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Instytut Informatyki

PRACA DYPLOMOWA MAGISTERSKA

Paweł Szostek

Metadata extraction from scholarly publications

Opiekun pracy
prof. dr hab. inż. Piotr Gawrysiak

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Podpis Przewodniczącego
Komisji Egzaminu Dyplomowego

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Chapter 1

Introduction

Digital libraries gained a lot of momentum in the recent years. The amount of publications stored there is enormous and constantly growing. Moreover, with time the purpose of the digital libraries has been evolving from a place where publications were stored, over search engines to quickly filter out publications relevant to certain topic, to frameworks used for analysis of collaboration patterns, calculation of productivity and efficiency factors such as H-index ([J. 05]) or G-index or looking for emerging trends and topics in science. All this research depends on a reliable source of full texts and metadata from analyzed articles.

Even though there was a huge progress in science as such, scholarly publishing relies on methods invented more than two decades ago, which is an immense time in digital world. The most common format in digital publishing is PDF (Portable File Format) which focuses on how the document is rendered in reader's browser, making it highly portable across hardware and software platforms, but also making it highly unsuitable for carrying metadata, understood here literally as *data about data*. Articles are very often distributed in this form

A modern, fully functional framework for digital libraries, in order to be useful and to provide high quality services, has to have access not only to the full texts of the articles and books that it stores, but also to their metadata. The metadata, data describing data, include such information as: document author(s), document title, document abstract, keywords, document references and others. The purpose of obtaining the metadata is twofold. Firstly, they are indispensable when implementing a search engine, being an invaluable tool for all researchers looking for articles needed in their research field. Secondly, a subset of metadata, i.e. article authors and references are needed for various ranking algorithms based on citation count, such H-index [J. 05], Impact Factor and other bibliometric indicators.

1.1 Problem statement

Regrettably, usually a digital library has to deal with the resources without any metadata provided by the publisher. In this case, the number of articles makes it barely possible to process them manually. It might also happen that the metadata available are not trustworthy or are faulty or partially missing. In these cases a digital library needs a method to obtain the metadata automatically or semi-automatically. The following thesis presents CERMINE - a system for extracting metadata and bibliographic references. This system was implemented jointly by the author and his team mates. However, their work will not be described extensively in this document and the authorship of each piece of the system will be marked explicitly.

1.2 Executive summary

This works presents CERMINE - a system for automatic extraction of metadata from scholarly publications, and GROTOAP2 - Ground-truth publication dataset. The system was developed by the author of this work as a part of his duties in Interdisciplinary Center for Mathematical and Computational Modeling at the University of Warsaw. The system has been recently presented at the Force2015 meeting ([For15]). Furthermore, an article on CERMINE was presented in the 11th IAPR International Workshop on Document Analysis Systems ([Dom14]). GROTOAP2 article was published in D-Lib magazine, volume 20. ([DB14]). Information on the access to the source code and other resources is included in the appendix D.

1.3 Related work

Extracting metadata from scholarly publications is a well-studied problem. In the past, the algorithms expected scanned documents as an input and were generally formulated as image recognition problem. Those were built in the period when scholarly communication was present mainly or uniquely in a printed form and each article, before becoming available in a digital way, had to be scanned. Nowadays, a digital library has to cope with born-digital documents, where the letter recognition stage is omitted and processing starts with building up words and lines of text based on single characters.

Chapter 2

Theory

2.1 Motivation

2.2 Statistical learning

The main objective of statistical learning is to find a non-trivial description of dependencies between data gathered by measuring objects and the objects themselves. The measurement, known also as input data, is known for all of the objects under research. The property that is being looked for, on the contrary, is known uniquely for a subset of objects. The main goal of the machine learning is to figure out, in an automated way, an algorithm allowing to reason values of the properties of interest for all available input objects.

As a classical example of machine learning we might take an application in the medical diagnosis. In this case, the input data are the data obtained by performing medical analysis and medical interview. The outcome of the algorithm is a probability of patient suffering from certain disease

2.3 Classification as supervised learning method

The goal of all classification is determine to which category a new observation belongs, being given a training set consisting of samples belonging to some predefined categories. Training samples have form of n-dimensional vectors, where n is the number of explanatory variables, known as well as *features*. Features are values that express some traits of the classified elements. They can be real-numbers (e.g. 1.23, 3.14), interger-numbers (e.g. 1,2,3) or categorical values (e.g. Circle, Square,

Trapezoid, Large, Medium, Small, 1,0 etc.).

In the thoery of statistical learning, classification is considered as an example of supervised learning tasks, i.e. learning on the basis of training set for which the categories of elements are available.

2.4 Support Vector Machines

One of the most successful and broadly known techniques in machine learning are Support Vector Machines, whose theory was developped by Cortez and Vapnik. The basic idea is given a set of two classes of N-dimension points to find a hyperplane which seperates an N-dimensional space into two subspaces, so that each of them contains points belonging to only one class. Since the two classes might not always be linearly separable, SVM introduces an idea of kernel-induced space which casts the points into a higher dimensional feature space where the new points are linearly-separable. In the section 2.4.1 there is a detailed description of the theoretical fundaments. In its original version the SVM classifier is a binary classifier, meaning that each point in the training sets belongs to one and only on of two classes and so the unknown points do.

CERMINE internally leverages SVM to classify its content based on the training database. This is why it is important to get acquainted with this algorithm in-depth.

2.4.1 Linearly separable Support Vector Machines

In the very basic example of SVM, namely a linear SVM, is to assign each new sample to one of the two classes, being given a set of learning samples. All the points, both being the learning samples and the unknown samples, are usually tuples of values of certain features.

Let us assume that we have a set of learning samples L, where each samples is labeled l_i, whereas i is the index of the learning sample and I is the set of these indices. Each training sample has d values, so is a d-dimensional tuple ($x_i \in \mathbb{R}^d$) and a class label y_i being on of two values $-1, 1$. We can sum up these assumptions with the following equation:

$$\forall i \in I \quad (x_i, y_i) : x_i \in \mathbb{R}^d, y_i \in \{-1, 1\} \tag{2.1}$$

For the sake of simplicity let us assume that the set of learning samples is linearly separable. We will label the separating hyperplane as H. Obiously, in a general case there is an infinite number of such hyper-planes what is shown in the figures 2.1 (in this case $I = 5$ and $d = 2$) and 2.2. The two dimensions are marked as $x[0]$ and $x[1]$.

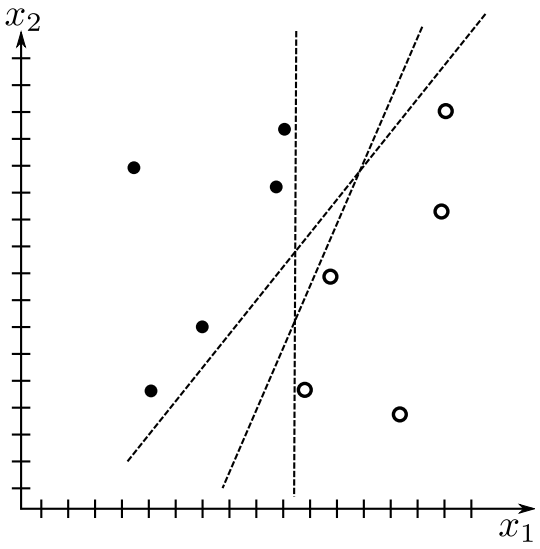


Figure 2.1: There might exist an infinite number of hyperplanes separating two groups of points. SVM's task is to find a hyperplane that maximizes distance to all data points.

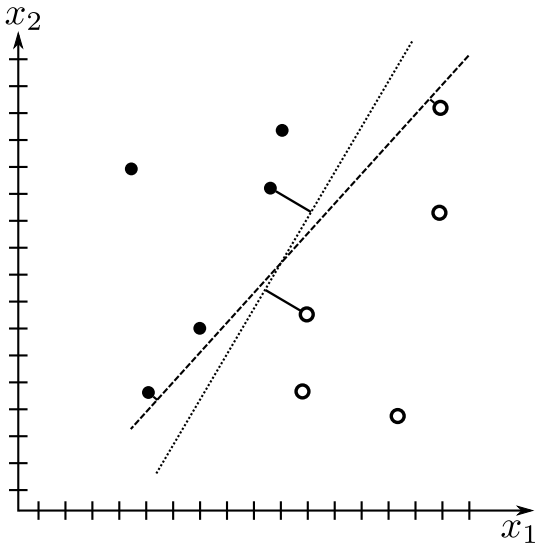


Figure 2.2: There were chosen two alternative lines separating the training points. The dotted line maximizes the distance to support points, whereas the dashed one is sub-optimal.

We can describe a hyperplane H with a general formula:

$$w \cdot x + b = 0 \tag{2.2}$$

Obviously, the number of such hyperplanes is infinite. Let us focus on a hyperplane H that is equally distanced to points from both class. Let us now focus on two hyperplanes parallel to each other that separate the space. Let us label them as H_{-1} and H^{+1}, whereas the former is stuck to a point from class -1 and the latter to a point belonging to class $+1$. They both maximize the distance to the objects of the other class and therefore are parallel to each other. These hyperplanes are shown in the figure 2.3.

We can describe them with the following equations:

$$w^T x_i + b = 1 \tag{2.3}$$

$$w^T x_i + b = -1 \tag{2.4}$$

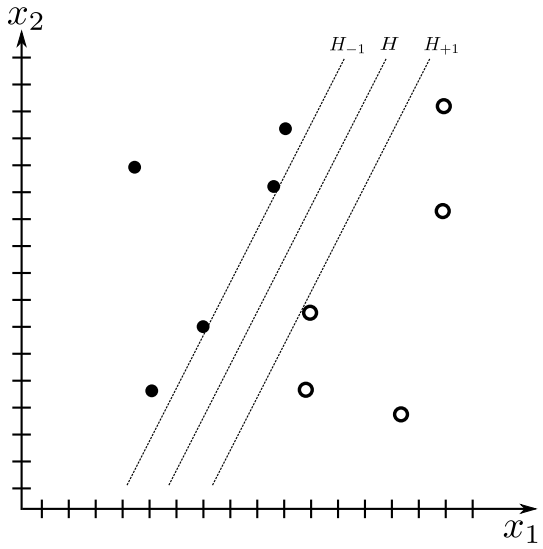


Figure 2.3: Hyperplane H separates perfectly points belonging to two classes. It is equally distanced to hyperplanes H_{-1} and H_{+1} which are stuck to objects of classes -1 and $+1$ respectively.

Because H_{-1} and H_{+1} are decision boundaries, there are no points in between them what can be summarized in the following equations:

$$w^T x_i + b \geq 1 \quad \forall\,(x_i, y_i) : y_i = 1 \tag{2.5}$$

$$w^T x_i + b \leq -1 \quad \forall\,(x_i, y_i) : y_i = -1 \tag{2.6}$$

We can unify equations 2.5 and 2.6 by a generalized equation:

$$y_i \left(w^T x_i + b\right) - 1 \geq 0 \tag{2.7}$$

For each data point we might caclulate the distance to any of the hyperplanes:

$$d\left((w, b), x_i\right) = \frac{y_i \left(x_i \cdot w + b\right)}{||w||} \geq \frac{1}{||w||} \tag{2.8}$$

To make the decision boundary most accurate, we are intuitively looking for a hyperplane that maximizes the distance to all the data points. This in turn minimizes the probability of an erronous classification of unknown data and avoids introducing a bias. According to the equation 2.8 this can be achieved by maximizing $\frac{1}{||w||}$ or alternatively by minimizing the $||w||$ vector. We can leverage the fact that $||w||$ is a non negative value and for sake of simplicity of calculations minimize $\frac{1}{2}||w||^2$ subject to $y_i \left(w^T x_i + b\right) \geq 1 \forall i$ (note that $||w||^2 = w^T w$).

This problem will be solved with the method of Lagrange multipliers. The Langragian is calculated as follows:

$$\mathcal{L} = \frac{1}{2} w^T w + \sum_{i=1}^{n} \alpha_i \left(1 - y_i \left(w^T x_i + b\right)\right) \tag{2.9}$$

In this equation α is a vector of Lagrange multipliers. The problem is reduced to finding a saddle point where the function has its maximum value. Thus, by setting the Langrangian to 0 with respect to w and b we get:

$$w = \sum_{i=1}^{n} \alpha_i \left(-y_i\right) x_i = 0 \Rightarrow w = \sum_{i=1}^{n} \alpha_i y_i x_i \sum_{i=1}^{n} \alpha_i y_i = 0 \tag{2.10}$$

If we substitute $w = \sum_{ix=1}^{n} \alpha_i y_i x_i$ in the formula for $\mathcal{L}$ we have

$$\begin{aligned}
\mathcal{L} &= \frac{1}{2} \sum_{i=1}^{n} \alpha_i y_i x_i^T \cdot \sum_{j=1}^{n} \alpha_j y_j x_j + \sum_{i=1}^{n} \alpha_i \left(1 - y_i \left(\sum_{j=1}^{n} \alpha_j y_j x_j^T x_i + b\right)\right) \\
&= \frac{1}{2} \sum_{i=1}^{n} \sum_{j=1}^{n} \alpha_i \alpha_j y_i y_j x_i^T x_j + \sum_{i=1}^{n} \alpha_i - \sum_{i=1}^{n} \alpha_i y_i \sum_{j=1}^{n} \alpha_j y_j x_j^T x_i - b \sum_{i=1}^{n} \alpha_i y_i \\
&= -\frac{1}{2} \sum_{i=1}^{n} \sum_{j=1}^{n} \alpha_i \alpha_j y_i y_j x_i^T x_j + \sum_{i=1}^{n} \alpha_i
\end{aligned}$$

This equation can be used to define a dual problem:

$$\begin{aligned}
\max \; & -\frac{1}{2} \sum_{i=1}^{n} \sum_{j=1}^{n} \alpha_i \alpha_j y_i y_j x_i^T x_j + \sum_{i=1}^{n} \alpha_i \\
& \text{subject to } \alpha_i \geq 0, \sum_{i=1}^{n} \alpha_i y_i = 0
\end{aligned}$$

The problem above is a quadratic programming problem that always has a solution. Points x_i with non-zero α_i are called support vectors. These are the points that determine the decision boundary.

2.4.2 Non-linearly separable Support Vector Machines

The assumption regardin linear separability of training points cannot be always met. In this section there will be presented an approach that does not require points to be linearly separable. The basic idea here is to allow misclassification, but to minimize the error on the same time. This method is known as Cost-SVM or soft margin method. In general, it allows the points to be on the *wrong* side of the hyperplane, but a penalty function is introduced. Let us label with ξ_i the error in classification

of the i-th point, i.e. its distance to the classification plane in case when it is misclassified. This variable is called *error variable* or *slack variable*. In addition, let us label with C a tradeoff parameter between error and margin. Now, the minimized function is expressed as follows:

$$\frac{1}{2}||w||^2 + C \cdot \sum_{i=1}^{n} \xi_i \tag{2.11}$$

with the following constrains:

$$y_i \left(w^T x_i + b \right) \geq 1 - \xi_i, \quad \xi_i > 0 \tag{2.12}$$

The dual problem becomes the following:

$$\text{max. } W(\alpha) = \sum_{i=1}^{n} \alpha_i - \frac{1}{2} \sum_{i=1}^{n} \sum_{j=1}^{n} \alpha_i \alpha_j y_i y_j x_i^T x_j$$

$$\text{subject to } C \geq \alpha_i \geq 0, \sum_{i=1}^{n} \alpha_i y_i x_i = 0$$

Non-linear Support Vector Machines

So far we considered only linear SVM, so these with linear decision boundary. While this solution is very simple from the computational and conceptual point of view, the results yielded by the method might be suboptimal. In this section we will present a generalized version of the algorithm, in which training points x_i will be transformed to a higher dimensional space. This will allow to perform a linear division of the transformed feature space equivalent to a non-linear operation in the original space i.e. a hyper-surface instead of a hyper-plane, e.g a curve in a 2-dimensional space. An example of such transformation is shown in the figure 2.4.

If we come back to the equation 2.11 we will se that the data points appear only as inner products ($x_i^T x_j$). This means that there is need to know the mapping to the higher dimensional feature space explicitely.
Let us define the kernel funtion $\mathcal{K}$ as follows:

$$\mathcal{K}(x_i, x_j) = \phi(x_i)^T \cdot \phi x_j \tag{2.13}$$

Under certain circumstances it is feasible to obtain analytically ϕ being given $\mathcal{K}$. As an example let's take $\mathcal{K}(u, v) = (1 + u^T v)^2$. Then when $n = 2$, i.e. $u = (u_1, u_2)$ and $v = (v_1, v_2)$ we get:

$$\begin{aligned}
\mathcal{K}(u, v) &= (1 + u^T v)^2 \\
&= 1 + u_1^2 v_1^2 + 2u_1 v_1 u_2 v_2 + u_2^2 v_2^2 + 2u_1 v_1 + 2u_2 v_2 \\
&= (1, u_1^2, \sqrt{2}u_1 u_2, u_2^2, \sqrt{2}u_1, sqrt2u_2)^T (1, v_1^2, \sqrt{2}v_1 v_2, v_2^2, \sqrt{2}v_1, sqrt2v_2) \\
&= \phi(u)^T \phi(v)
\end{aligned}$$

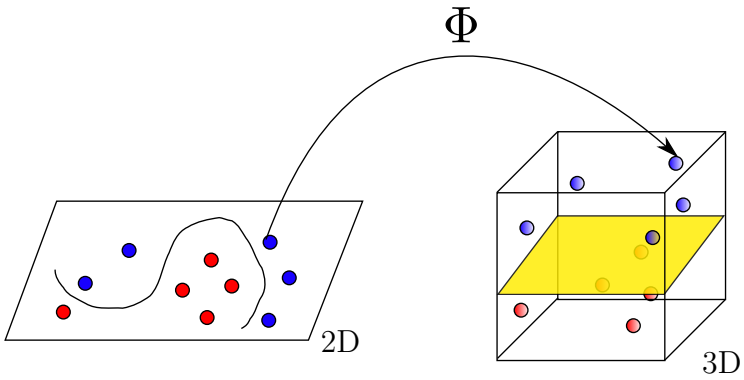


Figure 2.4: An example of a transformation from a two-dimensional to a three-dimensional space. In the original space the points are clearly not linearly separable. After applying a tranformation kernel, they can be separated with a plane marked with yellow color. With SVM several common kinds of kernels are applied to find the best way of transforming the input data into a problem with distinct borders.

A kernel function $\mathcal{K}$ must be symmetric, continuous and have a positive definite Gramian Matrix. If the kernel function does not satisfies these conditions, then the dual problem might have no solutions. There are three most commonly used kernel functions families: polynomial, sigmoid and radial (called also RBF). A polynomial kernel is expressed as follows:

$$\mathcal{K}(x_i, x_j) = (\gamma x_i^T x_j + c)^d \tag{2.14}$$

where the parameters are:

- c is a zero-degree term,
- d is the degree of the polynomial,
- γ is a generic coefficient used to parametrize the kernel.

When $d = 1$ we say that a kernel is linear. This case has been described in the section 2.4.1.
The most common variant of radial kernels is a gaussian distribution:

$$\mathcal{K}(x_i, x_j) = e^{-\gamma|x_i - x_j|^2} \tag{2.15}$$

where γ is often replaced with $\frac{1}{2\sigma^2}$, so it can be interpreted as a variation around distribution's deviation.

Chapter 3

System architecture

CERMINE is implemented in Java. While the choice of the implementation language is an important project decision, when developing our system we were constrained by a legacy of a digital library engine that CERMINE was derived from - Yadda ([Yad]). Yadda was implemented in Java and CERMINE followed this decision. The motivation behind this choice is an easier integration of both products and a wide choice of tools and libraries for Java facilitating implementation of a complex system.

3.1 CERMINE workflow

CERMINE workflow is composed of a multi-part pipeline, out of which every stage is treated as a separate module and can be maintained and developed independently. For implementation of the majority of non-trivial problems we used supervised and unsupervised machine learning algorithms, which gave us a lot of elasticity and allowed adapting to new document layouts.

CERMINE workflow consists of the following distinguishable stages:

1. **Character extraction** takes place at the very beginning of metadata extraction process. CERMINE uses `pdfbox` - an external library for manipulating PDF content - to extract a stream of characters together with their geometrical properties (size and position) from the input files.

2. **Text segmentation** builds up blocks of text from a set of characters using their position and size. This stage uses Docstrum algorithm, coded by Krzysztof Rusek and described in details in [O'G93]. It is therefore beyond the scope of this work and will not be mentioned hereafter.

3. **Resolution of the reading order** aims figuring out the order in which blocks of text are meant to be read. While this task is trivial to a human reader, it is tricky to implement an elastic algorithm suitable for different article layouts.

4. **Basic structure extraction** takes a PDF file on the input and produces a geometric hierarchical structure representing the document. The structure is composed of pages, zones, lines, words and characters. The reading order of all elements is determined. Every zone is labeled with one of four general categories: `METADATA`, `REFERENCES`, `BODY` and `OTHER`.

