



IDENTIFIER NAMESPACES IN MATHEMATICAL NOTATION

MASTER THESIS

by

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Abstract

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1 Introduction

1.1 Namespaces in Computer Science

In computer science, a *namespace* refers to a collection of terms that are managed together because they share functionality or purpose, typically for providing modularity and resolving name conflicts [1].

Namespaces are used in XML (eXtensible Markup Language), which is a framework for defining markup languages. XML lets users define a set of tags to represent information in some specific domain [2]. For example, XHTML is an XML language for hypertext markup and MathML is a language for describing mathematical notation.

However, different XML languages may use the same names for elements and attributes. For example, consider two XML languages: XHTML for specifying the layout of web pages, and some XML language for describing furniture. Both these languages have the `<table>` elements there, in XHTML table is used to present some data in a tabular form, while the second one uses it to describe a particular piece of furniture in the database.

The `<table>` elements have very different semantics in these languages and there should be a way to distinguish between these two elements. In XML this problem is solved with XML namespaces [3]: the namespaces are used to ensure the uniqueness of attributes and resolve ambiguity. It is done by binding a short namespace alias with some uniquely defined URI (Unified Resource Identifier), and then appending the alias to all attribute names that come from this namespace. In the example above, we can bind an alias `h` with XHTML's URI <http://www.w3.org/TR/xhtml1> and then use `<h:table>` to refer to XHTML's table. Likewise, in the furniture database language the element names can be prepended with a prefix `d`, where `d` is bound to some URI, e.g. <http://www.furniture.de/2015/db>.

Namespaces are also used in programming languages for organizing variables, procedures and other identifiers into groups and for resolving name collisions. In programming languages without namespaces the programmers have to take special care to avoid naming conflicts. For example, in the PHP programming language prior to version 5.3 [4] there is no notion of namespace, and the namespaces have to be emulated to ensure that the names are unique, and this often results in long names like `Zend_Search_Lucene_Analysis_Analyzer`¹.

Other programming languages have the notion of namespaces built in from the very first versions. For example, the Java programming language [5]

¹ http://framework.zend.com/apidoc/1.7/Zend_Search_Lucene/Analysis/Zend_Search_Lucene_Analysis_Analyzer.html

uses packages to organize identifiers into namespaces. In Java, packages solve the problem of ambiguity. For example, in the standard Java API there are two classes with the name `Date`: one in the package `java.util` and another in the package `java.sql`. To be able to distinguish between them, the classes are referred by their *fully qualified name*: an unambiguous name that uniquely specifies the class by combining the package name with the class name. Thus, to refer to a particular `Date` class in Java `java.util.Date` or `java.sql.Date` should be used.

It is not always convenient to use the fully qualified name in the code to refer to some class from another package. Therefore in Java it is possible to *import* the class by using the import statement which associates a short name alias with its fully qualified name. For example, to refer to `java.sql.Date` it is possible to import it by using `import java.sql.Date` and then refer to it by the alias `Date` in the class [5].

Although there is no strict requirement to organize the classes into well defined groups, it is a good software design practice to put related objects into the same namespace and by doing this achieve better modularity. There are design principles that tell software engineers how to best organize the source code: classes in a well designed system should be grouped in such a way that namespaces exhibit low *coupling* and high *cohesion* [6]. Coupling describes the degree of dependence between namespaces, and low coupling means that the interaction between classes of different namespaces should be as low as possible. Cohesion, on the other hand, refers to the dependence within the classes of the same namespace, and the high cohesion principle says that the related classes should all be put together in the same namespace.

1.2 Namespaces in Mathematical Notation

Can namespaces be extended for identifiers in mathematical formulae?

Informally, a mathematical formula is a rule that shows the relationship between different variables. For example, $x_{1,2} = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$ is a formula for solving a quadratic equation $ax^2 + bx + c = 0$.

To give a more formal definition of formula, we first need to define a first-order language that contains primitive symbols such as (1) parentheses, brackets and other boundary symbols (2) *constants* (1, 2, 3, ...) and variables (x , y , ...) (3) *functions* (+, \times , ...) and (4) *predicates*, e.g. binary relation symbols (“=”, “<”, “ \geq ”, ...) [7].

In this language, *constants* are symbols with pre-defined meaning from some alphabet and variables are symbols that can be assigned a value from

this alphabet. Any symbol can be a variable, for example, x , y , \mathbf{w} , or it can be a symbol with subscripts, for example, x_1, x_2, \dots or even w_{slope} .

A *well-formed term* t (or just *term*) in this language is defined as

$$t \equiv c \mid x \mid f(t_1, t_2, \dots, t_n) ,$$

which means that the term t can be a constant, a variable or an n -ary function $f(t_1, t_2, \dots, t_n)$. An *n -ary function* is an function that takes n terms t_1, t_2, \dots, t_n and produces a new term t . An *n -ary predicate* (or an *n -ary relation symbol*) is typically a boolean-valued function that can be evaluated to **True** or **False** depending on the values it gets.

Then an *atomic well-formed formula* (or just *formula*) in this language is a n -ary predicate with n terms evaluated to **True** [7].

For example, $x_{1,2} = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$ is a formula, because it represents an equation that always holds true for a quadratic equation $ax^2 + bx + c = 0$. The equality symbol “=” is a predicate that shows the relationship between variables x_1, x_2 and variables a, b, c .

In logic we can use any symbol for variables without changing the meaning of the formula. For example, the energy-mass equivalence relation $E = mc^2$ can be written as $x = yz^2$ and it still will still hold true and remain a valid formula. Nevertheless, there are research communities in mathematics that have developed a special system of naming these variables, and this naming system is called *mathematical notation* [8]. For each symbol in a formula, the notation assigns it a precise semantic meaning. Therefore, because of the notation, in Physics it is more common to write $E = mc^2$ rather than $x = yz^2$, because the notation assigns unambiguous meaning to the symbols “ E ”, “ m ” and “ c ”, and the meaning of these symbols is recognized among physicists.

However, notations may conflict. For example, while it is common to use symbol “ E ” to denote “Energy” in Physics, it also is used in Probability and Statistics to denote “Expected Value”, or in Linear Algebra to denote “Elimination Matrix”. We can compare the conflict of notations with the name collision problem in namespaces, and try to address this problem by extending the notion of namespaces to mathematical notation.

Thus, let us define a *notation* \mathcal{N} as a set of pairs $\{(i, s)\}$, where i is a symbol or *identifier* and s is its semantic meaning or *definition*, such that for any pair $(i, s) \in \mathcal{N}$ there does not exist another pair $(i', s') \in \mathcal{N}$ with $i = i'$. Two notations \mathcal{N}_1 and \mathcal{N}_2 *conflict*, if there exists a pair $(i_1, s_1) \in \mathcal{N}_1$ and a pair $(i_2, s_2) \in \mathcal{N}_2$ such that $i_1 = i_2$ and $s_1 \neq s_2$.

Then we can define *namespace* as a named notation, i.e. a pair (n, \mathcal{N}) where \mathcal{N} is a notation and n is its *name*: a string that uniquely identifies the notation. For example, $(\text{“Physics”}, \mathcal{N}_{\text{physics}})$ can refer to the notation used in Physics. For convenience, in this work we can use the Java syntax to refer to specific entries of a namespace. If (n, \mathcal{N}) is a namespace and i is an identifier such that $(i, s) \in \mathcal{N}$ for some s , then $\text{“}n.i\text{”}$ is a *fully qualified name* of the identifier i that relates i to the definition s . For example, given a namespace $(\text{“Physics”}, \{(E, \text{“energy”}), (m, \text{“mass”}), (c, \text{“speed of light”})\})$, “Physics.E” refers to “energy” – the definition of E in the namespace “Physics” .

Analogously to namespaces in Computer Science, formally a mathematical namespace can contain any set of identifier-definition pairs that satisfies the definition of the namespace, but typically namespaces of mathematical notation exhibit the same properties as well-designed Java packages: they have low coupling and high cohesion, meaning that all definitions in a namespace come from the same area of mathematical knowledge and the definitions from different namespace do not intersect heavily.

However, mathematical notation does not exist in isolation and it is usually observed indirectly by its usage in documents. Therefore we need to introduce a document-centric view on mathematical namespaces: suppose we have a collection of n documents $\mathcal{D} = \{d_1, d_2, \dots, d_n\}$ and a set of K namespaces $\{(n_1, \mathcal{N}_1), (n_2, \mathcal{N}_2), \dots, (n_K, \mathcal{N}_K)\}$. A document d_j can use a namespace (n_k, \mathcal{N}_k) by *importing* identifiers from it. To import an identifier, the document uses an import statement where the identifier i is referred by its fully qualified name. For example, a document $\text{“Energy-mass equivalence”}$ would import “Physics.E” , “Physics.m” , and “Physics.c” , and then these identifiers can be used in formulae of this document unambiguously.

TODO: Continue, re-introduce low coupling and high cohesion in terms of document collection. Then a namespace exhibits low coupling if it used in a small subset of documents $\mathcal{C} \subset \mathcal{D}$.

However, in real-life scientific document there are no import statements in the document preamble, and they contain only natural language texts along with some mathematical formulae. Yet we may still assume that these import exists, but they are implicit, i.e. they are latent and cannot be observed directly. Additionally, the namespaces themselves are also not observed.

How the identifier namespaces can be discovered? Typically in mathematical texts, when an identifier is first introduced, its definition is given in the natural language description that surrounds the formula. This description can be extracted and used to assign the meaning to the identifiers.

Once identifier definitions are extracted, a document can be represented as a set of identifier-definition pairs, and these pairs can be used to discover the namespaces.

In this work we study the problem of namespace discovery and the goal of this work is to **automatically discover a set of identifier namespaces given a collection of documents**.

In the next section we discuss how this problem can be addressed.

1.3 Discovery of Identifier Namespaces

How we can construct a set of namespaces given a collection of documents? It can be done by manually assigning each identifier/definition pair to some namespace. But this is expensive and very time consuming. Therefore in this work we suggest a different approach: use Machine Learning techniques for discovering namespaces automatically.

We illustrate this idea by first drawing an analogy between identifier namespaces and namespaces in programming languages. In a well-designed application, we can distinguish between two types of application packages [9]:

- *type 1*: domain-specific packages that deal with one particular concept or domain area, and
- *type 2*: packages that use other packages of the first type

For example, for an application `org.company.app` there can be several domain-specific packages: `org.company.app.domain.user` with classes related to users, `org.company.app.domain.account` with classes related to user accounts, and a system-related package `org.company.app.tools.auth` that deals with authentication and authorization. Then we also have a package `org.company.app.web.manage`, which belongs to the type 2: it handles web requests while relying on classes from `user` and `account` to implement the business logic and on `auth` for making sure the requests are authorized.

We can observe that the type 1 packages are mostly self-contained and not highly coupled between each other, but type 2 packages mostly use other packages of type 1: they depend on them.

This idea can be extended on the document-centric view on identifier namespaces. Each document can be seen as a class that imports identifiers defined in other documents. Then the documents can be grouped together based on the identifiers and the definitions they have, and then among these groups there are some groups of documents that are of *type 1* and the rest

are of *type 2*. The type 1 document groups contain information about closely related concepts, and they are very homogenous (they have high cohesion), and they are also not highly coupled with other document groups. By using the import metaphor, we can say that the type 1 document groups import only from few closely related namespaces. Other documents are of *type 2* and they do not have low coupling: they are not very homogenous and they import from several namespaces

With this intuition we can refer to *type 1* document groups as *namespace defining* groups. These groups can be seen as “type 1” packages: they define namespaces that are used by other *type 2* document groups. Once the namespace defining groups are found, we can learn the namespace of these document.

