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New Methods for Metadata Extraction from Scientific Literature

Ph.D. Thesis

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Abstract

Spreading the ideas and announcing new discoveries and findings in the scientific world is typically realized by publishing and reading scientific literature. Within the past few decades we have witnessed digital revolution, which moved scholarly communication to electronic media and also resulted in a substantial increase in its volume. Nowadays keeping track with the latest scientific achievements poses a major challenge for the researchers. Scientific information overload is a severe problem that slows down scholarly communication and knowledge propagation across the academia.

Modern research infrastructures facilitate studying scientific literature by providing intelligent search tools, proposing similar and related documents, building and visualizing interactive citation and author networks, assessing the quality and impact of the articles using citation-based statistics, and so on. In order to provide such high quality services the system requires the access not only to the text content of stored documents, but also to their machine-readable metadata. Since in practice good quality metadata is not always available, there is a strong demand for a reliable automatic method of extracting machine-readable metadata directly from source documents.

Our research addresses these problems by proposing an automatic, accurate and flexible algorithm for extracting wide range of metadata directly from scientific articles in born-digital form. Extracted information includes basic document metadata, structured full text and bibliography section.

Designed as a universal solution, proposed algorithm is able to handle a vast variety of publication layouts with high precision and thus is well-suited for analyzing heterogeneous document collections. This was achieved by employing supervised and unsupervised machine-learning algorithms trained on large, diverse datasets. The evaluation we conducted showed good performance of proposed metadata extraction algorithm. The comparison with other similar solutions also proved our algorithm performs better than competition for most metadata types.

Proposed method is a reliable and accurate solution to the problem of extracting the metadata from documents. It allows modern research infrastructures to provide intelligent tools and services supporting the process of consuming the growing volume of scientific literature by the readers, which results in facilitating the communication among the scientists and the overall improvement of the knowledge propagation and the quality of the research in the scientific world.
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Chapter 1

Overview

This chapter is an introduction to the research described in the thesis. First we sketch the background of the work and explain our motivations. Then we formulate the problem we focus on and outline the proposed solution and its features. Finally, we state the key contributions and briefly describe the thesis structure.

1.1 Background and Motivation

The background of the research described in the thesis is related to scholarly communication in digital era and the problems it encounters. Our main objective is to facilitate the communication among the scientists and improve the knowledge propagation in the scientific world. These goals are accomplished by equipping digital libraries and research infrastructures with means allowing them to support the process of consuming the growing volume of scientific literature by researchers and scientists.

Scholarly Communication

In the scientific world communicating the ideas, describing the planned, ongoing and completed research and finally reporting discoveries and project results is typically realized by publishing and reading scientific literature, mostly in the form of articles published in journals or conference proceedings. Originally scientific literature was distributed in the form of printed paper, but within the last 30 years we have witnessed the digital revolution which has moved this aspect of scientific communication to electronic media.

Along with the media change we have also observed a huge increase in the volume of available scientific literature. The exact total number of existing scientific articles is not known, but the statistics gathered from popular electronic databases show the scale we are dealing with. For example DBLP database\footnote{http://dblp.uni-trier.de/} which provides bibliographic information on scientific literature from computer science discipline only, currently contains approximately

\footnote{http://dblp.uni-trier.de/}
CHAPTER 1. OVERVIEW

3 million records. PubMed Central\footnote{http://www.ncbi.nlm.nih.gov/pmc/} is a full text free archive of 3.6 million biomedical and life sciences journal articles. PubMed\footnote{http://www.ncbi.nlm.nih.gov/pubmed}, a freely available index of biomedical abstracts, including the entire MEDLINE database, contains 25 million references. Finally, Scopus database\footnote{http://www.scopus.com/}, which collects publications from a much wider range of disciplines that DBLP or PubMed, currently contains 57 million records.

There also have been a number of attempts of estimating the total number of scientific articles or a specific subset of them. For example Bjork et al.\footnote{http://ip-science.thomsonreuters.com} estimated the number of peer-reviewed journal articles published by 2006 to be about 1,350,000 using data from the ISI citation database\footnote{http://academic.research.microsoft.com/}. Jinha \footnote{https://scholar.google.pl/} used this result and a number of assumptions related to a steady increase in the number of researchers, journals and articles, and arrived at the estimation of the total number of journal articles ever published to be more than 50 million as of 2009. Finally, Khabsa and Giles \footnote{http://academic.research.microsoft.com/} studied the volume of scholarly documents written in English and available on the web by analysing the coverage of two popular academic search engines: Google Scholar\footnote{http://www.ncbi.nlm.nih.gov/pmc/} and Microsoft Academic Search\footnote{http://academic.research.microsoft.com/}. Their estimates show that at least 114 million documents are accessible on the web, with at least 27 million available without any subscription or payment.

In addition to the total volume of already published scientific literature being huge, we are also observing a substantial increase in the number of new articles published every year. According to Larsen and von Ins \cite{larsen2013trends}, there are no indications that the growth rate in the number of published peer-reviewed journal articles has decreased within the last 50 years, and at the same time, the publication using new channels, such as conference proceedings, open archives and web pages, is growing fast. The statistical data obtained from DBLP and PubMed databases show similar trends (Figures 1.1 and 1.2).

Writing and publishing articles is only one side of scholarly communication. At the other end there are the consumers of the literature, usually also scientists and researchers, interested in new ideas and discoveries in their own field, or trying to get familiar with the state of the art in new fields. Keeping track of the latest scientific findings and achievements published in journals or conference proceedings is a crucial aspect of their work. Ignoring this task results in deficiencies in the knowledge related to the latest discoveries and trends, which in turn can lower the quality of their own research, make results assessment much harder and significantly limit the possibility to find new interesting research areas and challenges.

Unfortunately, due to the huge and still growing volume of scientific literature, keeping track with the latest achievements is a major challenge for the researchers. Scientific information overload is a severe problem that slows down the scholarly communication and knowledge propagation across the academia.
Digital Libraries

The digital era resulted not only in moving the literature from paper to digital media, but in fact changed the way modern research is conducted. Research infrastructures equip the users with the resources and services supporting all stages of the research in many disciplines. Digital libraries provide means for storing, organizing and accessing digital collections of research-related data of all kinds, such as documents, datasets or tools.

These modern infrastructures support the process of studying scientific literature by providing intelligent search tools, proposing similar and related documents (Figure 1.3), building and visualizing interactive citation and author networks (Figure 1.4), providing various citation-based statistics, and so on. This enables the users to effectively explore the map of science, quickly get familiar with the current state of the art of a given problem and reduce the volume of articles to read by retrieving only the most relevant and interesting positions.

Unfortunately, building the services supporting the readers is not a trivial task. Such intelligent, high-quality services and tools require reliable, machine-readable metadata of the digital library resources. Unfortunately, in practice a large portion of the resources is typically available to a great extent as unstructured text, intended for human readers, but poorly understood by machines. Good quality metadata is not always available, sometimes it is missing, full of errors or fragmentary, even for fairly recently published articles.

There are two complementary solutions to this problem. The easiest way to provide high quality metadata for scientific documents is to gather this information directly from the author when a document is submitted to the system for the first time. Since we are interested in a wide range of metadata, possibly including the metadata of all the
Figure 1.2: The number of records by year of publication and type in DBLP database. The data shows clear growing trend, in particular in both journal articles and conference proceedings categories.

On the other hand, digital libraries already have to deal with huge number of existing documents with missing or fragmentary metadata records. Since processing this huge volume by human experts would be extremely ineffective, we have to rely on automatic tools able to process large collections and provide reliable metadata for the documents in an unsupervised manner. Unfortunately, already existing metadata extraction tools are not accurate, flexible or comprehensive enough.

1.2 Problem Statement

The main goal of our research is to solve the problem of missing metadata information by providing an automatic, accurate and flexible algorithm for extracting wide range of metadata directly from scientific articles.

Even limited to analysing scientific literature only, the problem of extracting the document’s metadata remains difficult and challenging, mainly due to the vast diversity of possible layouts and styles used in articles. In different documents the same type of information can be displayed in different places using a variety of formatting styles and fonts.
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Figure 1.3: Example screenshots from Scopus system. Scopus enables the users to navigate through citation network using ”cited by” list. The system also proposes documents related to the current one based on references, authors or keywords.

For instance, a random subset of 125,000 documents from PubMed Central contains publications from nearly 500 different publishers, many of which use original layouts and styles in their articles.

In general solving the metadata extraction problem requires addressing the two major tasks: the analysis of the layout of the document, the difficulty of which varies with the input document formats, and understanding the roles played by all the fragments in the document.

The result of the research is an accurate automatic algorithm for extracting rich metadata directly from a scientific publication. Proposed algorithm takes a single publication in PDF format on the input, performs a thorough analysis of the document and outputs a structured machine-readable metadata record containing:

- a rich set of document’s basic metadata, such as title, abstract, keywords, authors’ full names, their affiliations and email addresses, journal name, volume, issue, year of publication, etc.,

- a list of references to other documents given in the article along with their metadata such as the document’s authors, title, journal name or year,

- structured full text with sections and subsections hierarchy.
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Figure 1.4: The visualization of a fragment of documents and authors network generated by COMAC (Common Map of Academia) [35].

Designed as a universal solution, the algorithm is able to handle a vast variety of scientific articles reasonably well, instead of being perfect in processing a limited number of document layouts only. We achieved this by employing supervised and unsupervised machine-learning algorithms trained on large, diverse datasets. This decision made the method well-suited for analysing heterogeneous document collections, and also resulted in increased maintainability of the system, as well as its ability to adapt to new, previously unseen document layouts.

Since our main objective was to provide a useful, accurate solution to a practical problem, machine learning-based solutions are accompanied with a number of rules and heuristics. This approach proved to work very well in practice, although perhaps lacks the simplicity and elegance of algorithms based purely on machine learning.

The evaluation we conducted showed good performance of the proposed metadata extraction algorithm. The comparison to other similar systems also proved our algorithm performs better than competition for most metadata types.

Proposed algorithm is very useful in the context of digital libraries for both automatic extraction of reliable metadata from large heterogeneous document collections and assisting the users in the process of providing metadata for the submitted documents.

The implementation of the algorithm is available as an open-source Java library\(^8\) and a web service\(^9\).

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\(^8\)https://github.com/CeON/CERMINE
\(^9\)http://cermine.ceon.pl
1.3 Key Contributions

The extraction algorithm we developed is based to a great extent on well-known supervised and unsupervised machine-learning techniques accompanied with heuristics. Nevertheless, the research contains the following innovatory ideas and extensions:

1. One of the key contributions is the architecture of the entire extraction workflow and the decomposition of the problem into smaller, well-defined tasks.

2. The page segmentation algorithm was enhanced with a few modifications increasing its accuracy.

3. We developed a large set of numeric features for text fragments of the document capturing all aspects of the content and appearance of the text and allowing to classify fragments with high accuracy.

4. We also developed a set of features for citation and affiliation tokens, which allow to parse affiliations and citations with high accuracy.

5. A clustering-based approach was proposed for extracting reference strings from the document.

6. We also proposed an algorithm based on normal scores of various statistics for selecting section header lines from the text content of the document.
7. Finally, we developed an efficient, scalable method of building gold standard publication datasets.

1.4 Thesis Structure

The thesis is structured as follows. In Chapter 2 we describe current state of the art with respect to scientific document analysis and automatic metadata extraction. Chapter 3 provides all the details related to the overall algorithm architecture, its internal decomposition into individual tasks and approaches employed for solving all of them. In Chapter 4 we thoroughly describe the datasets and methodology used to assess the quality of the algorithm and report the evaluation results, including the comparison with other similar systems. Chapter 5 summarizes the research. Appendix A provides the detailed results of the evaluation and all the tests performed, and finally Appendix B covers the practical aspects of the available algorithm implementation.
Chapter 2

State of the Art

In this chapter we present the current state of the art with respect to extracting metadata and content from scientific literature. We start with a brief description of document formats used for creating and storing academic articles (Section 2.1). In Section 2.2 we present machine learning techniques relevant to our work. Finally, in Section 2.3 we discuss various algorithms and approaches to the problem of metadata extraction and list existing systems and tools that can be used for analysing scientific articles.

2.1 Metadata and Content Formats

In this section we present a number of document formats useful for creating and storing academic articles, focusing on the most popular ones. Described formats are optimized for many different purposes, and as a result they differ a lot in the type of information they are able to store and the stage of the document’s life they are mostly useful in. In the context of automatic document analysis, the most important feature of a format is its machine-readability, which determines the ability of extracting the information from the documents by automatic tools.

In general we deal with three types of formats:

- formats optimized for creating and editing the documents, such as MS Word formats or LaTeX,

- formats optimized for presentation, mostly used for exchanging and storing the documents, but not for manipulating them, such as PDF,

- modern, machine-readable formats storing various aspects of documents, such as the content and physical and/or logical structure.

