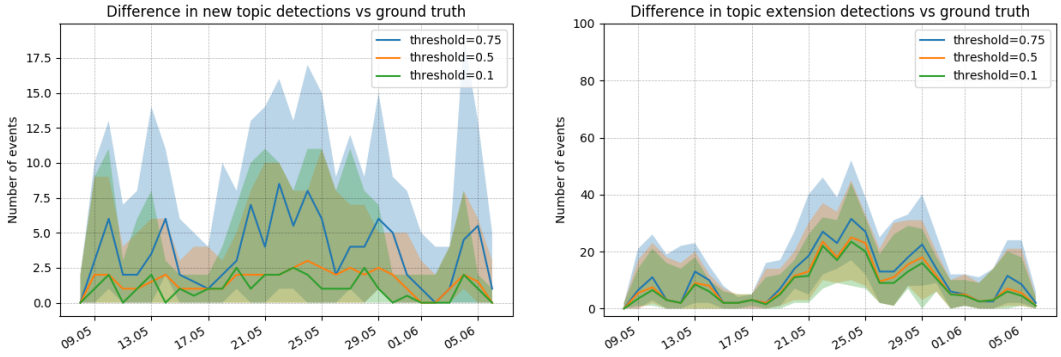


Figure 18: Differences in detected over true events with different thresholds

Figure 18 shows the effect of the threshold on the difference in decided over true events. We see how the initial threshold of 0.75 was set too high, as lower threshold values such as 0.1 provide a significant lower difference. While there is still a substantial variance per day the median of 0.1 and 0.5 is generally more stable and lower than with a threshold value of 0.75. The reason for the better performance of lower threshold values, is that the overlap between batches decreases with an increase in the volume of news articles. This is clearly visible during the peaks in Figure 18. Thus a high similarity threshold cannot be met, since there exists only an overlap of a few news articles for the same cluster between batches. The MP-Score is also improved for new events as can be seen in Figure 19. While there is more variance than in similar plots from Figure 14 and Figure 15, the median from using threshold=0.1 clearly surpasses any measure from using threshold=0.75. The high variance in the boxplot is due to the fact, that there are only a few new events per hour, if any. This means detecting no events, when there are none leads to a score of 1, while detecting one event, when there is none leads to a score of 0.

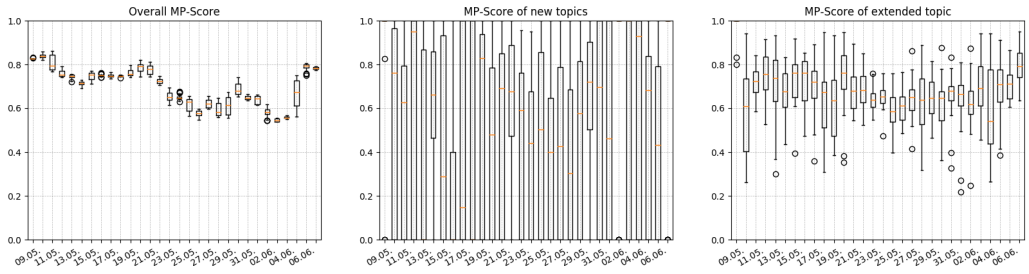


Figure 19: MP-Scores for online clustering with batch size n=3000 and threshold=0.1

Additional reasons for the general low performance in the quality of events might be due to the noise rate and the difference in the number of news articles. As described in the section about the cluster method evaluation, the noise rate for sample sizes between 1000 and 5000 ranges from 20% to 30%. This means a significant amount gets discarded as noise and thus potential new events might not even be detected, because too many of their news articles are discarded. Once an event is detected, detection in changes are more reliable than for new events, but as the variance in the MP-Score shows, there is still a fairly large error rate.

As a final note let us look at two specific examples. One where the detection was mostly accurate and a second where the detection failed.

TODO or OPTIONAL?

5.2.3 Conclusion

TODO rewrite with new findings e.g. not as bad as initially thought but still not very good.

While the overall clustering results in good scores, the detection of new events and changes in existing events gives rather poor results. Possible reasons have been explored such as the $min\_cluster\_size$, the noise rate or the general difference in the number of news articles, but there exist no simple solutions for any of them. As a result we conclude that the accuracy of the clustering method used in this approach is insufficient for the detection of events in a news stream. TODO elaborate a bit more

6 Conclusion

6.1 Lessons learned

Todo.

6.2 Future work

How can this work be improved further?

- Improving space complexity and noise ratio of HDBSCAN.
- Alternatively, use HDBSCAN as an approximation for the number of clusters and a different clustering algorithm for the actual creation of the clusters.