Thus we need to find groups of homogenous documents given a collection, and this is exactly what Cluster Analysis methods do.

In the next section we will argue why we can use traditional document clustering techniques and what are the characteristics that texts and identifiers have in common.

1.4 Namespace Discovery by Cluster Analysis

We believe that cluster analysis techniques developed for text documents should also work for cases when documents are represented by identifiers they contain.

First, let us consider the characteristics of text data. A natural language typically contains many different words. If \mathcal{V} is a set of all possible words, then usually $|\mathcal{V}| \approx 10^5$, but each individual document may contain only a small portion of these words [10]. Numbers of words across different documents may vary a lot, and the word distribution usually follows some power law distribution, e.g. Zipf’s law [10]. Power laws are commonplace [11], so it is safe to assume that number of identifiers across documents are also distributed according to some power law. Intuitively, it is true because there are many identifiers like x or n that are very frequent and used in all mathematical articles, while there are some quite specific identifiers like ℓ_∞ that do not occur very often. We verify this assumption in the implementation chapter (see Definition Extraction, section 4.2).

Additionally, natural languages suffer from lexical problems of variability and ambiguity, and the two main problems are synonymy and polysemy [12] [13]:

- two words are *synonymous* if they have the same meaning (for example, “word” and “term” are synonyms),
- a word is *polysemous* if it can have multiple meanings (for example, “trunk” can refer to a part of elephant or a part of a car).

We can note that identifiers have the same problems. For example, in Information Theory, the Shannon Entropy is usually denoted by “ H ”, but sometimes it is also denoted by “ I ” or by “ S ”, thus these identifiers may be seen as synonyms. Also, “ E ” can stand both for “Energy” and “Expected value”, so “ E ” is polysemous.

These problems have been studied in Information Retrieval and Natural Language Processing literature. One possible solution for the polysemy problem is *Word Sense Disambiguation* [14]: either replace a word with its sense [15] or append the sense to the word, for example if the polysemous word is “bank” with meaning “financial institution”, then we replace it with “bank_finance”. The same idea can be used for identifiers, for example if we have an identifier “ E ” which is defined as “energy”, then “ E ” can be replaced with “ E_{energy} ”.

Thus we see that text representation of documents and identifier representation of documents have many similarities and therefore we can apply the set of techniques developed for text representation for clustering documents based on identifiers.

For document clustering, documents are usually represented using Vector Space Models [16] [17]. Likewise, we can introduce “Identifier Space Model” analogously to Vector Space Models.

1.5 Thesis Outline

This work is organized as follows: In chapter 2 we discuss how extract definitions for identifiers in texts with mathematical formulae; in chapter 3 we review the vector space model, cluster analysis methods and how matrix factorization techniques can be used to extract semantic information from the corpus. Finally, we describe how the techniques are implemented (chapter 4) and evaluated (chapter 5).

2 Mathematical Definition Extraction

Mathematical expressions are hard to understand without the natural language description, therefore we want to extract identifiers from mathematical expressions and then find their definitions from the surrounding text.

For example, given the sentence “The relation between energy and mass is described by the mass-energy equivalence formula $E = mc^2$, where E is energy, m is mass and c is the speed of light” the goal is to extract the following identifier-definition relations: $(E, \text{“energy”})$, $(m, \text{“mass”})$ and $(c, \text{“the speed of light”})$.

Consider another example: “Let e be the base of natural logarithm”. We would like to extract $(e, \text{“the base of natural logarithm”})$.

Formally, a phrase that defines a mathematical expression consists of three parts [18]:

- *definiendum* is the term to be defined: it is a mathematical expression or an identifier;
- *definiens* is the definition itself: it is the word or phrase that defines the definiendum in a definition;
- *definitior* is a relator verb that links definiendum and definiens.

In this work we are interested in the first two parts: *definiendum* and *definiens*. Thus we define a *relation* as a pair $(\text{definiendum}, \text{definiens})$. For example, $(E, \text{“energy”})$ is a relation where E is a definiendum, and “energy” is a definiens.

In this chapter we will discuss how the relations can be discovered automatically. It is organized as follows: then discuss the Math-Aware POS Tagging procedure in section 2.1 and finally review the extraction methods in section 2.2 and briefly discuss how the quality of extracted identifiers is evaluated in section ??.

2.1 Math-aware POS tagging

Part-of-Speech Tagging (POS Tagging) is a typical Natural Language Processing task which assigns a POS Tag to each word in a given text [14]. While the POS Tagging task is mainly a tool for text processing, it can also be applicable to scientific documents with mathematical expressions, and can be adjusted to dealing with formulae [19] [20].

A *POS tag* is an abbreviation that corresponds to some part of speech. Penn Treebank POS Scheme [21] is a commonly used POS tagging scheme which defines a set of part-of-speech tags for annotating English words. For example, JJ is an adjective (“big”), RB as in adverb, DT is a determiner (“a”, “the”), NN is a noun (“corpus”) and SYM is used for symbols (“>”, “=”).

However the Penn Treebank scheme does not have special tags for mathematics, but it is flexible enough and can be extended to include additional tags. For example, we can include a math-related tag MATH. Usually it is done by first applying traditional POS taggers (like Stanford CoreNLP [22]), and then refining the results by re-tagging math-related tokens of text as MATH [19].

For example, consider the following sentence: “The relation between energy and mass is described by the mass-energy equivalence formula $E = mc^2$, where E is energy, m is mass and c is the speed of light”. In this case we will assign the MATH tag to “ $E = mc^2$ ”, “ E ”, “ m ” and “ c ”

However we can note that for finding identifier-definition relations the MATH tag alone is not sufficient: we need to distinguish between complex mathematical expressions and stand-alone identifiers - mathematical expressions that contain only one symbol: the identifier. For the example above we would like to be able to distinguish the expression “ $E = mc^2$ ” from identifier tokens “ E ”, “ m ” and “ c ”. Thus we extend the Penn Treebank scheme even more and introduce an additional tag ID to denote stand-alone identifiers.

Thus, in the example above “ $E = mc^2$ ” will be assigned the MATH tag and “ E ”, “ m ” and “ c ” will be annotated with ID.

In the next section we discuss how this can be used to find identifier-definition relations.

2.2 Extraction Methods

There are several ways of extracting the identifier-definition relations. Here we will review the following:

- Nearest Noun
- Pattern Matching
- Machine-Learning based methods
- Probabilistic methods

2.2.1 Nearest Noun Method

The Nearest Noun [23] [24] is the simplest definition extraction method. It assumes that the definition is a combination of ad It finds definitions by looking for combinations of adjectives and nouns (sometimes preceded by determiners) in the text before the identifier.

I.e. if we see a token annotated with ID, and then a sequence consisting only of adjectives (JJ), nouns (NN, NNS) and determiners (DET), then we say that this sequence is the definition for the identifier.

For example, given the sentence “In other words, the bijection σ normalizes G in ...” we will extract relation $(\sigma, \text{"bijection"})$.

2.2.2 Pattern Matching Methods

The Pattern Matching method [25] is an extension of the Nearest Noun method: In Nearest Noun, we are looking for one specific pattern where identifier is followed by the definition, but we can define several such patterns and use them to extract definitions.

For example, we can define the following patterns:

- IDE DEF
- DEF IDE
- let|set IDE denote|denotes|be DEF
- DEF is|are denoted|defined|given as|by IDE
- IDE denotes|denote|stand|stands as|by DEF
- IDE is|are DEF
- DEF is|are IDE
- and many others

In this method IDE and DEF are placeholders that are assigned a value when the pattern is matched against some subsequence of tokens. IDE and DEF need to satisfy certain criteria in order to be successfully matched: like in the Nearest Noun method we assume that IDE is some token annotated with ID and DEF is a phrase containing adjective (JJ), nouns (NN) and determiners (DET). Note that the first pattern corresponds to the Nearest Noun pattern.

The patterns above are combined from two sources: one is extracted from a guide to writing mathematical papers in English ([26]) by **TODO**, and another is extracted from Graphs and Combinatorics papers from Springer by **TODO**.

The pattern matching method is often used as the baseline method for identifier-definition extraction methods [18] [27] [20].

2.2.3 Machine Learning Based Methods

The definition extraction problem can be formulated as a binary classification problem: given a pair (identifier, candidate-definition), does this pair correspond to real identifier-definition relation?

To do this we find all candidate pairs: identifiers are tokens annotated with ID, and candidate definitions are nouns and noun phrases from the same sentence as the definition.

Once the candidate pairs are found, we extract the following features [27] [24]:

- boolean features for each of the patterns from section 2.2.2 indicating if the pattern is matched,
- indicator if there’s a colon or comma between candidate and identifier,
- indicator if there’s another math expression between candidate and identifier,
- indicator if candidate is inside parentheses and identifier is outside,
- distance (in words) between the identifier and the candidate,
- the position of candidate relative to identifier,
- text and POS tag of one/two/three preceding and following tokens around the candidate,
- text of the first verb between candidate and identifier,
- many others.

Once the features are extracted, a binary classifier can be trained to predict if an unseen candidate pair is a relation or not. For this task the popular choices of classifiers are Support Vector Machine classifier with linear kernel [27] [24] and Conditional Random Fields [27], but, in principle, any other binary classifier can be applied as well.

2.2.4 Probabilistic Approaches

In the Mathematical Language Processing approach [20] a definition for an identifier is extracted by ranking candidate definitions by the probability of defining the identifier, and only the most probable candidates are retained.

The main idea of this approach is that the definitions occur very closely to identifiers in sentences, and the closeness can be used to model the probability distribution over candidate definitions.

The candidates are ranked by the following formula:

$$R(n, \Delta, t, d) = \frac{\alpha R_{\sigma_d}(\Delta) + \beta R_{\sigma_s}(n) + \gamma \text{tf}(t, s)}{\alpha + \beta + \gamma}$$

where α, β, γ are weighting parameters.

Finally, for weights α, β, γ the following parameters were chosen in [20]: $\alpha = \beta = 1$ and $\gamma = 0.1$.

3 Namespaces as Document Clusters

In this chapter, we discuss how the process of namespace discovery can be automated.

First, in section ?? we describe identifier namespaces and we compare the namespace discovery with cluster analysis techniques applied to textual data and see how clustering algorithms can be useful. Next, in section 3.1 we review the Vector Space Model (VSM): the traditional way of representing a collection of documents as vectors, and then in section ?? we introduce the Identifier VSM - which is a way to represent identifier-definition relations in the vector space. Finally we go over common similarity and distance functions that are useful for document clustering in section 3.2 and discuss how similarity search can be made faster by using inverted index ??.

3.1 Vector Space Model

Vector Space Model is a statistical model for representing documents in some vector space. It is an Information Retrieval model [10], but it is also used for various Text Mining tasks such as Document Classification [28] and Document Clustering [16] [17].

In Vector Space Model we make two assumptions about the data: (1) *Bag of Words assumption*: the order of words is not important, only word counts; (2) *Independence assumption*: we treat all words as independent. Both assumptions are quite strong, but nonetheless this method often gives good results.

Let $\mathcal{V} = \{t_1, t_2, \dots, t_m\}$ be a set of n terms. Then documents can be represented as m -vectors $\mathbf{d}_i = (w_1, w_2, \dots, w_m)$, where w_j is the weight of term t_j in the document \mathbf{d}_i , and the document collection can be represented by a *term-document matrix* D , where columns of D are document vectors $\mathbf{d}_1, \mathbf{d}_2, \dots, \mathbf{d}_n$ and rows of D are indexed by terms t_1, t_2, \dots, t_m (see fig. 1).