One of the most popular formats used for creating and editing documents are of course those related to Microsoft Word\footnote{https://products.office.com/en-us/word}, a widely used word processor. Microsoft Word uses several file formats, and the default one varies with the version of the software.
In the 1990s and early 2000s the default format was .DOC. It is a very complex binary format, where a document is in fact a hierarchical file system within a file. The format was optimized for the software performance during editing and viewing the files, and not for machine understanding. For many years .DOC format specification was closed. Some specifications for Microsoft Office 97 were first published in 1997 under a restrictive license, and remained available until 1999. Since 2006 the specification was available under a restrictive license on request. In 2008 Microsoft released a .DOC format specification under the Microsoft Open Specification Promise. Unfortunately, due to the format complexity and missing descriptions of some features, automatic analysis of .DOC files still requires some amount of reverse engineering.

Starting from Microsoft Office 2007, the default format is Office Open XML, which comprises formats for word processing documents, spreadsheets and presentations as well as specific formats for mathematical formulae, graphics, bibliographies etc. The format uses WordprocessingML as the markup language for word processing documents. In comparison to .DOC, OOXML is much more machine-readable thanks to the usage of XML and open specifications.

Another format used for creating and editing documents, popular especially in academia, is LaTeX. As opposed to Microsoft Word, writers using LaTeX write in plain text and use markup tagging to define styles, the document structure, mathematical formulae, citations, and so on. LaTeX uses the TeX typesetting program for formatting its output, and is itself written in the TeX macro language. LaTeX documents can be processed by machines, although it is often used as an intermediate format only.

Portable Document Format (PDF) is currently the most popular format for exchanging and storing the documents, including the contents of scientific publications. The format is optimized for presentation, PDF documents look the same no matter what application software, operating system or hardware is used for creating or viewing them.

A PDF document is in fact a collection of objects that together specify the appearance of a list of pages and their content. A single page contains a PDF content stream which is a sequence of text, graphics and image objects printed on the page, along with all the information related to the position and appearance of all the objects.

A text object in a PDF stream specifies the text to be painted on the page, as well as the font, size, position, and other geometric features used to print the text. Listing 2.1 shows an example text object, which results in writing a string “PDF” using 10-point font identified by F13 font source (typically Helvetica), 360 typographic points from the bottom of the page and 288 typographic points from its left edge.

A text object can contain three types of operators:

- text state operators, used to set and modify text state parameters, such as character spacing, word spacing, horizontal scaling, text font and text font size,
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- text positioning operators, which control the placement of chunks that are subsequently painted, for example they can be used to move the current position to the next line with or without an offset,

- text showing operators, used to paint the text accordingly to the current state and position parameters.

Listing 2.1: Example PDF text object

```
BT
/F13 10 Tf
288 360 Td
(PDF ) Tj
ET
```

Depending on the software and method used to create a PDF file, a single text-showing operator can be used to print a single character, word, line, or any other chunk of continuous text without line breaks. Spaces may be included in the text strings painted on the pages, or may be a result of moving the current cursor to a different position. Some text decorations, such as underline or strikethrough, can be produced using specialized fonts or printed independently on top of the text as geometric objects.

What is more, PDF format does not preserve any information related to the logical structure of the text, such as words, lines, paragraphs, enumerations, column layout, sections, section titles or even the reading order of text chunks. This information has to be deduced from the geometric features of the text chunks. The text in a PDF file may be also present not in the form of text operators, but as images of scanned pages. In such cases only optical character recognition can be used to extract the text content from a file. All these issues make PDF format very difficult to understand by machines.

Another format specifying the precise positions and the appearance of the text in a document is TrueViz [46], an XML-based, machine-readable format. TrueViz stores the geometric structure of the document containing pages, zones, lines, words and characters, along with their positions, dimensions, font information and the reading order.

Modern XML-based machine-readable formats can be used for storing both structured metadata and the content of the documents, preserving various characteristics related to the appearance and meaning of the text. For example NLM JATS [5] (Journal Article Tag Suite) defines a rich set of XML elements and attributes for describing scientific publications. Documents in JATS format can store a wide range of structured metadata of the document (title, authors, affiliations, abstract, journal name, identifiers, etc.), the full text (the hierarchy of sections, headers and paragraphs, structured tables, equations, etc.), the document’s bibliography in the form of a list of references along with their identifiers and metadata, and also the information related to the text formatting.

[5]http://jats.nlm.nih.gov/
Other similar XML-based formats are: the format developed by Text Encoding Initiative (TEI\textsuperscript{6} which is semantic rather than presentational, and Dublin Core Schema\textsuperscript{7}, a small set of vocabulary terms that can be used to describe documents.

In our algorithm we use three formats described above. PDF, as the most popular format for storing the documents in digital libraries, is the input format to the entire algorithm. TrueViz is used as an intermediate format to serialize the geometric model of the input document inferred from the PDF file. The output format is NLM JATS, as a widely used machine-readable format able to store both the metadata of the document as well as structured full text in hierarchical form.

2.2 Relevant Machine Learning Techniques

This section describes briefly machine learning tasks and techniques related to extracting metadata from documents. We focus mainly on the algorithms used in our work.

2.2.1 General Classification

Classification is one of the most useful technique in the context of extracting information from documents. Classification can be used to determine the roles played in the document by its fragments of various granularity.

Classification refers to the problem of assigning a category (a label from a known label set) to an instance. In supervised machine learning this is achieved by learning a model (a classification function) from a set of instances with known labels, called the training set, and applying the learned function to new instances with unknown labels. Instances are typically represented by features of various types (binary, numerical, categorical).

There are many known classification algorithms, for example: linear classifiers (including LDA, naive Bayes, logistic regression, Support Vector Machines), which make classification decisions based on a linear combination of instance features, k-Nearest Neighbors algorithm, in which the decision is based on the labels of instances close to the input instance according to some metric, or decision trees, which make a decision based on a sequence of ”questions” related to the values of individual features.

Our extraction algorithm makes extensive use of Support Vector Machines. SVM\textsuperscript{8, 76, 14} is a powerful classification technique able to handle a large variety of input and work effectively even with training data of a small size. SVM is a binary classifier (able to handle label sets containing exactly two elements) based on finding the optimal separation hyperplane between the observations of two classes. It is little prone to overfitting, generalizes well, does not require a lot of parameters and can deal with highly dimensional data. SVM is widely used for content classification and achieves very good results in practice.

Let the classification instances be represented by vectors of real-valued features. Let us also assume that the label set contains exactly two elements. SVM is a linear model of

\textsuperscript{6}http://www.tei-c.org
\textsuperscript{7}http://dublincore.org/schemas/
the form

\[ y(x) = w^T \phi(x) + b \]

where

- **x** is a feature vector representing the classification instance,
- **\( \phi(x) \)** denotes a fixed feature-space transformation,
- **w** and **b** are parameters determined during the training based on the training instances,
- new instances are classified according to the sign of \( y(x) \).

The training set contains \( N \) vectors \( x_1, ..., x_N \) with corresponding target values (labels) \( t_1, ..., t_N \), where \( t_n \in \{-1, 1\} \). If we assume the training set is linearly separable, then there exists at least one choice of the parameters \( w \) and \( b \) such that the function \( y \) satisfies \( y(x_n) > 0 \) for points having \( t_n = 1 \) and similarly, \( y(x_n) < 0 \) for points having \( t_n = -1 \). In short, we have \( t_n y(x) > 0 \) for all training data points. There of course might exist many choices of the parameters separating the classes entirely. The objective of the training phase is to find the parameters resulting in the best separation.

In SVM we are interested in finding the parameters which maximize the margin in the training set, which is the smallest distance between the decision boundary and any of the points of a given class. Formally, the task of the training is to find

\[ \arg \max_{w,b} \frac{1}{||w||} \min_n [t_n(w^T \phi(x_n) + b)] \]

Since the direct solution of this problem would be very complex, we often convert this into an equivalent problem easier to solve by rescaling \( w \) and \( b \), so that we have \( t_n(w^T \phi(x_n) + b) = 1 \) for the point that is the closest to the decision boundary. For all data points we then have \( t_n(w^T \phi(x_n) + b) \geq 1 \) and the optimization problem now becomes the equivalent

\[ \arg \min_{w,b} \frac{1}{2} ||w||^2 \text{ subject to } t_n(w^T \phi(x_n) + b) \geq 1 \]

If the feature space \( \phi(x) \) is not linearly separable, then there is no hyperplane separating the training data points of two classes. To deal with this, we allow some data points to be on the wrong side of the hyperplane, but we use a penalty which increases with the distance to the decision boundary. We introduce slack variables, \( \xi_n \geq 0 \), one per training instance, and the condition \( t_n(w^T \phi(x_n) + b) \geq 1 \) becomes \( t_n(w^T \phi(x_n) + b) \geq 1 - \xi_n \). Our new optimization problem now becomes the following:
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\[
\arg \min_{\mathbf{w}, b, \xi} \quad \frac{1}{2} \|\mathbf{w}\|^2 + C \sum_{n=1}^{N} \xi_n \\
\text{subject to} \quad t_n (\mathbf{w}^T \phi(x_n) + b) \geq 1 - \xi_n \\
\xi_n \geq 0
\]

where \( C > 0 \) is the regularization parameter (the penalty parameter of the error term).

For practical reasons, we usually operate not on \( \phi(x) \) function directly, but on a kernel function \( K(x_i, x_j) = \phi(x_i)^T \phi(x_j) \). The most popular kernel functions are:

- linear: \( K(x_i, x_j) = x_i^T x_j \)
- polynomial: \( K(x_i, x_j) = (\gamma x_i^T x_j + r)^d, \gamma > 0 \)
- radial basis function (RBF): \( K(x_i, x_j) = \exp(-\gamma \|x_i - x_j\|^2), \gamma > 0 \)
- sigmoid: \( K(x_i, x_j) = \tanh(\gamma x_i^T x_j + r) \)

The kernel function, as well as its parameters \( \gamma, r \) and/or \( d \) are typically set prior to the training. Usually some procedure is adopted in order to determine the best kernel function and its parameters. One of the most widely used is a grid search, in which various combinations of parameters are used to assess the classifier performance on a validation set and the parameters giving the best scores are chosen.

Since SVM is a binary classifier, usually we need a strategy of dealing with multiple target classes. Two most popular strategies are one-vs.-all and one-vs.-one. In one-vs.-all strategy we train a single classifier per class, with the instances of the given class as positive samples and all other samples as negatives. In one-against-one approach \([41]\) we train a single classifier per each pair of classes using only the samples of these classes, resulting in \( k(k-1)/2 \) classifiers for \( k \) classes. During the classification a voting strategy might be used. Early works of applying this strategy to SVM-based classification include, for example \([43]\).

### 2.2.2 Sequence Classification

A special case of classification, sequence classification, is also often encountered in document analysis domain. In sequence classification we are interested in analysing a sequence of instances rather than independent instances.

More formally, the input is a sequence of instances and we are interested in finding a sequence of corresponding class labels from a known label set. We would like to predict a vector \( \mathbf{y} = y_0, y_1, \ldots, y_T \) of class labels given an observed feature vector \( \mathbf{x} \), which is typically divided into feature vectors \( \mathbf{x}_0, \mathbf{x}_1, \ldots, \mathbf{x}_T \). Each \( \mathbf{x}_s \) contains various information about the instance at position \( s \).

Sequence classification can be approached as any other classification problem by simply treating sequence elements as independent classification instances, and the successor and/or
predecessor relations might be reflected in the instances features. On the other hand, sequences can also be seen as special cases of graphs and analysed with graphical modelling tools. In graphical modelling we model probabilistically arbitrary graphs, which represent the conditional dependence structure between random variables (labels and features).

A lot of effort in learning with graphical models has focused on generative models that explicitly model a joint probability distribution $p(y, x)$ over both features and output labels and usually have the form $p(y) p(x|y)$. One very popular approach from this family are Hidden Markov Models (HMM).

HMM models a chain of variables, where every variable can be in a certain state (states correspond to the labels) and emit observations (observations correspond to the features). In HMM we assume that each state depends only on its immediate predecessor, and each observation variable depends only on the current variable’s state. The model comprises the initial probability distribution for the state of the first variable in a sequence, the transition probability distribution from one variable’s state to the next variable and emission probability distributions. The classification is performed with the use of Viterbi algorithm, which infers the most probable label sequence based on observed features.

Apart from generative models, another family of approaches are discriminative models, which instead of modelling the joint probability focus only on the conditional distribution $p(y|x)$. This approach does not include modelling $p(x)$, which is not needed for classification and often hard to model because it may contain many highly dependent features. Modelling the dependencies among inputs can lead to complex and unmanageable models, but ignoring them can result in reduced performance. Because dependencies that involve only variables in $x$ play no role in the discriminative models, they are better suited to including rich, overlapping features.

A very popular model in the discriminative family is Conditional Random Fields (CRF) [44]. CRF combines the advantages of classification and graphical modeling, bringing together the ability to model multivariate, highly dependent data with the ability to leverage a large number of input features for prediction. CRF can be seen as a discriminative variant of HMM.