5. **Metadata extraction** part analyses parts of the geometric hierarchical structure labeled as `METADATA` and extracts a rich set of document's metadata from it.

6. **References extraction** part analyses parts of the geometric hierarchical structure labeled as `REFERENCES` and the result is a list of document's parsed bibliographic references.

7. **Content extraction** part analyses parts of the geometric hierarchical structure labeled as `BODY` and extracts document's body structure composed of sections, subsections and paragraphs.

A diagram of the above mentioned workflow can be found in the figure 3.1.

3.2 Structure extraction

3.2.1 Character extraction

PDF document as such consists of a stream of characters, whereas position of each character in the stream doesn't have to be related, and usually is not, to its position in the text. Extraction of the characters is achieved using iText library. This part of the system was entirely implemented by Dominika Tkaczyk and will not be described in this work.

3.2.2 Page segmentation

Page segmentation is a task of clustering a set of characters into blocks of text. Implemented system uses internally the Docstrum algorithm, described in details in [O'G93]. It is a bottom-up approach based on nearest-neighborhood clustering of connected components extracted from the document. K-nearest neighbors for each component are found and text lines are found based on a threshold of the angle

between component centroids. Then, histograms of components spacing are used to detect inter-character distance in a word and between words. The algorithm has a set of thresholds that have to be set based on experiments with various documents. The algorithm was implemented by Krzysztof Rusek and tuned by Dominika Tkaczyk and therefore will not be described in this document in details.

3.2.3 Reading order resolving

Resolution of Reading Order is a process aiming to transform text zones from a two-dimensional space (as they are laid out on the paper) to a single-dimensional space, i.e. as they are read by a human. Usually this is done by going from left to right and from top to bottom, but there are a lot of cases that made this naïve approach less efficient. This includes multi-column layout, page numbers, textual elements of figures, figures' and equations' labels.

As already described in [Dom14], a PDF file contains a stream of characters that undergoes processes of extraction and segmentation. This results in a list of pages consisting of zones, lines, words and chunks of text. These elements need to be put together in the same order as that would be done by a human reader.

To this end, a bottom-up strategy is applied: firstly characters are sorted within words and words within lines in ascending order according to X coordinate value. Afterwards, lines are sorted with Y coordinate as the key. As next we need to figure out zones' order. Below we describe a heuristic responsible for setting order of text zones. Its fundamental principle was borrowed from [AD09]. A schematic diagram of this phase, together with the symbols used, can be found in the figure 3.2.

1. For each pair of zones inside a single page boundaries a free space between them is calculated. On the figure 3.2 this space is illustrated as the black area between two zones. The full implementation of the algorithm is included in the appendix C. Below we detail the steps taken.
   (a) Formally the free space S can be expressed as $S = A_d - (A_1 + A_2)$, where A_1 and A_2 are areas of the two zones and A_d is area of the smallest rectangle in which two objects can fit. This rectangle has its sides parallel to the X and Y axes.
   (b) To include preference for vertical clustering (and to avoid joining blocks horizontally when working with multi-column layouts) cosine of the angle α between the vector $\vec{v}$ connecting two objects' geometrical centers and vector $\vec{x}$ being a projection of the vector $\vec{v}$ on the X axis is calculated. This was illustrated in the figure 3.3. The formula $\cos\alpha = \frac{\vec{v}\cdot\vec{x}}{|\vec{v}||\vec{x}|}$ is employed.

(c) Free space S is multiplied by sum of coefficient M and $\cos\alpha$. Coefficient M is introduced in order to prevent situations where more than two zones have the same width and lay in-line with respect to the Y axes. Then, for each of them the calculated distance would be equal to zero. In such cases we prefer to join these two groups between which the Euclidean distance is minimized.

2. A list L containing triples (O_1, O_2, D) is created (where O_1 and O_2 are zones on the page and D is the distance between zones). Initially there are $\binom{N}{2}$ elements in the list, where N is the total number of zones on a page.graphics

3. List L is sorted in ascending order with respect to the distance D.

4. Until this list is empty, the first triple is picked (i.e. with the smallest distance D) and two associated objects, O_1 and O_2, are merged into a new object O_{1-2}.

5. For each element E in the list L recalculate the distance D to the new group iff E was based on O_1 or O_2 (i.e. is in form of $(O_*, *, D)$ or $(*, O_*, D)$). Then, a new triple (O_1O_2, X, D) is inserted in the list L, where O_{1-2} is the new group.

6. The list L is sorted in ascending order.

```
private double distance(BxObject obj1, BxObject obj2) {

    double x0 = Math.min(obj1.getX(), obj2.getX());
    double y0 = Math.min(obj1.getY(), obj2.getY());
    double x1 = Math.max(obj1.getX() + obj1.getWidth(),
           obj2.getX() + obj2.getWidth());
    double y1 = Math.max(obj1.getY() + obj1.getHeight(),
           obj2.getY() + obj2.getHeight());
    double dist = ((x1 - x0) * (y1 - y0) - obj1.getArea() - obj2.getArea());

    double obj1CenterX = obj1.getX();
    double obj1CenterY = obj1.getY() + obj1.getHeight() / 2;
    double obj2CenterX = obj2.getX();
    double obj2CenterY = obj2.getY() + obj2.getHeight() / 2;

    double obj1obj2VectorCosineAbs = Math.abs((obj2CenterX - obj1CenterX) /
        Math.sqrt((obj2CenterX - obj1CenterX) * (obj2CenterX - obj1CenterX) +
        (obj2CenterY - obj1CenterY) * (obj2CenterY - obj1CenterY)));
    final double M_COEFF = 0.5;
    return dist * (M_COEFF + obj1obj2VectorCosineAbs);
}
```

3.3 Initial zone classification

Once the workflow stages described in sections 3.2.1, 3.2.2 and 3.2.3 are done, the document can undergo two phases of classification. For the sake of clarity, in this document all classes from the first phase of classification will be written in upper case, while those from the second phase will be typed in lower case. In CERMINE primarily all the zones are classified to one of the four general classes: `METADATA`, `REFERENCES`, `BODY` and `OTHER`. After this stage, more specific classifiers and algorithms can perform fine-grained analysis on the zones falling into each class. Semantics of these classes is as following

- `METADATA` contains all the data which do not constitute the proper content. This includes publication elements such as: title, author name, affiliation, bibliographic information, abstract etc.

- `BODY` contains text of the publication. This includes the chapters, figures, tables, equations, plots, acknowledgments, headings, contribution statements, conflict statements and attachments.
- `REFERENCES` contains article's references,
- `OTHER` contains misclassified zones and page numbers. It is a result of a non-ideal dataset, being tagged only to some extent. When training the classifier, those unclassified zones are labeled as `OTHER`. This in turn introduces some kind on additional noise. We decided that it is better to exclude a handful of zones from the further processing and classify them as `OTHER`, rather than to classify them incorrectly to one of the remaining classes. Employed dataset contains 3.6% of unknown labels, therefore we might expect a similar number of zones classified to `OTHER` in the classifier's output.

Initial classification uses Support Vector Machines as classification algorithm, with the parameters given in the table 4.1. A way to obtain these parameters is described in 4.1.5.

3.4 Metadata classification

Once the initial coarse-grained classification is done, we employ a second classifier which is specialized in classifying metadata, i.e. those zones, which initially got the `METADATA` label. This class consists of 19 labels:

- `abstract` - document's abstract, usually one or more zones placed in the first page of the document;
- `acknowledgments` - sections containing information about document's acknowledgments or funding;
- `affiliation` - authors' affiliations sections, which sometimes contain contact information (emails, addresses) as well;
- `author` - a list of document's authors,
- `bib_info` - zones containing all kinds of bibliographic information, such as journal/publisher name, volume, issue, DOI, etc.; often includes pages' headers or footers; headers and footers containing document's title or author names are also labeled as bib_info;
- `body_content` - the text content of the document, contains paragraphs and section titles;

- `conflict_statement` - conflict statement declarations;
- `copyright` - copyright or license-related sections;
- `correspondence` - the authors' contact information, such as emails or addresses;
- `dates` -important dates related to the document, such as received, revised, accepted or published dates;
- `editor` - the names of the document's editors;
- `equation` - equations placed in the document;
- `figure` - zones containing figures' captions and other text fragments belonging to figures;
- `glossary` - important terms and abbreviations used in the document;
- `keywords` - keywords listed in the document;
- `page` number -zones containing the numbers of pages;
- `table` - the text content of tables and table captions;
- `title` - the document's title;
- `title_author` - zones containing both document's title and the list of authors;
- `type` -the type of the document, usually mentioned on the first page near the title, such as *research paper*, *case study* or *editorial*;
- `unknown` - used for all the zones that do not fall in any of the above categories.

3.5 References extraction

Reference extraction path is responsible for processing zones that were labeled as `REFERENCE` during the initial classification; its purpose is to extract bibliographic references together with their metadata.

To this end, the blocks of text are divided into strings containing one bibliographic reference each. This phase employs unsupervised learning whose task is to cluster all lines of references into two group - one group containing only first lines of references and the second group containing other lines. The clustering algorithm uses 5 features based on the text layout.

Afterwards, individual references are parsed and corresponding bibliographical data are yield back. This algorithm is based on Conditional Random Fields, thus a supervised learning algorithm, and is implemented on the top of GRMM and Mallet packages.

Reference extraction was implemented by Mateusz Fedoryszak and is described in details in [Dom14].

3.6 Content extraction

CERMINE is capable of extracting article's raw text. To this end, it processes all the zones labeled by the initial classifier as `BODY` and outputs the text that they contain according to the reading order.

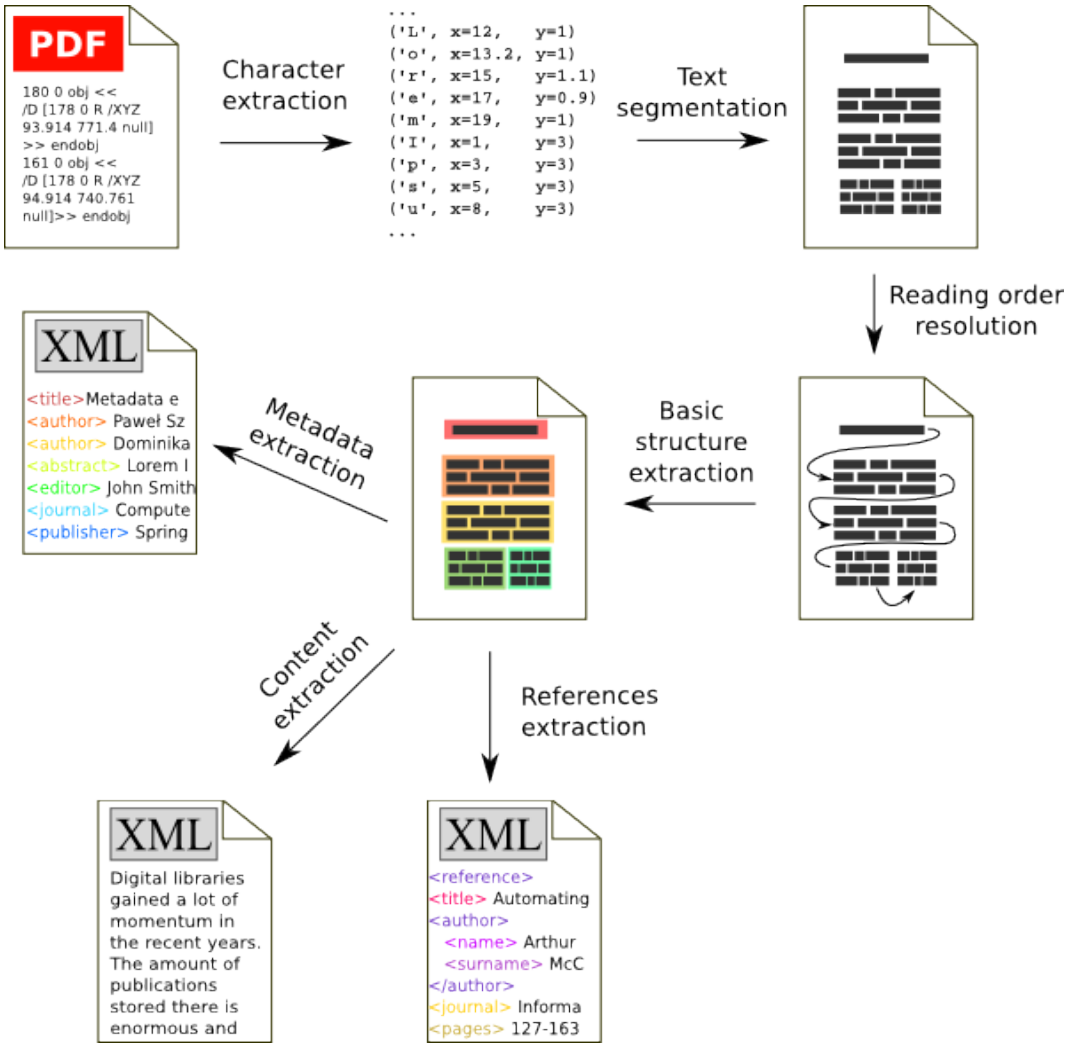


Figure 3.1: A schematic diagram of CERMINE's workflow.

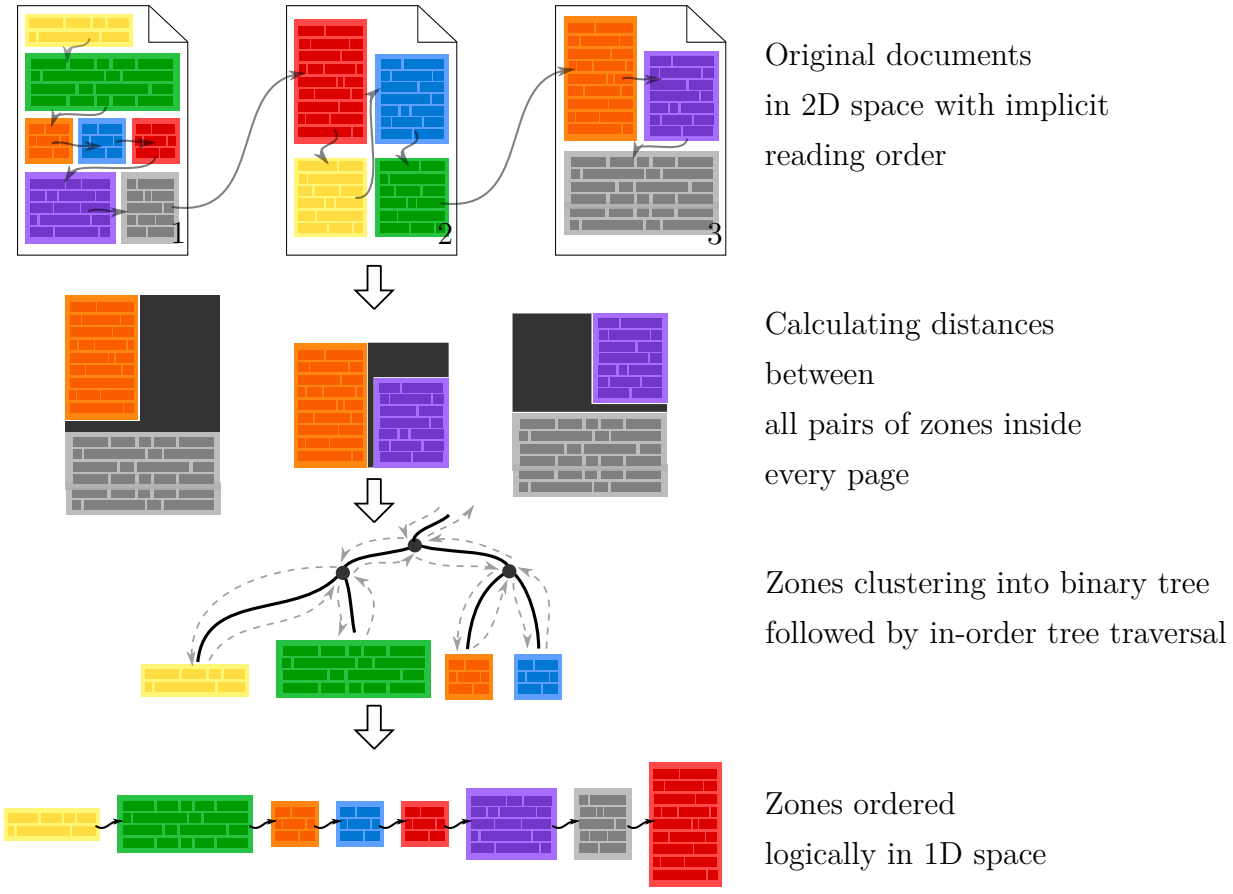
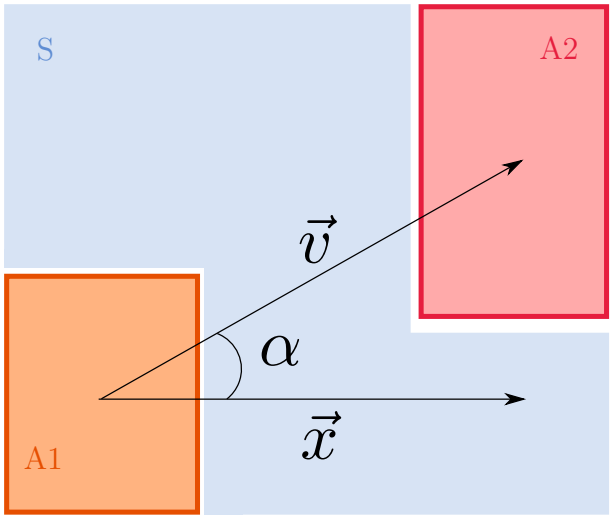


Figure 3.2: A schematic diagram of reading order resolving. Firstly, distances between text zones are calculated. Then, zones are hierarchically grouped according to distances between them. Finally, the tree is in-order traversed and a list of zones in created.



$$D = S \cdot (M + \frac{\vec{v} \cdot \vec{x}}{|\vec{v}||\vec{x}|})$$

Figure 3.3: An example of calculating distance between two zones. To include preference for vertical clustering a cosine of the angle α between the vector $\vec{v}$ and vector $\vec{x}$ (horizontal axis) is calculated. Parameter M is used to prevent zeroing of the distance for zones laying in the same vertical axis.

Chapter 4

Classification workflow

4.1 Classification training workflow

4.1.1 Generating samples

TrueViz documents are an input for the classification training workflow. As depicted in 5.2 they consists of text together with its geometrical properties and class. The zones are used to generate training samples, which are values of plethora of features for particular zones together with the classification information. Semantics of the feature values is as following: *if the final classifier gets an input that has the same values of features, it should be classified in the same way as the training sample.* The role of a classifier is to extrapolate in a compact way data from the training samples to unseen cases.

4.1.2 Data scaling

A very important step towards learning a classifier is scaling of the input data. The main motivation behind that, as mentioned in [CL10], is not to allow variables in greater numerical ranges to dominate those in smaller numerical ranges. What is more, large values might cause numerical problems. One has to take into account that the closer to zero floating point variables are, the more precisely are they represented. Scaling recommended by [CL10] is in range [-1, +1] or [0, 1]. The latter is used in CERMINE. Obviously, both learning and testing data have to be scaled using the same transformation. Thus, it is necessary to retain extreme values encountered in learning process. In CERMINE scaling for learning purposes was realized with `svm-scale`, a software tool delivered together with the `libsvm`

package.

4.1.3 Data sampling

When the decision classes are unequally represented in the training data. The approaches used to deal this problem can be divided into three groups ([Cho10]):

1. Changing class distribution by modifying the data itself in order to rebalance it. It can be reached by either getting rid of samples from over-represented classes or by cloning samples from the under-represented classes. The former can greatly reduce the time spent on the optimization phase. The latter prohibits not common samples from falling out of the training set, making the resulting classifier more versatile.

2. Adjusting the classifier itself by applying different misclassification costs for different classes. These costs might be for instance inversely linear to number of samples in each class.

3. Ensemble learning methods, i.e. using multiple classifiers trained with multiple training data and then combining output of the classifier, for instance by a simple voting.

In CERMINE two first of the mentioned approaches were tested and the second one is included in the final code.

4.1.4 Transformation to svmlight format

Various SVM packages, including libsvm, require that the data are represented as vectors of real numbers. Thus, if the data contains categorical attributes (such as `red`, `green`, `blue` or `big`, `small`) they have to be converted to numerical values. There are two common approached to this problem:

- Using a single value to encode the category. This can be very easily implemented by using the integer value behind enumeration in C implementation

- Using N different numbers to represent a category with N possible values. According to [CL10], this approach yields more stable results

Svmlight format is a text file format that requires every training sample to be in a separate line (thus, they must be split with new line characters). Each line consists of a certain number of fields separated with white signs, e.g. spaces. Each line has to begin with a number representing the decision class followed by feature

values. There are no constrains regarding encoding of the decision classes, as long as this encoding is coherent. Feature values have a form of $f_n : v_n$, where f_n is the feature number and v_n is its value. Not every feature has to be listed, but only these whose values are non-zero. This format is beneficial for the scenarios where features are sparse.