There are following term weighting schemes [10]:

- binary: 1 if a term is present, 0 otherwise;
- term frequency (TF): number of occurrences of the term in a document;
- document frequency (DF): number of documents containing the term
- TF-IDF: combination of TF and inverse DF.

Term Frequency (TF) weights terms by local frequency in the document. That is, the term is weighed by how many times it occurs in the document. Sometimes a term is used too often in a document, and we want

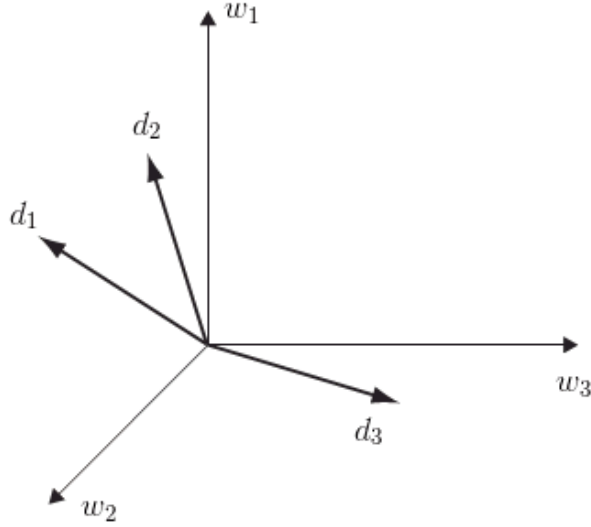


Fig. 1: **TODO redraw in vector** Documents $\mathbf{d}_1, \mathbf{d}_2, \mathbf{d}_3$ in a document space with dimensions t_1, t_2, t_3

to reduce its influence, and this is typically done by applying some sublinear transformation to TF, for instance, a square root or a logarithms.

Document Frequency (DF) weights terms by their global frequency in the collection, which is the number of documents that contain the token. But more often we are interested in domain specific words than in neutral words, and these domain specific words tend to occur less frequently and they usually have more discriminative power: that is, they are better in telling one document apart from another. So we use **Inverse Document Frequency (IDF)** to give more weight to rare words rather than to frequent words.

A good weighting system gives the best performance when it assigns more weights to terms with high TF, but low DF [29]. This can be achieved by combining both TF and IDF schemes. Usually a sublinear TF is used to avoid the dominating effect of words that occur too frequently. As the result, terms appearing too rarely or too frequently are ranked low. The TF and IDF are combined together in **TF-IDF** weighting scheme:

$$\text{tf-idf}(t, \mathbf{d}) = (1 + \log \text{tf}(t, \mathbf{d})) \cdot \log \frac{n}{\text{df}(t)},$$

where $\text{tf}(t, \mathbf{d})$ is term frequency of term t in document \mathbf{d} and $\text{df}(t)$ is the document frequency of term t in the document collection.

The Vector Space Model can be adjusted to represent documents by identifiers they contain instead of words. To do that we replace the vocabulary \mathcal{V} with a set of identifiers $\mathcal{I} = \{i_1, i_2, \dots, i_m\}$, but documents are still represented as m -vectors $\mathbf{d}_j = (w_1, w_2, \dots, w_m)$, where w_k is a weight of identifier i_k in the document \mathbf{d}_j . Likewise, we can define an identifier-document matrix D as a matrix where columns are document vectors and rows are indexed by the identifiers.

Identifiers, as terms, suffer from the problems of synonymy and polysemy, and we solve this problem by extracting definitions for all the identifiers. There are several ways of incorporating the extracted definitions into the model:

- do not include definition information at all, use only identifiers;
- use “weak” identifier-definition association: include identifiers and definitions as separate dimensions;
- use “strong” association: append definition to identifier.

To illustrate how it is done, consider three relations (E , “energy”), (m , “mass”) and (c , “speed of light”), and three documents $d_1 = \{E, m, c\}$, $d_2 = \{m, c\}$, $d_3 = \{E\}$. Then

- no definitions: dimensions are (E, m, c) and the identifier-document matrix is

$$D = \left[\begin{array}{c|ccc} & d_1 & d_2 & d_3 \\ \hline E & 1 & 0 & 1 \\ m & 1 & 1 & 0 \\ c & 1 & 1 & 0 \end{array} \right];$$

- “weak” association: dimensions are $(E, m, c, \text{energy}, \text{mass}, \text{speed of light})$, and the matrix is

$$D = \left[\begin{array}{c|ccc} & d_1 & d_2 & d_3 \\ \hline E & 1 & 0 & 1 \\ m & 1 & 1 & 0 \\ c & 1 & 1 & 0 \\ \text{energy} & 1 & 0 & 1 \\ \text{mass} & 1 & 1 & 0 \\ \text{speed of light} & 1 & 1 & 0 \end{array} \right];$$

- “strong” association: dimensions are (E_energy , m_mass , c_speed of light), and the matrix is

$$D = \left[\begin{array}{c|ccc} & d_1 & d_2 & d_3 \\ \hline E_energy & 1 & 0 & 1 \\ m_mass & 1 & 1 & 0 \\ c_speed \text{ of light} & 1 & 1 & 0 \end{array} \right].$$

3.2 Similarity Measures and Distances

Once the documents are represented in some vector space, we need to define how to compare these documents to each other. There are two ways of doing this: using a similarity function that tells how similar two objects are (the higher values, the more similar the objects), or using a distance function, sometimes called “dissimilarity function”, which is the opposite of similarity (the higher the values, the less similar the objects).

We consider Euclidean distance, inner product, cosine similarity and Jac-card coefficient.

3.2.1 Euclidean Distance

The Euclidean distance function is the most commonly used distance function in vector spaces. Euclidean distance corresponds to the geometric distance between two data points in the vector space. For example, if we have two points \mathbf{x} and \mathbf{z} , then the Euclidean distance is the length of the line that connects these two points. The square of the Euclidean distance is defined as

$$\|\mathbf{x} - \mathbf{z}\|^2 = (\mathbf{x} - \mathbf{z})^T (\mathbf{x} - \mathbf{z}) = \sum_i (x_i - z_i)^2.$$

This distance is useful for low-dimensional data, but it does not always work well in high dimensions, especially with sparse vector such as document vectors [30].

3.2.2 Inner product

The inner product between two vectors can be used as a similarity function: the more similar two vectors are, the larger is their inner product. Geometrically the inner product between two vectors \mathbf{x} and \mathbf{z} is defined as

$\mathbf{x}^T \mathbf{z} = \|\mathbf{x}\| \|\mathbf{z}\| \cos \theta$ where θ is the angle between vectors \mathbf{x} and \mathbf{z} . In Linear Algebra, however, the inner product is defined as a sum of element-wise products of two vectors: given two vectors \mathbf{x} and \mathbf{z} , the inner product is $\mathbf{x}^T \mathbf{z} = \sum_{i=1}^n x_i z_i$ where x_i and z_i are i th elements of \mathbf{x} and \mathbf{z} , respectively. The geometric and algebraic definitions are equivalent [31].

3.2.3 Cosine Similarity

Inner product is sensitive to the length of vectors, and thus it may make sense to consider only the angle between them: the angle does not depend on the magnitude, but it is still a very good indicator of vectors being similar or not.

The angle between two vectors can be calculated from the geometric definition of inner product: $\mathbf{x}^T \mathbf{z} = \|\mathbf{x}\| \|\mathbf{z}\| \cos \theta$. By rearranging the terms we get $\cos \theta = \mathbf{x}^T \mathbf{z} / (\|\mathbf{x}\| \|\mathbf{z}\|)$.

We do not need the angle itself and can use the cosine directly [10]. Thus can define *cosine similarity* between two documents \mathbf{d}_1 and \mathbf{d}_2 as

$$\text{cosine}(\mathbf{d}_1, \mathbf{d}_2) = \frac{\mathbf{d}_1^T \mathbf{d}_2}{\|\mathbf{d}_1\| \|\mathbf{d}_2\|}.$$

If the documents have unit lengths, then cosine similarity is the same as dot product: $\text{cosine}(\mathbf{d}_1, \mathbf{d}_2) = \mathbf{d}_1^T \mathbf{d}_2$.

The cosine similarity can be converted to a distance function. The maximal possible cosine is 1 for two identical documents. Therefore we can define *cosine distance* between two vectors \mathbf{d}_1 and \mathbf{d}_2 as $d_c(\mathbf{d}_1, \mathbf{d}_2) = 1 - \text{cosine}(\mathbf{d}_1, \mathbf{d}_2)$. The cosine distance is not a proper metric [32], but it is nonetheless useful.

The cosine distance and the Euclidean distance are connected [32]. For two unit-normalized vectors \mathbf{d}_1 and \mathbf{d}_2 the Euclidean distance between them is $\|\mathbf{d}_1 - \mathbf{d}_2\|^2 = 2 - 2 \mathbf{d}_1^T \mathbf{d}_2 = 2 d_c(\mathbf{d}_1, \mathbf{d}_2)$. Thus we can use Euclidean distance on unit-normalized vectors and interpret it as cosine distance.

3.2.4 Jaccard Coefficient

Finally, the Jaccard Coefficient is a function that compares how similar two sets are. Given two sets A and B , it is computed as $J(A, B) = \frac{|A \cap B|}{|A \cup B|}$. It is also applicable to document vectors with binary weights, and it can be defined as $J(\mathbf{d}_1, \mathbf{d}_2) = \frac{\mathbf{d}_1^T \mathbf{d}_2}{\|\mathbf{d}_1\|^2 + \|\mathbf{d}_2\|^2 - \mathbf{d}_1^T \mathbf{d}_2}$ [10].

3.3 Document Clustering Techniques

Cluster analysis is a set of techniques for organizing collection of items into coherent groups. In Text Mining clustering is often used for finding topics in a collection of document [17]. In Information Retrieval clustering is used to assist the users and group retrieved results into clusters [33].

There are several types of clustering algorithms: hierarchical (agglomerative and divisive), partitioning, density-based, and others.

3.3.1 Agglomerative clustering

The general idea of agglomerative clustering algorithms is to start with each document being its own cluster and iteratively merge clusters based on best pair-wise cluster similarity.

Thus, a typical agglomerative clustering algorithms consists of the following steps:

1. let each document be a cluster on its own
2. compute similarity between all pairs of clusters and store the results in a similarity matrix
3. merge two most similar clusters
4. update the similarity matrix
5. repeat until everything belongs to the same cluster

These algorithms differ only in the way they calculate similarity between clusters. It can be **Single Linkage**, when the clusters are merged based on the closest pair; **Complete Linkage**, when the clusters are merged based on the worst-case similarity – the similarity between the most distant objects on the clusters; **Group-Average Linkage**, based on the average pair-wise similarity between all objects in the clusters; and **Ward's Method** when the clusters to merge are chosen to minimize the within-cluster error between each object and its centroid is minimized [16].

Among these algorithms only Single Linkage is computationally feasible for large data sets, but it doesn't give good results compared to other agglomerative clustering algorithms. Additionally, these algorithms are not always good for document clustering because they tend to make mistakes at early iterations that are impossible to correct afterwards [34].

3.3.2 K-Means

Unlike agglomerative clustering algorithms, K-Means is an iterative algorithm, which means that it can correct the mistakes made at earlier iterations. Lloyd’s algorithm is the most popular way of implementing K-Means [35]: given a desired number of clusters K , it iteratively improves the Euclidean distance between each data point and the centroid, closest to it.