In general CRF can be used to model arbitrary graphs. A special case, a linear-chain CRF models sequences of variables and is a distribution $p(y|x)$ that takes the form

$$p(y|x) = \frac{1}{Z(x)} \exp \left( \sum_{t=1}^{T} \sum_{k=1}^{K} \lambda_k f_k(y_{t-1}, y_t, x, t) \right)$$

where

- $\{f_k(y, y', x, i)\}_{k=1}^{K}$ is a set of real-valued feature functions, which typically are based on two consecutive class labels and the entire observations sequence,
- $\lambda = \{\lambda_k\} \in R^K$ is a vector of feature weights which are learned during the training phase,
- $Z(x)$ is a normalization function to make $p(y|x)$ a valid probability.
\[ Z(\mathbf{x}) = \sum_y \sum_{t=1}^{T} \sum_{k=1}^{k} \lambda_k f_k(y_{t-1}, y_t, \mathbf{x}, t) \]

After we have trained the model, we can predict the labels of a new input \( \mathbf{x} \) using the most likely labeling by calculating

\[ \arg \max_y p(y|x) \]

In the case of a linear-chain CRF, finding the most probable label sequence can be performed efficiently and exactly by variants of the standard dynamic programming algorithm for HMM, Viterbi algorithm.

CRF is trained by a maximum likelihood estimation, that is, the parameters are chosen such that the training data has the highest probability under the given model.

### 2.2.3 Clustering

Clustering is another very useful technique in document analysis. It can be employed whenever we wish to group a set of objects into disjoint subsets called clusters, such that the objects in the same cluster have similar characteristics. Two widely used clustering techniques are: hierarchical clustering and k-means clustering.

Hierarchical clustering not only groups objects into clusters, but also results in a hierarchy of clusters. In a bottom-up approach each object starts as a single-element cluster, and the clusters are iteratively merged accordingly to a certain strategy. In a top-down approach we start with a single cluster containing the entire set and the clusters are then iteratively split. Both approaches result in a tree-like hierarchy, where the root is a cluster containing the entire set, the leaves represent the individual elements and the remaining nodes are clusters of various granularity.

In order to decide which clusters should be combined or where a cluster should be split we need a measure of distance between sets of observations. This is typically based on a distance metric between individual points. Some commonly used metrics are:

- minimum distance between pairs of observations (single linkage clustering): \( d(A, B) = \min\{d(a, b) : a \in A, b \in B\} \)
- maximum distance between pairs of observations (complete linkage clustering): \( d(A, B) = \max\{d(a, b) : a \in A, b \in B\} \)
- average distance between pairs of observations (average linkage clustering):

\[ d(A, B) = \frac{1}{|A||B|} \sum_{a \in A} \sum_{b \in B} d(a, b) \]
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In k-means clustering the number of target clusters has to be known in advance. The clusters are represented by the means of the observations and each data point belongs to the closest mean according to a given distance metric.

More formally, given a set of observations \( (x_1, x_2, \ldots, x_n) \), where each observation is a real vector, k-means clustering aims to partition the observations into \( k \leq n \) sets \( S = S_1, S_2, \ldots, S_k \) so that the within-cluster sum of squares is minimized. In other words, its objective is to find:

\[
\arg \min_S \sum_{i=1}^{k} \sum_{x \in S_i} ||x - \mu_i||^2
\]

where \( \mu_i \) is the mean of vectors in \( S_i \).

K-means algorithm works in iterations. At the beginning we choose \( k \) vectors as the initial centroids of the clusters. Then every point in the data set is assigned to the nearest cluster centroid and the centroids are recalculated as the means of their assigned points. This is repeated until there are any changes in the points assignments. The algorithm converges to a local minimum, but there is no guarantee a global minimum will be found. To obtain better results the algorithm can be repeated several times with different initial centroids.

2.3 Document Analysis

In this section we describe the state of the art in the area of scientific literature analysis. The section covers a number of tasks related to the problem, including layout analysis and information extraction.

Extracting metadata and content from scientific articles and other documents is a well-studied problem. Older approaches expected scanned documents on the input and were prepared for executing full digitization from bitmap images. Nowadays we have to deal with growing amount of born-digital documents, which do not require individual character recognition.

Extracting information from documents is a complex problem and usually has to be divided into smaller subtasks. Typical tasks related to the extraction problem include:

- Preprocessing, which can be understood as parsing the input document and preparing a model of it for further analysis. The difficulty depends heavily on the input format. In the case of scanned documents, an OCR has to be performed. For PDFs the input text objects need to be parsed. Highly machine-readable formats, such as NLM JATS or TrueViz are comparatively easy to process.

- Page segmentation, in which we detect basic objects on the pages of the document, for example text lines or blocks (zones). Similarly as before, depending on the format it might be sufficient to parse the input XML-based file, or a more complicated analysis of mutual positions of chunks or characters has to be performed.
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- Reading order resolving, in which we determine the order, in which all the text elements should be read. In western culture the text is usually read from the top to the bottom and from left to right, but the resolver has to take into account the column layout, various decorations such as page numbers, headers or footers, text elements floating around images and tables, etc.

- Region classification, in which we detect the roles played by different regions in the document. The classification may be performed on the instances of various kinds (such as zones, lines or text chunks, images, other graphical objects) and can be based on many different features related to both text content and the way the objects are displayed on the document’s pages.

- Parsing, which assigns sequences of labels to text string. Parsing is typically used to detect metadata in shorter fragments of the text, such as citation or affiliation strings, author full names, etc.

In the following subsections we discuss the state of the art in the following tasks: page segmentation (Section 2.3.1), reading order resolving (Section 3.2.3), document content classification (Section 2.3.3), sequence parsing (Section 2.3.4). Finally, in Section 2.3.5 we describe available systems and tools for processing scientific publications and extracting useful metadata and content from them.

2.3.1 Page Segmentation

Page segmentation refers to the task of detecting objects of various kinds in a document’s pages. The objects we are interested in can be zones (regions separated geometrically from other parts, such as blocks of text or images), text lines and/or words. Most approaches assume an image of the page is present on the input, and require additional OCR phase, as well as noise removal. Some of the algorithms can be adapted to analyzing born-digital documents, where the input is rather a bag of characters or chunks appearing on the page.

One of the most famous and widely used page segmentation algorithm is XY-cut proposed by Nagy et al. [57]. XY-cut is a top-down algorithm which recursively divides the input page into blocks. The result of the algorithm is a tree, in which the root represents the entire document page and the leaf nodes are the final blocks. The tree is built from the top, by recursively dividing the current rectangular region into two rectangular parts by cutting it horizontally or vertically. The place of a cut is determined by detecting valleys (empty horizontal or vertical space touching both up and down, or left and right fragment edge). By default the widest valley is chosen as the cut and the entire process stops when there are no more valleys wider than a predefined threshold. XY-cut is a simple and efficient algorithm, though sensitive to the skew of the page.

Run-length smearing algorithm (RLSA) proposed by Wong et al. [79] expects an image of the page on the input and analyses the bitmap of white and black pixels. It is based on a simple observation, that zones typically are dense and contain a lot of black pixels separated only by a small number of white pixels. The first phase of the algorithm is
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called smearing. During smearing the sequences of pixels (rows or columns of the bitmap) are analysed and black pixels separated by only a low number (less than some predefined threshold) of white pixels are joined together by transforming the separating white pixels into black ones. Smearing is performed vertically and horizontally separately with different thresholds and the resulting bitmaps are then combined in a logical AND operation. Then, one additional horizontal smearing is performed using a smaller threshold, which results in a smoothed final bitmap. Next, connected component analysis is performed on the pixels to obtain document zones. Finally, each block’s mean height and mean run-length of black pixels is compared to the mean values calculated over all blocks on the page. Based on this each block is classified into one of four classes: text, horizontal black line, vertical black line or image.

The whitespace analysis algorithm proposed by Baird [5] is based on analysing the structure of the white background in document images. First, the algorithm finds a set of maximal white rectangles called covers, the union of which completely covers the background. Then, the covers are sorted using a sorting key based on the rectangle area combined with a weighting function, which assigns higher weight to tall and long rectangles (as meaningful separators of text blocks). Next, we gradually construct the union of the covers in the resulting order, covering more and more of the white background. At each step, connected components within the remaining uncovered parts are considered candidates for text blocks. This process stops at some point, determined by a stopping rule, which results in the final segmentation. The stopping rule is defined as a predicate function of two numerical properties of segmentations: the sorting key of the covers and the fraction of the cover set used so far.

Breuel [10] describes two geometric algorithms for solving layout analysis-related problems: finding a set of maximal empty rectangles covering the background whitespace of a document page image and finding constrained maximum likelihood matches of geometric text lines in the presence of obstacles. The combination of these algorithms can be used to find text lines in a document in the following manner: after finding the background rectangles, they are evaluated as candidates for column separators (called gutters or obstacles) based on their aspect ratio, width, text columns width and proximity to text-sized connected components, and finally, the whitespace rectangles representing the gutters are used as obstacles in a robust least square text-line detection algorithm. This approach is not sensitive to font size, font style, or scan resolution.

The Docstrum algorithm proposed by O’Gorman [58] is a bottom-up page segmentation approach based on the analysis of the nearest-neighbor pairs of connected components extracted from the document image. After noise removal, $K$ nearest neighbors are found for each connected component. Then, the histograms of the distances and angles between nearest-neighbor pairs are constructed. The peak of the angle histogram gives the dominant skew (the text line orientation angle) in the document image. This skew estimate is used to compute within-line nearest neighbor pairs. Next, text lines are found by computing the transitive closure on within-line nearest neighbor pairs using a threshold. Finally, text-lines are merged to form text blocks using a parallel distance threshold and a perpendicular distance threshold. The algorithm uses a significant number of threshold values
and behaves the best if they are tuned for a particular document collection.

The Voronoi-diagram based segmentation algorithm proposed by Kise et al. [39] is also a bottom-up approach. It is based on a generalization of Voronoi diagram called area Voronoi diagram, where the regions are generated by a set of non-overlapping figures of any shape rather than individual points, and the distance between a point and a figure is defined as a minimal distance between the point and any point belonging to a figure. At the beginning the algorithm computes the connected components and samples the points from the boundaries of them. Then, an area Voronoi diagram is generated using sample points obtained from the borders of the connected components. The Voronoi edges that pass through any connected component are deleted to obtain an area Voronoi diagram. Finally, superfluous Voronoi edges are deleted to obtain boundaries of document components. An edge is considered superfluous if the minimum distance between its associated connected components is small, the area ratio of the two connected components is above a certain threshold or at least one of its terminals is neither shared by another Voronoi edge nor lies on the edge of the document image. The algorithm works well even for non-Manhattan layouts and is not sensitive to line skew or text orientation.

The above six algorithms were evaluated and compared by Shafait et al. [61]. They propose a pixel-accurate representation of a document’s page along with several performance measures to identify and analyze different classes of segmentation errors made by page segmentation algorithms. The algorithms were evaluated using a well-known University of Washington III (UW-III) database [26], which consists of 1,600 English document images with Manhattan layouts scanned from different archival journals with manually edited ground-truth of entity bounding boxes, including text and non-text zones, text lines and words. On average, Docstrum along with the Voronoi-based algorithm achieved the lowest error rates in most categories. Docstrum is also the only algorithm, which by default detects both text lines and zones.

In addition, International Conference on Document Analysis and Recognition (ICDAR) hosted a number of page segmentation competitions starting from 2001. The last competition for tools and systems of general segmentation purpose took place in 2009 [4]. Its aim was to evaluate new and existing page segmentation methods using a realistic dataset and objective performance measures. The dataset used comprised both technical articles and magazine pages and was selected from the expanded PRImA dataset [3].

In 2009 four systems were submitted to the competition. DICE (Document Image Content Extraction) system is based on classifying individual pixels into machine-print text, handwriting text and photograph [6], followed by a post-classification methodology [2] which enforces local uniformity without imposing a restricted class of region shapes. The Fraunhofer Newspaper Segmenter system is based on white [10] and black [83] separator detection followed by a hybrid approach for page segmentation [32]. The REGIM-ENIS method is designed primarily for degraded multi-script multi-lingual complex official documents, containing also tabular structures, logos, stamps, handwritten text and images. Finally, Tesseract [62], an extension of the Tesseract OCR system, in which the page layout analysis method uses bottom-up methods, including binary morphology and connected component analysis, to estimate the type (text, image, separator, or unknown) of connected
According to the competition results, the Fraunhofer Newspaper Segmenter method performed the best, improving on both the state-of-the-art methods (ABBYY FineReader and OCRopus) and the best methods of the ICDAR2007 page segmentation competition.

The segmentation algorithms can be adapted to process born-digital documents, although in some cases it might be non-trivial. In the case of born-digital document we often deal with characters, their dimensions and positions, but we lack the pixel-accurate representation of the pages, and thus the algorithms analysing individual pixels, such as RLSA or Voronoi would require preprocessing.

2.3.2 Reading Order Resolving

Another task related to document layout analysis is reading order resolving. Reading order resolving aims at determining the order, in which all the elements on a given page should be read. One might be interested in the order of elements of various types, such as zones, lines, or words. An accurate solution has to take into account many different aspects of the document layout, such as: column layout, presence of images and other text fragments not belonging to the main text flow, various language scripts, etc.