4.1.5 Parameter optimization

It impossible to tell *a priori* which kernel function is the most appropriate for the given training data. There are kernels that behave usually well (and RBF is one of them) and these should be a choice when the learning process is constrained by time.

SVM classifier have a handful of free variables and kernel type is one of them. In general, when optimizing a classifier one has to find a triple (K, C, γ) that maximizes classifier's accuracy for the given training data. In this triple K is the kernel type, C is a generic cost of misclassifying data and γ is a kernel parameter. One of the techniques of obtaining them is an extensive parameter space search by checking classifier's accuracy in every point on a parameter grid. Commonly this kind of search is called *grid search* and does not allow to omit any of the points in the parameter space without a risk of missing a possibly optimal point.

For every point in the space a k-fold cross-validation is applied. It means that for a set of parameters the training set is divided into k subsets, each of equal or nearly-equal size. At every step $k - 1$ of these subsets constitute the training set and the remaining k-th set is treated as the unknown data employed to verify correctness of the trained classifier. The trained classifier is applied to classification of the pseudo-unknown data and finally their *de facto* is compared to the output of the classification. After k iterations the mean efficiency is calculated and it serves as a criterion for evaluating the current (K, C, γ) triple.

In the case of CERMINE grid search was performed on 16'384 samples from GROTOAP2. The training set was limited to this size to limit to make possible evaluation with reasonable time constraints. For both classifiers four kernels were tested with $log_{10}C$ and $log_{10}\gamma$ varying with a unit step in range $[-5, 15]$ and $[-15, 3]$ respectively, resulting in 399 points tested for every classifier. In total there were 3192 $(= 399 \cdot 4 \cdot 2)$ points tested in the first pass, which yielded candidates for accuracy maxima. Later, a fine-grained search was performed with the best kernels so far (both RBF) around the candidates for maximum in distance of 10dB with a step equal to 2.5dB resulting in additional 81 points being checked for each of the classifier. Results of this procedure are presented in the figures 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9 and 4.10. Optimal parameters for the classifiers are presented in the table 4.1.

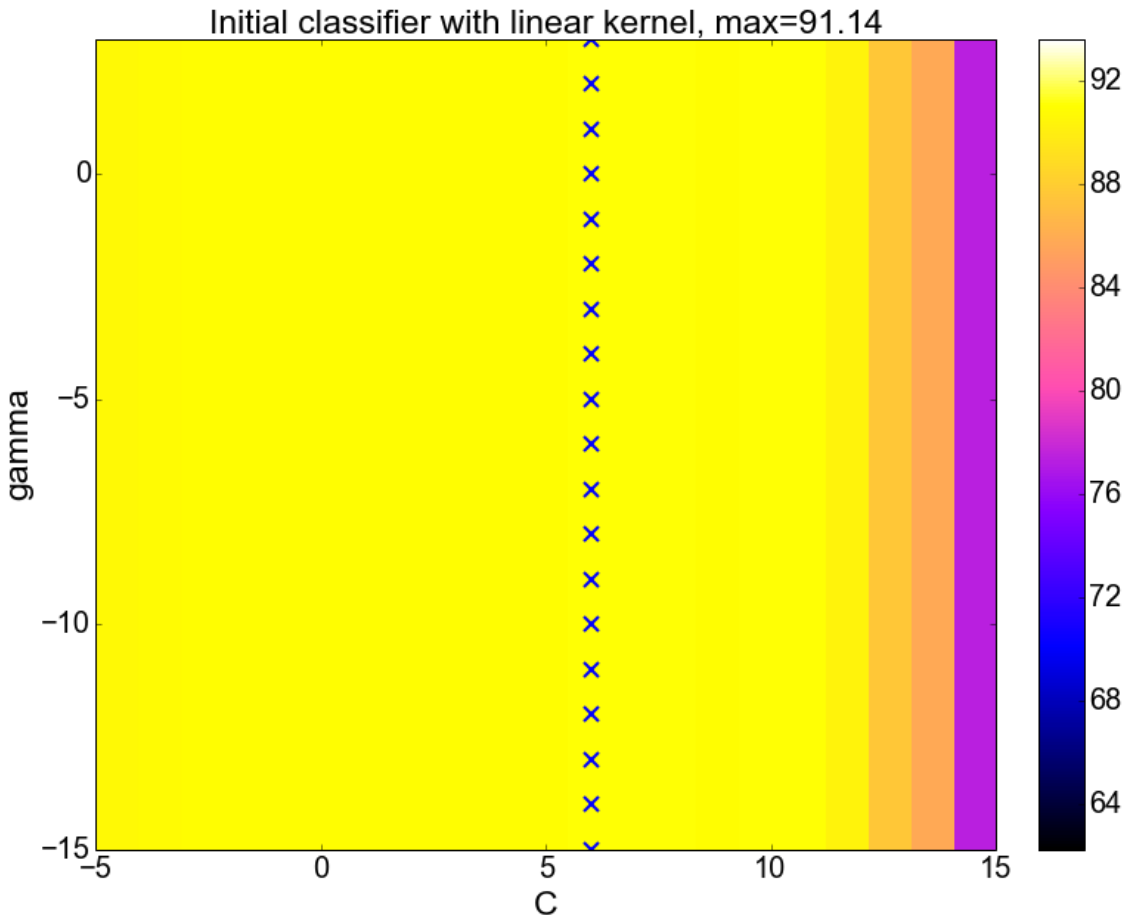


Figure 4.1: Grid search over two-dimensional parameter space (C, γ) with linear kernel for the initial classifier. The maximal accuracy in 5-fold cross-validation is equal to 91.14 and is found for $log_{10}C = 6$

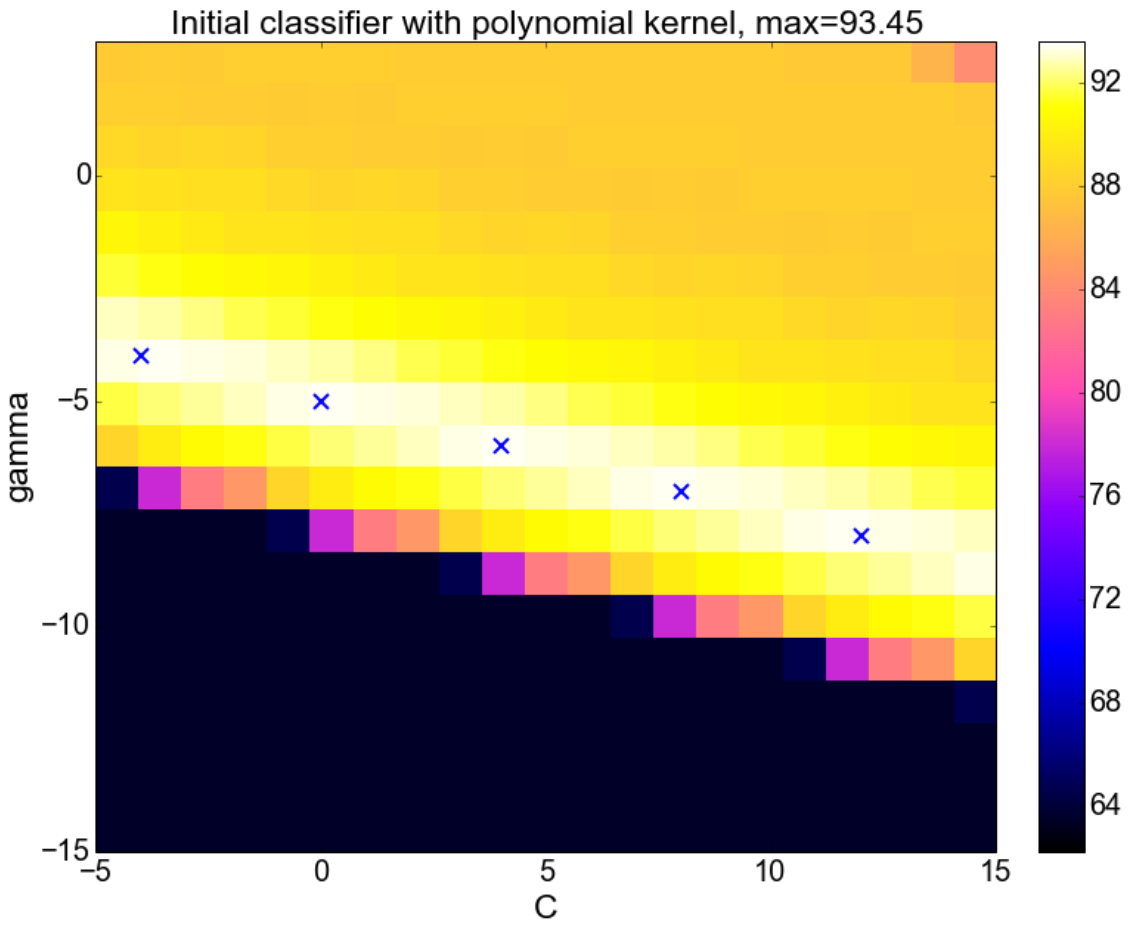


Figure 4.2: Grid search over two-dimensional parameter space (C, γ) with polynomial 4^{th}-degree kernel for the initial classifier. In the investigated interval there are 5 maxima. Classifier accuracy over 5-fold validation is equal to 93.45 and is found for instance for $log_{10}C = 3$ and $log_{10}\gamma = -7$.

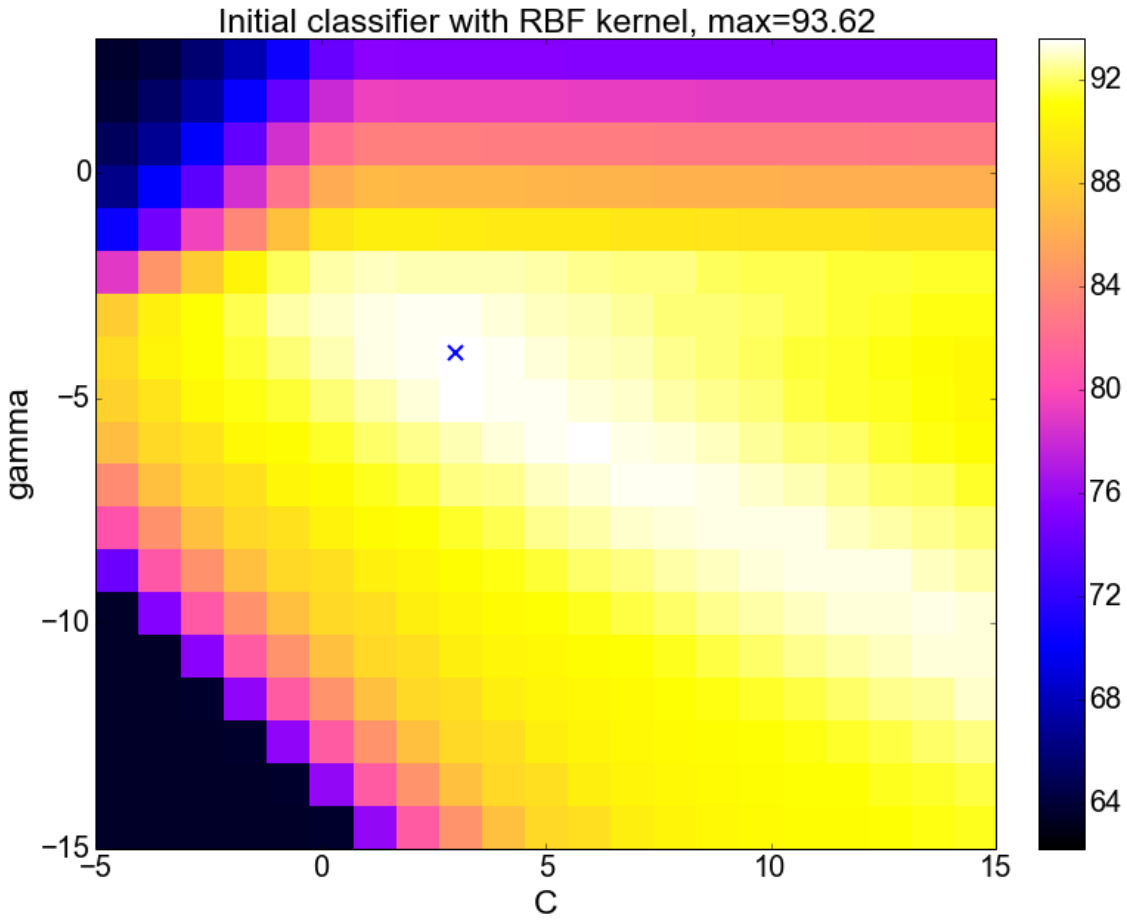


Figure 4.3: Grid search over two-dimensional parameter space (C, γ) with a radial-basis function kernel for the initial classifier. The maximal accuracy in 5-fold cross-validation is equal to 93.62 and is found for $log_{10}C = 3$ and $log_{10}\gamma = -4$. This was the highest accuracy found in the first pass. The second pass refined the maximum around the initial result.

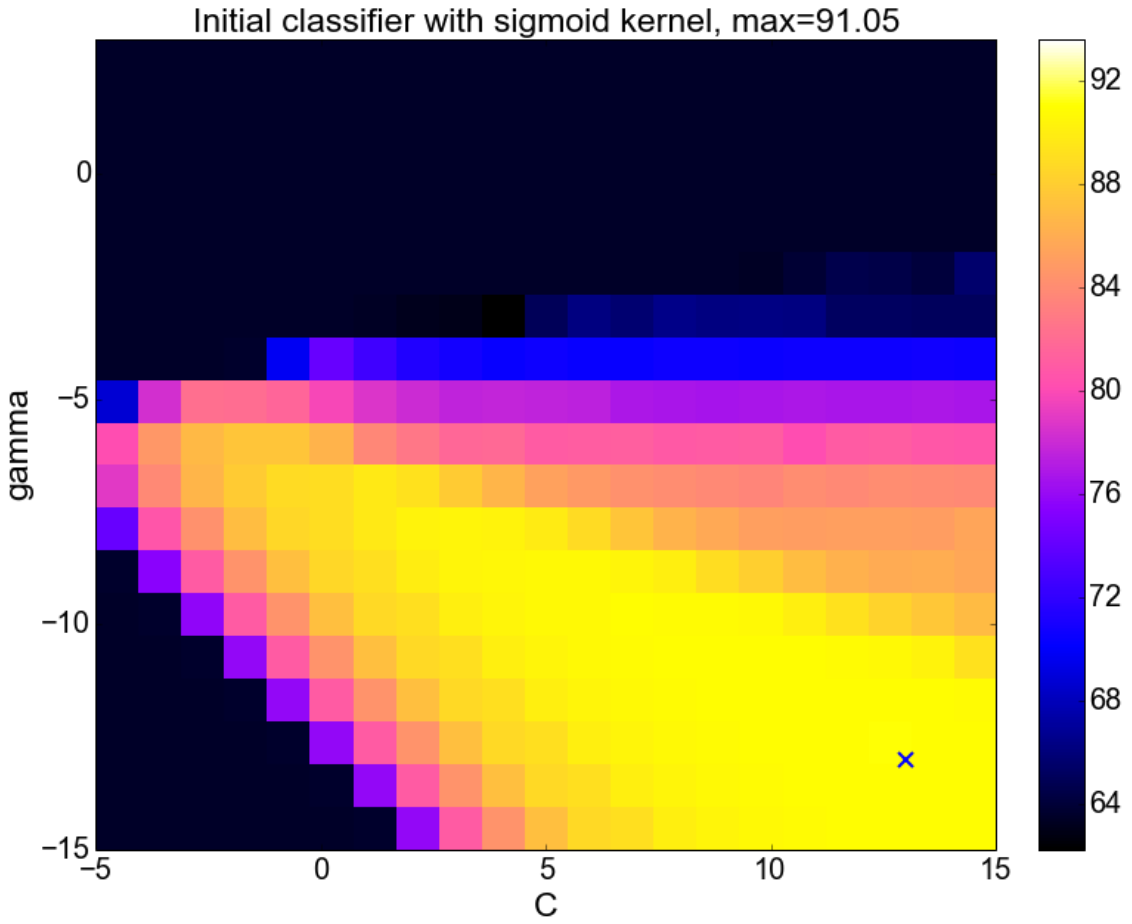


Figure 4.4: Grid search over two-dimensional parameter space (C, γ) with a sigmoid kernel for the initial classifier. The maximal accuracy in 5-fold cross-validation is equal to 91.05 and is found for $log_{10}C = 13$ and $log_{10}\gamma = -13$

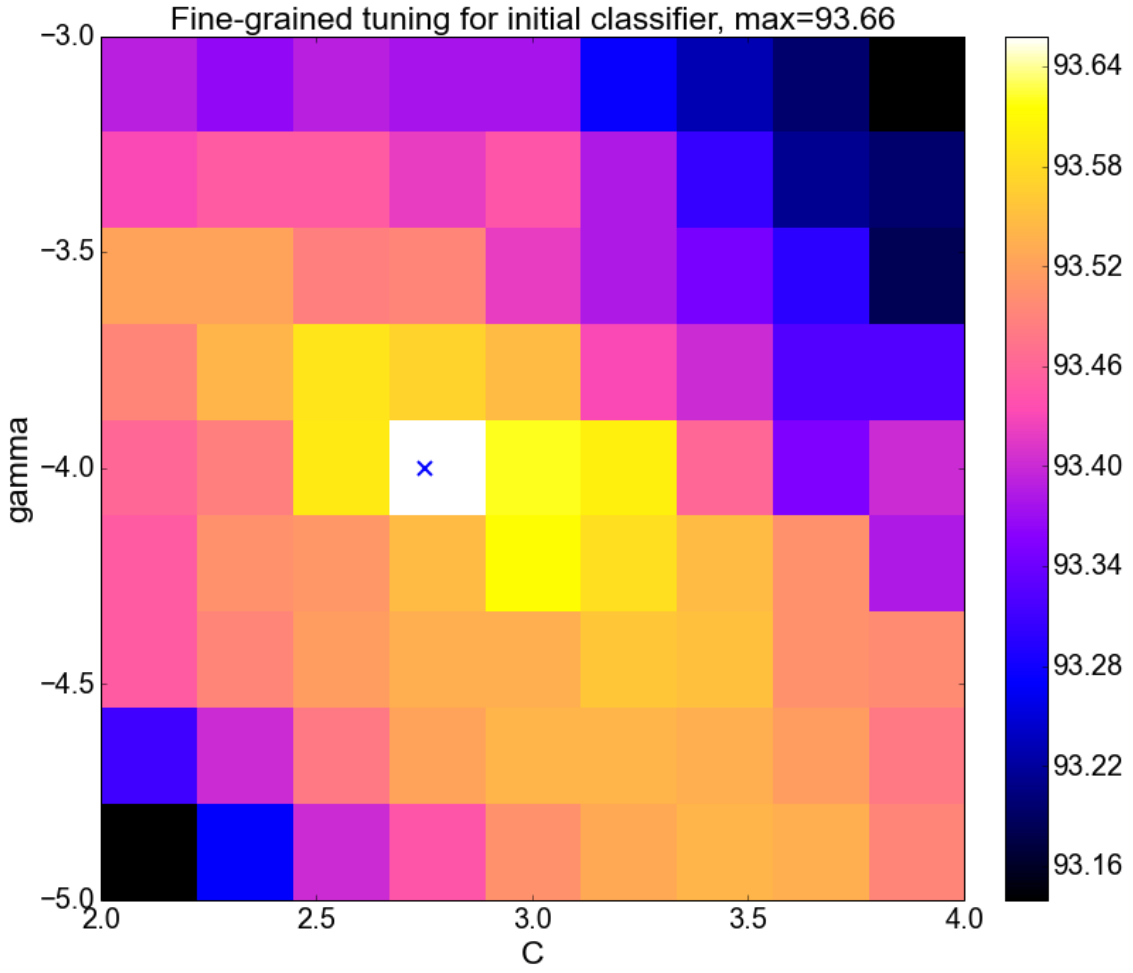


Figure 4.5: Fine-grain search around initial classifier with RBF kernel for the initial classifier (the color-mapping scheme is not coherent with the previous plots). Initial coarse-grain search yielded the maximum in ($log_{10}C = 3$, $log_{10}\gamma = -4$) equal to 93.62. This search refines the search with $log_{10}step = 0.25$ yielding maximum in ($log_{10}C = 2.75$, $log_{10}\gamma = -4$) equal to 93.66. This parameters are used for training of the final classifier.