Let $\mathcal{D} = \{\mathbf{d}_1, \mathbf{d}_2, \dots, \mathbf{d}_n\}$ be the document collection, where documents \mathbf{d}_i are represented as a document vector space \mathbb{R}^m and K is the desired number of clusters. Then we define k cluster centroids $\boldsymbol{\mu}_j$ that are also in the same document vector space \mathbb{R}^m . Additionally for each document \mathbf{d}_i we maintain the assignment variable $c_i \in \{1, 2, \dots, k\}$, which specifies to what cluster centroid $\boldsymbol{\mu}_1, \boldsymbol{\mu}_2, \dots, \boldsymbol{\mu}_k$ the document \mathbf{d}_i belongs.

The algorithm consists of three steps: (1) seed selection step, where each $\boldsymbol{\mu}_j$ is randomly assigned some value, (2) cluster assignment step, where we iterate over all document vectors \mathbf{d}_i and find its closest centroid, and (3) move centroids step, where the centroids are re-calculated. Steps (2) and (3) are repeated until the algorithm converges. The pseudocode for K -Means is presented in the listing 1.

Algorithm 1 Lloyd’s algorithm for K -Means

```

function K-MEANS(no. clusters  $k$ , documents  $\mathcal{D}$ )
  for  $j \leftarrow 1 \dots k$  do                                     ▷ random seed selection
     $\boldsymbol{\mu}_j \leftarrow \text{random } \mathbf{d} \in \mathcal{D}$ 
  while not converged do
    for each  $\mathbf{d}_i \in \mathcal{D}$  do                                     ▷ cluster assignment step
       $c_i \leftarrow \arg \min_j \|\mathbf{d}_i - \boldsymbol{\mu}_j\|^2$ 
    for  $j \leftarrow 1 \dots k$  do                                     ▷ move centroids step
       $\mathcal{C}_j \leftarrow \{\mathbf{d}_i \text{ s.t. } c_i = j\}$ 
       $\boldsymbol{\mu}_j \leftarrow \frac{1}{|\mathcal{C}_j|} \sum_{\mathbf{d}_i \in \mathcal{C}_j} \mathbf{d}_i$ 
  return ( $c_1, c_2, \dots, c_n$ )

```

Usually, K -Means shows very good results for document clustering, and in several studies it (or its variations) shows the best performance [34] [36].

However for large document collections Lloyd’s classical K -Means takes a lot of time to converge. The problem is caused by the fact that it goes through the entire collection many times. Mini-Batch K -Means [37] uses Mini-Batch Gradient Descent method, which is a different optimization technique that converges faster.

K -Means uses Euclidean distance, which does not always behave well in high-dimensional sparse vector spaces like document vector spaces. However, as discussed in section 3.2, if document vectors are normalized, the Euclidean distance and cosine distance are related, and therefore Euclidean K -means is the same as “Cosine Distance” K -Means.

K -Means is the most popular clustering algorithms and there are many extensions. For example, Bisecting K -Means [34] is a combination of partitioning and hierarchical (divisive) algorithms. It’s a variant of K -Means that gradually splits the document space in halves until the desired number of clusters is obtained. Bisecting K -Means can achieve good performance while giving the user additional insight into the clustering process. Additionally, in the results it produces clusters of comparable sizes.

The algorithm is simple: (1) start with a single cluster; (2) choose a cluster to split (for example, the largest one); (3) apply traditional K -Means to this cluster with $K = 2$ to split it; (4) repeat until have desired number of clusters.

Scatter/Gather is another popular variation of K -means, initially used for clustering documents for Information Retrieval systems [33]. This variation includes: special smart seed selection procedure and several cluster refinement operations. Additionally, in Scatter/Gather cluster centroids are concatenations of all terms in the cluster documents, not a mean value; finally, the cosine similarity is used instead of Euclidean distance.

There are two cluster refinement operations: split and join. The split operation selects the clusters that are not coherent enough and clusters them again using K -Means. The coherence is measured via *self-similarity* of a cluster, which is the mean similarity of all documents in the cluster to its centroid, or the mean pair-wise similarity between all documents of the cluster.

The join operation merges the clusters that are very similar to each other. The similarity is measured by computing “typical” terms for each cluster (usually the most frequent terms of the centroid) and examining which clusters have significant overlaps between their typical terms.

However, when there are many documents, the centroids tend to contain a lot of words, which leads to a significant slowdown. To solve this problem, some terms of the centroid can be truncated. There are several possible ways of truncating the terms: for example, we can keep only the top c terms, or remove the least frequent words such that at least 90% (or 95%) of the original vector norm is retained [38].

3.3.3 DBSCAN

DBSCAN is a density-based clustering algorithm that can discover clusters of complex shapes based on the density of data points [39].

The *density* associated with a data point is obtained by counting the number of points in a region of radius ε around the point, where ε is defined by the user. If a point has a density of at least some user defined threshold **MinPts**, then it is considered a *core point*. The clusters are formed around these core points, and if two core points are within the radius ε , then they belong to the same cluster. If a point is not a core point itself, but it belongs to the neighborhood of some core point, then it is a *border point*. But if a point is not a core point and it is not in the neighborhood of any other core point, then it does not belong to any cluster and it is considered *noise*.

DBSCAN works as follows: it selects an arbitrary data point p , and then finds all other points in ε -neighborhood of p . If there are more than **MinPts** points around p , then it is a core point, and it is considered a cluster. Then the process is repeated for all points in the neighborhood, and they all are assigned to the same cluster, as p . If p is not a core point, but it has a core point in its neighborhood, then it's a border point and it is assigned to the same cluster and the core point. But if it is a noise point, then it is marked as noise or discarded (see listing 2).

The details of implementation of REGION-QUERY are not specified, and it can be implemented differently. For example, it can use Inverse Index to make the similarity search faster [10] [30].

The DBSCAN algorithm uses the Euclidean distance, but can be adapted to use any other distance or similarity function. For example, to modify the algorithm to use the cosine similarity (or any other similarity function) the REGION-QUERY has to be modified to return $\{x : \text{similarity}(x, p) \geq \varepsilon\}$.

Shared Nearest Neighbors Similarity (SNN Similarity) [30] is a special similarity function that is particularly useful for high-dimensional spaces, it works well with DBSCAN, and it is applicable to document clustering and topic discovery [40].

SNN Similarity is specified in terms of the K nearest neighbors. Let $\text{NN}_{K, \text{sim}}(p)$ be a function that returns top K closest points of p according to some similarity function **sim**. Then the SNN similarity function is defined as

$$\text{snn}(p, q) = |\text{NN}_{K, \text{sim}}(p) \cup \text{NN}_{K, \text{sim}}(q)|.$$

The extension of DBSCAN that uses the SNN Similarity is called SSN Clustering algorithm. The user needs to specify the SSN similarity function

Algorithm 2 DBSCAN

```

function DBSCAN(database  $\mathcal{D}$ , radius  $\varepsilon$ , MinPts)
  result  $\leftarrow \emptyset$ 
  for all  $p \in \mathcal{D}$  do
    if  $p$  is visited then
      continue
    mark  $p$  as visited
     $\mathcal{N} \leftarrow \text{REGION-QUERY}(p, \varepsilon)$   $\triangleright \mathcal{N}$  is the neighborhood of  $p$ 
    if  $|\mathcal{N}| < \text{MinPts}$  then
      mark  $p$  as NOISE
    else
       $\mathcal{C} \leftarrow \text{EXPAND-CLUSTER}(p, \mathcal{N}, \varepsilon, \text{MinPts})$ 
      result  $\leftarrow \text{result} \cup \{\mathcal{C}\}$ 
  return result

function EXPAND-CLUSTER(point  $p$ , neighborhood  $\mathcal{N}$ , radius  $\varepsilon$ , MinPts)
   $\mathcal{C} \leftarrow \{p\}$ 
  for all  $x \in \mathcal{N}$  do
    if  $x$  is visited then
      continue
    mark  $x$  as visited
     $\mathcal{N}_x \leftarrow \text{REGION-QUERY}(x, \varepsilon)$   $\triangleright \mathcal{N}_x$  is the neighborhood of  $x$ 
    if  $|\mathcal{N}_x| \geq \text{MinPts}$  then
       $\mathcal{N} \leftarrow \mathcal{N} \cup \mathcal{N}_x$ 
   $\mathcal{C} \leftarrow \mathcal{C} \cup \{x\}$ 
  return  $\mathcal{C}$ 

function REGION-QUERY(point  $p$ , radius  $\varepsilon$ )
  return  $\{x : \|x - p\| \leq \varepsilon\}$   $\triangleright$  all points within distance  $\varepsilon$  from  $p$ 

```

by setting parameter K and choosing the base similarity function $\text{sim}(\cdot, \cdot)$ (typically Cosine, Jaccard or Euclidean). The algorithm itself has the same parameters as DBSCAN: radius ε (such that $\varepsilon < K$) and the core points density threshold MinPts . The REGION-QUERY function is modified to return $\{q : \text{snn}(p, q) \geq \varepsilon\}$. For pseudocode, see the listing 3.

Algorithm 3 SNN Clustering Algorithm

```

function SNN-CLUSTER(database  $\mathcal{D}$ ,  $K$ , similarity function  $\text{sim}$ , radius  $\varepsilon$ ,  $\text{MinPts}$ )
  for all  $p \in \mathcal{D}$  do                                      $\triangleright$  Pre-compute the  $K$ NN lists
     $\text{NN}[p] \leftarrow \text{NN}_{K, \text{sim}}(p)$ 
  for all  $(p, q) \in (\mathcal{D} \times \mathcal{D})$  do                        $\triangleright$  Pre-compute the SNN similarity matrix
     $A[p, q] \leftarrow |\text{NN}[p] \cup \text{NN}[q]|$ 
  return DBSCAN( $A, \varepsilon, \text{MinPts}$ )

```

The algorithm’s running time complexity is $O(n^2)$ time, where $n = |\mathcal{D}|$, but it can be sped up by using the Inverted Index [30].

3.4 Latent Semantic Analysis

In section 1.4 we have discussed the lexical variability and ambiguity problems in natural language: synonymy and polysemy. We can treat these problems as “statistical noise” and apply dimensionality reduction techniques to find the optimal dimensionality for the data and thus reduce the amount of noise there. This technique is called Latent Semantic Analysis (LSA) [41] or Latent Semantic Indexing [12], and it is often used for document clustering [17] [42].

There are three major steps in Latent Semantic Analysis [43]: (1) preprocess documents; (2) construct a term-document matrix D using the Vector Space Model; (3) de-noise D by reducing its dimensionality with Singular Value Decomposition (SVD).

The first two steps are the same as for traditional Vector Space Models and in the result we obtain a term-document matrix D . If D has rank r , then the SVD of D is $D = U\Sigma V^T$, where U is an $m \times r$ orthogonal matrix; Σ is a diagonal $r \times r$ matrix with singular values ordered by their magnitude; and V is an $n \times r$ orthogonal matrix.

The dimensionality reduction is done by finding the best k -rank approximation of D , which is obtained by keeping only the first k singular values of Σ and setting the rest to 0. Typically, not only Σ is truncated, but also U and V , and therefore, the k -rank approximation of D using SVD is written

as $D \approx D_k = U_k \Sigma_k V_k^T$ where U_k is an $m \times k$ matrix with first k columns of U , Σ_k is an $k \times k$ diagonal matrix with singular values, and V_k is an $n \times k$ matrix with first k columns of V . This decomposition is called *rank-reduced* SVD and when applied to text data it reveals the “true” latent semantic space. The parameter k corresponds to the number of “latent concepts” in the data. The idea of LSA is very nicely illustrated by examples in [12] and [41].