XY-cut algorithm, described in the previous section, can be naturally extended to output extracted zones in their natural reading order. In XY-cut algorithm every cut divides the current page fragment into two blocks positioned left-right or up-down to each other. If we assume that the text should be read from left to right and from top to bottom, then it is enough to always assign left or top part to the left child in the constructed tree, and similarly, right and bottom part should be always assigned to the right child. After the tree is complete, an in-order leaves traversal gives the resulting reading order of the extracted zones.

There are, however, a few serious problems with this approach. First of all, the algorithm is not able to process non-manhattan layouts (such as pages containing L-shaped zones). This is not a big problem in the case of scientific publications, since most of them use manhattan layout. There is also an issue of choosing the right threshold for the minimum width of the valley, which might vary from one document to another. The most problematic is the issue of choosing the best cut when there are a number of possible valleys to choose from. The default decision in XY-cut is to cut the regions along the widest valley, which works well for page segmentation, but often results in incorrect reading order. For example a multi-column page might get cut horizontally in the middle dividing all the columns, because the gaps between paragraphs or sections happen to occur in one horizontal line creating a valley wider than the gap between the columns.

Various approaches addressing these issues have been proposed. For example Ishitani et al. [31] describe a bottom up approach, in which some objects on the page are merged prior to applying XY-cut, using three heuristics based on local geometric features, text orientation and distance among vertically adjacent layout objects. As observed by Meunier [56], this aims at reducing the probability of dealing with multiple cutting alternatives, but it does not entirely prevent them from occurring. Meunier proposes a different approach, in
which an optimal sequence of XY cuts is determined using dynamic programming and a score function, which prefers column-based reading order. This results in a cutting strategy which favors vertical cuts against horizontal ones, based on the heights of blocks.

Another example of a reading order algorithm is the approach proposed by Breuel [9]. It is based on topological sorting and can be used for determining the reading order of text lines. At the beginning, four simple rules are used to determine the order between a subset of line pairs on a page, giving a partial order. The rules are based on mutual coordinate positions and overlap, for example: line segment $a$ comes before line segment $b$ if their ranges of x-coordinates overlap and if line segment $a$ is above line segment $b$ on the page. Finally, a topological sorting algorithm is applied to find a global order consistent with previously determined partial order.

As opposed to previous methods, Aiello et al. [1] propose to employ linguistic features in addition to the geometric hints. In their approach the input is first divided into two parts: metadata and body. The reading order is determined separately for these subsets, and finally the two orders are combined using rules. Each reading order is determined in two steps performed by the following modules: a spatial reasoning module, based on spatial relations, and a natural language processing module, based on lexical analysis. The modules are applied in order: first, the spatial reasoning module identifies a number of possible reading orders by solving a constraint-satisfaction problem, where constraints correspond to rules such as “documents are usually read from top to bottom and from left to right”. The natural language processing module identifies the linguistically most probable reading orders among those returned by the first module using part-of-speech tagging and assessing the probabilities of POS sequences of possible reading orders.

Finally, Malerba et al. [50] propose a learning-based method for reading order detection. In their approach the domain specific knowledge required for this task is automatically acquired from a set of training examples by applying logic programming techniques. The input of the learning algorithm is the description of chains of layout components defined by the user, and the output is a logical theory which defines two predicates: ”first to read” and ”successor”. The algorithm uses only spatial information of the page elements. In the recognition phase learned rules are used to reconstruct the reading order, which in this case contains reading chains and may not define a total ordering.

### 2.3.3 Content Classification

Content classification, the purpose of which is to find the roles played by different objects in the document, is a crucial task in analysing the documents. The problem has been addressed by numerous researchers. Proposed solutions differ a lot in the approach used (usually rule- or machine learning-based), classified objects (zones, lines or text chunks), used features and characteristics (geometrical, formatting, textual, etc.) and target labels. Some examples of the target labels include: title, authors, affiliation, address, email, abstract, keywords, but also header, footer, page number, body text, citation.

Rule-based systems were more popular among the older algorithms. Such approach does not require building a training set and performing the training, but since the rules are
usually constructed manually, it does not generalize well and is not easily maintainable. Rule-based approaches are well-suited for homogeneous and stable document sets, with only few different documents layouts.

An example of a rule-based classification is PDFX system described by Constantin et al. [12]. In this approach page elements are converted to geometric and textual features and hand-made rules are used to label them. The target label set contains: front matter labels (title, abstract, author, author footnote), body matter labels (body text, h1 title, h2 title, h3 title, image, table, figure caption, table caption, figure reference, table reference, bibliographic item, citation) and other (header, footer, side note, page number, email, URI).

Flynn et al. [20] describe a system which also can be seen as a variant of the rule-based approach. Their algorithm uses a set of templates associated with document layouts. A template can be understood as a set of rules for labelling page elements. A document is first assigned to a group of documents of similar layout and then corresponding template is used to assign labels to elements. The target label set depends on the layout, some examples include: title, author, date.

Also in the algorithm proposed by Giuffrida et al. [23] hand-made rules are used to label text chunks. In this approach, text strings annotated with spatial and visual properties, such as positions, page number and font metrics, are used as ”facts” in a knowledge base. Basic document metadata, including title, authors, affiliations, relations author-affiliation, is extracted by a set of hand-made rules that reason upon those facts. Some examples of rules include: ”the title is written in the top half of the first page with the biggest font”, or ”authors’ list follows the title immediately”.

Mao et al. [51] also propose a rule-based system for extracting basic metadata, including the title, authors, affiliations and abstract, from scanned medical journals. The system is used for MEDLINE database. Its iterative process includes human intervention, which corrects the zone labelling obtained from the previous rules. Corrected results are then used to develop specialized geometric and contextual features and new rules from a set of issues of each journal.

Rule-based approaches are especially popular for locating the regions containing references. This is related to the fact that fairly common and clear differences between these sections and other document parts can be easily expressed by hand-made rules and heuristics.

For example Pdf-extract system uses a combination of visual cues and content traits to detect references sections. The rules are to a great extent based on the observation that the reference section of a scientific document tends to have a significantly higher ratio of proper names, initials, years and punctuation with comparison to other regions.

In the approach proposed by Gao et al. [21] a rule-based method is used to locate citation regions in electronic books. The rules are based on the percentage of text lines in the page containing certain Chinese words such as ”reference”, ”bibliography”, years and family names.

Also in the system described by Gupta et al. [25] the reference blocks are found by

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[8]http://labs.crossref.org/pdfextract/
estimating the probability that each paragraphs belongs to references using parameters based on paragraph length, presence of keywords, author names, years and other text clues.

Kern and Klampfl [36] also propose a heuristics-based approach for locating the references sections. Their algorithm first iterates over all blocks in the reading order and uses regular expressions and a dictionary of references section titles to find the reference headers. Then all the lines are collected until another section heading, for example "Acknowledgement", "Autobiographical", "Table", "Appendix", "Exhibit", "Annex", "Fig", "Notes", or the end of the document, is found. Headers and footers lines are recognized based on the comparison of the blocks across neighboring pages based on their content and geometrical position and they are not added to the references content.

Supervised machine learning-based approaches are far more popular for classifying the document fragments. They are more flexible and generalize better, in particular when we have to deal with diverse document collections. Proposed methods differ in classification algorithms, document fragments that undergo the classification (text chunks, lines or blocks) and extracted features. Some examples of the classification algorithms used for this task include: Hidden Markov Models, Support Vector Machines, neural classifiers, Maximum Entropy, Conditional Random Fields.

For example, Cui and Chen [15] propose a classification approach in which text blocks (small pieces of text, often smaller than one logical line) are classified with an HMM classifier using features based on location and the font information. The target labels include: title, author, affiliation, address, email and abstract. A straightforward HMM-based approach would just label the stream of text blocks, but the authors modified it to take into account the structure of the lines containing the classified blocks. Based on the location of the text chunks, the HMM state transition matrix is divided into two separate matrices: one for the state transition probability within the same line and the other for the state transition probability between lines. A modified Viterbi algorithm uses these new matrices to find the most probable label sequence.

Han et al. [27] perform a two-stage classification of document header text lines with the use of Support Vector Machines and only text-related features. They use a rich set of labels: title, author, affiliation, address, note, email, date, abstract, introduction, phone, keyword, web, degree, pubnum and page. In the first step the lines are classified independently of each other using features related to text and dictionaries. The second step makes use of the sequential information among lines by extending the feature vectors with the classes of a number of preceding and following lines. Iteratively a new classifier is trained using extended feature vectors and lines are reclassified, until the process converges (there are only few changes in the class assignments).

Another example of an SVM-based approach is described by Kovacevic et al. [42]. In their method the lines of text on the first page of documents are classified into the following classes: title, authors, affiliation, address, email, abstract, keywords and publication note using both geometric (formatting, positions) and text-related (lexical, NER) features. The authors experimented with different models (decision trees, Naive Bayes, k-Nearest Neighbours and Support Vector Machines) and different strategies for multi-class classification.
Based on the results obtained during the classification experiments, an SVM model with a one-vs.-all strategy was chosen, as giving the best performance on a manually produced test set.

Lu et al. [48] also use SVM to classify the lines of the text in scanned scientific journals. They use the following classes: title, author, volume, issue, start page, end page, start page index and start page image and geometric, formatting and textual features of the text lines. The approach is tested on scanned historical documents nearly two centuries old.

Marinai [52] proposes a Multi-Layer Perceptron (MLP) classifier to identify regions that could contain the title and the authors of the paper by classifying the text blocks. The features include: graphical features (related to the position on the page, the width and height of the region, which page it is on), textual features (the number of characters, bold or italics characters), and neighbor features (such as the number of neighboring regions and their distance).

Team-Beam algorithm proposed by Kern et al. [37] uses an enhanced Maximum Entropy classifier for assigning labels to document fragments. The approach works in two stages: first the blocks are classified as title, subtitle, journal, abstract, author, email, affiliation, author-mixed or other, and then the tokens within blocks related to author metadata are classified as given name, middle name, surname, index, separator, email, affiliation-start, affiliation, other. The algorithm uses and enhanced version of Maximum Entropy classifier, which takes the classification decision of preceding instances into account to improve the performance and to eliminate unlikely label sequences. The features used for classification are derived from the layout, the formatting, the words within and around a text block, and common name lists.

In the approach proposed by Lopez [47] the regions of the document are classified using 11 different CRF models cooperating together at various levels of a document’s structure. Each specialized model aims at solving a concrete classification task. The main model classifies the fragments of the entire document into header, body, references, etc. Other models are used for classifying the header fragments, parsing affiliation, author and dates strings, classifying body parts into titles, paragraphs and figures, parsing references and so on. Each model has its own set of features and training sets. The features are based on position-, lexical- and layout-related information.

Cuong et al. [16] also use CRF for labelling the fragments of the documents. In their approach the input is a document in plain text, and therefore they do not use geometric hints present for example in the PDF files. They describe methods for solving three tasks: reference parsing (where the reference tokens are labelled as title, author, year, etc.), section labelling (where the sequence of document’s sections are given the functional label, such abstract, acknowledgement, background, categories, conclusions, discussions, evaluation, general terms, introduction, methodology, references, related works) and finally assigning labels such as author and affiliation to the lines of the document’s header. The instances are classified using a higher order semi-Markov Conditional Random Fields to model long-distance label sequences, improving upon the performance of the linear-chain CRF model.

Finally, Zou et al. [84] propose a binary SVM classifier for locating the references sections in the document. The text zones are classified using both geometric and textual
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features.

2.3.4 Sequence Parsing

Parsing refers to extracting metadata from strings by annotating their fragments with labels from a particular label set. In the context of scientific documents analysis parsing can be used for example to extract metadata such as title, authors, source or date from citation strings, dividing authors’ fullnames into given names and surnames, recognizing days, months and years in date strings or extracting institution name, address and country name from an affiliation string.

Similarly as in the case of content classification, there are two widely used families of approaches used for parsing. One popular family of methods is based on regular expressions or knowledge bases. The advantage of these techniques is that they usually can be implemented in a straightforward manner without gathering any training data or performing the training.

For example Gupta et al. [25] propose a simple regexp-based approach for classifying fragments of citation strings as particular metadata classes: authors, title, publication and year of publication. The regular expressions are hand-made and the algorithm is also enhanced by using a publication database of a domain of interest (zoology) to lookup the title in case the default approach failed.

Jonnalagadda and Topham [34] describe NEMO system, which is able to parse affiliations using rules and a number of dictionaries. The parsing includes extracting fragments related to country, email address, URL, state, city, street address and organization name. The fragments are extracted in consecutive steps using 30 different manually verified dictionaries, such as the dictionaries in Geoworldmap database\(^9\) the mapping between internet domains and countries, stop words list, organization-related keywords, address-related keywords or zip code dictionary.