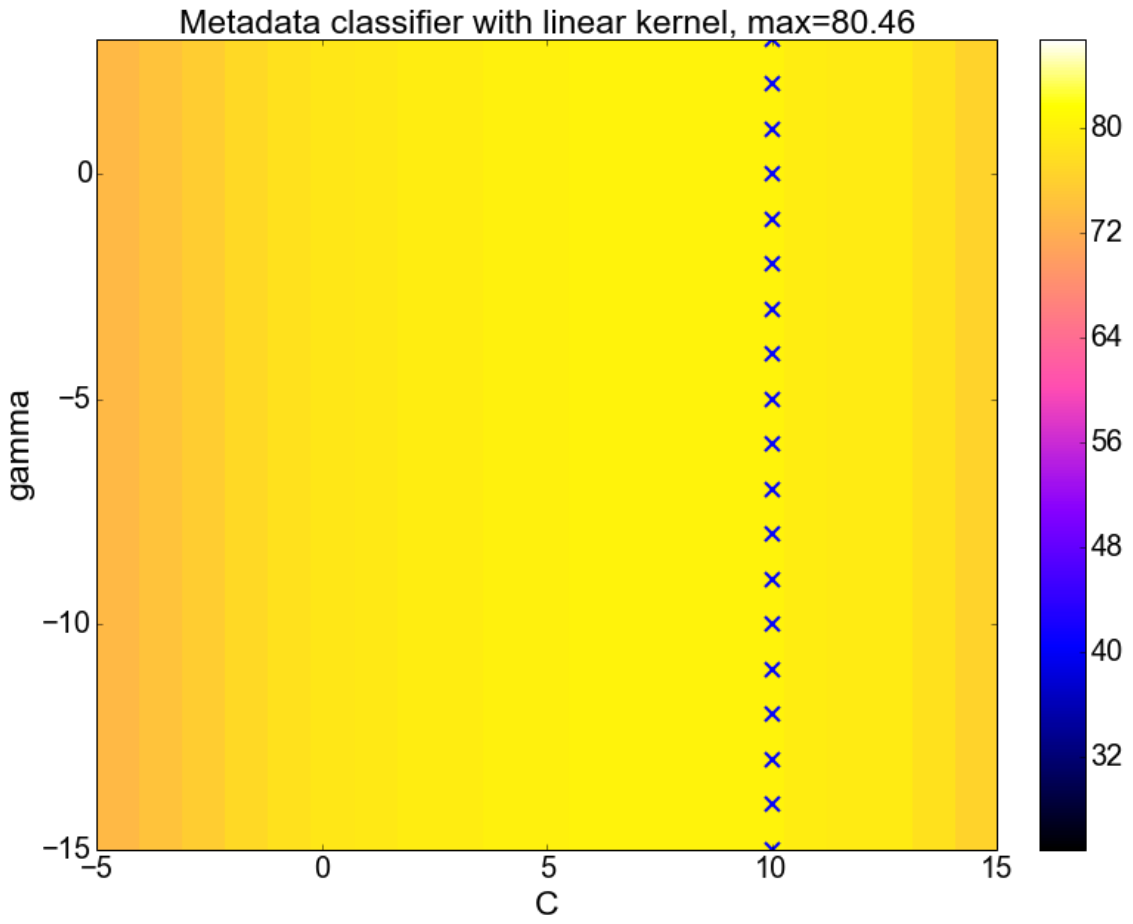


Figure 4.6: Grid search over two-dimensional parameter space (C, γ) with linear kernel for the metadata classifier. The maximal accuracy in 5-fold cross-validation is equal to 80.46 and is found for $log_{10}C = 19$

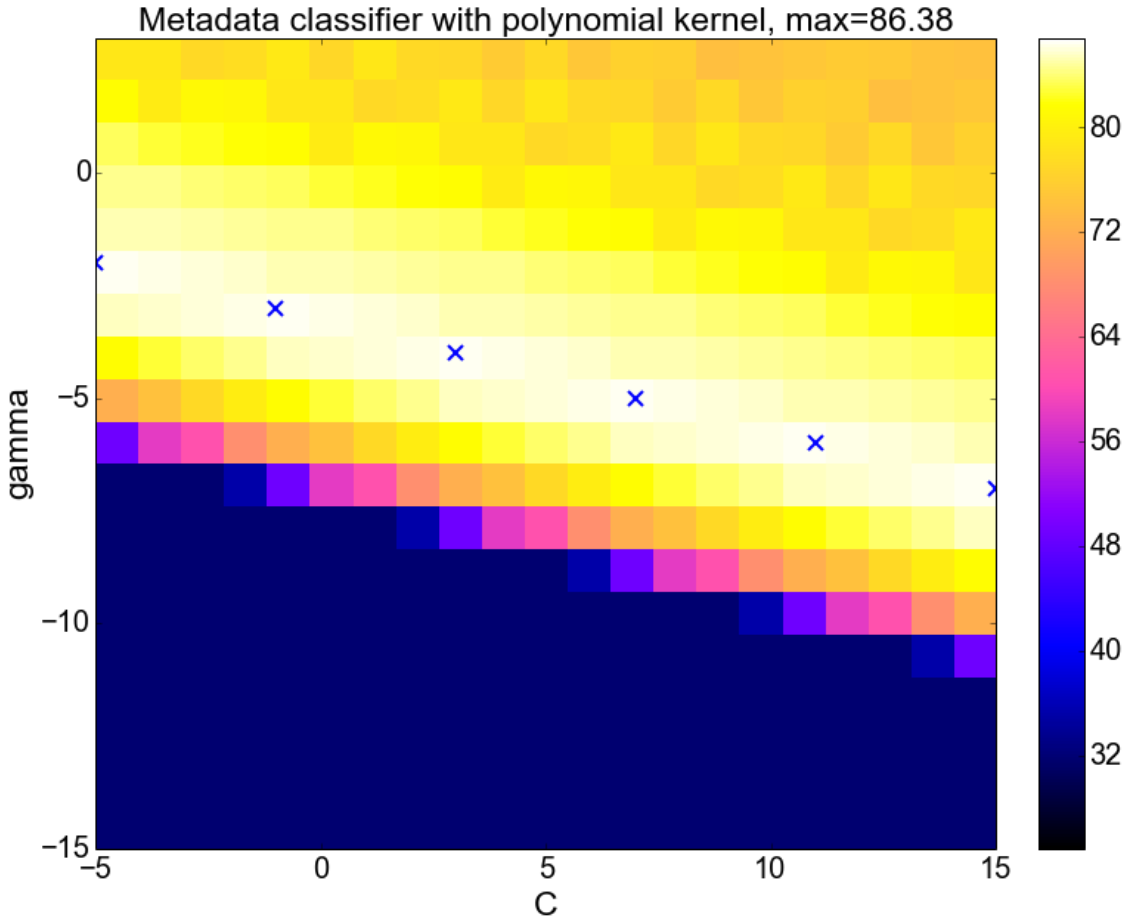


Figure 4.7: Grid search over two-dimensional parameter space (C,γ) with polynomial 4^{th}-degree kernel for the metadata classifier. In the investigated interval there are 5 maxima. Classifier accuracy over 5-fold validation is equal to 86.38 and is found for instance for $log_{10}C = 7$ and $log_{10}\gamma = -5$.

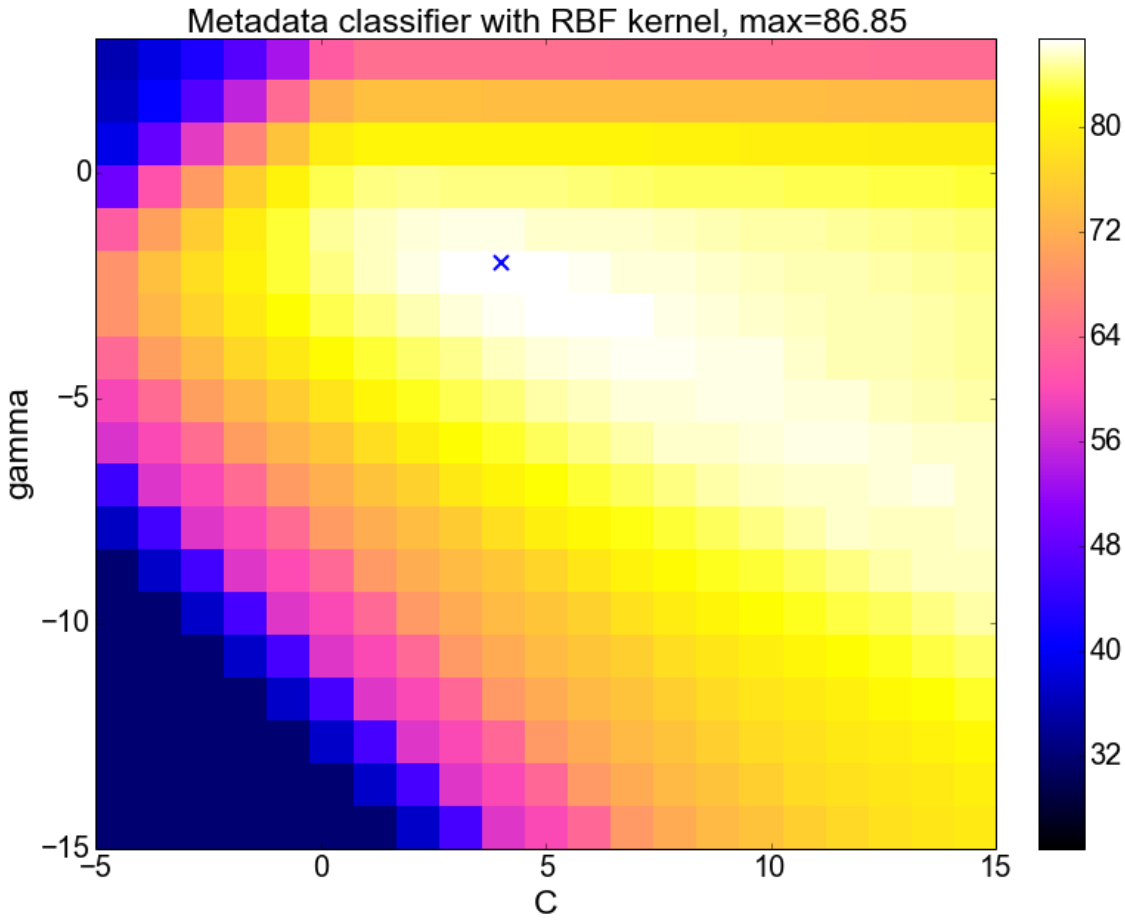


Figure 4.8: Grid search over two-dimensional parameter space (C, γ) with a radial-basis function kernel for the metadata classifier. The maximal accuracy in 5-fold cross-validation is equal to 86.85 and is found for $log_{10}C = 4$ and $log_{10}\gamma = -2$. This was the highest accuracy found in the first pass. The second pass refined the maximum around the initial result.

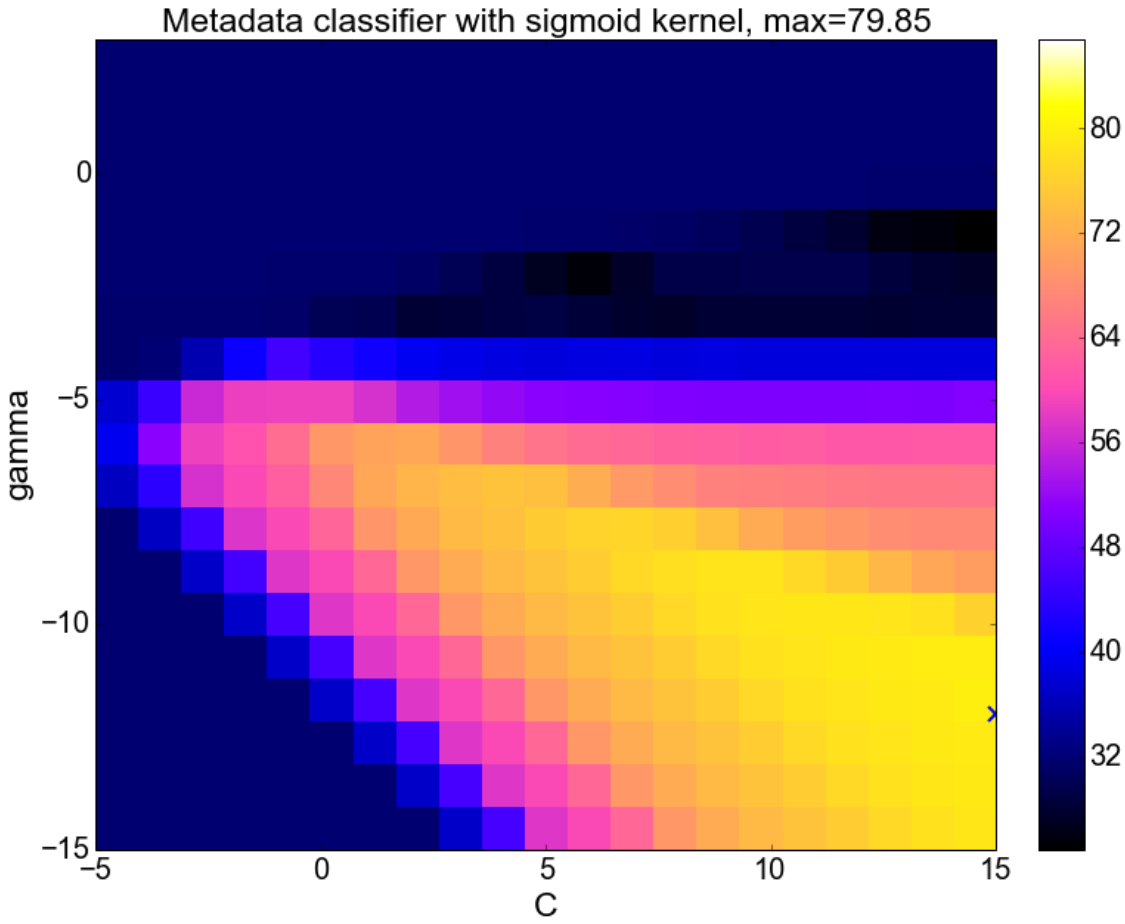


Figure 4.9: Grid search over two-dimensional parameter space (C, γ) with a sigmoid kernel for the initial classifier. The maximal accuracy in 5-fold cross-validation is equal to 79.85 and is found for $log_{10}C = 15$ and $log_{10}\gamma = -12$

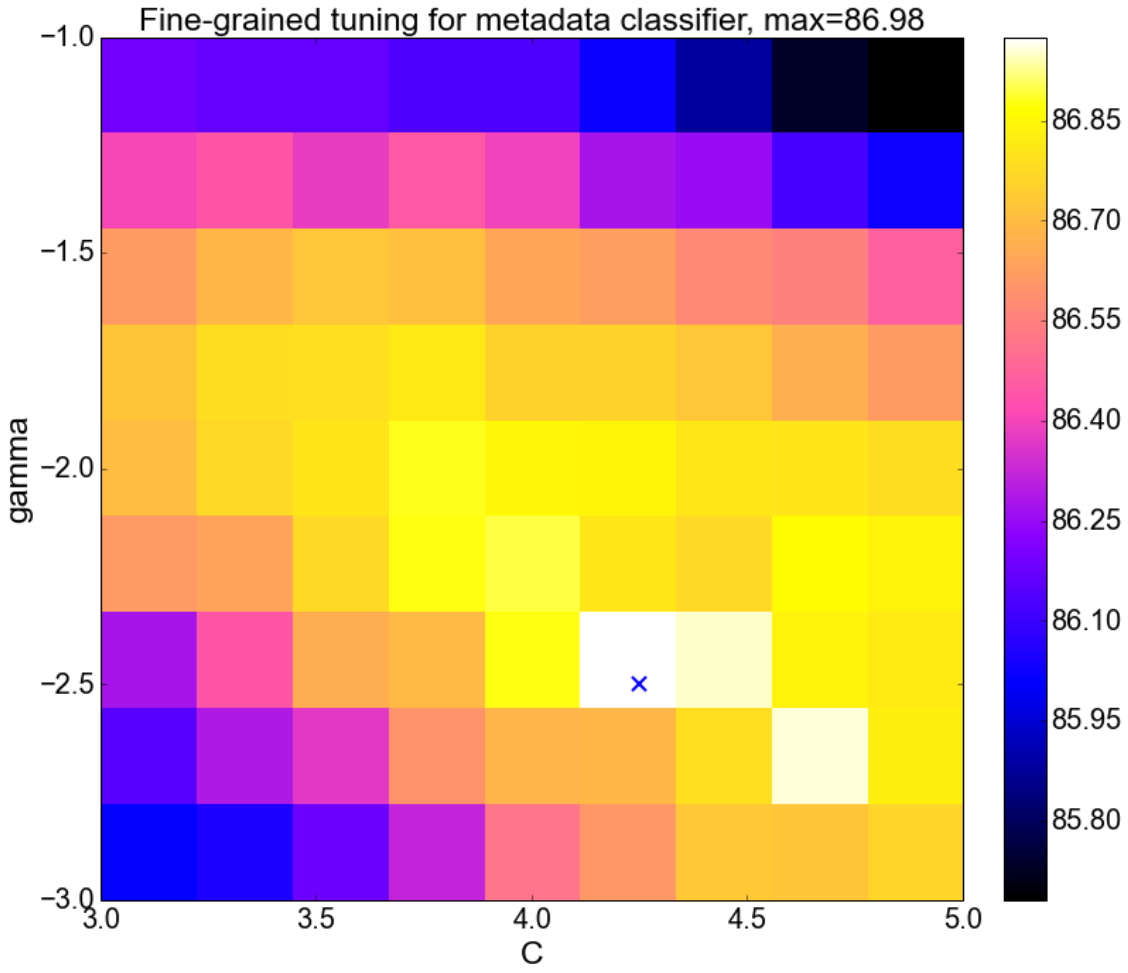


Figure 4.10: Fine-grain search around initial classifier with RBF kernel for the metadata classifier (the color-mapping scheme is not coherent with the previous plots). Initial coarse-grain search yielded the maximum in ($log_{10}C = 4$, $log_{10}\gamma = -2$) equal to 86.85. This search refines the search with $log_{10}step = 0.25$ yielding maximum in ($log_{10}C = 4.25$, $log_{10}\gamma = -2.5$) equal to 86.98. This parameters are used for training of the final classifier.

	Initial classifier	Metadata classifier
SVM type	C_SVC	C_SVC
kernel type	RBF	RBF
γ	-4.0	-2.5
C	2.75	4.25
$coef_0$	0.5	0.5
mean accuracy	93.66	86.98

Table 4.1: Results of the grid search in parameter space for the initial and metadata classifiers. Values above were used to train the classifiers and to perform final evaluation of the systems.

4.1.6 Training of the final classifier

After the optimal parameters have been found using a grid search, we train the classifiers to perform the final evaluation. This process is characterized in the appendix A. To this end, we used classes `SVMInitialZoneClassificationEvaluator` and `SVMMetadataClassificationEvaluator` that build the classifier and perform cross-validation at a time. Its results are presented in the chapter 6.

4.2 Feature selection

In both stages of classification we employed a set of features including almost one hundred elements. In appendix B there is a detailed description of how their values are calculated. Briefly, they can be divided into following groups:

Sequence features

This group contains only two features: *PreviousZoneFeature* and *LastButOneZoneFeature*. It leverages the fact that the zones are classified after the process of reading order resolution is done. The features contain numerical value of two previous labels. In turn, this allows to incorporate sequence information into classification, which is not done in SVM by design (as opposed to for instance Hidden Markov Model).

Formatting features

This group of features contains information about graphical properties of text. It can be very helpful since certain elements in scholarly publications are usually typed with bigger font size.

Layout features

These features encode information about graphical layout on the page. This includes properties of the zone itself (e.g. *WidthFeature*, *HeightFeature*, *LineMeanWidthFeature*) as well as features of the area between text zones (e.g. *HorizontalRelativeProminenceFeature*, *VerticalRelativeProminenceFeature*, *IsHighestOnThePage*, *IsGreatestOnThePage*, *DistanceFromNearestNeighbourFeature*).

Semantic features

This group of features encodes appearence of certain key-words that very often characterize certain parts of articles written with scientific english, e.g. *keywords*, *terms*, *distributed*, *reproduction*, *open*, *commons*, *license*, *creative*, *copyright*, *cited*, *distribution*, *access*, *references*, *author*, *bibliography*, *figure*, *table*, *editor*, *email*, *correspondence*, *address*, *abstract*, *author details*, *university*, *department*, *school*, *institute*, *affiliation*, *affiliation*, *research article*, *review article*, *editorial*, *review*, *debate*, *case report*, *research*, *original research*, *methodology*, *clinical study*, *commentary*, *article*, *hypothesis*.

Special features

This group contains features that do not fit other groups described above. This includes e.g. *IsAnywhereElseFeature*, BracketCountFeature, CharCountFeature, CommaCountFeature.

Chapter 5

Dataset

5.1 Motivation

Despite a strong need of performing automated analyses of scholarly publications, there are no big and reliable datasets of annotated publications available publicly. Such a dataset would greatly facilitate the process of building a classifier to perform the processes of metadata extraction, which, even when boiled down to scientific publishing, is error prone and not trivial. By far this is caused by two factors:

- scientific publishing is inherently *blessed* by richness of layouts, formats and designs. No one is to be blamed for this variety which is to the most extreme degree natural. Any tool that aims to be reliable needs to take this diversity of styles into account.
- PDF, being a *de facto* standard in the scientific publishing, is a format designed to carry content as it displayed. However, it is not suitable for carrying metadata. Its main design goal was to hold geometrical metadata allowing a faithful reproduction of the source document's display with different tools and platforms. It holds no relevant metadata and the structure of the input document is broken down to the level of single characters

Each publisher or even each journal follows its own layout. For instance, in the Open Access subset of PubMed Central there are more than 800 publishers, each of them very likely following a different layout. We need to keep in mind that the articles included there are biology-related which is only a fraction of scientific publishing. It's safe to assume that there are thousands of publishers worldwide. We decided to put together a diverse set of articles that could serve as a basis for automatic approach for content analysis.