LSA can be used for clustering as well, and this is usually done by first transforming the document space to the LSA space and then doing applying transitional cluster analysis techniques there [38]. Once D is decomposed as $D \approx U_k \Sigma_k V_k^T$ it is enough to keep only the low dimensional representation $\hat{D} = V_k \Sigma_k$: the calculation of inner product between two documents i and j in the reduced semantic space corresponds to computing the inner product between i th and j th rows of \hat{D} [12]. Since the Euclidean distance is defined in terms of inner product, it can also be used directly on the rows of \hat{D} .

Therefore, a generic LSA-based clustering algorithm consists of the following steps:

1. Build a term-document matrix D from the document collection;
2. Select number of latent concepts k and apply rank-reduced SVD on D to get $\hat{D} = V_k \Sigma_k$;
3. Apply the cluster algorithm on the rows of $V_k \Sigma_k$.

LSA has some drawbacks. Because SVD looks for an orthogonal basis for the new reduced document space, there could be negative values that are harder to interpret, and what is more, the cosine similarity can become negative as well. However, it does not significantly affect the cosine distance: it still will always give non-negative results.

Apart from SVD there are many other different matrix decomposition techniques that can be applied for document clustering and for discovering the latent structure of the term-document matrix [44], and one of them in Non-Negative Matrix Factorization (NMF) [45]. Using NMF solves the problem of negative coefficients: when it is applied to non-negative data such as term-document matrices, NMF produces non-negative rank-reduced approximations.

The main conceptual difference between SVD and NMF is that SVD looks for orthogonal directions to represent document space, while NMF does not require orthogonality [46] (see fig. 2).

The NMF of an $m \times n$ term-document matrix D is $D \approx D_k = UV^T$ where U is an $m \times k$ matrix, V is an $n \times k$ matrix and k is the number

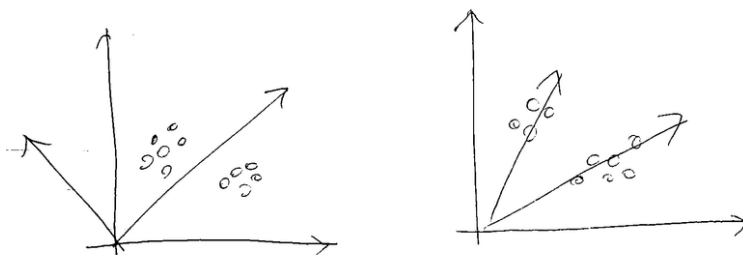


Fig. 2: **TODO redraw** Directions found by SVD (on the left) vs directions by NMF (on the right)

of semantic concepts in D . Non-negativity of elements in D_k is very good for interpretability: it ensures that documents can be seen as a non-negative combination of the key concepts.

Additionally, NMF is useful for clustering: the results of NMF can be directly interpreted as cluster assignment and there is no need to use separate clustering algorithms [46]. When D is a term-document matrix and $D \approx UV^T$, then elements $(V)_{ij}$ represent the degree to which document i belongs to cluster j .

The document clustering using NMF consists of the following steps [46]:

1. Construct the term-document matrix D and perform NMF on D to get U and V
2. Normalize rows \mathbf{v}_i of V by using $\mathbf{v}_i \leftarrow \mathbf{v}_i / \|\mathbf{v}_i\|$;
3. Assign document \mathbf{d}_i to cluster x if $x = \arg \max_j (V)_{ij}$.

If the desired number of clusters K is larger than the rank k of the reduced matrix D_k , the clustering can be performed directly on the rows of V , for example, by using K -Means.

4 Implementation

In section 4.1 we describe the data set that we use, then we describe how we extract identifiers from this dataset (section 4.2) and how this dataset is cleaned (section 4.2.1). Next, the implementation of clustering algorithms is described in the section 4.2.1. After the clusters are found, we combine them into a hierarchy in the section 4.5.

Finally, in the section 4.6 we explore how the same set of techniques can be applied to source code in Java.

4.1 Data set

Wikipedia is a big online encyclopedia where the content are written and edited by the community. It contains a large amount of articles on a variety of topics, including articles about Mathematics and Mathematics-related fields such as Physics. It is multilingual and available in several languages, including English, German, French, Russian and others. The content of wikipedia pages are authored in a special markup language and the content of the entire encyclopedia is freely available for download.

The techniques discussed in this work are mainly applied to the English version of Wikipedia. At the moment of writing (July 18, 2015) English Wikipedia contains about 4.9 million articles². However, just a small portion of these articles are math related: there are only 30.000 pages that contain at least one `<math>` tag.

Apart from the text data and formulas Wikipedia articles have information about categories, and we can exploit this information as well. The category information is encoded directly into each Wikipedia page with a special markup tag. For example, the article “Linear Regression”³ belongs to the category “Regression analysis” and `[[Category:Regression analysis]]` tag encodes this information. However there are other indirect ways to associate a page with some category, for example, by using Wiki templates. A template is a user-defined macro that is executed by the Wikipedia engine, and the content of a template can include category association tags. It is hard to extract the content information from the template tag and therefore we use category information available in a structured machine-processable form in DBpedia [47]. Additionally, DBpedia provides extra information such as parent categories (categories of categories) that is very easy to process and incorporate into analysis.

² <https://en.wikipedia.org/wiki/Wikipedia:Statistics>

³ https://en.wikipedia.org/wiki/Linear_regression

Wikipedia is available in other languages, not only English. While the most of the analysis is performed on the English Wikipedia, we also apply some of the techniques to the Russian version [48] to compare it with the results obtained on the English Wikipedia. Russian Wikipedia is smaller than the English Wikipedia and contains 1.9 million articles⁴, among which only 15 000 pages are math-related (i.e. contain at least one `<math>` tag).

4.2 Definition Extraction

Before we can proceed to discovering identifier namespaces, we need to extract identifier-definition relations. For this we use the probabilistic approach, discussed in the section 2.2.4. The extraction process is implemented using Apache Flink [49] and it is based on the open source implementation provided by Pagael and Schubotz in [20]⁵.

The first step is to keep only mathematical articles and discard the rest. This is done by retaining only those articles that contain at least one `<math>` tag. Once the data set is filtered, then all the \LaTeX formulas from the `<math>` tags are converted to MathML, an XML-based representation of mathematical formulae [50].

The dataset is stored in a big XML file in the Wiki XML format. It makes it easy to extract the title and the content of each document, and then process the documents separately. The formulas are extracted by looking for the `<math>` tags. However some formulas for some reasons are typed without the tags using the unicode symbols, and such formulas are very hard to detect and therefore we choose not to process them. Once all `<math>` tags are found, they (along with the content) are replaced with a special placeholder `FORMULA_%HASH%`, where `%HASH%` is MD5 hash [51] of the tag's content represented as a hexadecimal string. After that the content of the tags is kept separately from the document content.

The next step is to find the definitions for identifiers in formulas. We are not interested in the semantics of a formula, only in the identifiers it contains. In MathML `<ci>` corresponds to identifiers, and hence extracting identifiers from MathML formulas amounts to finding all `<ci>` tags and retrieving their content. It is enough to extract simple identifiers such as “ t ”, “ C ”, “ μ ”, but there also are complex identifiers with subscripts, such as “ x_1 ”, “ ξ_i ” or even “ β_{slope} ”. To extract them we need to look for tags `<msub>`. We do not process superscripts because they are usually powers (for example, “ x^2 ”),

⁴ https://en.wikipedia.org/wiki/Russian_Wikipedia

⁵ <https://github.com/rbzn/project-mlp>

and therefore they are not interesting for this work. There are exceptions to this, for example, “ σ^2 ” is an identifier, but these cases are rare and can be ignored.

Since MathML is XML, the identifiers are extracted with XPath queries [2]:

- `//m:mi[not(ancestor::m:msub)]/text()` for all `<ci>` tags that are not subscript identifiers;
- `//m:msub` for subscript identifiers.

Once the identifiers are extracted, the rest of the formula is discarded. As the result, we have a “Bag of Formulae”: analogously to the Bag of Words approach (see section 3.1) we keep only the counts of occurrences of different identifiers and we do not preserve any other structure.

The content of Wikipedia document is authored with Wiki markup – a special markup language for specifying document layout elements such as headers, lists, text formatting and tables. Thus the next step is to process the Wiki markup and extract the textual content of an article, and this is done using a Java library “Mylyn Wikitext” [52]. Almost all annotations are discarded at this stage, and only inner-wiki links are kept: they can be useful as candidate definitions. The implementation of this step is taken entirely from [20] with only a few minor changes.

Once the markup annotations are removed and the text content of an article is extracted, we then apply Natural Language Processing (NLP) techniques. Thus, the next step is the NLP step, and for NLP we use the Stanford Core NLP library (StanfordNLP) [22]. The first part of this stage is to tokenize the text and also split it by sentences. Once it is done, we then apply Math-aware POS tagging (see section 2.1). For English documents from the English Wikipedia we use StanfordNLP’s Maximal Entropy POS Tagger [53]. Unfortunately, there are no trained models available for POS tagging the Russian language for the StanfordNLP library and we were not able to find a suitable implementation of any other POS taggers in Java. Therefore we implemented a simple rule-based POS tagger ourselves. The implementation is based on a PHP function from [54]: it is translated into Java and seamlessly integrated into the StanfordNLP pipeline. The English tagger uses the Penn Treebank POS Scheme [21], and hence we follow the same convention for the Russian tagger.

For handling mathematics we introduce two new POS classes: “ID” for identifiers and “MATH” for formulas. These classes are not a part of the Penn Treebank POS Scheme, and therefore we need to label all the instances of

these tags ourselves during the additional post-processing step. If a token starts with “`FORMULA_`”, then we recognize that it is a placeholder for a math formula, and therefore we annotate it with the “`MATH`” tag. Additionally, if this formula contains only one identifier, this placeholder token is replaced by the identifier and it is tagged with “`ID`”. We also keep track of all identifiers found in the document and then for each token we check if this token is in the list. If it is, then it is re-annotated with the “`ID`” tag.

At the Wikipedia markup processing step we discard almost all markup annotations, but we do keep inner Wikipedia links, because these links are good definition candidates. To use them, we introduce another POS Tag: “`LINK`”. To detect all inner-wiki links, we first find all token subsequences that start with “[`[`” and end with “[`]`”, and then these subsequences are concatenated and tagged as “`LINK`”.

Successive nouns (both singular and plurals), possibly modified by an adjective, are also candidates for definitions. Therefore we find all such sequences on the text and then concatenate each into one single token tagged with “`NOUN_PHRASE`”.

The next stage is selecting the most probable identifier-definition pairs, and this is done by ranking definition candidates. The definition candidates are tokens annotated with “`NN`” (noun singular), “`NNS`” (noun plural), “`LINK`” and “`NOUN_PHRASE`”. We rank these tokens by a score that depends how far it is from the identifier of interest and how far is the closest formula that contains this identifier (see section 2.2.4). The output of this step is a list of identifier-definition pairs along with the score, and only the pairs with scores above the user specified threshold are retained. The implementation of this step is also taken entirely from [20] with very minor modifications.

4.2.1 Data Cleaning

The Natural Language data is famous for being noisy and hard to clean [55]. The same is true for mathematical identifiers and scientific texts with formulas. In this section we describe how the data was preprocessed and cleaned at different stages of Definition Extraction.