7 Index

7.1 Bibliography

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7.2 Glossary

api An application programming interface allowing access to data or features of an application. 36

clustering The task of grouping a set of objects based on their similarity. 36

docker A tool to package the application with all its dependencies as a single deployable unit and run it on independently from the underlying host. 36

dockerized An application environment running as a single or a collection of docker containers. 36

vectorizer A vectorizer transform a text into a numeric vector. 36

7.3 List of Figures

7.4 List of Tables

8 Appendix

8.1 Algorithm for MP-Score

```
import collections


def calculate_mp_score(true_clusters, predicted_clusters):
    """
    Calculate the mp_score of a clustering based on the contents of the clusters and the overall difference in
    predicted over true number of clusters. The calculation is based on three steps:
        1. Create an similarity matrix by calculating the difference between each cluster of both clusterings.
        2. Select the most relevant values from the similarity matrix and make sure no two clusters are being used
           at the same time.
        3. Calculate the weighted average, where the weight is based on the true and predicted amount of elements
           in a cluster.

    Parameters
    ----------
    true_clusters: array[clusters]
        2-dimensional array of true clusters

    predicted_clusters: array[clusters]
        2-dimensional array of predicted clusters
    """

    # If both clusters are empty, they are identical.
    if len(true_clusters) == 0 and len(predicted_clusters) == 0:
        return 1

    similarity_matrix = create_similarity_matrix(true_clusters, predicted_clusters)
    unique_indices = select_max_values(similarity_matrix)
    return calculate_weighted_average(unique_indices, true_clusters, predicted_clusters)


def create_similarity_matrix(true_clusters, predicted_clusters):
    similarity_matrix = []
    for true_cluster in true_clusters:
        true_set = set(true_cluster)
        n_true = float(len(true_set))
        row = []
        for predicted_cluster in predicted_clusters:
            cluster_set = set(predicted_cluster)

            # Calculate the similarity using the jaccard index
            similarity = len(true_set.intersection(cluster_set)) / len(
                true_set.union(cluster_set)
            )
            row.append(similarity)

        similarity_matrix.append(row)
    return similarity_matrix


def select_max_values(precision_matrix):
    unique_indices = dict()
    row_index = 0
```

```
    nrows = len(precision_matrix)

    while row_index < nrows:
        ignore_indices = set()
        max_value_found = False

        while not max_value_found:
            max_value = 0
            column = 0
            for col_index, value in enumerate(precision_matrix[row_index]):
                if value >= max_value and col_index not in ignore_indices:
                    max_value = value
                    column = col_index

            if (
                max_value > 0
                and column in unique_indices
                and unique_indices[column]["row_index"] != row_index
                and unique_indices[column]["max_value"] > 0
            ):
                if unique_indices[column]["max_value"] < max_value:
                    # The column is already used, but we found a better
                    # candidate. We use the new candidate and set the
                    # cursor to the old one to find a new max value.
                    old_row_index = unique_indices[column]["row_index"]
                    unique_indices[column]["row_index"] = row_index
                    row_index = old_row_index
                    unique_indices[column]["max_value"] = max_value
                    max_value_found = True
                else:
                    # The column is already used by a better candidate.
                    ignore_indices.add(column)
            else:
                # If max_value is greater than 0, we store the value as a
                # new candidate. Otherwise either the row does not match
                # any other column or the max_value was low and got
                # overridden by previous tries and no other match is available.
                if max_value > 0:
                    # The column is free to use
                    unique_indices[column] = {
                        "row_index": row_index,
                        "max_value": max_value,
                    }
                max_value_found = True
                row_index += 1

    return unique_indices


def calculate_weighted_average(unique_indices, true_clusters, predicted_clusters):
    mp_score = 0

    elements_per_true_cluster = [len(cluster) for cluster in true_clusters]
    elements_per_predicted_cluster = [len(cluster) for cluster in predicted_clusters]

    total_true_elements = sum(elements_per_true_cluster)
    total_pred_elements = sum(elements_per_predicted_cluster)
    total_elements = total_true_elements + total_pred_elements

    if total_elements > 0:
        for column, value in unique_indices.items():
```

```
115             # The row of the similarity matrix equals the index of the true cluster,
    while the column is the index of the predicted cluster
116             weight = (
117                 elements_per_true_cluster[value["row_index"]]
118                 + elements_per_predicted_cluster[column]
119             ) / (total_elements)
120             mp_score += value["max_value"] * weight
121 
122     return mp_score
```

Listing 6: Calculate the MP-Score between two clusterings.