5.2 Related work

The vast majority of the data sets publicly available is based on images, i.e. there are no born-digital documents available. As an example here we might give MARG, which contains scanned first pages of biomedical articles. This makes its usability in our case very limited. PRImA is a data set containing images of various documents, whose category goes beyond scientific publishing. Again, these are images which aren't helpful in case of chosen architecture. Conversely, The UW-III data set contains both articles' images and born-digital data. It is not available freely, though. What is more, we preferred to focus in our work on pure scientific articles as those are the target input of the designed system.

5.3 Pubmed database

Pubmed [Puba] is a collection of more than 24 millions articles from MEDLINE, life science journals and online books maintained by the US National Library of Medicine. This collection is digitized which means that the articles are stored in form of PDF files and can serve as a source of full texts without a need for performing Optical Character Recognition. The PMC Open Access Subset (abbreviated to PMC-OAS) is a part of the collection of Pubmed central available publicly with any fees. These articles are kept protected by copyrights, but can be used under the Creative Commons license that allows for more liberal usage of the resources. For the time of creating this report (June 2014) there were more than 400,000 articles available.

5.4 Dataset creation

With very limited budget it is clearly impossible to create a rich set of annotated articles by human means. A predecessor of the thereafter described data set was created at ICM in [DCR+12]. GROTOAP (*GROund Truth for Open Access Publications*) created there is a collection of 113 articles in digital form with corresponding ground-truth files. This data set was created semi-automatically. First, a handful of articles was tagged manually and supplied to a predecessor of CERMINE as a training input. Then, the remaining part of articles was tagged by the trained classifier and corrected by experts later on, guaranteeing high precision and accuracy.

Its downside was that the included articles cover not more than 15 different layouts, which is certainly not enough when aiming to build a tool applicable to the whole spectrum of publishers and layouts. Initial tests have proven that this data

set did not provide sufficient diversity for the classifier to perform well enough. This is why it was decided to create a dataset, called GROTOAP2, that could serve as a base for classifiers.

5.5 GROTOAP2 properties

GROTOAP2 is made of ground-truth files in TrueViz format, which extends XML, containing publications' content structured hierarchically and tagged according to its role. This is accompanied by geometrical data on 4 levels of granularity: text zone, text line, word and character whose role is to reflect how the content should be displayed according to the PDF files. Since function of a piece of text can be distinguished not only by the text itself, but also by its appearance, i.e. the geometrical features, a dataset applicable for training a classifier must preserve the information related to dimensions and positions of the objects.

In GROTOAP2 there are in total 13210 articles made of 119334 pages and 1640973 zones coming from 208 different publishers and 1170 different journals. The data set is distributed under the CC-BY license and can be downloaded from the server of Center for Open Science [CeO]. It is available together with a list of URLs for the corresponding PDF files (which are not included in the data set itself) and scripts downloading both input XMLs and the PDFs.

5.6 The methodology of creating GROTOAP2

As stated before, it was assumed that GROTOAP2 has to be based on open access articles. Pubmed was chosen as source of input data, as a great majority of contained articles is associated with extracted metadata. Sometimes their quality might be put in doubt, but the process was designed to automatically filter them out. The method presented here is scalable to immense sets as the human factor was ruled out.

Each article in the Pubmed dataset comes as a tarball containing the article itself (in PDF file format), a metadata file (in XML file format) and possible some resource files, mainly including pictures extracted from the PDF. A sample content of a metadata XML is showed in the listing 5.1. A complete description of possible elements can be found in [Pubb].

```
<?xml version="1.0" encoding="UTF-8"?>
<front>
  <journal-meta>
    <journal-id journal-id-type="nlm-ta">Genome Biol</journal-id>
    <journal-title>Genome Biology</journal-title>
```

```
    <issn pub-type="ppub">1465-6906</issn>
    <issn pub-type="epub">1465-6914</issn>
    <publisher>
      <publisher-name>BioMed Central</publisher-name>
    </publisher>
  </journal-meta>
  <article-meta>
    <article-id pub-id-type="pmid">18341703</article-id>
    <article-id pub-id-type="pmc">2397496</article-id>
    <article-id pub-id-type="publisher-id">gb-2008-9-3-213</article-id>
    <article-id pub-id-type="doi">10.1186/gb-2008-9-3-213</article-id>
    <article-categories>
      <subj-group subj-group-type="heading">
        <subject>Minireview</subject>
      </subj-group>
    </article-categories>
    <title-group>
      <article-title>On the nature of thumbs</article-title>
    </title-group>
    <contrib-group>
      <contrib id="A1" corresp="yes" contrib-type="author">
        <name>
          <surname>Wagner</surname>
          <given-names>Gunter P</given-names>
        </name>
        <xref ref-type="aff" rid="I1">1</xref>
        <email>gunter.wagner@yale.edu</email>
      </contrib>
      <contrib id="A2" contrib-type="author">
        <name>
          <surname>Vargas</surname>
          <given-names>Alexander O</given-names>
        </name>
        <xref ref-type="aff" rid="I1">1</xref>
      </contrib>
    </contrib-group>
    <aff id="I1">
      <label>1</label>
      Department of Ecology and Evolutionary Biology, Yale University, Prospect Street, New Haven, CT
          06520-8106, USA.
    </aff>
    <pub-date pub-type="ppub">
      <year>2008</year>
    </pub-date>
    <pub-date pub-type="epub">
      <day>4</day>
      <month>3</month>
```

```
        <year>2008</year>
      </pub-date>
      <volume>9</volume>
      <issue>3</issue>
      <fpage>213</fpage>
      <lpage>213</lpage>
      <permissions>
        <copyright-statement>Copyright 2008 BioMed Central Ltd</copyright-statement>
        <copyright-year>2008</copyright-year>
        <copyright-holder>BioMed Central Ltd</copyright-holder>
      </permissions>
      <abstract abstract-type="short">
        <p>Differential Hox gene expression make the thumb special</p>
      </abstract>
      <abstract>
        <p>Asymmetric regulation of Hox gene expression pre-dates the appearance of tetrapod digits, and
            was co-opted in the development of 'thumbness'. This asymmetric expression correlates with
            independent morphological evolutionary variation of digit 1.</p>
      </abstract>
    </article-meta>
</front>
```

Listing 5.1: Sample content of a PUBMED XML file

The general strategy for creating ground-truth files out of the PMC-OAS was to match content of the metadata files to blocks of text extracted and segmented from the provided PDF files resulting in a tagged TrueViz file. This allowed us to mix together both data, metadata and geometric properties of the articles.

textbfThe role played by a given document fragment can be deduced not only from its text content, but also from the way the text is displayed for the readers. As a result, document zone classifier can benefit a lot from using not only the text content of objects, but also geometric features, such as object dimensions, positions on the page and in the document, formatting, object neighborhood, distance between objects, etc. A dataset useful for training such a classifier must therefore preserve the information related to object size, position and distance.

PMC-AOS metadata files are not perfect, though. Full understanding of their structure was achieved by thorough and laborious manual analysis of many randomly picked sample files. There are many situations that one has to take into account:

- structure of the documents varies between documents,
- random fields might be missing or be incomplete,
- same content (e.g. article's title) might be located under different paths, e.g. contributor's e-mail address might be found under `/article/front/article-meta/contrib` or `/article/front/article-meta/contrib-group/contrib/address/email`.

- same content might have different level of granularity, e.g. editor's name might be given as a flat string, whereas author's name might be divided into surname and given names,
- elements of the same kind be found under different parents, e.g. figures might be located in `/article/floats-wrap//fig`, `/article/floats-group//fig`, `/article/back//fig`, `/article/body//fig`, `/article/back/app-group//fig`

As being said, we created the data set in an automatic way ([DB14]):

1. First, a large set of files was downloaded from Open Access Subset of PubMed Central. We obtained both source articles in PDF and corresponding NLM files containing metadata, full text and references.
2. PDF files were automatically processed by tools provided by CERMINE and their hierarchical geometric structure along with the natural reading order was constructed.
3. The text content of every extracted zone was compared to labeled data from corresponding NLM files, which resulted in attaching the most probable labels to zones.
4. Files containing a lot of zones with unknown labels, that is zones for which the automatic labeling process was unable to determine the label, were filtered out.
5. A small random sample of the remaining documents was inspected by a human expert. We were able to identify a number of repeated problems and errors and develop heuristic-based rules to correct them.
6. From the corrected files the final dataset was chosen randomly.

We use xpath to extract text entries from predefined paths. These paths are common for the documents in the Pubmed dataset. Each path is mapped to a label in our labeling system. The task consists in finding a mapping between NLM entries and PDF zones, so that each zone could obtain a label dependent on its path in the NLM file.

For each pair `(pdf_zone, nlm_entry)` Smith-Waterman distance is calculated. Afterwards, for each zone a set of different approaches are followed in order to assign a correct label:

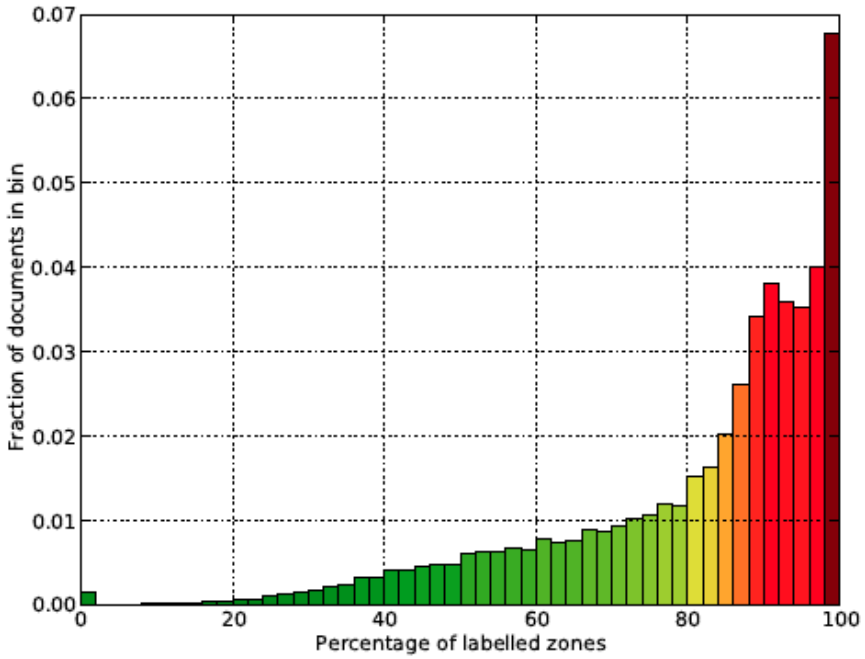
1. Take NLM entry with the highest ratio of SW distance to the number of tokens. If both PDF zone and NLM entry are not empty and their size expressed in number of tokens is comparable (ratio not smaller than 0.7) and length of the common substring constitutes more than 70% of the NLM entry, then assign corresponding label,

2. if the previous approach failed, take the entry with the highest SW distance. If the length of the common substring is bigger than 50% of the number of tokens in the PDF zone, then assign corresponding label,

3. if the previous approaches failed, a *cumulative* distance is calculated. This makes it possible to assign a label to these zones that form together one NLM entry, but were segmented into several parts. This applies mostly to `BODY` zones. For each and each entry and each zone is calculated. For each zone these values are aggregated by summing them up. From all the cumulative distance the biggest one is taken. If it is greater than 0.5, the corresponding label is assigned.

5.7 Filtering

After the matching stage we obtained initial set of TrueViz files whose quality was very diverse, i.e. spanning from fully labeled to almost unlabeled. There are two reasons for that:



1. NLM files in PMC vary in quality. Those with less detailed metadata resulted in barely labeled TrueViz files,

2. with certain layouts our segmentation algorithm was failing, producing very finely-grained text zones with just a handful of letters each. In these cases it was barely possible to match NLM metadata with the actual text, what again lead to sparsely labeled TrueViz files.

In order to assure good quality of the final set we needed to filter out documents with TrueViz files of bad quality. In the figure **??** one can see a distribution of documents with a given fraction of labeled zones. Based on this distribution we decided to keep these documents having the percentage of labeled zone equal or greater than 90%.

5.8 TrueViz file format

We decided to choose TrueViz file format as the data set's main data format. This was to maintain the choice taken when working on GROTOAP data set. The motivation behind this choice is discussed in details in [DCR+12]. TrueViz is a plain text file based on the XML format that holds in an extremely inefficient way the content of a document together with its geometrical properties and classification metadata. An example of a dumb file containing a single character is shown on the listing 5.2.

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE Document SYSTEM "Trueviz.dtd">
<Document>
  <Page>
    <Zone>
      <ZoneID Value="52"/>
      <ZoneCorners>
        <Vertex x="45.4" y="743.8"/>
        <Vertex x="197.4" y="751.3"/>
      </ZoneCorners>
      <ZoneNext Value="53"/>
      <ZoneInsets Bottom="" Left="" Right="" Top=""/>
      <ZoneLines Value=""/>
      <Classification>
        <Category Value="BIB_INFO"/>
        <Type Value=""/>
      </Classification>
      <Line>
        <LineID Value="506"/>
        <LineCorners>
          <Vertex x="45.4" y="743.8"/>
          <Vertex x="197.4" y="751.3"/>
        </LineCorners>
        <LineNext Value="507"/>
```