Often identifiers contain additional semantic information visually conveyed by special diacritical marks or font features. For example, the diacritics can be hats to denote “estimates” (e.g. “ \hat{w} ”), bars to denote the expected value (e.g. “ \bar{X} ”), arrows to denote vectors (e.g. “ \vec{x} ”) and others. As for the font features, boldness is often used to denote vectors (e.g. “ \mathbf{w} ”) or matrices

(e.g. “ \mathbf{X} ”), calligraphic fonts are used for sets (e.g. “ \mathcal{H} ”), double-struck fonts often denote spaces (e.g. “ \mathbb{R} ”), and so on.

Unfortunately there is no common notation established across all fields of mathematics and there is a lot of variance. For example, a vector can be denoted by “ \vec{x} ”, “ \boldsymbol{x} ” or “ \mathbf{x} ”, and a real line by “ \mathbb{R} ”, “ \mathbf{R} ” or “ \Re ”. In natural languages there are related problems of lexical ambiguity such as synonymy, when different words refer to the same concept, and it can be solved by replacing the ambiguous words with some token, representative of the concept. Therefore this problem with identifiers can be solved similarly by reducing identifiers to their “root” form. This can be done by discarding all additional visual information, such that “ \bar{X} ” becomes “ X ”, “ \mathbf{w} ” becomes “ w ” and “ \Re ” becomes “ R ”. The disadvantage of this approach is that we lose the additional semantic information about the identifier that otherwise could be useful.

The diacritic marks can easily be discarded because they are represented by special MathML instructions that can be ignored when the identifiers are retrieved. But, on the other hand, the visual features are encoded directly on the character level: the identifiers use special unicode symbols to convey font features such as boldness or Fraktur, so it needs to be normalized by converting characters from special “Mathematical Alphanumeric Symbols” unicode block [56] back to the standard ASCII positions (“Basic Latin” block). Some identifiers (such as “ \hbar ” or “ ℓ ”) are expressed using the characters from a special “Letterlike Symbols” table, and these characters are normalized as well.

Additionally, there is a lot of noise on the annotation level in MathML formulas: many non-identifiers are captured as identifiers inside `<ci>` tags. Among them there are many mathematic-related symbols like “ \wedge ”, “ $\#$ ”, “ ∇ ”, “ \int ”; miscellaneous symbols like “ \diamond ” or “ \circ ”, arrows like “ \rightarrow ” and “ \Rightarrow ”, and special characters like “ \lceil ”.

To filter out these one-symbol false identifiers we fully exclude all characters from the following unicode blocks: “Spacing Modifier Letters”, “Miscellaneous Symbols”, “Geometric Shapes”, “Arrows”, “Miscellaneous Technical”, “Box Drawing”, “Mathematical Operators” (except “ ∇ ” which is sometimes used as an identifier) and “Supplemental Mathematical Operators” [56]. Some symbols (like “ $=$ ”, “ $+$ ”, “ \sim ”, “ $\%$ ”, “ $?$ ”, “ $!$ ”) belong to commonly used unicode blocks which we cannot exclude altogether. For these symbols we manually prepare a stop list for filtering them.

It also captures multiple-symbol false positives: operators and functions like “`sin`”, “`cos`”, “`exp`”, “`max`”, “`trace`”; words commonly used in formu-

las like “const”, “true”, “false”, “vs”, “iff”; auxiliary words like “where”, “else”, “on”, “of”, “as”, “is”; units like “mol”, “dB”, “mm”. These false identifiers are excluded by a stop list as well: if a candidate identifier is in the list, it is filtered out. The stop list of false positives is quite similar for both English and Russian: for the Russian wikipedia we only need to handle the auxiliary words such as “где” (“where”), “иначе” (“else”) and so on. The names for operators and functions are more or less consistent across both data sources.

Then, at the next stage, the definitions are extracted. However many shortlisted definitions are either not valid definitions or too general. For example, some identifiers become associated with “if and only if”, “alpha”, “beta”, “gamma”, which are not valid definitions. Other definitions like “element” (“элемент”), “number” (“число”) or “variable” (“переменная”) are valid, but they are too general and not descriptive. We maintain a stop list of such false definitions and filter them out from the result. The elements of the stop list are also consistent across both data data sets, in the sense that the false definition candidates are same but expressed in different languages.

The Russian language is highly inflected, and because of this extracted definitions have many different forms, depending on grammatical gender, form (singular or plural) and declensions. This highly increases the variability of the definitions, and to reduce it lemmatize the definitions: they are reduced to the same common form (nominative, singular and masculine). This is done using Pymorphy2: a python library for Russian and Ukrainian morphology [57].

At the next stage the retrieved identifier/definition pairs are used for document clustering. Some definitions are used only once and we can note that they are not very useful because they do not have any discriminative power. Therefore all such definitions are excluded.

4.2.2 Dataset Statistics

During the data cleaning at the identifier extraction step some false identifiers are discarded, and after that some documents become empty: they contain no identifiers at all, and these documents are no longer considered for the analysis. Additionally, we discard all the documents that have only one identifier. This leaves only 22 515 documents out of 30 000, and they contain 12 771 distinct identifiers, which occur about 2 million times.

The most frequent identifiers are x (125 500 times), p (110 000), m (105 000 times) and n (83 000 times), but about 3 700 identifiers occur only once and

1 950 just twice. Clearly, the distribution of identifiers follows some power law distribution (see fig. 3).

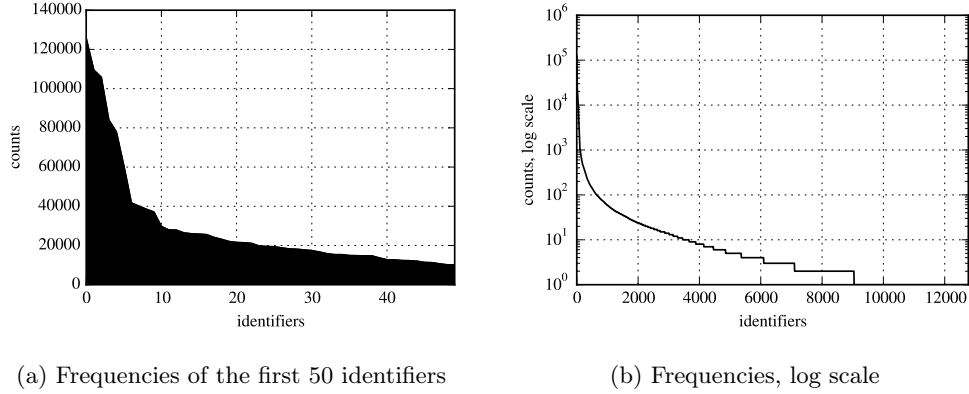


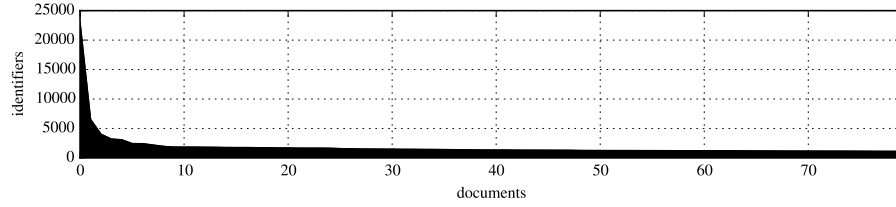
Fig. 3: Distribution of frequencies of identifiers

The distribution of counts for identifiers inside the documents also appears to follow a long tail power law distribution: there are few articles that contain many identifiers, while most of the articles do not (see fig. 4a). The biggest article (“Euclidean algorithm”) has 22 766 identifiers, and the second largest (“Lambda lifting”) has only 6 500 identifiers. The mean number of identifiers per document is 33. The distribution for number of distinct identifiers per document is less skewed (see fig. 4b). The largest number of distinct identifiers is 287 (in the article “Hooke’s law”), and it is followed by 194 (in “Dimensionless quantity”). The median number of identifiers per document is 10.

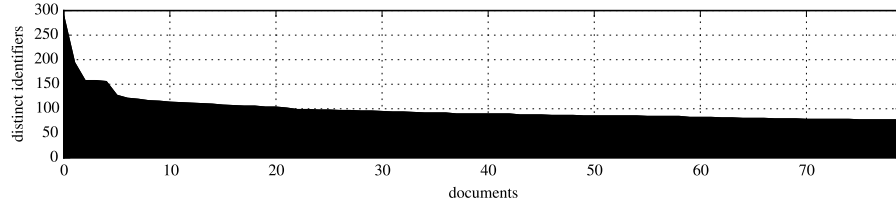
For 12 771 identifiers the algorithm extracted 115 300 definitions, and the number of found definitions follows a long tail distribution as well (see fig. 4c), with the median number of definitions per page being 4.

The following is the list of the most common identifier-definition pairs extracted from the English Wikipedia:

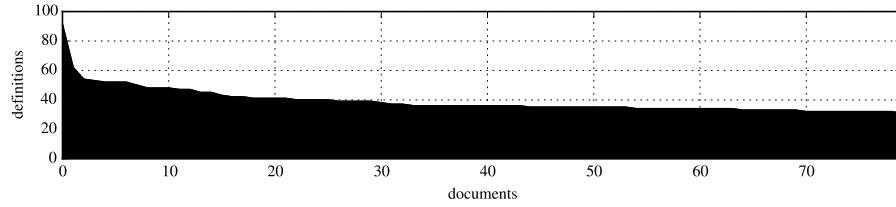
- t : “time” (1086)
- m : “mass” (424)
- θ : “angle” (421)
- T : “temperature” (400)
- r : “radius” (395)
- v : “velocity” (292)



(a) Identifier frequencies per document for first 80 most largest documents



(b) No. of distinct identifiers per document for first 80 most largest documents



(c) Definitions per document

Fig. 4: Frequencies per documents

- ρ : “density” (290)
- G : “group” (287)
- V : “volume” (284)
- λ : “wavelength” (263)
- R : “radius” (257)
- n : “degree” (233)
- r : “distance” (220)
- c : “speed of light” (219)
- L : “length” (216)
- n : “length” (189)
- n : “order” (188)
- n : “dimension” (185)
- n : “size” (178)
- M : “mass” (171)

- d : “distance” (163)
- X : “topological space” (159)

In Russian Wikipedia only 5 300 articles contain enough identifiers, and the remaining 9 500 are discarded.

The identifiers and definitions extracted from the Russian Wikipedia exhibit the similar properties. The most frequently occurring identifier is x with 13 248 occurrences, but the median frequency of an identifier is only 3 times. The article with the largest number of identifiers is “Уравнения Максвелла” (“Maxwell’s equations”) which contains 1 831 identifiers, while the median number of identifiers is just 3; the article with the largest number of distinct identifiers is also “Уравнения Максвелла” with 112 unique identifiers, and the median number of distinct identifiers in the data set is 5. Finally, the largest number of extracted definitions is 44 (again, for “Уравнения Максвелла”) with 2 being the median number of definitions per page.

The following is the list most frequent relations extracted from the Russian wikipedia:

- t : “функция” (“function”) (215)
- t : “время” (“time”) (130)
- X : “множество” (“set”) (113)
- m : “масса” (“mass”) (103)
- c : “скорость свет” (“speed of light”) (89)
- G : “группа” (“group”) (87)
- T : “температура” (“temperature”) (69)
- h : “постоянный планка” (“Plank constant”) (68)
- ρ : “плотность” (“density”) (57)
- M : “многообразие” (“manifold”) (53)
- K : “поле” (“field”) (53)
- X : “пространство” (“space”) (50)
- v : “скорость” (“speed”) (50)
- X : “топологический пространство” (“topological space”) (46)
- G : “граф” (“graph”) (44)
- R : “радиус” (“radius”) (38)
- R : “кольцо” (“ring”) (36)
- G : “гравитационный постоянный” (“gravitational constant”) (34)
- E : “энергия” (“energy”) (34)
- m : “модуль” (“modulo”) (33)
- S : “площадь” (“area”) (32)
- k : “постоянный больцмана” (“Boltzmann constant”) (30)

4.3 Document Clustering

At the Document Clustering stage we want to find cluster of documents that are good namespace candidates.