Day et al. [17] propose a knowledge-based approach for parsing citations in order to extract the following metadata: author, title, journal, volume, issue, year, and page. The method is based on a hierarchical knowledge representation framework called INFOMAP. First the data from the Journal Citation Reports (JCR) indexed by the ISI and digital libraries is collected and fed into the knowledge base. The format of INFOMAP is a tree-like knowledge representation scheme that organizes knowledge of reference concepts in a hierarchical fashion, which contains characteristic patterns occurring in citations. To extract metadata from a citation, the template matching engine uses dynamic programming to match it with the syntax templates.

Vilarinho et al. [77] also propose a knowledge-based approach for citation parsing. In their method, the knowledge base stores typical words for each citation metadata type, which is then used to assign labels to the citation tokens. After that, tokens left unassociated in the previous step are further analyzed and labels are assigned to them based on rules related to their neighbourhood and relative position in the citation string.

\(^9\)http://www.geobytes.com/geoworldmap/
Unfortunately, similarly as in the case of general classification, rule-based approaches are poorly adaptable and do not generalize well. For this reason, machine learning-based approaches, which are much more flexible, are far more popular for sequence parsing. These methods typically leverage the sequence-related information in addition to the tokens themselves, either by decoding them in the features or using dedicated algorithms for sequence labelling.

For example Zhang et al. [82] propose SVM for classifying the reference’s tokens into the following classes: citation number, author names, article title, journal title, volume, pagination and publication year. Their method uses structural SVM [75], an extension of SVM designed for predicting complex structured outputs, such as sequences, trees and graphs. The features are related to dictionaries of author names, article titles and journal titles, patterns for name initials or years, the presence of digits and letters and the position of the token. Additionally, two kinds of contextual features are used: the features of the neighboring tokens and the labels assigned to those tokens.

Hetzner [28] proposes to parse citation strings using HMM in order to extract: author, booktitle, date, editor, institution, journal title, location, note, number, pages, publisher, techtitle, title and volume. The model includes two HMM states per each metadata class: a ”first” state for the first token in the subsequence and a ”rest” state, along with a set of separator states (which represent words and punctuation that are not part of metadata fields) for every metadata class pair, and a terminating ”end” state. The tokens are mapped to a small alphabet of emission symbols, which is composed of symbols representing punctuation, particular words, classes of words and word features.

Yin et al. [80] propose to parse citations using a bigram HMM, where emission symbols are token words. Different from the traditional HMM, which typically uses word frequency, this model also considers the words’ bigram sequential relation and position information in text fields. In particular, a modified model is used for computing the emission probability, while keeping the structure of HMM unchanged. In the new model, the probability of emitting symbol at given state composes of beginning emission probability (the probability that the state emits word as the first word) and inner emission probability (the probability that the state emits the word as the inner word).

Ojokoh et al. [59] propose even more advanced approach based on a trigram HMM, where a state of a current token depends on the states of two preceding tokens, instead of one. A modified Viterbi algorithm is used to infer the most probable sequence of token labels. Only 20 symbols are used for the emission alphabet, these are based on specific characters (for example a comma, a dot, a hyphen), regular expressions (for example checking whether the token is a number), also a dictionary of state names and a list of common words found in specific metadata fields.

Definitely the most popular technique for citation parsing is linear-chain CRF. In practice, it achieves better results than HMM and is more flexible as able to handle a lot of overlapping features of the tokens, whereas in HMM the tokens have to be mapped to a dictionary of emission symbols.

ParsCit described by Councill et al. [13] is an open-source library for citation parsing based on CRF. The labels assigned to the citation tokens include: author, booktitle, date,
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editor, institution, journal, location, note, pages, publisher, tech, title and volume. The features are related to the token identity, punctuation, numbers, letters, cases, dictionaries (for example dictionaries of publisher names, place names, surnames, female and male names, and months).

Also Gao et al. [21] use CRF to parse citations in Chinese electronic books in order to extract: author, editor, title, publisher, date, page number, issue, volume, conference, book, note, location and URL. The parsing is supported by a knowledge base storing the most common words in citation strings, the punctuation marks used to separate fields, Chinese family names, English names, publishing houses in China, journal names, conference names, places and dates, and so on. Apart from textual features, layout-related features are also used. Finally, the tool takes advantage of document layout consistency to enhance citation parsing through clustering techniques. The main citation format used in the book is detected and used to correct minor mistakes occurred during parsing.

Kern and Klampfl [36] also propose a citation parsing algorithm based on CRF. The model uses the following labels of the tokens: author given name, author surname, author other, editor, title, date, publisher, issue, book, pages, location, conference, source, volume, edition, issue, url, note, and other. In order to integrate sequence-related information, the algorithm takes the classification decision of four preceding instances into account. In addition to the typical text-related features, the model also incorporates layout and formatting information using a set of binary features specifying whether the font of the tokens inside a sliding window from -2 to +2 tokens is equal to the font of the current token.

Another example of a CRF-based approach is the citation parser proposed by Zhang et al. [81]. The algorithm extracts: author (further separated into surname and given name), title, source (for example journal, conference, or other source of publication), volume, pages (further separated into first page and last page), and year. The features are based on traits such as whether the token contains a capital letter, all capital letters, a digit, all digits, and other symbols (such as Roman and Greek characters, hyphens, etc.), as well as the length of the token.

In Enlil system described by Do et al. [18] linear-chain CRF classifier is used to parse both author names and affiliation strings in order to recognize the name (author or organization name), symbol (characters marking the relations between authors and affiliations) and separator. The features are both text- (such as token identity, punctuation, number) and layout-related (fonts, subscript, superscript).

CRF is also used extensively in GROBID system described by Lopez [47] to parse various entities, for example citations, affiliations, author names or date strings. Each task has its own CRF model, training set and a set of features, which are based on position, lexical and layout information.

Cuong et al. [16] is another example of a CRF-based citation parser. In their approach the citation tokens are labelled as: author, booktitle, date, editor, institution, journal, location, note, pages, publisher, tech, title or volume. The tokens are classified using a higher order semi-Markov Conditional Random Fields to model long-distance label sequences, improving upon the performance of the linear-chain CRF.
Finally, Zou et al. [84] compared two algorithms for citation parsing. One relies on sequence statistics and trains a CRF. The other focuses on local feature statistics and trains an SVM to classify each individual word, which is followed by a search algorithm that systematically corrects low confidence labels if the label sequence violates a set of predefined rules. The approaches achieved very similar high accuracies.

### 2.3.5 Extraction Systems

This section describes tools and systems able to extract various types of metadata and content from scientific literature. The approaches differ in the scope of extracted information, methods used, input and output formats, availability and licenses.

Typically at the beginning of the document processing some kind of layout analysis is performed, and then the regions of the document are classified using various algorithms. The metadata extracted from documents usually contains the title, authors, affiliations, emails, abstract, keywords, and so on. These fragments are usually located in the document using rules or machine learning. Extracting bibliography-related information typically includes locating the references sections in the document using rules or machine learning, splitting their content into individual references and parsing them. The analysis of the middle part of the document might require locating the paragraphs, tables, figures, section titles, sometimes determining the hierarchy of sections or the roles of the sections as well.

For example Flynn et al. [20] propose a metadata extraction approach which can be seen as a variant of a rule-based approach. First input PDF documents are OCR’ed using a commercial tool ScanSoft’s OmniPage Pro, which results in a XML-based representation containing the layout and the text organized in pages, regions, paragraphs, lines and words, accompanied by information such as font face, font size and font style, alignment and spacings. The metadata is then extracted using independent templates, each of which is a set of simple rules associated with a particular document layout. Processed document is first assigned to a group of documents of similar layout, and then the corresponding template is used to extract the document’s metadata.

Mao et al. [51] propose a rule-based system for extracting title, author, affiliation, and abstract from scanned medical journals. The system is used for MEDLINE database. The documents are first OCR’ed, and then undergo an iterative process which includes human intervention for correction the zone labelling resulting from applied rules. Corrected results are then used to develop geometric and contextual features and rules optimized for the set of issues of a given journal.

Hu et al. [29] describe a machine learning-based approach for extracting titles from general documents, including presentations, book chapters, technical papers, brochures, reports and letters. As a case study, Word and PowerPoint document are used. During pre-processing, the units (text chunks with uniform format) are extracted from the top region of the first page of a document. These units are then transformed to features and classified as title begin, title end or other. Two types of features were used: format features (font size, alignment, boldface, the presence of blank lines) and linguistic features (keywords specific for titles and other document parts, number of words). Four models were employed.
(Maximum Entropy Model, Perceptron with Uneven Margins, Maximum Entropy Markov Model, and Voted Perceptron). The authors have observed that Perceptron-based models perform better in terms of extraction accuracy.

Cui and Chen [15] describe a system for extracting title, author, affiliation, address, email and abstract from PDF documents. In this approach, text extraction and page segmentation is done with the use of pdf2html, a third-party open-source tool. The resulting HTML document contains a set of text blocks, which are small pieces of text, often less than one logical line, along with their location and font information. These blocks are labelled with the target metadata classes with the use of an enhanced HMM classifier.

Han et al. [27] extract metadata (title, author, affiliation, address, note, email, date, abstract, introduction, phone, keyword, web, degree and page) from the headers of scientific papers in plain text format. The metadata is extracted by classifying the text lines with the use of a two-stage SVM classification based on text-related features.

Another example of an SVM-based approach is the metadata extractor used in CRIS systems described by Kovacevic et al. [42]. In this approach PDF articles are first converted to HTML, which preserves the formatting and layout-related information. Then, the lines of text in the first page of the document are classified using both geometric and text-related features. Extracted metadata contains: title, authors, affiliation, address, email, abstract, keywords and publication note.

Lu et al. [48] analyse scanned scientific journals in order to obtain volume metadata (such as name, number), issue metadata (volume number, issue number, etc.) and article metadata (title, authors, volume, issue and pages range). In their approach scanned pages are first converted to text using OCR techniques. Then, rule-based pattern matching on the feature vectors of the text lines is used to recognize and analyze volume and issue title pages, while article metadata is extracted using SVM and geometric, formatting, distance, layout and textual features of text lines. The approach is tested on scanned historical documents nearly two centuries old.

Marinai [52] first extracts characters from PDF documents using JPedal package, which results in a set of basic objects on each page accompanied with additional information such as their position and font size. Then, the blocks are merged in the horizontal and vertical directions, avoiding to join separate columns or paragraphs, using simple rule-based heuristics. Each region is then transformed to feature vectors and a Multi-Layer Perceptron (MLP) classifier is used to identify regions that could contain the title and the authors of the paper. The classifier uses features related to both the layout and the text. Additionally, the information gathered from DBLP citation database is used to assist the tool by checking the extracted metadata.

Enlil, described by Do et al. [18], is a tool able to extract authors, affiliations and relations between them from scientific publications in PDF format. In this approach a PDF file is first OCRred with the use of OmniPage, which results in an XML version of the document that stores both the textual and spatial information for each word that appears on each page. The system is built on top of SectLabel module from ParsCit [49], which is used to detect authors and affiliations blocks in the text by classifying text lines using
CRF. The lines classified as author or affiliation are then tokenized into chunks and the
tokens are labelled using a linear-chain CRF classifier with the following classes: name,
symbol and separator. The model uses both text- and layout-related features. Finally, a
binary SVM classifier is applied to author-affiliation pairs to extract the relations between
them. The features used in this model are related to the information provided by the
 parsing module and the distances between the author and the affiliation fragments.

In the citation extraction system described by Gupta et al. [25] the documents are first
scanned, OCRed and converted into PDF format. The PDF documents are then converted
into HTML using Abby PDF Reader. Then reference block is found by estimating the
probability that each paragraph belongs to references using parameters based on paragraph
length, presence of keywords, the author names, the presence of the year and other text
clues. Regular expressions are then used to extract metadata from citation strings. The
algorithm also uses external publication database to correct the extraction results.

Zou et al. [84] propose a two-step process using statistical machine learning algorithms
for extracting bibliography data from medical articles in HTML format. The algorithm
first locates the references with a binary SVM classifier using geometric and text features
for text zones. For reference parsing two algorithms were used: CRF and SVM followed by
a search algorithm that systematically corrects low confidence labels if the label sequence
violates a set of predefined rules.

Gao et al. [22] describe CEBBIP, a tool able to extract the chapter and section hierarchy
from Chinese books. The overall approach is based on the observation that within a book,
some features related to formatting and fonts are shared among elements of the same type,
such as the headings, footnotes or citations. At the beginning the tool performs page layout
analysis by merging small page objects (eg. characters, words, lines) into bigger ones in a
bottom-up manner using position and font-related heuristics. Then the global typographies
characteristics, such as columns, header and footer, page body area, text line directions,
line spacing of body text, and fonts used in various components (headings, paragraphs,
etc.) are extracted. For example, to detect headers and footers, similarities of the text
and geometric position between the top/bottom lines on neighboring pages is exploited.
Columns are identified by detecting the recurring white spaces in multiple pages. Then the
page objects are clustered based on general typesetting, and the output clusters serve as
the prototypes of similar blocks. After that, the system uses a learning-based classification
method to label the blocks in each cluster as headings, figure/table captions, footnotes.
The table of contents hierarchy is extracted from the ”Table of contents” section with the
use of heuristics and associated with the headings extracted from the text.