```
        <LineNumChars Value=""/<name />
        <Word>
          <WordID Value="4796"/>
          <WordCorners>
            <Vertex x="45.4" y="743.9"/>
            <Vertex x="77.0" y="751.3"/>
          </WordCorners>
          <WordNext Value="4797"/>
          <WordNumChars Value=""/>
          <Character>
            <CharacterID Value="26121"/>
            <CharacterCorners>
              <Vertex x="45.4" y="743.9"/>
              <Vertex x="49.5" y="751.3"/>
            </CharacterCorners>
            <CharacterNext Value="26122"/>
            <GT_Text Value="F"/>
          </Character>
        </Word>
      </Line>
    </Zone>
  </Page>
</Document>
```

Listing 5.2: Sample content of a TrueViz file with one letter of content - *F*

The resulting TrueViz files are obviously much bigger than the input PDF file. This is the price that has to be paid for the readability that it offers.

Each of the text zones in a document is labeled with one out of 22 categories:

- `abstract` - document's abstract,
- `acknowledgments` - acknowledgment for article's funding
- `affiliation` - authors' affiliations,
- `author` - document authors,
- `author_title` - zones containing both document's title and the list of authors; This zone has been introduced, as very often our segmentation algorithm
- `bib_info` - bibliographic information that did not fall into any other category, usually concerning the journal issue e.g. journal name, publisher name, volume, DOI,
- `body_content` - the text of the document that did not match any other category,

- `conflict_statement` - conflict statement declaration,
- `copyright` - copyright section,
- `correspondence` - contact information to the article's authors, usually includes e-mail addresses, but physical address is also possible,
- `dates` - dates related to the document life-cycle - reception date, review date, publishing date etc.,
- `editor` - name of document's editor,
- `equation` - mathematical equation,
- `figure` - figure captions and figures elements which are embedded in a PDF as text, e.g. axes labels,
- `glossary` - article's glossary,
- `keywords` - article's keywords,
- `page_number` - page number of the volume;
- `references` - article's references with all the data (titles, names, years) put into one bag,
- `table` - table's content and caption;
- `title` - article title;
- `type` -the type of the document, usually mentioned on the first page near the title, such as *research paper*, *case study* or *editorial*;
- `unknown` - used for the text zones that couldn't be assigned to any other category. This might be because they are very rare or couldn't be matched to the any metadata.

This list is richer than the set of labels used by CERMINE, as we were not targeting such a fine-grained granularity in the system output. On the other hand, Pubmed XMLs are very rich and contain a huge number of metadata elements. It would be pity to create a data set which would loose silently these data. This is why we decided to keep extended set of categories in GROTOAP2. In the appendix E one can see distributions of these catogories for the chosen documents.

The `acknowledgment` section has a very similar distribution, `affiliation` is mostly focused in two or three zones with a pretty short tail, `author` section has a very narrow distribution with most of the articles having only one such zone. On

the contrary, `author_title` is in most cases represented by 4 or 5 zones. `editor` is, as expected, in the majority of cases present in only one zone per document. It's interesting to see what is the distribution of `unknown` zones, i.e. those whose content couldn't be matched with the data from Pubmed XML. The most numerous bins are `1` and `2`, containing in total more than 12000 documents. This can be seen as an indicator of good quality of the data set.

Figure 5.1 shows the fraction of documents in the data set that contain given label. One can see that all the documents contain labels `bib_info`, `body_content`, `references` and `affiliation`.

Figure 5.2 shows the total count of labels across all the documents (logarithmic scale). One can see that `table` is the most numerous label, followed by `body_content`. This is caused by inability to cluster very small and distant text zones together, as they usually appear so in the tables embedded in the PDF documents.

Figures 5.4 and 5.3 show the contribution in the data set of the top 15 publishers and top 25 journals respectively. In total there are 208 publishers included and 1170 journals. As expected, the biggest publisher is a medical one (BioMed Central), but the remaining ones might be associated with a general scientific publishing. As different journals are stuck to their layouts, we might be sure that the variety of the layouts in the data set is sufficient to allow good mean performance on unknown articles.

Figures 5.5 and 5.6 show the distribution of number of pages and publication years respectively. The first distribution reaches its maximum at 8 pages, which is a standard in the scientific publishing. The second distribution is focused around the year 2010, but has a tail reaching year 1995. Therefore we might expect that the classifier trained using this set will show better performance for more recent publications.

5.9 Dataset evaluation

Evaluation of the created dataset is precisely described in [DB14]. Evaluation was not done by the author of this thesis. It was entirely performed by author's team mates from the Interdisciplinary Center for Mathematical and Computation Modeling. Nevertheless, its results and methodology will be quoted here in order to make the description more complete.

For the purpose of evaluation there was a handful of 50 documents picked. Those documents were automatically labeled and then errors were rectified. Subsequently, the corrected documents and the original ones were compared and the factors of precision and recall were calculated. Table 5.1 shows the values obtained

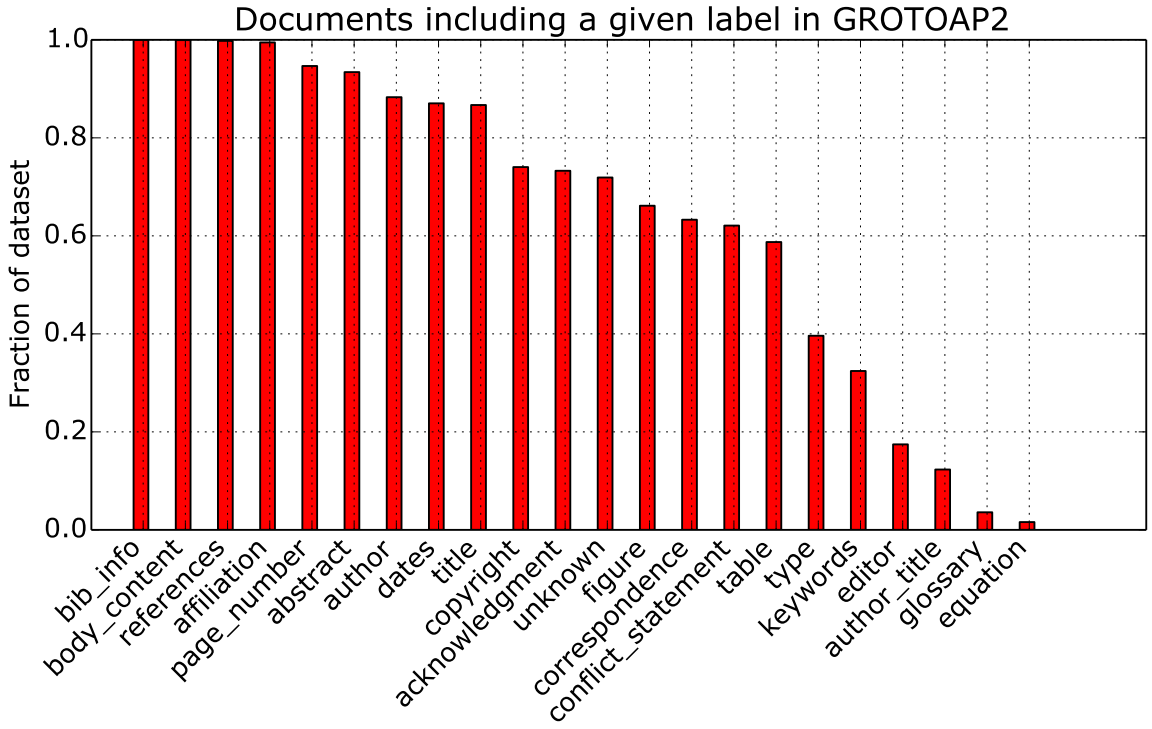


Figure 5.1: Barplot of fraction of documents containing given label

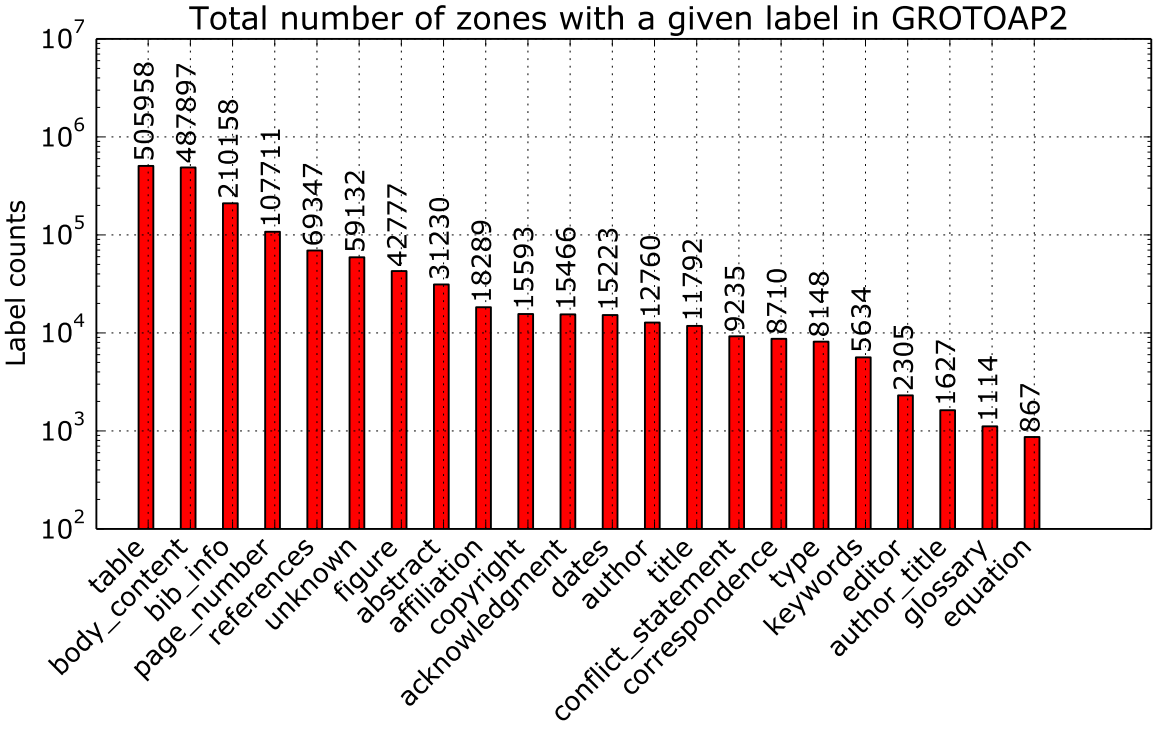


Figure 5.2: Barplot of total count of zones labeled with given label in GROTOAP2

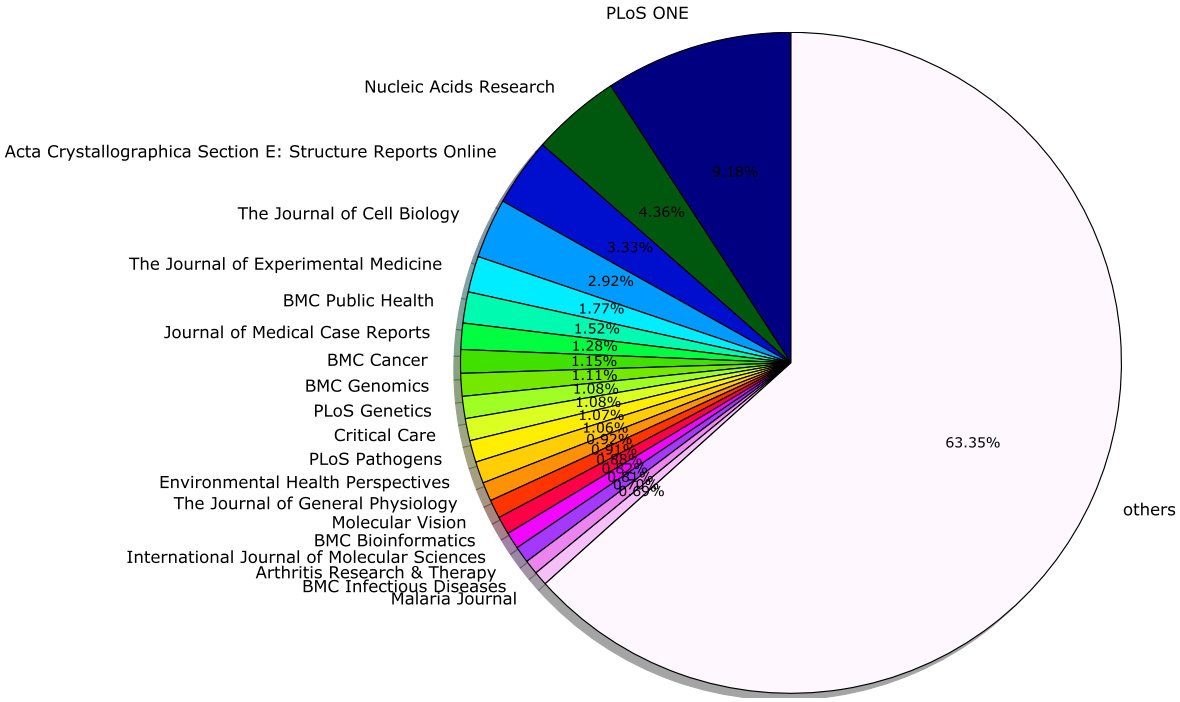


Figure 5.3: Top 25 journals in the GROTOAP2 dataset

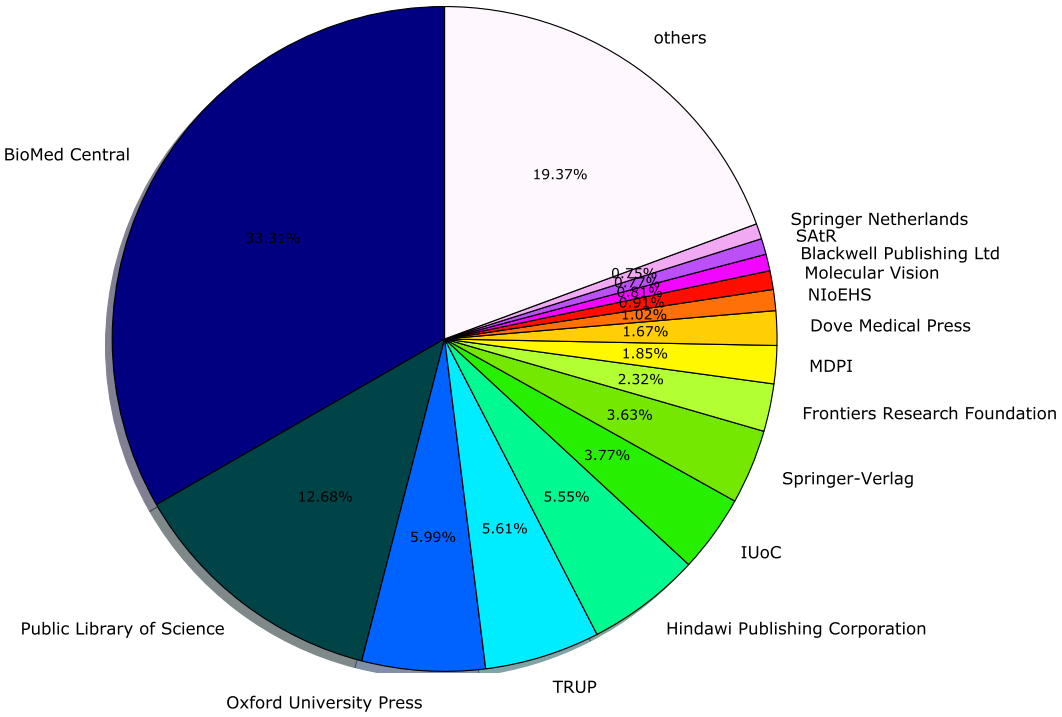


Figure 5.4: Top 15 publishers in the GROTOAP2 dataset

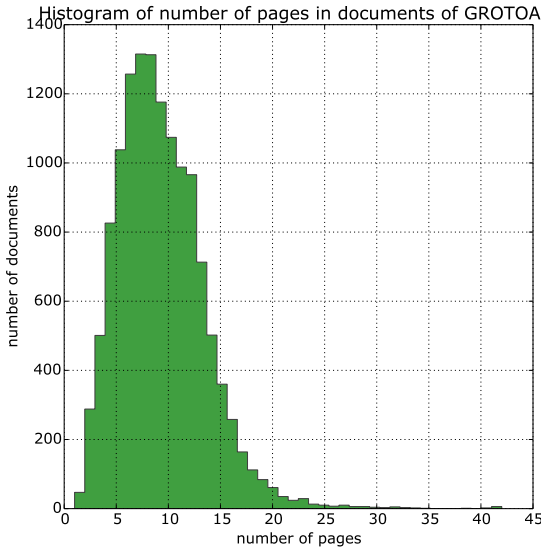


Figure 5.5: Histogram of number of pages of the documents in the GROTOAP2 dataset

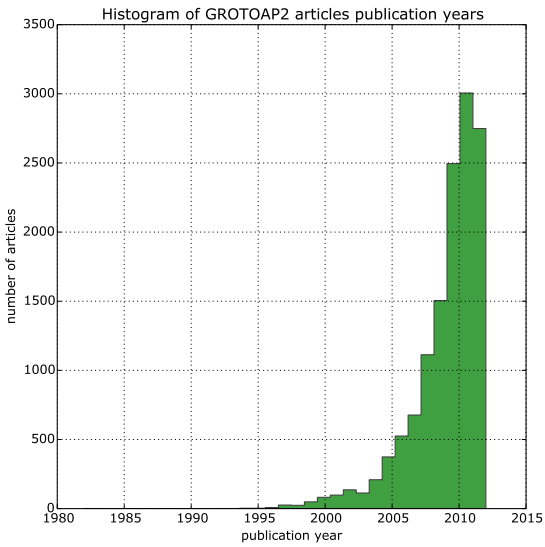


Figure 5.6: Histogram of publication year of the documents in the GROTOAP2 dataset

for each label.

Another evaluation of the dataset was done by comparing CERMINE performance in two scenarios: trained with GROTOAP and a random handful of 1000 documents from GROTOAP2. Test documents were randomly selected from the Pubmed Central collection. Table 5.2 shows results of the evaluation. One can notice that the F-score of classifier based on GROTOAP2 has grown by 16.93%.

label	precision	recall	label	precision	recall
abstract	0.98	0.98	equation	-	-
acknowledgment	1.00	0.90	figure	0.99	0.46
affiliation	0.95	0.95	glossary	1.00	1.00
author	1.00	0.98	keywords	1.00	0.94
author_title	1.00	1.00	page_number	0.98	0.97
bib_info	0.96	0.94	references	0.99	0.95
body	0.88	0.99	table	0.98	0.96
conflict_statement	0.82	0.89	title	1.00	1.00
copyright	0.93	0.78	type	0.89	0.47
correspondence	1.00	0.97	unknown	0.62	0.94
dates	0.94	1.00	*	0.95	0.91
editor	1.00	1.00			

Table 5.1: Evaluation metrics for the GROTOAP2 zone labeling process. The automatically generated metrics were manually compared with the actual labels on a subset of GROTOAP2. For each class precision and recall were calculated. Source: [DB14]

	GROTOAP	GROTOAP2
precision	77.13%	82.22%
recall	55.99%	76.96%
F-score	62.41%	79.34%

Table 5.2: Evaluation of GROTOAP2 using CERMINE trained with GROTOAP and GROTOAP2.

Chapter 6

Evaluation

6.1 Results

	BODY	METADATA	REFERENCES	OTHER	precision	recall
BODY	**1**					
METADATA		**2**				
REFERENCES			**3**			
OTHER				**4**		

Table 6.1: Confusion matrix for the initial zone classification in GROTOAP2 in a 5-fold cross-validation. Rows and columns contain desired and obtained labels respectively.

	abstract	affiliation	author	bib_info	copyright	correspondence	dates	editor	keywords	title	title_author	type	unknown	precision	recall
abstract	o														
affiliation		o													
author			o												
bib_info				o											
copyright					o										
correspondence						o									
dates							o								
editor								o							
keywords									o						
title										o					
title_author											o				
type												o			
UNKNOWN													o		

Table 6.2: Confusion matrix for the initial zone classification in GROTOAP2 in a 5-fold cross-validation. Rows and columns contain desired and obtained labels respectively.

6.2 Future work

6.2.1 GROTOAP2

GROTOAP2 is a rich data set created in a semi-automatized way from Open Access publications. It contains 13210 articles representing a big variety of layouts and issued by more than 200 publishers. We find this set very useful for every data mining algorithm willing to extract metadata, data and other various features from scholarly articles in an automated way. GROTOAP2 can be easily applied to testing or learning every algorithm designed for processing born-digital documents. We believe that GROTOAP2 can be made more versatile by:

- growing its size by an order or two orders of magnitude.
- Improving the algorithm used to assign NML metadata to text zones by tuning the magic constants used there.
- Tuning the segmentation algorithm and improving segmentation quality. This would result in removing the `author_title` tag.
- Dividing the `body_content` into subcategories based on the level of their headers.
- Including fine-grained author metadata, e.g. first name, middle name, surname.
- Introducing association between authors and theirs affiliations, i.e. pointing out which author is associated with which affiliation.
- Including fine-grained bibliographic reference data, making it applicable for reference-extraction algorithms.

Most of the above-mentioned cases are related to loosing as little information as possible from the original Pubmed XML files.

6.2.2 CERMINE

CERMINE is a robust system for metadata extraction. It can be used to accurately extract fine-grained metadata from scientific articles en masse. CERMINE can be very useful in every digital library application, as it is flexible and doesn't depend on any particular layout. What is more, it can be easily adapted in a semi-automatic way to some particular layout, if such need arises.

We consider that there are many ways to improve the system, e.g.:

- increase classification accuracy and recall. This can be done by:
  - choosing a different classification algorithm,
  - using an ensemble of algorithms,
  - performing lexical analysis on the zones classified as unknown,
  - increasing quality of the training set.
- extract detailed bibliographic references,
- extract figures and tables,
- perform sentiment analysis with respect to the included references,
- improve segmentation algorithm's on unusual layouts.

Appendix A

Decription of the training workflow

Below one can find description of the complete procedure for training the system classifiers.

1. Get CERMINE source code. It is available publicly on the Web.

   ```
   git clone https://github.com/pszostek/CERMINE.git
   cd CERMINE
   ```

2. Build CERMINE using maven by running the following Bash script from the CERMINE main directory. It assumes that the `PATH` variable contains a path to `mvn`.

   ```
   #!/usr/bin/env bash
   curdir=$PWD
   cd cermine-impl && mvn package -DskipTests && mvn assembly:single && cd
       $curdir
   cd cermine-tools && mvn package -DskipTests && mvn assembly:single && cd
       $curdir
   ```

3. Create files with samples for the classifiers using GROTOAP2. To this end, one need to run the following script. Note that the `GROTOAP2_PATH` variable has to point to a directory containing cxml files from the dataset.

   ```
   #!/usr/bin/env bash
   BASE=$(dirname $(pwd))
   ```

```
java -Djava.util.Arrays.useLegacyMergeSort=true -cp \
    $BASE/cermine-tools/target/cermine-tools-1.2-SNAPSHOT-jar-with-dependencies.jar:\
    $BASE/cermine-impl/target/cermine-impl-1.2-SNAPSHOT-jar-with-dependencies.jar:\
    $BASE/cermine-impl/target/cermine-impl-1.2-SNAPSHOT.jar
        pl.edu.icm.cermine.libsvm.LibSVMExporter $GROTOAP2_PATH
```

4. Scale down the samples' feature values so that those with relatively huge absolute values do not dominate those with smaller values. This is a step recommended in [CL10]. It can be done by using the svm-scale tool from `libsvm` package.

```
svm-scale -l -1 -u 1 -s range1 meta_GROTOAP2 > meta_GROTOAP2.scale
svm-scale -l -1 -u 1 -s range1 initial_GROTOAP2 > initial_GROTOAP2.scale
```

5. Find the best parameters for the classifiers using `grid.py` from the `libsvm` package. The below script can facilitate iterating over different kernel types. One need to pick the classifier with the lowest error rate.

```
#!/usr/bin/env bash
for classifier in meta initial; do
        for kernel in $(seq 0 3); do
                printf "kernel=$kernel: "
                if [ $kernel -eq 1 ]; then
                        degree=" -d 4 "
                else
                        degree=""
                fi
                /root/grid.py -t $kernel -gnuplot /usr/local/bin/gnuplot
                    -svmtrain /root/libsvm-3.18/svm-train $degree
                    ${classifier}_GROTOAP.dat.scale
        done
done
```

6. Using the optimal parameters, train the classifiers and save them to files. The below command has to be run from the main CERMINE directory. The variables `KERNEL_I`, `G_I`, `C_I` and `D_I` indicate respectively the kernel type, the γ parameter, the C parameter and possibly polynomial degree of the initial zone classification kernel. Variables `KERNEL_M`, `G_M`, `C_M` and `D_M` indicate respectively the kernel type, the γ parameter, the C parameter and possibly polynomial degree of the metadata classification kernel.

```
#!/usr/bin/env bash
java -Djava.util.Arrays.useLegacyMergeSort=true -cp \
    ./cermine-tools/target/cermine-tools-1.2-SNAPSHOT-jar-with-dependencies.jar\
    ./cermine-impl/target/cermine-impl-1.2-SNAPSHOT-jar-with-dependencies.jar\
    ./cermine-impl/target/cermine-impl-1.2-SNAPSHOT.jar\
    pl.edu.icm.cermine.tools.classification.svm.SVMInitalBuilder -input\
        initial_GROTOAP2.dat.scale -output CERMINE_initial_classifier\
        -kernel $KERNEL_I -g $G_I -C $C_I [-degree $D_I]

java -Djava.util.Arrays.useLegacyMergeSort=true -cp \
    ./cermine-tools/target/cermine-tools-1.2-SNAPSHOT-jar-with-dependencies.jar\
    ./cermine-impl/target/cermine-impl-1.2-SNAPSHOT-jar-with-dependencies.jar\
    ./cermine-impl/target/cermine-impl-1.2-SNAPSHOT.jar\
    pl.edu.icm.cermine.tools.classification.svm.SVMMetadataBuilder -input\
        meta_GROTOAP2.dat.scale -output CERMINE_meta_classifier\
        -kernel $KERNEL_M -g $G_M -C $C_M [-degree $D_M]
```

7. Parameters from the previous step can be used to evaluate the classifier. CERMINE contains full classes that perform n-fold cross-validation. To obtain full validation reports, one need to run the commands that follow.