Before we can do this, we need to vectorize our dataset: i.e. build the Identifier Space (see section 3.1) and represent each document in this space.

There are three choices for dimensions of the Identifier space:

- identifiers alone,
- “weak” identifier-definition association,
- “strong” association: use identifier-definition pairs.

In the first case we are only interested in identifier information and discard the definitions altogether.

In the second and third cases we keep the definitions and use them to index the dimensions of the Identifier Space. But there is some variability in the definitions: for example, the same identifier “ σ ” in one document can be assigned to “Cauchy stress tensor” and in other it can be assigned to “stress tensor”, which are almost the same thing. To reduce this variability we perform some preprocessing: we tokenize the definitions and use individual tokens to index dimensions of the space. For example, suppose we have two pairs (σ , “Cauchy stress tensor”) and (σ , “stress tensor”). In the “weak” association case we have will dimensions (σ , Cauchy, stress, tensor), while for the “strong” association case we will have (σ_Cauchy , σ_stress , σ_tensor).

Additionally, the effect of variability can be decreased further by applying a stemming technique for each definition token. In this work we use Snowball stemmer for English [58] implemented in NLTK [59]: a python library for Natural Language Processing.

Using `TfidfVectorizer` from scikit-learn [60] we vectorize each document.

We use the following settings:

- A `use_idf=True, min_df=2`
- B `use_idf=False, min_df=2`
- C `use_idf=False, sublinear_tf=True, min_df=2`

In the first case we use inverse document frequency (IDF) to assign additional collection weight for "terms" (see section 3.1), while in second and in third we use only term frequency (TF). In the second case we apply a sublinear transformation to the TF component to reduce the influence of

frequently occurring words. In all three cases we keep only "terms" that are used in at least two documents.

The output is a document-identifier matrix (analogous to "document-term"): documents are rows and identifiers/definitions are columns. The output of `TfidfVectorizer` is row-normalized, i.e. all rows has unit length.

Once we the documents are vectorized, we can apply clustering techniques to them. We use K -Means (class `KMeans` in scikit-learn) and Mini-Batch K -Means (class `MiniBatchKMeans`) [60]. Note that if rows are unit-normalized, then running K -Means with Euclidean distance is equivalent to cosine distance (see section 3.3.2).

Bisecting K -Means (see section 3.3.2) was implemented on top of scikit-learn: at each step we take a subset of the dataset and apply K -Means with $K = 2$ to this subset. If the subset is big (with number of documents $n > 2000$), then we use Mini-Batch K -means with $K = 2$ because it converges much faster.

Scatter/Gather, an extension to K -means (see section 3.3.2), was implemented manually using `scipy` [61] and `numpy` [62] because scikit-learn's implementation of K -Means does not allow using user-defined distances.

DBScan (section 3.3.3) and SNN Clustering (also section 3.3.3) algorithms were also implemented manually: available DBScan implementations usually take distance measure rather than a similarity measure. The similarity matrix created by similarity measures are typically very sparse, because usually only a small fraction of the documents are similar to some given document. Similarity measures can be converted to distance measures, but in this case the matrix will no longer be sparse, and we would like to avoid that. Additionally, available implementations are usually general purpose implementations and do not take advantage of the structure of the data: in text-like data clustering algorithms can be sped up significantly by using an inverted index.

Dimensionality reduction techniques are also important: they not only reduce the dimensionality, but also help reveal the latent structure of data. In this work we use Latent Semantic Analysis (LSA) (section 3.4) which is implemented using randomized Singular Value Decomposition (SVD) [63]. The implementation of randomized SVD is taken from scikit-learn [60] - method `randomized_svd`. Non-negative Matrix Factorization is an alternative technique for dimensionality reduction (section 3.4). Its implementation is also taken from scikit-learn [60], class `NMF`.

To assess the quality of produced clusters we use wikipedia categories. It is quite difficult to extract category information from raw wikipedia text,

therefore we use DBPedia [47] for that: it provides machine-readable information about categories for each wikipedia article. Additionally, categories in wikipedia form a hierarchy, and this hierarchy is available as a SKOS ontology.

A cluster is said to be “pure” if all documents have the same category. Using categories information we can find the most frequent category of the cluster, and then we can define purity as

$$\text{purity}(C) = \frac{\max_i \text{count}(c_i)}{|C|},$$

where C is a cluster, and c_i is some category.

Then we can calculate the overall purity of a cluster assignment and use this to compare results of different clustering algorithms. However it is not enough just to find the most pure cluster assignment: because as the number of clusters increases the overall purity also grows. Thus we can also optimize for the number of clusters with purity p of size at least n .

When the number of clusters increase, the purity always grows (see fig. 5), but at some point the number of pure clusters will start decreasing (see fig. 6).

4.4 Parameter Tuning

There are many different clustering algorithms, each with its own set of parameter. In this section we describe how we find the settings that find the best namespaces.

The following things can be changed:

- Ways to incorporate definition information (no definitions, soft association, hard association);
- Weighting schemes for the identifier-document matrix D : TF, sublinear TF, TF-IDF;
- There are different clustering algorithms: agglomerative clustering, DB-SCAN, SNN clustering, K -Means, Bisecting K -Means, Scatter/Gather, each algorithm has its own set of parameters;
- Dimensionality of D can be reduced via SVD or NMF, parameter k controls the rank of output.

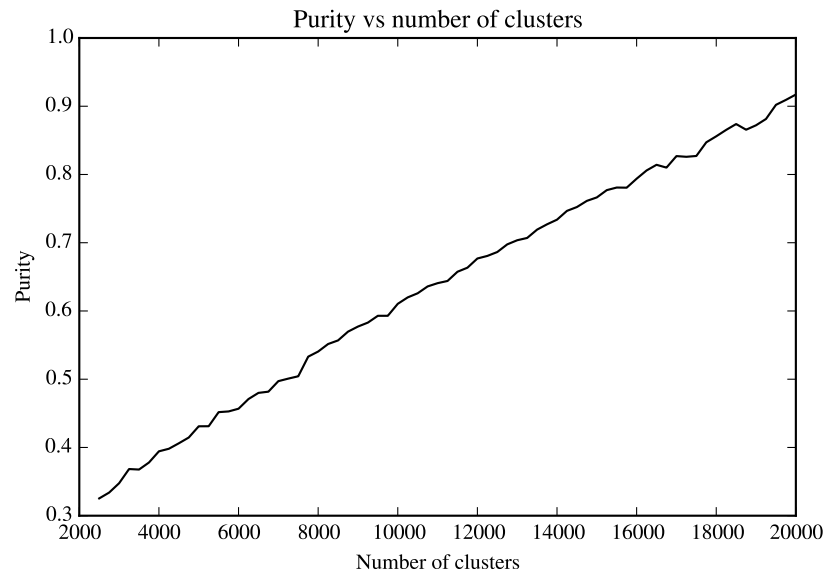


Fig. 5: K in K -Means vs overall purity of clustering: the purity increases linearly with K ($R^2 = 0.99$)

The approach for finding

Distance and similarity measures used Euclidean distance, cosine similarity, jaccard similarity, SNN Similarity

The approach for finding the best parameter set is a grid search: different combination are tries and the best result is kept.

Agglomerative: Wald linkage: takes forever never finished

Only identifiers

Usual K-Means

some clusters are useful, but most of them aren't

For example

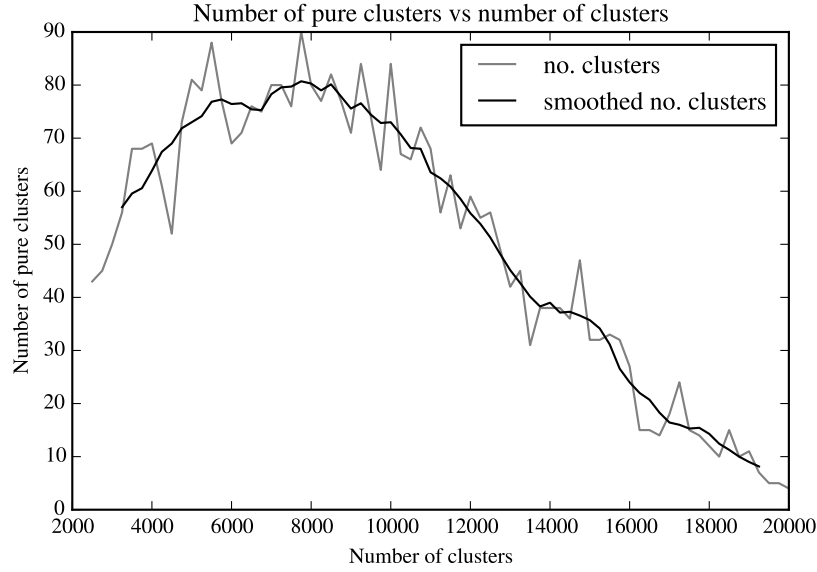


Fig. 6: K in K -Means vs the number of pure clusters: it grows initially, but after $K \approx 8\,000$ starts to decrease

Article	Identifiers
APL (programming language)	n, O, R
Binary search tree	O, n
Boolean satisfiability problem	O, n
Complexity	O, n
Earley parser	O, n
Heapsort	O, n, Ω
Lisp (programming language)	O, n
Priority queue	O, n
Sieve of Eratosthenes	O, n
Smoothsort	O, n
Comb sort	Ω, n, p, O
Divide and conquer algorithm	O, n, Ω
Stack (abstract data type)	O, n, t
Skip list	n, p, O
Graph minor	O, n, h
Flex lexical analyser	O, n
Gift wrapping algorithm	O, n, h
Perlin noise	n, O
Pseudo-polynomial time	n, O, m
Hirzebruch surface	O, n, m, p
Beap	n, O
Pairing heap	O, n, Ω
Cost efficiency	O, n, p

(54 documents in total) These articles appear to relate to

DBSCAN SNN

$k = 10$ dist = jaccard

$\varepsilon=7$ points MinPts=5 points

Article	Identifiers
Epsilon Eridani in fiction	M_{\odot}
Solar mass	M_{\odot}
Orders of magnitude (mass)	M_{\odot}
Carbon-burning process	M_{\odot}
Baryonic dark matter	M_{\odot}
PSR J1614–2230	M_{\odot}
Kennicutt–Schmidt law	M_{\odot}
Portal:Star/Selected article/19	M_{\odot}
NGC 6166	M_{\odot}
Celestial Snow Angel	M_{\odot}
Huge-LQG	M_{\odot}
High-velocity cloud	M_{\odot}
NGC 4845	M_{\odot}
Pulsating white dwarf	M_{\odot}
Robust associations of massive baryonic objects	M_{\odot}
Black Widow Pulsar	M_{\odot}
Betelgeuse	M_{\odot}
Andromeda Galaxy	M_{\odot}

In general doesn't give clusters

TODO add some numbers and graphs

WEAK ASSOCIATION

K-Means weak association

DBSCAN k=15, eps=8, min_pts=5

Article	Identifiers
Papyrus 66	<i>P</i> papyrus
Alexandrian text-type	<i>P</i> , papyrus
Western text-type	<i>P</i> , papyrus
Codex Ephraemi Rescriptus	<i>P</i> , papyrus
Bodmer Papyri	<i>P</i> , papyrus
Categories of New Testament manuscripts	<i>P</i> , papyrus
Papyrus 4	<i>P</i> , papyrus
Papyrus 75	<i>P</i> , papyrus
Uncial 0308	<i>P</i> , <i>M</i> , papyrus, 47
Codex Athous Lavrensis	<i>P</i> , papyrus
Papyrus 92	<i>P</i> , papyrus
Papyrus 90	<i>P</i> , papyrus
Papyrus 9	<i>P</i> , papyrus
Papyrus 15	<i>P</i> , papyrus
Papyrus 16	<i>P</i> , papyrus
Papyrus 20	<i>P</i> , papyrus
Papyrus 39	<i>P</i> , papyrus
Papyrus 49	<i>P</i> , papyrus
Papyrus 65	<i>P</i> , papyrus
Papyrus 111	<i>P</i> , papyrus
Uncial 0243	<i>P</i> , papyrus
Minuscule 1739	<i>P</i> , papyrus
Minuscule 88	<i>P</i> , papyrus
Authorship of the Epistle to the Hebrews	<i>P</i> , papyrus
Egerton Gospel	<i>P</i> , papyrus
Rylands Library Papyrus P52	<i>P</i> , papyrus
Codex Vaticanus	<i>P</i> , papyrus

K-Means

TODO: think of different ways to represent it - maybe truncate some definitions?