CEBBIP is also able to extract the bibliographic data [21]. In this approach a rule-based
method is used to locate citation data in a book and the data is segmented into citation
strings of individual references with the use of heuristics based on the citation markers and
spaces. A learning-based approach (CRF) is employed to parse citation strings. Finally, the
tool takes advantage of document layout consistency to enhance citation data segmentation
and parsing through clustering techniques. The main citation format used in the book is
detected and used to correct the parsing results.

Giuffrida et al. [23] extract the content from PostScript files using a tool based on
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*Pstotext*, which results in a set of strings of text annotated with spatial/visual properties, such as positions, page number and font metrics. These strings become "facts" in a knowledge base. Basic document metadata, including title, authors, affiliations, relations author-affiliation, is extracted by a set of hand-made rules that reason upon those facts.

The same system also uses rules to extract the titles of the sections from the text of the document. The algorithm first determines whether the section titles are numbered. If the sections are numbered, various schemes of numbering are examined. If the sections are not numbered, heuristics based on the text size and line space are used. Additionally the algorithm looks for titles commonly appearing in the documents, such as "Introduction", "Overview", "Motivation" or "References" to find hints for the font size typical for the titles in a given document.

**PDFX**, described by Constantin *et al.* [12], is a rule-based system able to extract basic metadata, structured full text and unparsed reference strings from scientific publications. PDFX can be used for converting scholarly articles in PDF format to their XML representation by annotating fragments of the input documents. The analysis comprises two main stages. During the first one the geometric model of the article’s content is constructed to determine the organization of textual and graphical units on every page using a library from the Utopia Documents PDF reader. The model comprises pages, words and bitmap images, along with their features such as bounding box, orientation, textual content or font information. During the second stage, different logical units are identified by rules based on their discriminative features. The following block types are used: *title, author, abstract, author footnote, reference, body, (sub)section, (sub)section heading, figure, table, caption, figure/table reference*. PDFX is a closed source system, available only as a web service [10].

**Pdf-extract** [11] is an open-source tool for identifying and extracting semantically significant regions of scholarly articles in PDF format. Pdf-extract can be used to extract the title and a list of unparsed bibliographic references of the document. The tool uses a combination of visual cues and content traits to perform structural analysis in order to determine columns, headers, footers and sections, detect references sections and finally extract individual references. Locating the references section is based on the observation, that it tends to have a significantly higher ratio of proper names, initials, years and punctuation than other sections. The reference section is divided into individual references also based on heuristics.

**Team-Beam** algorithm proposed by Kern *et al.* [37] is able to extract a basic set of metadata (title, subtitle, the name of the journal, conference or venue, abstract, the names of the authors, the e-mail addresses of the authors and their affiliations) from PDF documents using an enhanced Maximum Entropy classifier. In their approach first the PDF file is processed by PDFBox library [12]. Then, clustering techniques are used in order to build words, lines and text blocks from the output obtained from PDFBox library. The structure is built from the bottom, and each type is built by two steps: merge (done by

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[10]http://pdfx.cs.man.ac.uk/
[11]http://labs.crossref.org/pdfextract/
[12]https://pdfbox.apache.org/

32
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hierarchical clustering) and split (k-means clustering for splitting incorrectly merged objects). Then, reading order is determined using the approach described in [1]. Next, a machine learning approach is employed to extract the metadata in two stages: first the blocks of text are classified into metadata types and then the tokens within blocks related to author metadata are classified in order to extract given names, middle names, surnames, etc.

Team-Beam also contains a bibliography extraction component described by Kern and Klampfl [36]. In this approach, the references section is located using heuristics related to a list of typical section titles. The individual references are extracted based on a simple version of k-means clustering algorithm applied to the text lines. The only feature used is the minimal x-coordinate of a line’s bounding box. The algorithm clusters the line set into two subsets, representing the first lines of the references and the rest. Finally, the references are parsed using a CRF token classifier.

Team-Beam provides also the functionality of extracting the body text of the article along with the table of contents hierarchy [40] based on an unsupervised method. After performing the segmentation and detecting the reading order, the text blocks are categorized by a sequential pipeline of detectors, each of which labels a specific type of block: decorations, such as page numbers, headers, and footers (done by analysing the similarity between blocks on the neighbouring pages), figure and table captions (based on heuristics), main text (hierarchical clustering applied to blocks based on alignment, font, and width-related features), section headings (heuristics based on fonts, distances and regular expressions), sparse blocks and tables (again heuristics). Each of these detectors is completely model-free and unsupervised.

Lopez [47] describes GROBID, a system useful for analysing scientific publication in PDF format. GROBID uses pdf2xml/Xpdf for processing PDF files and CRF in order to extract a rich set of document’s metadata, full text with section titles, paragraphs and figures, and a list of parsed bibliographic references with their metadata. The extraction is performed by a cascade of 11 specialized CRF models, which start by labelling the parts of the document as header, body, references, etc., and then focuses on each part. There are separate models specializing in classifying the header parts, parsing affiliations, author data, dates, selecting the header title lines, paragraphs, figures, extracting individual references and parsing them. Each model has its own set of features and training data. The features are based on position, lexical and layout information. The system is available as open-source.

ParsCit system, described by Councill et al. [13], is an open-source system for extracting parsed references from plain text files. Reference sections are identified using heuristics, which search for particular section titles such as ”References” or ”Bibliography”. If such a label is found too early in the document, the process continues. The references sections are then split into individual strings also using heuristics. Regular expressions are used for detecting characteristic markers indicating the beginning of the reference, and if no such markers are found, the system splits the lines based on their length and other indicators.

13https://github.com/kermitt2/grobid
related to whether the line ends with a dot and whether it contains tokens characteristic for
author names. Reference parsing is realized by a CRF model labelling token sequence in the
reference string. The tokens’ features are related to punctuation, numbers, letters, cases
and dictionaries (such as publisher names, place names, surnames, female and male
names, months).

ParsHed, described by Cuong et al. [16], is a ParsCit’s module able to extract the basic
metadata (title, authors, abstract, etc.) from the document’s plain text. The extraction is
done by classifying the header’s text lines using higher order semi-Markov Conditional
Random Fields, which model long-distance label sequences, improving upon the performance
of the linear-chain CRF model.

SectLabel, described by Luong et al. [49] is also a ParsCit’s module, useful for extract-
ing a logical structure of a document, both in PDF or plain text formats. In this approach,
PDFs are first converted to XML using Nuance OmniPage, and the output XML includes
the coordinates of paragraphs, lines and words within a page, alignment, font size, font
face or format. SectLabel performs then two tasks: logical structure classification and
generic section classification. For both tasks CRF with lexical and formatting features is
used. In the first task the ordered sequence of document’s text lines is labeled with the
following categories: address, affiliation, author, bodyText, categories, construct, copyright,
email, equation, figure, figureCaption, footnote, keywords, listItem, note, page, reference,
sectionHeader, subsectionHeader, subsubsectionHeader, table, tableCaption and title. In
the second task, the sequence of the headers of the sections is labelled with a class de-
noting the purpose of the section, including: abstract, categories, general terms, keywords,
introduction, background, related work, methodology, evaluation, discussion, conclusions,
acknowledgments, and references. ParsCit is also an open source system14.

Unfortunately, as of now, there has not been any competition for evaluating the tools
extracting rich metadata from scientific publications. Semantic Publishing Challenge15,16
hosted in 2015 by European Semantic Web Conference17 contained some tasks related to
analysing scientific articles. Our algorithm [65] was the winner in Task 2, which included
the problems of extracting authors, affiliations and citations from PDF documents [30].

The extraction systems available online, namely GROBID, ParsCit, PDFX and Pdf-
extract, are the most similar to our work in terms of potential applications in the context of
digital libraries and research infrastructures. Unfortunately, they all have major drawbacks.
Pdf-extract is rule-based and focuses almost only on extracting the references without
parsing them. PDFX is also rule-based and closed-source, available only as a web service.
The open-source version of ParsCit processes only plain text documents, ignoring the
layout, and also does not output structured document metadata record, but rather the
annotated input text along with the confidence scores. Finally, GROBID does not extract
the section hierarchy and uses the same machine-learning method for all tasks, without
taking into account the specifics of particular problems.

14http://aye.comp.nus.edu.sg/parsCit/
15http://2015.eswc-conferences.org/program/semwebeval
16https://github.com/ceurws/lo/lo/wiki/SemPub2015
17http://2015.eswc-conferences.org/
Our research brings together various advantages of the previous works, resulting in one accurate solution. The algorithm is comprehensive and analyses the entire document, including the document’s header, body and references. It processes born-digital PDF documents and focuses not only on the textual features, but also on the layout and appearance of the text, which carries a lot of valuable hints for classification. Extensive use of machine learning-based algorithms makes the system well-suited for heterogeneous document collections, increases its flexibility and the ability to adapt to new, previously unseen document layouts. Careful decomposition of the extraction problem allows for treating each task independently of others, with each solution selected and tuned for the task’s specific needs. The system is open-source and available as a Java library\textsuperscript{18} and a web service\textsuperscript{19}. In Section 4 we report the results of the comparison of our method to four similar systems available online: GROBID, ParsCit, PDFX and Pdf-extract.

\textsuperscript{18}https://github.com/CeON/CERMINE
\textsuperscript{19}http://cermine.ceon.pl
Chapter 3

Document Content Extraction

In this chapter we describe the algorithm for extracting basic metadata, structured body content and the bibliography from academic articles in born-digital form. The chapter provides the details related to the algorithm’s architecture, all the individual tasks it performs during the analysis of a document, and the approaches employed for solving them.

The extraction algorithm [70, 71, 72, 69] is based on a modular workflow composed of a number of paths and steps. The purpose of each step is to address a single task with clearly defined input and output. Thanks to such modular architecture individual steps can be maintained separately, which allows for evaluation, testing, adjustment and replacement of individual components without touching other parts of the workflow.

The algorithm is designed as a universal solution, able to handle a vast variety of scientific publications reasonably well, instead of being perfect in processing a limited number of document layouts only. This was achieved by employing supervised and unsupervised machine-learning algorithms trained on large and diverse datasets. The result is also increased maintainability of the system, as well as its ability to adapt to new, previously unseen document layouts.

The chapter is organized as follows. Section 3.1 describes the overall architecture of the extraction algorithm, as well as its input and output. The remaining sections contain detailed descriptions of all algorithm parts, including: layout analysis (Section 3.2), document content classification (Section 3.3), metadata extraction (Section 3.4), bibliography extraction (Section 3.5) and structured body extraction (Section 3.6).

3.1 Algorithm Overview

The extraction algorithm accepts a single scientific publication on the input, inspects the entire content of the document and outputs a single record containing: the document’s metadata information, parsed bibliography and structured body content.

The input document format is PDF [60]. The algorithm is optimized for processing born-digital documents and does not perform optical character recognition. As a result,
PDF documents containing scanned pages in the form of images are not properly processed. The output format is NLM JATS\(^1\). The output contains all the information the algorithm is able to extract from a given document structured into three parts: *front* (the document’s metadata), *body* (the middle part of the document, its proper text in a structured form containing the hierarchy of sections) and *back* (the bibliography section).

The algorithm is composed of the following stages (Figure 3.1):

- Layout analysis (Section 3.2) — The initial part of the entire algorithm. During layout analysis the input PDF file is analysed in order to extract all text fragments and their geometric characteristics.

- Document region classification (Section 3.3) — The goal of the classification is to assign a single label to each text fragment of the document. The labels denote the function a given fragment plays in the document.

- Metadata extraction (Section 3.4) — In this stage structured metadata is extracted from previously labelled document.

- Bibliography extraction (Section 3.5) — The purpose of this stage is to extract parsed bibliography in a structured form from previously labelled document.

- Body extraction (Section 3.6) — The goal of this stage is to extract full text and section hierarchy from labelled document.

### 3.2 Document Layout Analysis

Document layout analysis is the initial phase of the extraction algorithm. Its goal is to detect all the text fragments in the input PDF document, compute their geometric characteristics and produce a geometric hierarchical model of the document.

The input is a single file in PDF format and the output is a geometric hierarchical model of the document. The model holds the entire text content of the article, while also preserving the information related to various aspects of the way elements are displayed in the input PDF file.

Intuitively, the output model represents the document as a list of pages, each page contains a list of text zones (blocks), each zone contains a list of lines, each line contains a list of words, and finally each word contains a list of characters. Each element in this hierarchical structure can be described by its text content and the position on its page. The order of the elements in the lists corresponds to the natural reading order of the text, that is the order, in which the fragments should be read. In this tree structure every text element belongs to exactly one element of higher level.

A single page of a given document is a rectangle-shaped area, where the text elements are placed. The position of any point \( p \) on the page is defined by two coordinates: \( p_X \) (the

\(^1\)http://jats.nlm.nih.gov/
Figure 3.1: The architecture of the extraction algorithm. The algorithm accepts a single PDF file on the input. The first stage of the process is layout analysis, followed by assigning functional classes to all the text fragments of the document during document region classification. Finally, in three parallel stages the following information is extracted: document’s metadata, structured body content and parsed bibliographic references.
horizontal distance to the left edge of the page) and $p_Y$ (the vertical distance to the top edge of the page). The origin of the coordinate system is the left upper corner of the page, and the coordinates are given in typographic points (1 typographic point equals to 1/72 of an inch). The positions of all the text elements are defined with respect to this coordinate system.