```
#!/usr/bin/env bash
java -Djava.util.Arrays.useLegacyMergeSort=true -cp \
    ./cermine-tools/target/cermine-tools-1.2-SNAPSHOT-jar-with-dependencies.jar\
    ./cermine-impl/target/cermine-impl-1.2-SNAPSHOT-jar-with-dependencies.jar\
    ./cermine-impl/target/cermine-impl-1.2-SNAPSHOT.jar\
    pl.edu.icm.cermine.evaluation.SVMInitialClassificationEvaluator -full\
        -input initial_GROTOAP2.dat \
        -kernel $KERNEL_I -g $G_I -C $C_I [-degree $D_I]

java -Djava.util.Arrays.useLegacyMergeSort=true -cp \
    ./cermine-tools/target/cermine-tools-1.2-SNAPSHOT-jar-with-dependencies.jar\
    ./cermine-impl/target/cermine-impl-1.2-SNAPSHOT-jar-with-dependencies.jar\
    ./cermine-impl/target/cermine-impl-1.2-SNAPSHOT.jar\
    pl.edu.icm.cermine.evaluation.SVMMetadataClassificationEvaluator -full\
        -input metadata_GROTOAP2.dat \
        -kernel $KERNEL_I -g $G_I -C $C_I [-degree $D_I]
```

Appendix B

Description of classification features

Below the reader can find description of all the features used in the zone classification process.

Feature Name	Type	Description
Affiliation	`bool`	Tells if the zone contains one of the {*author details*, *university*, *department*, *school*, *institute*, *affiliation*}
Author	`bool`	Tells if a text zone contains a word starting with *author*
Bibinfo	`int`	Number of occurences of {*cite*, *pages*, *article*, *volume*, *publishing*, *journal*, *doi*, *cite this article*, *citation*, *issue*, *issn*}
BracketRelativeCount	`float`	Ratio of the number of brackets to the number of all characters
BracketedLineRelativeCount	`float`	Ratio of number of lines starting with a bracket to the number of all lines
CharCount	`int`	Counts number of characters in a zone
CharCountRelative	`float`	Ratio of number of characters in a zone to the number of character on its page
CommaCount	`int`	Counts number of commas in a zone

CommaRelativeCount	`int`	Ratio of commas to all characters in a zone
ContainsPageNumber	`bool`	Does the zone consists of a number or is like *Page %d* or *page %d*, where %d is a number
CuePhrasesRelativeCount	`float`	Ratio of cue phrases from {*although*, *therefore*, *therein*, *hereby*, *nevertheless*, *to this end*, *however*, *moreover*, *nonetheles*} to all words
Date	`bool`	Tells if the zone contains a string being a date with months expressed as text or as a number, with either European or American order
DigitCount	`int`	Number of digits is in the zone
DigitRelativeCount	`float`	Ratio of digits to all characters in the zone
DistanceFromNearestNeighbour	`float`	Distance to the nearest neighbour zone or returns Double.MAX_VALUE if there is no other zone on the page
DotCount	`int`	Counts number of dots (.) in the zone
DotRelativeCount	`float`	Ratio of number of dots to all characters in the zone
Email	`bool`	Tells if the zone contains a valid e-mail address
EmptySpaceRelative	`float`	Calculates a ratio of the surface taken by the characters' bounding boxes to the area of the zone
FontHeightMean	`float`	Calculates average font size in the zone
FreeSpaceWithinZone	`float`	Difference between zone's area and total area taken by the characters
Height	`int`	Height of a zone
HeightRelative	`float`	Ratio of zone's height to the page's height
HorizontalRelativeProminence	`float`	Area taken by the zone and free area to the West and East of the page. This features tries to fit `int`o the page a bounding box of the same height as the zone and sticking either to neighbour zones or to the page boundaries in E and W

IsAnywhereElse	`bool`	Tells if this zone is duplicated anywhere in the investigated document
IsFirstPage	`bool`	Tells if the zone is located on the first page of the document
IsFontBiggerThanNeighbours	`bool`	Tells whether the font of the zone is bigger than in neighbour zones
IsGreatestFontOnPage	`bool`	Tells if the zone has the greatest font on the page
IsHighestOnThePage	`bool`	Tells if the zone is the highest on the page
IsItemize	`bool`	Tells if the zone contains any kind of indexing charactersic for section or enumeration numbering
IsWidestOnThePage	`bool`	Tells if the zone is the widest on the page
IsLastButOnePage	`bool`	Tells if the zone is located on the last but one page
IsLastPage	`bool`	Tells if the zone is located on the last page
IsLeft	`bool`	Tells if the zone is in the left part of the page
IsLongestOnThePage	`bool`	Tells if the zone contains maximal number of characters among all the zones in the page
IsLowestOnThePage	`bool`	Tells if the zone is most southern on the page (southern bounding box border is taken `into` account)
IsOnSurroundingPages	`bool`	Tells if the same zone is on the previous or on the next page
IsPageNumber	`bool`	Tells if a zone is entirely a number
IsRight	`bool`	Tells if a zone is on the east side of the page
IsSingleWord	`bool`	Tells if a zone is one word
LastButOneZone	`bool`	Tells if the zone is last but one wrt. to the reading order
LineCount	`int`	Number of lines in the zone
LineRelativeCount	`float`	Ratio of lines in the to all lines on the page
LineHeightMean	`float`	Mean height of the zone
LineWidthMean	`float`	Mean width of the zone's lines

LineXPositionMean	`float`	Mean distance of zone's lines to the zone's bounding box
LineXPositionDiff	`float`	The feature looks at the left border of all lines within a zone and finds the most-eastern and most-western among them. A positive difference between these two values is returned
LineXWidthPositionDiff	`float`	Difference between mean value of lines' left border X coordinate and zone's
LetterCount	`int`	Number of letters in the zone
LetterRelativeCount	`float`	Ratio of letters in the zone to all letters on the page
LowercaseCount	`int`	Number of letters in lower case in the zone
LowercaseRelativeCount	`float`	Number of letters in lower case in the zone
PageNumber	`int`	Page number wrt. the reading order
PreviousZone	`int`	Value of label assigned to the previous zone wrt. the reading order
Proportions	`float`	Width to height ratio
PunctuationRelativeCount	`float`	Ratio of punctuation marks to all characters in the zone
References	`int`	Number of characteristic enumeration indices in the zone, e.g. *1.*.
StartsWithDigit	`bool`	Tells if the zone's first character is a digit
UppercaseCount	`int`	Number of upper case characters in the zone
UppercaseRelativeCount	`float`	Ratio of upper case letters to all characters
UppercaseWordCount	`int`	Number of words starting with upper case
UppercaseWordRelativeCount	`float`	Ratio of upper case words to all words
VerticalProminence	`float`	Space taken by the zone and free area to the North and South of the page. This features tries to fit `into` the page a bounding box of the same height as the zone and sticking either to neighbor zones or to the page boundaries in N and S

Width	`int`	Width of the bounding box in pixels
WordCount	`int`	Number of words in the zone
WordCountRelative	`float`	Ratio of number of words in the zone to all words in the page
WordWidthMean	`float`	Mean width of words in the zone expressed as pixels
WordLengthMean	`float`	Mean width of words in the zone expressed as number of characters
WordLengthMedian	`int`	Median of number of characters in all words
WhitespaceCount	`int`	Number of white characters in the text
WhitespaceRelativeCountLog	`float`	Feature calculated as $-log\frac{S}{L}$ where S is zone's empty area and L is zone's text length
WidthRelative	`float`	Ratio of zone's width to page's width
XPosition	`int`	X coordinate
XPositionRelative	`float`	Ratio of zone's X coordinate to page's width
YPosition	`int`	Y coordinate
YPositionRelativeFeature	`float`	Ratio of zone's Y coordinate to page's height

Appendix C

Reading order resolving

```
public class HierarchicalReadingOrderResolver implements ReadingOrderResolver {

    static final int GRIDSIZE = 50;
    static final double BOXES_FLOW = 0.5;
    static final double EPS = 0.0001;
    static final int MAX_ZONES = 1000;
    static final Comparator<BxObject> Y_ASCENDING_ORDER = new
        Comparator<BxObject>() {

        @Override
        public int compare(BxObject o1, BxObject o2) {
                if((o1.getY() - o2.getY()) > EPS ) {
                        return 1;
                } else if(Math.abs(o1.getY() - o2.getY()) < EPS) {
                        return 0;
                } else {
                        return -1;
                }
        }
    };

    static final Comparator<BxObject> X_ASCENDING_ORDER = new
        Comparator<BxObject>() {
```

```
    @Override
    public int compare(BxObject o1, BxObject o2) {
            if(o1.getX()-o2.getX() > EPS) {
                    return 1;
            } else if(Math.abs(o1.getX() - o2.getX()) < EPS) {
                    return 0;
            } else {
                    return -1;
            }
    }
};

static final Comparator<BxObject> YX_ASCENDING_ORDER = new
    Comparator<BxObject>() {

    @Override
    public int compare(BxObject o1, BxObject o2) {
        int yCompare = Y_ASCENDING_ORDER.compare(o1, o2);
        return yCompare == 0 ? X_ASCENDING_ORDER.compare(o1, o2) : yCompare;
    }
};

@Override
public BxDocument resolve(BxDocument messyDoc) {
    BxDocument orderedDoc = new BxDocument();
    List<BxPage> pages = messyDoc.getPages();
    for (BxPage page : pages) {
        List<BxZone> zones = page.getZones();
        for (BxZone zone : zones) {
            List<BxLine> lines = zone.getLines();
            for (BxLine line : lines) {
                List<BxWord> words = line.getWords();
                for (BxWord word : words) {
                    List<BxChunk> chunks = word.getChunks();
                    Collections.sort(chunks, X_ASCENDING_ORDER);
                }
                Collections.sort(words, X_ASCENDING_ORDER);
            }
```

```
            Collections.sort(lines, Y_ASCENDING_ORDER);
        }
        List<BxZone> orderedZones;
        if (zones.size() > MAX_ZONES) {
            orderedZones = new ArrayList<BxZone>(zones);
            Collections.sort(orderedZones, YX_ASCENDING_ORDER);
        } else {
            orderedZones = reorderZones(zones);
        }
        page.setZones(orderedZones);
        orderedDoc.addPage(page);
    }
    setIdsAndLinkTogether(orderedDoc);
    return orderedDoc;
}

/**
 * Builds a binary tree from list of text zones by doing a hierarchical
     clustering and converting the result tree to
 * an ordered list.
 *
 * @param zones is a list of unordered zones
 * @return a list of ordered zones
 */
private List<BxZone> reorderZones(List<BxZone> unorderedZones) {
    if (unorderedZones.isEmpty()) {
        return new ArrayList<BxZone>();
    } else if (unorderedZones.size() == 1) {
        List<BxZone> ret = new ArrayList<BxZone>(1);
        ret.add(unorderedZones.get(0));
        return ret;
    } else {
        BxZoneGroup bxZonesTree = groupZonesHierarchically(unorderedZones);
        sortGroupedZones(bxZonesTree);
        TreeToListConverter treeConverter = new TreeToListConverter();
        List<BxZone> orderedZones = treeConverter.convertToList(bxZonesTree);
        assert unorderedZones.size() == orderedZones.size();
        return orderedZones;
```

```
    }
}

/**
 * Generic function for setting IDs and creating a linked list by filling
     references. Used solely by
 * setIdsAndLinkTogether(). Can Handle all classes implementing Indexable
     interface.
 *
 * @param list is a list of Indexable objects
 */
private <A extends Indexable<A>> void setIdsGenericImpl(List<A> list) {
    if (list.isEmpty()) {
        return;
    }
    if (list.size() == 1) {
        A elem = list.get(0);
        elem.setNext(null);
        elem.setPrev(null);
        elem.setId("0");
        elem.setNextId("-1");
        return;
    }

    //unroll the loop for the first and last element
    A firstElem = list.get(0);
    firstElem.setId("0");
    firstElem.setNextId("1");
    firstElem.setNext(list.get(1));
    firstElem.setPrev(null);
    for (int idx = 1; idx < list.size() - 1; ++idx) {
        A elem = list.get(idx);
        elem.setId(Integer.toString(idx));
        elem.setNextId(Integer.toString(idx + 1));
        elem.setNext(list.get(idx + 1));
        elem.setPrev(list.get(idx - 1));
    }
    A lastElem = list.get(list.size() - 1);
```

```
    lastElem.setId(Integer.toString(list.size() - 1));
    lastElem.setNextId("-1");
    lastElem.setNext(null);
    lastElem.setPrev(list.get(list.size() - 2));
}

/**
 * Function for setting up indices and reference for the linked list. Causes
     objects of BxPage, BxZone, BxLine,
 * BxWord and BxChunk to be included in the document's list of elements and
     sets indices according to the
 * corresponding list order.
 *
 * @param doc is a reference to a document with properly set reading order
 */
private void setIdsAndLinkTogether(BxDocument doc) {
    setIdsGenericImpl(doc.asPages());
    setIdsGenericImpl(doc.asZones());
    setIdsGenericImpl(doc.asLines());
    setIdsGenericImpl(doc.asWords());
    setIdsGenericImpl(doc.asChunks());
}

/**
 * Builds a binary tree of zones and groups of zones from a list of
     unordered zones. This is done in hierarchical
 * clustering by joining two least distant nodes. Distance is calculated in
     the distance() method.
 *
 * @param zones is a list of unordered zones
 * @return root of the zones clustered in a tree
 */
private BxZoneGroup groupZonesHierarchically(List<BxZone> zones) {
    /*
     * Distance tuples are stored sorted by ascending distance value
     */
    List<DistElem<BxObject>> dists = new
        ArrayList<DistElem<BxObject>>(zones.size()*zones.size()/2);
```

```
    for (int idx1 = 0; idx1 < zones.size(); ++idx1) {
        for (int idx2 = idx1 + 1; idx2 < zones.size(); ++idx2) {
            BxZone zone1 = zones.get(idx1);
            BxZone zone2 = zones.get(idx2);
            dists.add(new DistElem<BxObject>(false, distance(zone1, zone2),
                    zone1, zone2));
        }
    }
    Collections.sort(dists);
    DocumentPlane plane = new DocumentPlane(zones, GRIDSIZE);
    while (!dists.isEmpty()) {
        DistElem<BxObject> distElem = dists.get(0);
        dists.remove(0);
        if (!distElem.isC() && plane.anyObjectsBetween(distElem.getObj1(),
            distElem.getObj2())) {
            dists.add(new DistElem<BxObject>(true, distElem.getDist(),
                distElem.getObj1(), distElem.getObj2()));
            continue;
        }

        BxZoneGroup newGroup = new BxZoneGroup(distElem.getObj1(),
            distElem.getObj2());
        plane.remove(distElem.getObj1()).remove(distElem.getObj2());
        dists = removeDistElementsContainingObject(dists, distElem.getObj1());
        dists = removeDistElementsContainingObject(dists, distElem.getObj2());
        for (BxObject other : plane.getObjects()) {
            dists.add(new DistElem<BxObject>(false, distance(other,
                    newGroup), newGroup, other));
        }
        Collections.sort(dists);
        plane.add(newGroup);
    }

    assert plane.getObjects().size() == 1 : "There should be one object left
        at the plane after grouping";
    return (BxZoneGroup) plane.getObjects().get(0);
}
```

```
/**
 * Removes all distance tuples containing obj
 */
private List<DistElem<BxObject>>
    removeDistElementsContainingObject(Collection<DistElem<BxObject>> list,
    BxObject obj) {
    List<DistElem<BxObject>> ret = new ArrayList<DistElem<BxObject>>();
    for (DistElem<BxObject> distElem : list) {
        if (distElem.getObj1() != obj && distElem.getObj2() != obj) {
            ret.add(distElem);
        }
    }
    return ret;
}

/**
 * Swaps children of BxZoneGroup if necessary. A group with smaller sort
     factor is placed to the left (leftChild).
 * An object with greater sort factor is placed on the right (rightChild).
     This plays an important role when
 * traversing the tree in conversion to a one dimensional list.
 *
 * @param group
 */
private void sortGroupedZones(BxZoneGroup group) {
    BxObject leftChild = group.getLeftChild();
    BxObject rightChild = group.getRightChild();
    if (shouldBeSwapped(leftChild, rightChild)) {
        // swap
        group.setLeftChild(rightChild);
        group.setRightChild(leftChild);
    }

    if (leftChild instanceof BxZoneGroup) // if the child is a tree node,
        then recurse
    {
        sortGroupedZones((BxZoneGroup) leftChild);
    }
```

```
    if (rightChild instanceof BxZoneGroup) // as above - recurse
    {
        sortGroupedZones((BxZoneGroup) rightChild);
    }
}

private boolean shouldBeSwapped(BxObject first, BxObject second) {
    double cx, cy, cw, ch, ox, oy, ow, oh;
    cx = first.getBounds().getX();
    cy = first.getBounds().getY();
    cw = first.getBounds().getWidth();
    ch = first.getBounds().getHeight();

    ox = second.getBounds().getX();
    oy = second.getBounds().getY();
    ow = second.getBounds().getWidth();
    oh = second.getBounds().getHeight();

    // Determine Octant
    //
    // 0 | 1 | 2
    // __|___|__
    // 7 | 9 | 3 First is placed in 9th square
    // __|___|__
    // 6 | 5 | 4

    if (cx + cw <= ox) { //2,3,4
            return false;
    } else if (ox + ow <= cx) { //0,6,7
            return true; //6
    } else if (cy + ch <= oy) {
        return false; //5
    } else if (oy + oh <= cy) {
        return true; //1
    } else { //two zones
        double xdiff = ox+ow/2 - cx-cw/2;
        double ydiff = oy+oh/2 - cy-ch/2;
        if (xdiff + ydiff < 0) {
```

```
            return true;
        }
        return false;
    }
}

/**
 * A distance function between two TextBoxes.
 *
 * Consider the bounding rectangle for obj1 and obj2. Return its area minus
     the areas of obj1 and obj2, shown as
 * 'www' below. This value may be negative.
 * (x0,y0) +------+wwwwwwwwwwwwwwwww
 * | obj1 |wwwwwwwwwwwwwwwww
 * +------+wwwwwwwww+------+
 * wwwwwwwwwwwwwwwww| obj2 |
 * wwwwwwwwwwwwwwwww+------+ (x1,y1)
 *
 * @return distance value based on objects' coordinates and physical size on
     a plane
 *
 */
private double distance(BxObject obj1, BxObject obj2) {

    double x0 = Math.min(obj1.getX(), obj2.getX());
    double y0 = Math.min(obj1.getY(), obj2.getY());
    double x1 = Math.max(obj1.getX() + obj1.getWidth(),
            obj2.getX() + obj2.getWidth());
    double y1 = Math.max(obj1.getY() + obj1.getHeight(),
            obj2.getY() + obj2.getHeight());
    double dist = ((x1 - x0) * (y1 - y0) - obj1.getArea() - obj2.getArea());

    double obj1CenterX = obj1.getX();
    double obj1CenterY = obj1.getY() + obj1.getHeight() / 2;
    double obj2CenterX = obj2.getX();
    double obj2CenterY = obj2.getY() + obj2.getHeight() / 2;
```

```
        double obj1obj2VectorCosineAbs = Math.abs((obj2CenterX - obj1CenterX) /
            Math.sqrt((obj2CenterX - obj1CenterX) * (obj2CenterX - obj1CenterX) +
            (obj2CenterY - obj1CenterY) * (obj2CenterY - obj1CenterY)));
        final double MAGIC_COEFF = 0.5;
        return dist * (MAGIC_COEFF + obj1obj2VectorCosineAbs);
    }
}
```

Appendix D

Project resources

D.1 CERMINE repository

CERMINE was a collaborative project implemented as a part of author's work in ICM UW. Repository for the project can be found under `https://github.com/CeON/CERMINE/`. In total there were 217 commits added between 25.06.2012 and 10.01.2015 by the author of this work under usernames "Pawel Szostek" and "pszostek". They can be easily listed with the procedure below:

```
#!/usr/bin/env bash
git clone https://github.com/CeON/CERMINE.git
cd CERMINE
git log --author="Pawel Szostek"
git log --author="pszostek"
```

D.2 CERMINE interface

CERMINE interface was created as a side project to make the engine available for public use. It can be found under `http://cermine.ceon.pl/`.

D.3 GROTOAP2

GROTOAP2 can be downloaded from the servers of the Center for Open Science (CeON) under `http://cermine.ceon.pl/grotoap2/`

Appendix E

GROTOAP2 labels distributions

Figures E.1, E.2, E.3, E.4, E.5, E.6, E.7, E.8, E.9, E.10, E.11, E.12, E.13, E.14, E.15, E.16, E.17, E.18, E.19, E.20, E.21, E.22 show the density of different labels across the data set. One can see that in most of the documents the abstract is enclosed in only one zone. Nevertheless, there is a tail of the distribution going up to 40 zones. This can mean that there are articles where abstract is excessively long or that the segmentation algorithm failed.

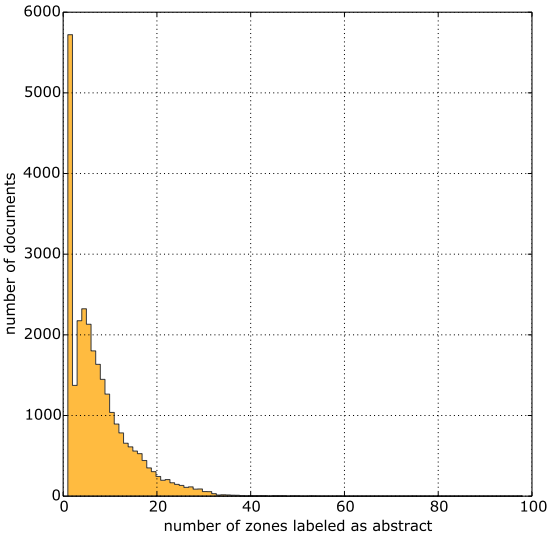


Figure E.1: Histogram of number of zones labeled as `abstract`

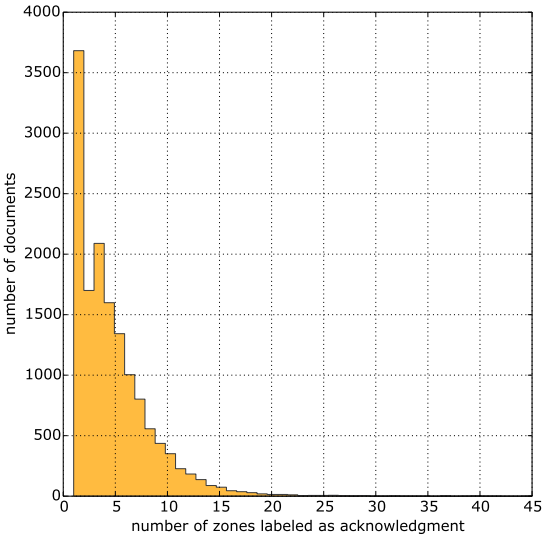


Figure E.2: Histogram of number of zones labeled as `acknowledgment`

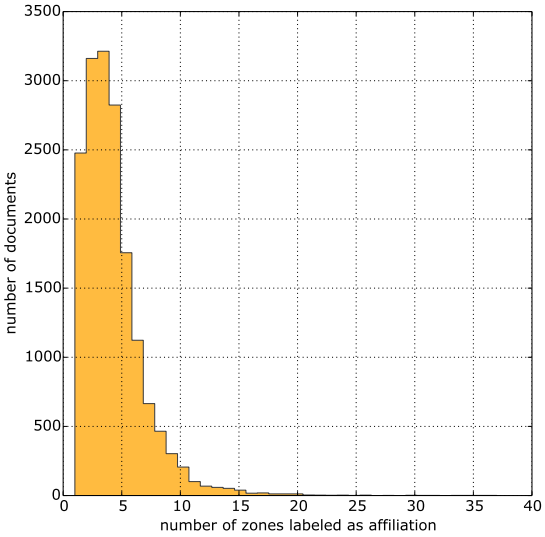


Figure E.3: Histogram of number of zones labeled as `affiliation`

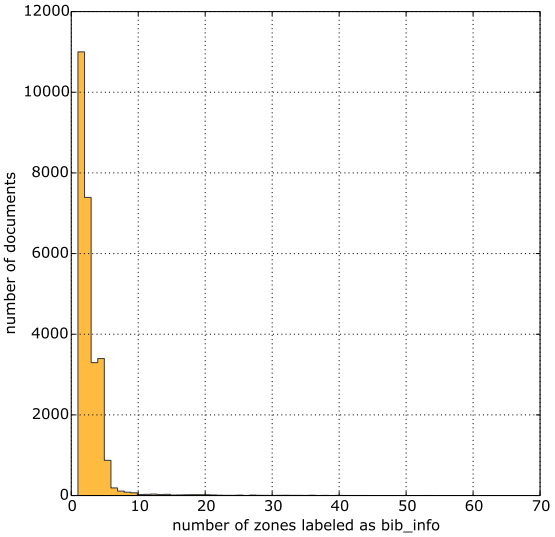


Figure E.4: Histogram of number of zones labeled as `bib_info`

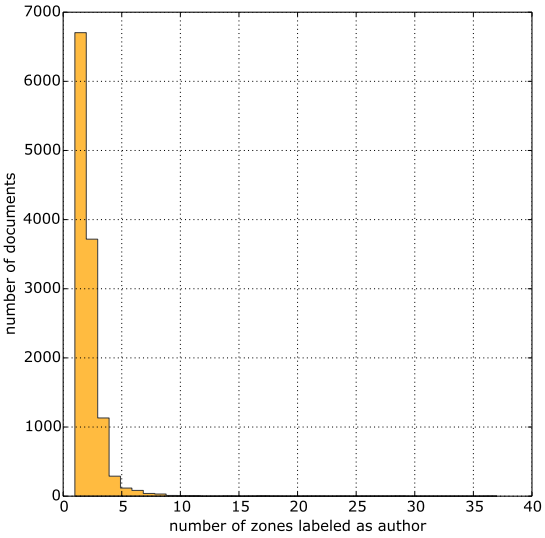


Figure E.5: Histogram of number of zones labeled as `author`

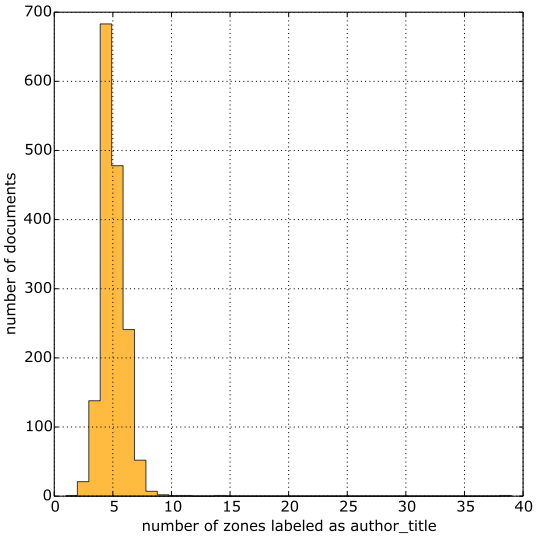


Figure E.6: Histogram of number of zones labeled as `author_title`

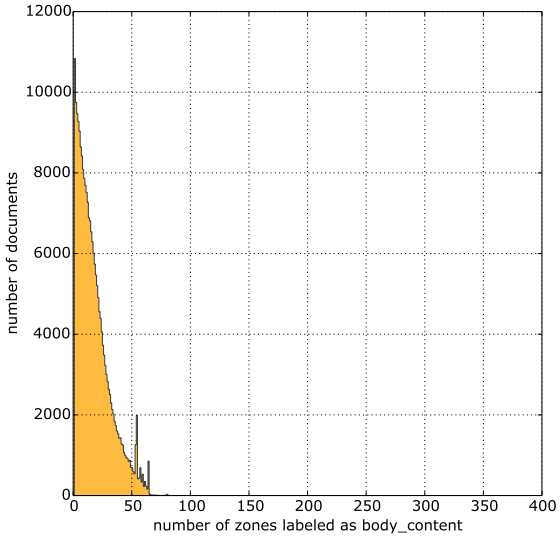


Figure E.7: Histogram of number of zones labeled as `body_content`

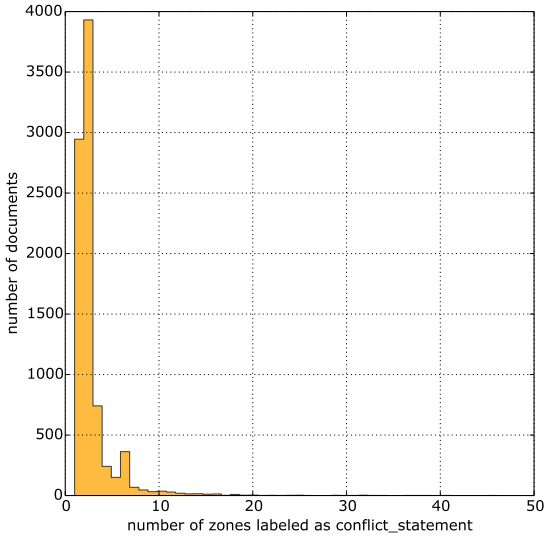


Figure E.8: Histogram of number of zones labeled as `conflict_statement`

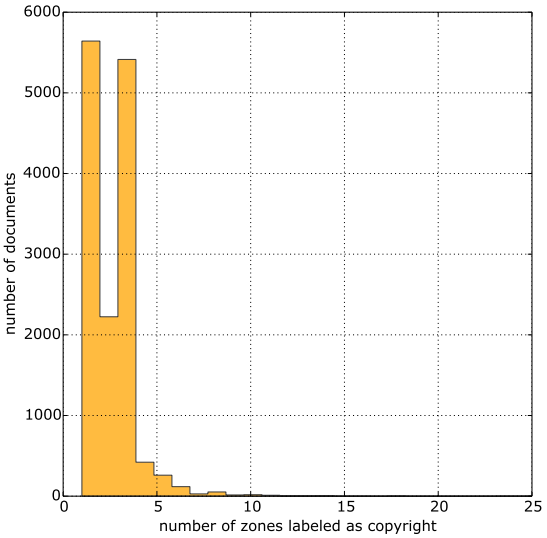


Figure E.9: Histogram of number of zones labeled as `copyright`

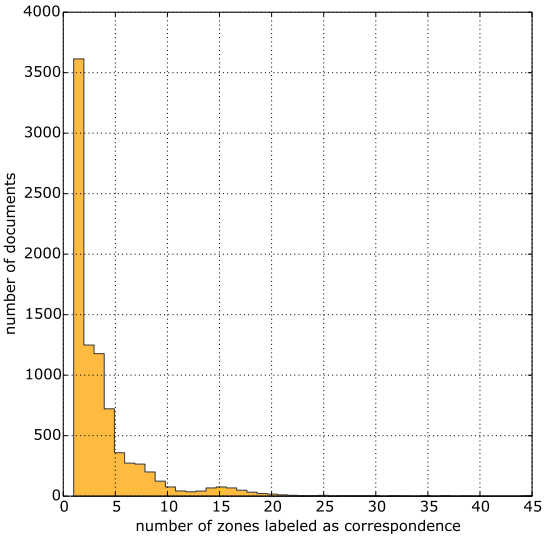


Figure E.10: Histogram of number of zones labeled as `correspondence`

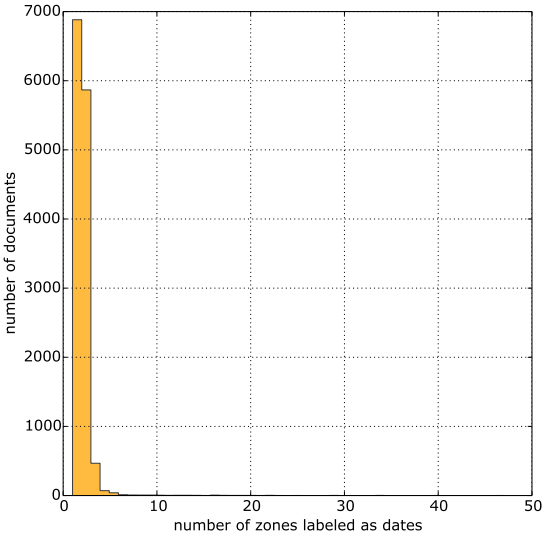


Figure E.11: Histogram of number of zones labeled as `dates`

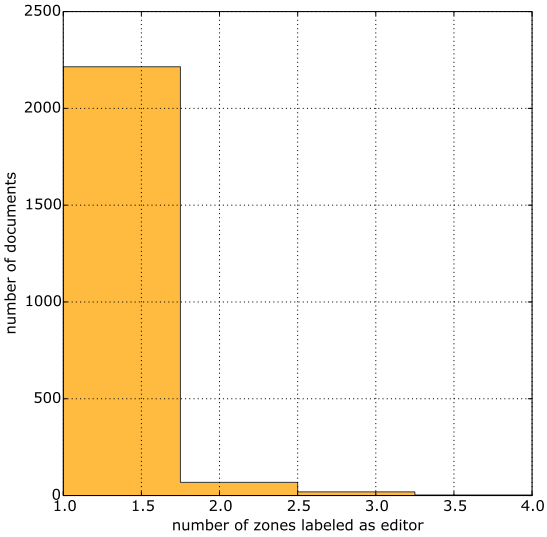


Figure E.12: Histogram of number of zones labeled as `editor`

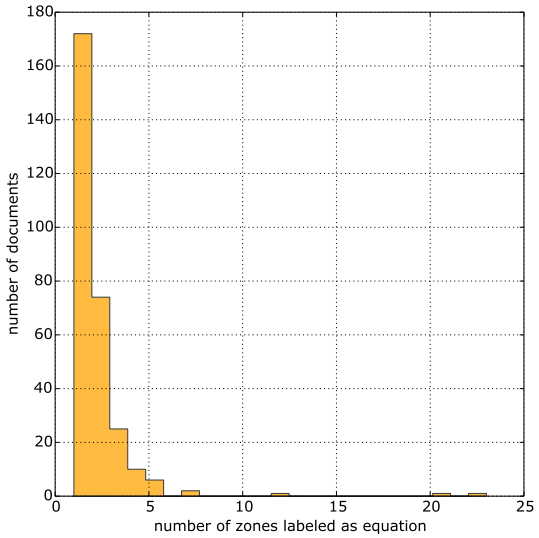


Figure E.13: Histogram of number of zones labeled as `equation`

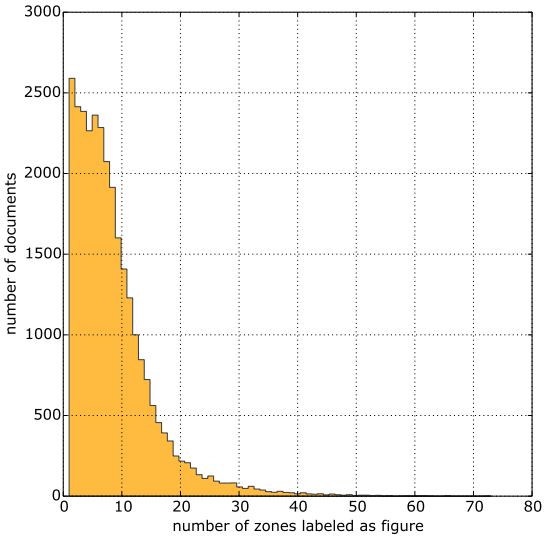


Figure E.14: Histogram of number of zones labeled as `figure`

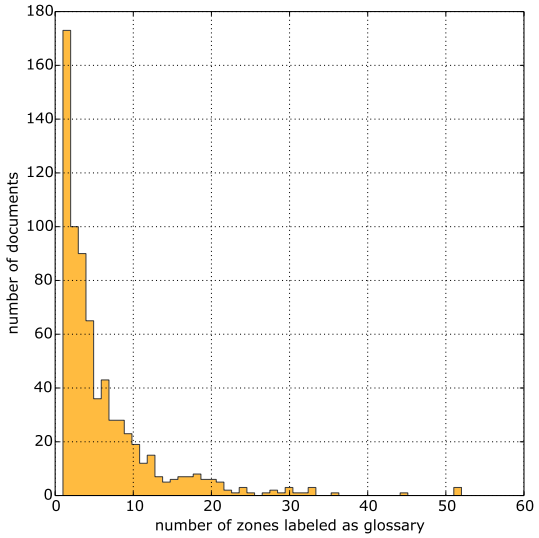


Figure E.15: Histogram of number of zones labeled as `glossary`

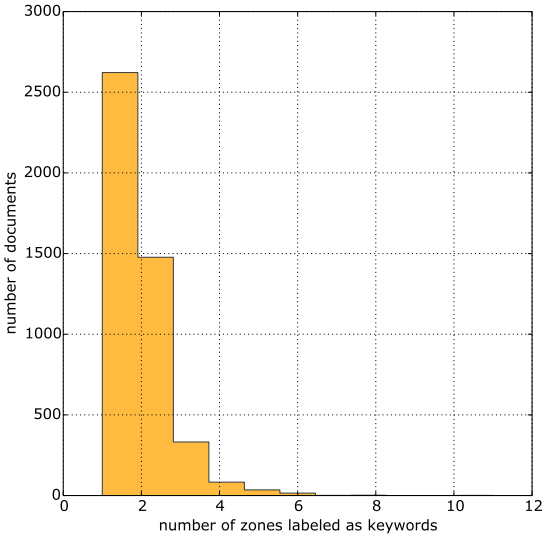


Figure E.16: Histogram of number of zones labeled as `keywords`

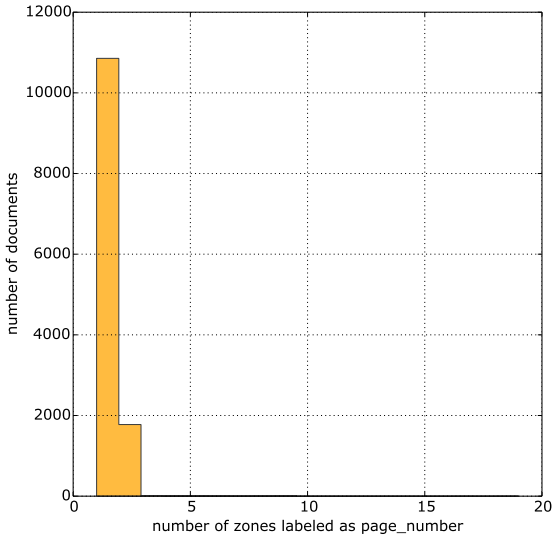


Figure E.17: Histogram of number of zones labeled as `page_number`

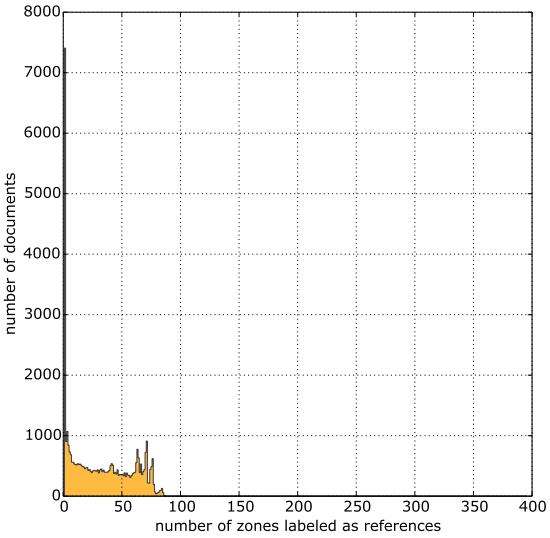


Figure E.18: Histogram of number of zones labeled as `reference`

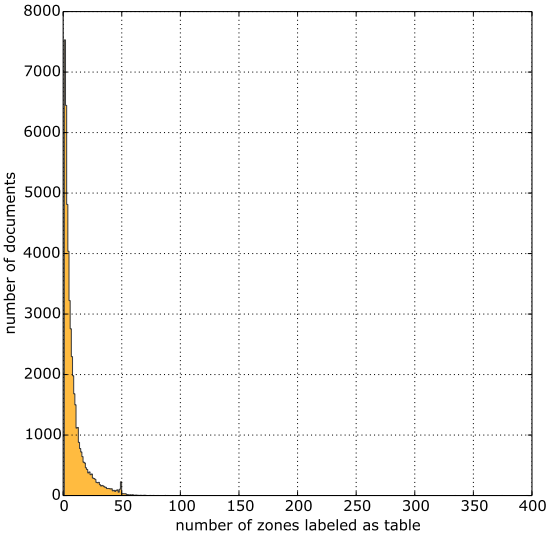


Figure E.19: Histogram of number of zones labeled as `table`

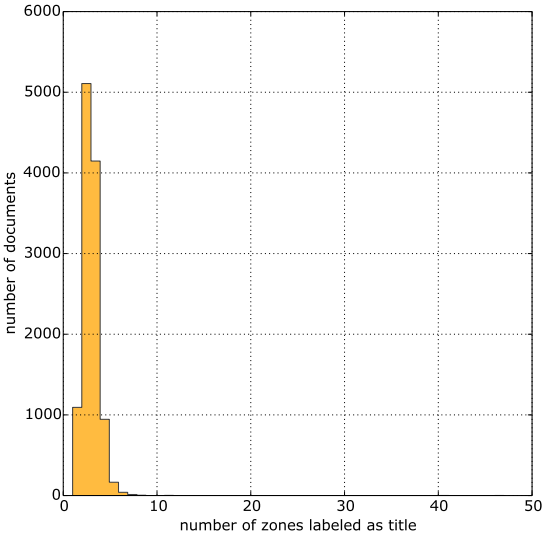


Figure E.20: Histogram of number of zones labeled as `title`

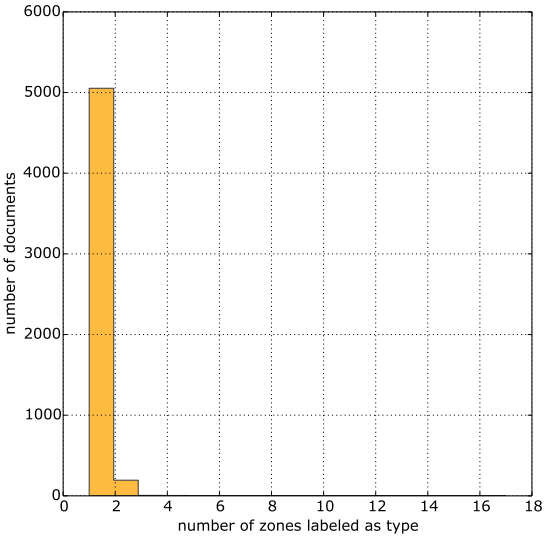


Figure E.21: Histogram of number of zones labeled as `type`

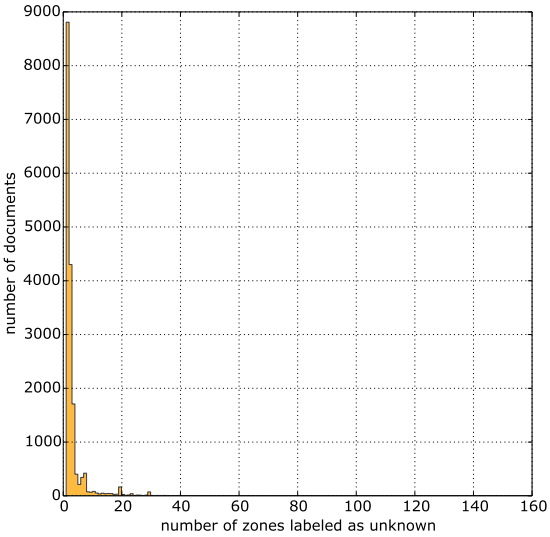


Figure E.22: Histogram of number of zones labeled as `unknown`

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