Article	Identifiers
Direct shear test	$angle, \varphi, friction$
Truncated dodecadodecahedron	$golden, ratio, \phi$
Golden triangle (mathematics)	$golden, section, \theta, \phi$
Petrophysics	$percentage\varphi, symbol, S_w$
Greedy algorithm for Egyptian fractions	$golden, terms, d, \phi, denominator, possible, expa$
Pi Josephson junction	$\pi, junction, \varphi$
Snub dodecahedron	$golden, ratio, \tau, 2\xi, -, V, \xi$
Lucas number	$golden, terms, \phi, m, L, number, values, ratio, L$
54 (number)	$golden, \varphi, ratio$
Special right triangles	$\pi, c, b, ratio, c., \phi, m, golden, radians, n, line, in$
Universal code (data compression)	$golden, code, ratio, power, \phi, l, n, q, p$
Existential instantiation	$csymbol\varphi variable$
Perles configuration	$goldenratio\phi$
Wythoff array	$goldenratio\phi column m number n \varphi fib$
Golomb sequence	$a_n, n, golden, ratio, \phi$
Almost integer	$constant\pi, gel fonds, \varphi, exampl$
16:10	$golden, ratio, \phi$
Leonardo number	$golden, ratio, \phi, computations, \psi, L, n$
Rogers–Ramanujan continued fraction	$golden.function.sratioG\phi Hqmodu$
Great rhombic triacontahedron	$goldenratio\phi$
108 (number)	$golden\varphi ratio$
Random Fibonacci sequence	$golden.BratioM_nprobability\phi f_nsequence n randominc$
Rhombic triacontahedron	$goldenratio\phi r_i Sedger_m V$
Exact trigonometric constants	$function\pi ratio\phi image golden values x V$
Bilunabiro tunda	$goldenratio\phi$
Feigenbaum constants	$mapzratioplaces f \phi goldenc_n \alpha \delta varia$

Found some interesting clusters but in general doesn't show good results.

Need to use semantic menthols

Batch, k = 2500 .. 10000 with step 50 SVD with n=600

HEre results

4.5 Building Hierarchy

After the namespaces are found, we need to organize them into a hierarchical structure. It is hard to fully automatically, and we choose to use existing hierarchies for mathematical knowledge, and then map the found namespaces to these hierarchies.

The first hierarchy that we use is “Mathematics Subject Classification” (MSC) hierarchy [64] by the American Mathematical Society, and it is used

for categorizing mathematical articles. In this scheme there are 64 top-level categories such as “Mathematical logic”, “Number theory”, or “Fourier analysis”. It also includes some physics categories such as “Fluid mechanics” or “Quantum Theory”. The following top level categories are excluded: “General”, “History and biography” and “Mathematics education”.

Each top-level category contains second-level categories and third-level categories. In this work we exclude all subcategories those code ends with 99: they are usually “Miscellaneous topics” or “None of the above, but in this section”.

Additionally, we excluded the following second level categories because they interfere with PACS, a hierarchy for Physics:

- Quantum theory → Axiomatics, foundations, philosophy
- Quantum theory → Applications to specific physical systems
- Quantum theory → Groups and algebras in quantum theory
- Partial differential equations → Equations of mathematical physics and other areas of application
- Statistics → Sufficiency and information
- Functional analysis → Other (nonclassical) types of functional analysis
- Functional analysis → Miscellaneous applications of functional analysis

The second hierarchy is “Physics and Astronomy Classification Scheme” (PACS) [65], which is a scheme for categorizing articles about Physics. Like in MSC, we remove the top-level category “GENERAL”.

Finally, we also use the ACM Classification Scheme [66] available as a SKOS [67] ontology at their website [68]. The SKOS ontology graph was processed with RDFLib [69].

We use the following top level categories: “Hardware”, “Computer systems organization”, “Networks”, “Software and its engineering”, “Theory of computation”, “Information systems”, “Security and privacy”, “Human-centered computing”, “Computing methodologies”.

After obtaining and processing the data, the three hierarchies are merged into one. Then each found namespace is mapped to the most suitable second-level category.

However these categories are only good for the English wikipedia and a different hierarchy is needed for Russian. One of such hierarchies is “Государственный рубрикатор научно-технической информации” (ГРНТИ) – “State categorizer of scientific and technical information”, which is a state-recommended scheme for categorizing scientific articles published in Russian [70]. The dataset is retrieved from the official website <http://grnti.ru/> [71].

This is done by keywords matching: we extract all words from the category (this includes top level category name, subcategory name and all sub-sub categories concatenated). From the cluster we also extract the category information. Then we try to do keyword matching using cosine similarity between the cluster and each category. The cluster is assigned to the category with the best cosine.

If the cosine score is low (below 0.2) or there is only one keyword matched, then the cluster is assigned to the “OTHERS” category.

4.6 Java Language Processing

TODO: also refer back to the introduction

we have compared the identifier namespaces with namespaces in programming languages and with packages in the Java programming language in particular. We motivated the assumption that there exist “namespace defining” groups of documents by arguing that these groups also exist in programming languages. Thus, the same set of techniques for namespace discovery should be applicable to source code as well.

If a programming language is statically typed, like Java or Pascal, usually it is possible to know the type of a variable from the declaration of this variable. Therefore we can see variable names as “identifiers” and variable types as “definitions”. Clearly, there is a difference between variable types and identifier definitions, but we believe that this comparison is valid because the type carries additional semantic information about the variable and in what context it can be used – like the definition of an identifier.

The information about variables and their types can be extracted from a source code repository, and each source file can be processed to obtain its Abstract Syntax Tree (AST). By processing the ASTs, we can extract the variable declaration information. Thus, each source file can be seen as a document, which is represented by all its variable declarations.

In this work we process Java source code, and for parsing it and building ASTs we use a library `JavaParser` [72]. The Java programming language was chosen because it requires the programmer to always specify the type information when declaring a variable. It is different for other languages when the type information is usually inferred by the compilers at compilation time.

In Java a variable can be declared in three places: as an inner class variable (or a “field”), as a method (constructor) parameter or as a local variable inside a method or a constructor. We need to process all three

types of variable declarations and then apply additional preprocessing, such as converting the name of the type from short to fully qualified using the information from the import statements. For example, `String` is converted to `java.lang.String` and `List<Integer>` to `java.util.List<Integer>`, but primitive types like `byte` or `int` are left unchanged. Secondly,

Consider an example in the listing 1. There is a class variable `threshold`, a method parameter `in` and two local variables `word` and `posTag`. The following relations will be extracted from this class: (“threshold”, `double`), (“in”, `domain.Word`), (“word”, `java.lang.String`), (“posTag”, `java.lang.String`). Since all primitives and classes from packages that star with `java` are discarded, at the end the class `WordProcessor` is represented with only one relation (“in”, `domain.Word`).

Listing 1: A java class

```
package process;

import domain.Word;

public class WordProcessor {

    private double threshold;

    public boolean isGood(Word in) {
        String word = in.getWord();
        String posTag = in.getPosTag();
        return isWordGood(word) && isPosTagGood(posTag);
    }

    // ...

}
```

In the experiments we applied this source code analysis to the source code of Apache Mahout 0.10 [73], which is an open-source library for scalable Machine Learning and Data Mining.

As on 2015-07-15, this dataset consists of 1560 java classes with 45878 variable declarations. After discarding declarations from the standard Java API, primitives and types with generic parameters, only 15869 declarations were retained.

The following is top-15 variable/type declarations:

- (“conf”, `org.apache.hadoop.conf.Configuration`), 491 times
- (“v”, `org.apache.mahout.math.Vector`), 224 times
- (“dataModel”, `org.apache.mahout.cf.taste.model.DataModel`), 207 times

- (“fs”, org.apache.hadoop.fs.FileSystem), 207 times
- (“log”, org.slf4j.Logger), 171 times
- (“output”, org.apache.hadoop.fs.Path), 152 times
- (“vector”, org.apache.mahout.math.Vector), 145 times
- (“x”, org.apache.mahout.math.Vector), 120 times
- (“path”, org.apache.hadoop.fs.Path), 113 times
- (“measure”, org.apache.mahout.common.distance.DistanceMeasure), 102 times
- (“input”, org.apache.hadoop.fs.Path), 101 times
- (“y”, org.apache.mahout.math.Vector), 87 times
- (“comp”, org.apache.mahout.math.function.IntComparator), 74 times
- (“job”, org.apache.hadoop.mapreduce.Job), 71 times
- (“m”, org.apache.mahout.math.Matrix), 70 times

5 Evaluation

In section 4.4 we describe how we select the best clustering algorithm.

5.1 Result analysis

Hierarcical methods are too slow, and SLINK is not good. Bisecting K -Means is good for explaining steps but not very practical

MiniBatch K means is preferred to usual KMeans: fast but same results

NMF takes a lot of time to decompose a matrix with large k

$k = 100$ 30 min, but with results inferior to SVD $k = 250$ 2 hours, with results comparable to SVD

The complexity of NMF is $O(kn)$

The best definition embedding technique is soft association The best clustering algorithm is K -Means with $K = 10000$ on the semantic space produced by rank-reduced SVD with $k = 200$

5.2 Building Hierarchy

How to evaluate???

5.3 Experiment Conclusions

6 Conclusions

The results are super.

6.1 Future Work

the work is done assuming that document imports only from one namespace but it can import from several. can solve that by dividing the document in parts (e.g. by paragraphs) and then applying the same analysis independently to each paragraph - instead of each document.

Can use additional information from wiki articles. For example, can extract some keywords from the article and use it in clustering

Or interwiki pages.

Pages that describe certain namespaces may be quite interconnected. There are link-based clustering methods e.g. Botafogo and Schneiderman 1991

Can extract wiki graph and use this for clustering . There are hybrid approaches that use both usual textual representation + links [16]

It can be interesting to apply these techniques to a larger dataset, for example, arXiv.

Other dim red techniques for LSA, e.g. Local NMF [74] There should also be randomized NMF that works faster.

Try other clustering techniques: spectral clustering [75] other ways to embed identifiers like word2vec [76] or GloVe [77]

How to extend this method to situations when no additional information about document category is known. I.e. need to replace the notion of purity with some other objective for discovering namespaces and namespace-defining clusters

Micro-clustering (<http://arxiv.org/abs/1507.03067>) Micro-Clustering: Finding Small Clusters in Large Diversity

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