The model stores text elements of various granularity: characters, words, lines and zones. Every text element belongs to exactly one document page and represents a fragment of a text written on the page. The position of the element on its page is defined by two points: left upper and right lower corner of its bounding box, which is a rectangle with edges parallel to the page’s edges enclosing a given text element.

Formally the levels in the model can be defined in terms of sets. For any set $S$ let’s denote its partition as $P(S)$. In other words, $P(S)$ is any set meeting the following conditions:

- $\forall p \in P(S) \quad p \subset S$
- $\emptyset \notin P(S)$
- $\bigcup_{p \in P(S)} p = S$
- $\forall p, r \in P(S) \quad (p \neq r \Rightarrow p \cap r = \emptyset)$

For a given document $D$ let’s define the following sets:

- **Characters.** Let $C_D$ be the set of all characters visible in the document. For every character $c \in C_D$ we define its text $T(c) \in \Sigma_D$, where $\Sigma_D = \{',', b', ..., A', B', ...\}$ is the alphabet used within document $D$, and its bounding box given by two points: left upper corner $B_1(c) \in R^2$ and right lower corner $B_2(c) \in R^2$.

- **Words.** Let $W_D = P(C_D)$ be the set of all words in the document. Intuitively, a word is a continuous sequence of characters placed in one line with no spaces between them. Punctuation marks and typographical symbols can be separate words or parts of adjacent words, depending on the presence of spaces.

- **Lines.** Let $L_D = P(W_D)$ be the set of all lines in the document. Intuitively, a line is a sequence of words that forms a consistent fragment of the document’s text. Words placed geometrically in the same line of the page, which are parts of neighbouring columns, should not belong to the same line in the model. Hyphenated words that are divided into two lines should appear in the model as two separate words that belong to different lines.

- **Zones.** Let $Z_D = P(L_D)$ be the set of all zones in the document. Intuitively, A zone is a consistent fragment of the document’s text, geometrically separated from surrounding fragments and not divided into columns.

- **Pages.** Finally, let $P_D = P(Z_D)$ be the set of all pages in the document.
We can also define a parent function, which for any character, word, line or zone returns the element’s parent in the structure:

$$\text{par} : C_D ∪ W_D ∪ L_D ∪ Z_D \to W_D ∪ L_D ∪ Z_D ∪ P_D$$

such that

- $$\forall c ∈ C_D \quad (\text{par}(c) ∈ W_D \land c ∈ \text{par}(c))$$
- $$\forall w ∈ W_D \quad (\text{par}(w) ∈ L_D \land w ∈ \text{par}(w))$$
- $$\forall l ∈ L_D \quad (\text{par}(l) ∈ Z_D \land l ∈ \text{par}(l))$$
- $$\forall z ∈ Z_D \quad (\text{par}(z) ∈ P_D \land z ∈ \text{par}(z))$$

The sets $$C_D, W_D, L_D, Z_D$$ and $$P_D$$ are totally ordered sets. The order corresponds to the natural reading order of the elements in the document, that is the order in which the text should be read. The order of the elements respects the set hierarchy, in particular

$$\forall S ∈ \{C_D, W_D, L_D, Z_D\} \quad \forall e_1, e_2 ∈ S \quad (e_1 ≤ e_2 \Rightarrow \text{par}(e_1) ≤ \text{par}(e_2))$$

For every word, line and zone we also define a bounding box as a minimal rectangle enclosing all contained elements:

- $$\forall w ∈ W_D \quad (B_1(w) = B_{min}(w) \land B_2(w) = B_{max}(w))$$
- $$\forall l ∈ L_D \quad (B_1(l) = B_{min}(l) \land B_2(l) = B_{max}(l))$$
- $$\forall z ∈ Z_D \quad (B_1(z) = B_{min}(z) \land B_2(z) = B_{max}(z))$$

where

- $$B_{min}(x) = (\min\{B_{1,x}(y) \mid y ∈ x\}, \min\{B_{1,y}(y) \mid y ∈ x\})$$
- $$B_{max}(x) = (\max\{B_{2,x}(y) \mid y ∈ x\}, \max\{B_{2,y}(y) \mid y ∈ x\})$$

The model of a document described in this section is built incrementally by three steps executed in a sequence: character extraction (Section 3.2.1), page segmentation (Section 4.2) and reading order resolving (Section 3.2.3). Each steps updates the structure with new information. Table 3.1 summarizes the basic information about the steps.

### 3.2.1 Character Extraction

Character extraction is the first step of the entire extraction process. Its purpose is to parse the input PDF file and build initial simple geometric model of the input document, which stores only the pages and individual characters.

Let $$D$$ be the given input document. The purpose of character extraction is to:
### Table 3.1: The decomposition of layout analysis stage into individual steps.

| Step                        | Goal                                                                 | Implementation          |
|-----------------------------|----------------------------------------------------------------------|-------------------------|
| 1. Character extraction    | Extracting individual characters along with their page coordinates and dimensions from the input PDF file. | iText library           |
| 2. Page segmentation       | Constructing the document’s geometric hierarchical structure containing (from the top level) pages, zones, lines, words and characters, along with their page coordinates and dimensions. | enhanced Docstrum       |
| 3. Reading order resolving | Determining the reading order for all structure elements.           | bottom-up heuristics    |

- **determine** $P_D$ — a set of document’s pages along with their order,
- **determine** $C_D$ — a set of characters visible in the document,
- **assign** characters to pages, that is find a function $\text{anc}_{cp} : C_D \rightarrow P_D$, which for given character $c \in C_D$ returns the page the character is displayed on.

Character extraction does not find other elements of the model, and does not determine the order of the characters. The output of character extraction is a list of pages, each of which contains a set of characters.

The implementation of character extraction is based on open-source PDF parsing library iText\[^2\]. The document’s pages and their order are explicitly given in the source of the input file. To extract characters, we iterate over all text-related PDF operators, keeping track of the current text state and text positioning parameters. During the iteration we extract text strings from text-showing operators along with their bounding boxes. The strings are then split into individual characters and their individual widths and positions are calculated. Finally, all the coordinates are translated from the PDF coordinate system to the system used in our geometric model. The mapping between characters and pages is determined directly by the position of the text-showing operators in the input PDF file.

Due to the features of the PDF format and iText library, the resulting bounding boxes are in fact not the smallest rectangles enclosing the characters, but often are slightly bigger, depending on the font and size used. In particular the bounding boxes of the characters printed in the same line using the same font have usually the same vertical position and height. Figure 3.2 shows an example fragment of a page from a scientific publication with

\[^2\]http://itextpdf.com/
Figure 3.2: An example fragment of a page from a scientific publication. The rectangles are the bounding boxes of individual characters.

characters’ bounding boxes, as returned by iText library. Fortunately, these approximate coordinates are sufficient for further steps of the algorithm.

For performance reasons we enhanced character extraction with an additional cleaning phase, which in some rare cases reduces the number of extracted characters. In general the PDF text stream can contain text-showing operators, which do not result in any text visible to the document’s reader. For example a text string might be printed in a position outside of the current page, or text fragments can be printed in the same place, causing one fragment to cover the other. We also encountered PDF files, in which text-showing operators were used for printing image fragments, which resulted in tens of thousands tiny characters on one page, that do not contribute to the proper text content of the document. In such rare cases it is very difficult to extract a logical, useful text from the PDF stream. What is more, the number of characters is a significant factor of the algorithm performance (more details are given in Section 4.7). The algorithm attempts to detect such problems during character extraction step and reduce the number of characters by removing suspicious characters, if needed.

The cleaning phase comprises the following steps. First, we remove those characters, that would not be visible on the page, because their coordinates are outside of the pages limits. Then, we detect and remove duplicates, that is characters with the same text and bounding boxes. Finally, we check whether the density of the characters on each page is within a predefined threshold. If the overall density exceeds the limit, we use a small sliding window to detect highly dense regions and all the characters from these regions are removed.

Individual characters extracted in this step are the input for the page segmentation step.
3.2.2 Page Segmentation

The goal of page segmentation is to extract the remaining levels of the model described previously: words, lines and zones. It is achieved by grouping characters into larger objects in a bottom-up manner.

Let $D$ be the given document, $P_D$ — a list of document’s pages and $C_D$ — a set of extracted characters. From character extraction step we also have the function $\text{anc}_{cp} : C_D \rightarrow P_D$, which assigns a parent page to every character.

The purpose of page segmentation is to find:

- $W_D$: a partition of the set $C_D$ corresponding to the words of the document,
- $L_D$: a partition of the set $W_D$ corresponding to the text lines of the document,
- $Z_D$: a partition of the set $L_D$ corresponding to the text zones of the document.

The function $\text{par}$, which is defined by the partitions, should satisfy the following condition:

$$\text{anc}_{cp} = \text{par} \circ \text{par} \circ \text{par} \circ \text{par}$$

Page segmentation does not determine the order of the elements. The result of page segmentation is a partial model, in which the analysed document is represented by a list of pages, each of which contains a set of zones, each of which contains a set of lines, each of which contains a set of words, each of which contains a set of characters.

Figure 3.3: An example fragment of a page from a scientific publication. The rectangles mark the bounding boxes of words.

Figure 3.3 shows a group of words with their bounding boxes printed on a page of a scientific publication. As the picture shows, punctuation marks as well as hyphenation characters usually belong to the proper word preceding them. In general words in the model should be understood geometrically rather than logically — as a continuous sequence of characters without a space or other white character.
Figure 3.4: An example fragment of a page from a scientific publication. The rectangles mark the bounding boxes of lines.

Figure 3.5: An example fragment of a page from a scientific publication. The rectangles mark the bounding boxes of zones.

Page segmentation is implemented with the use of a bottom-up Docstrum algorithm. Docstrum is an accurate algorithm able to recognize both text lines and zones. The algorithm can be fairly easily adapted to process born-digital documents: it is sufficient to treat individual characters as connected components, which in the original algorithm are calculated from a page image.

In our case the algorithm’s input is a single page containing a set of characters, which are clustered hierarchically based on geometric traits. The algorithm is based to a great extent on the analysis of the nearest-neighbor pairs of individual characters.
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Figure 3.6: An example fragment of a text zone in a scientific article. The figure shows five nearest neighbours of a given character (red dotted lines), neighbours placed in the same line used to determine in-line spacing (blue solid lines), and neighbours placed approximately in the line perpendicular to the text line orientation used to determine between-line spacing (green dashed lines).

1. First, five nearest components for every character on the page are identified (red dotted lines in Figure 3.6). The distance between two characters is the Euclidean distance between the centers of their bounding boxes.

2. In order to calculate the text orientation (the skew angle) we analyze the histogram of the angles between the elements of all nearest-neighbor pairs. The peak value is assumed to be the angle of the text. Since in the case of born-digital documents the skew is almost always horizontal, this step would be more useful for documents in the form of scanned pages. All the histograms used in Docstrum are smoothed to avoid detecting local abnormalities. An example of a smoothed histogram is shown in Figure 3.7.

3. Next, within-line spacing is estimated by detecting the peak of the histogram of distances between the nearest neighbors. For this histogram we use only those pairs, in which the angle between components is similar to the estimated text orientation angle (blue solid lines in Figure 3.6).

4. Similarly, between-line spacing is also estimated with the use of a histogram of the distances between the nearest-neighbor pairs. In this case we include only those pairs, that are placed approximately in the line perpendicular to the text line orientation (green dashed lines in Figure 3.6).

5. Next, line segments are found by performing a transitive closure on within-line nearest-neighbor pairs. To prevent joining line segments belonging to different columns, the components are connected only if the distance between them is sufficiently small.

6. The zones are then constructed by grouping the line segments on the basis of heuristics related to spatial and geometric characteristics. Each line segment pair is ex-
amined and the decision is made whether they should be in the same zone. If both horizontal and vertical distance are within predefined limits, the current zones of the line segments are merged.

7. Finally, line segments belonging to the same zone and placed in one line horizontally are merged into final text lines.

![Distance Histogram](image)

Figure 3.7: An example of a nearest-neighbour distance histogram. The figure shows both original and smoothed versions of the histogram. The peak distance chosen based on the original data would be the global maximum, even though the histogram contains two close peaks of similarly high frequency. Thanks to smoothing both local peaks are taken into account, shifting the resulting peak slightly to the left and yielding more reliable results.

All the threshold values used in the algorithm have been obtained by manual experiments performed on a validation dataset. The experiments also resulted in adding a few improvements to the Docstrum-based implementation of page segmentation:

- the distance between connected components, which is used for grouping components into line segments, has been split into horizontal and vertical distance (based on estimated text orientation angle),

- fixed maximum distance between lines that belong to the same zone has been replaced with a value scaled relatively to the line height,
merging of lines belonging to the same zone has been added,

• rectangular smoothing window has been replaced with Gaussian smoothing window,

• merging of highly overlapping zones has been added,

• words determination based on within-line spacing has been added.

Section 4.2 reports the results of the comparison of the performance of the original Docstrum and the enhanced version used in our algorithm.

The resulting hierarchical structure is the input for the next step, reading order resolving.

3.2.3 Reading Order Resolving

The purpose of reading order resolving is to determine the right sequence, in which all the structure elements should be read. More formally, its task is to find a total order for the sets of zones, lines, words and characters. The order of the pages is explicitly given in the input PDF file.

An example document page with a reading order of the zones is shown in Figure 3.8. The reading order is very important in the context of the body of the document and bibliography sections, but much less meaningful for the areas of the document containing metadata.

Algorithm 3.1 shows the pseudocode of reading order resolving step. The algorithm is based on a bottom-up strategy:

1. At the beginning the characters are sorted within words horizontally, from left to right (line 6 in Algorithm 3.1).

2. Similarly, the words are sorted within lines also horizontally, from left to right (line 8 in Algorithm 3.1).

3. Next, the lines are sorted vertically within zones, from top to bottom (line 10 in Algorithm 3.1).

4. In the final step we sort zones. Sorting zones is done with the use of simple heuristics similar to those used in PDFMiner tool\(^3\). We make use of an observation that the natural reading order in most modern languages descends from top to bottom, if successive zones are aligned vertically, otherwise it traverses from left to right. There are few exceptions to this rule, for example Arabic script, and such cases would currently not be handled properly by the algorithm.

The zones are sorted in the following steps:

\(^3\)http://wwwunixuserorg/euske/python/pdminer/
1. We use the following formula to calculate the distance between all pairs of zones on a given page:

\[
d(z_1, z_2) = (\text{area}(\{z_1, z_2\}) - \text{area}(z_1) - \text{area}(z_2)) \times (0.5 + \min(\cos_L(z_1, z_2), \cos_M(z_1, z_2)))
\]

where

- for any zone \( z \in Z_D \) area(\( z \)) is the area of the zone’s bounding box,
- for any zone set \( S \subset Z_D \) placed in the same page, area(\( S \)) is the area of the smallest rectangle containing all the zones in \( S \),
- \( \cos_L(z_1, z_2) \) is the cosine of the slope connecting the centers of left edges of the zones,
- \( \cos_M(z_1, z_2) \) is the cosine of the slope connecting the centers of the zones.
We use the angle of the slope of the vector connecting zones to make sure that in general zones aligned vertically are closer than those aligned horizontally.

2. Using this distance we apply a hierarchical clustering algorithm, repeatedly joining the closest zones and zone sets. This results in a binary tree, where the leaves represent individual zones, other nodes can be understood as groups of zones and the root represents the set of all zones on the page (line 12 in Algorithm 3.1).

3. Next, we visit every node in the tree and swap the children if needed (lines 13-17 in Algorithm 3.1). The decision process for every node is based on a sequence of rules. The first matched rule determines the decision result:

(a) if two groups can be separated by a vertical line, their order is determined by the x-coordinate (case 1 in Figure 3.9),

(b) if two groups can be separated by a horizontal line, their order is determined by the y-coordinate (case 2 in Figure 3.9),

(c) if the groups overlap, we calculate $xDiff$ and $yDiff$, which are horizontal and vertical distance between the centers of the right and left child of the node. The children are swapped if $xDiff + yDiff < 0$ (case 3 and 4 in Figure 3.9).

4. Finally, an in-order tree traversal gives the desired zones order (line 18 in Algorithm 3.1).

Reading order resolving concludes the layout extraction stage of the extraction algorithm. The result is a fully featured geometric model of the document, containing the entire text content of the input file as well as the geometric characteristics related to the way the text is displayed in the input PDF file.
Algorithm 3.1 Reading order resolving algorithm

1: function SortDocument(document)
2:     for page ∈ Pages(document) do
3:         for zone ∈ Zones(page) do
4:             for line ∈ Lines(zone) do
5:                 for word ∈ Words(line) do
6:                     SortHorizontally(word) \(\triangleright\) sort characters from left to right
7:                 end for
8:             end for
9:         end for
10:     end for
11:     SortVertically(zone) \(\triangleright\) sort lines from top to bottom
12:     tree ← BuildTree(Zones(page)) \(\triangleright\) build hierarchical tree by clustering
13:     for node ∈ Nodes(tree) do
14:         if ShouldBeSwapped(LeftChild(node), RightChild(node)) then
15:             SwapChildren(node) \(\triangleright\) swap children if needed
16:         end if
17:     end for
18:     sort(page, tree) \(\triangleright\) sort zones accordingly to in-order tree traversal
19: end function

22: function ShouldBeSwapped(leftNode, rightNode)
23:     leftGroup ← Zones(leftNode)  \(\triangleright\) group of zones represented by left node
24:     rightGroup ← Zones(rightNode) \(\triangleright\) group of zones represented by right node
25:     if MaxX(leftGroup) ≤ MinX(rightGroup) then
26:         return false \(\triangleright\) groups can be separated by a vertical line
27:     end if
28:     if MaxX(rightGroup) ≤ MinX(leftGroup) then
29:         return true \(\triangleright\) groups can be separated by a vertical line
30:     end if
31:     if MaxY(leftGroup) ≤ MinY(rightGroup) then
32:         return false \(\triangleright\) groups can be separated by a horizontal line
33:     end if
34:     if MaxY(rightGroup) ≤ MinY(leftGroup) then
35:         return true \(\triangleright\) groups can be separated by a horizontal line
36:     end if
37:     return DiffX(rightGroup, leftGroup) + DiffY(rightGroup, leftGroup) < 0
38: end function
Case 1

Case 2

Case 3

Case 4

Figure 3.9: Different cases of the mutual position of two zone groups. In each case the blue solid group will precede the red dashed one in the resulting reading order. Case 1: if the groups can be separated by a vertical line, the first is the group closer to the left. Case 2: if the groups can be separated by a horizontal line, the first is the group closer to the top of the page. Case 3: if the groups cannot be fully separated by any line, and $xdiff$ and $ydiff$ are both positive or both negative, the first is the group closer to the left upper corner of the page. Case 4: if the groups cannot be fully separated by any line, and $xdiff$ and $ydiff$ have different signs, the decision is based on the sign of $xDiff + yDiff$.

3.3 Document Region Classification

The goal of content classification is to determine the role played by every zone in the document by assigning a general category to it. We use the following classes: metadata (document’s metadata, containing title, authors, abstract, keywords, and so on), references (the bibliography section), body (publication’s text, sections, section titles, equations, figures and tables, captions) and other (acknowledgments, conflicts of interests statements, page numbers, etc.).

Formally, the goal of document region classification is to find a function

$$\text{class} : Z_D \rightarrow \{\text{metadata, references, body, other}\}$$

The classification is performed by a Support Vector Machine classifier using a large set of zone features of various nature. SVM is a very powerful classification technique able to handle a large variety of input and work effectively even with training data of a small size. The algorithm is little prone to overfitting. It does not require a lot of parameters and...
can deal with highly dimensional data. SVM is widely used for content classification and achieves very good results in practice.

The features we developed capture various aspects of the content and surroundings of the zones and can be divided into the following categories:

- geometric — based on geometric attributes, some examples include: zone’s height and width, height to width ratio, zone’s horizontal and vertical position, the distance to the nearest zone, empty space below and above the zone, mean line height, whether the zone is placed at the top, bottom, left or right side of the page;

- sequential — based on sequence-related information, some examples include: the label of the previous zone (according to the reading order), the presence of the same text blocks on the surrounding pages, whether the zone is placed in the first/last page of the document;

- formatting — related to text formatting in the zone, examples include: font size in the current and adjacent zones, the amount of blank space inside zones, mean indentation of text lines in the zone;

- lexical — based upon keywords characteristic for different parts of narration, such as: affiliations, acknowledgments, abstract, keywords, dates, references, or article type; these features typically check, whether the text of the zone contains any of the characteristic keywords;

- heuristics — based on heuristics of various nature, such as the count and percentage of lines, words, uppercase words, characters, letters, upper/lowercase letters, digits, whitespaces, punctuation, brackets, commas, dots, etc; also whether each line starts with enumeration-like tokens, or whether the zone contains only digits.

The features used by the classifier were selected semi-automatically from a set of 103 features with the use of the zone validation dataset. The final version of the classifier uses 54 features. More details about the selection procedure and results can be found in Section 4.3.1.

The best SVM parameters were also estimated automatically using the zone validation dataset. More detailed results can be found in Section 4.3.2.

Since our problem is a multiclass classification problem, it is reduced to a number of binary classifiers with the use of "one vs. one" strategy.

Document region classification allows to split the content of the input file into three areas of interest: metadata, body and references, which are later on analysed in three parallel specialized extraction paths.

## 3.4 Metadata Extraction

The geometric model of the input document enhanced with zone categories is the input to metadata extraction stage, which is a part of the algorithm specializing in extracting
the proper metadata of the document. During metadata extraction only zones labelled as metadata are analysed.

The algorithm is able to extract the following information:

• title (string): the title of the document,

• authors (a list of strings): the full names of all the authors, in the order given in the document,

• affiliations (a list of tuples): a list of parsed affiliations of the authors of the document, in the order given in the document; a single affiliation contains:
  – raw text of the affiliation (string),
  – organization name (string),
  – address (string),
  – country (string and two-character country ISO code).

• relations author-affiliation,

• emails (a list of strings): a list of emails of the authors of the document,

• relations author-email,

• abstract (string): the abstract provided by the authors,

• keywords (a list of strings): the article’s keywords listed in the document,

• journal (string): the name of the journal in which the article was published,

• volume (string): the volume in which the article was published,

• issue (string): the issue in which the article was published,

• year (string): the year of publication,

• pages (string): the pages range of the published article,

• DOI (string): DOI identifier of the document.

The algorithm analyses only the content of the input document, and only the information explicitly given in the document are extracted. No information is acquired from external sources or inferred based on the text of the document. All information listed above is optional, and there is no guarantee that it will appear in the resulting metadata record.

The default output format is NLM JATS. Listing 3.2 shows an example metadata record.
Listing 3.1: Example document metadata record in NLM JATS format

```xml
<article>
  <front>
    <journal-meta>
      <journal-title-group>
        <journal-title>Dhaka Univ. J. Pharm. Sci.</journal-title>
      </journal-title-group>
    </journal-meta>
    <article-meta>
      <title-group>
        <article-title>Phytochemical and Biological investigations of Phoenix paludosa Roxb.</article-title>
      </title-group>
      <contrib-group>
        <contrib contrib-type="author">
          <string-name>Farzana Alam</string-name>
          <xref ref-type="aff" rid="2">2</xref>
        </contrib>
        <contrib contrib-type="author">
          <string-name>Mohammad S. Rahman</string-name>
          <xref ref-type="aff" rid="1">1</xref>
        </contrib>
        <contrib contrib-type="author">
          <string-name>Md. Shahanur Alam</string-name>
          <xref ref-type="aff" rid="2">2</xref>
        </contrib>
        <contrib contrib-type="author">
          <string-name>Md. Khalid Hossain</string-name>
          <xref ref-type="aff" rid="1">1</xref>
        </contrib>
        <contrib contrib-type="author">
          <string-name>Md. Aslam Hossain</string-name>
          <xref ref-type="aff" rid="1">1</xref>
        </contrib>
        <contrib contrib-type="author">
          <string-name>Mohammad A. Rashid</string-name>
          <email>rashidma@univdhaka.edu</email>
          <xref ref-type="aff" rid="0">0</xref>
          <xref ref-type="aff" rid="1">1</xref>
        </contrib>
      </contrib-group>
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        <addr-line>Dhaka-1000</addr-line>
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      <aff id="1">
        <label>1</label>
        <institution>Centre for Biomedical Research, University of Dhaka</institution>
        <addr-line>Dhaka-1000</addr-line>
      </aff>
    </article-meta>
  </front>
</article>
```
CHAPTER 3. DOCUMENT CONTENT EXTRACTION

Table 3.2 lists the steps executed during the metadata extraction stage. The details of the implementations are provided in the following sections: metadata zone classification (Section 3.4.1), authors and affiliations extraction (Section 3.4.2), affiliation parsing (Section 4.4) and metadata cleaning (Section 3.4.4).
| Step                          | Goal                                                                 | Implementation |
|-------------------------------|----------------------------------------------------------------------|----------------|
| 1. Metadata zone classification | Classifying the zones labelled previously as metadata into specific metadata classes. | SVM            |
| 2. Authors and affiliations extraction | Extracting individual author names, affiliation strings and determining the relations between them. | heuristics     |
| 3. Affiliation parsing         | Extracting organization, address and country from affiliation strings. | CRF            |
| 4. Metadata cleaning          | Extracting atomic metadata information from labelled zones, cleaning and forming the final record. | simple rules   |

Table 3.2: The decomposition of metadata extraction stage into independent steps.

### 3.4.1 Metadata Classification

Metadata classification is the first step in the metadata extraction stage. Its goal is to classify all zones labelled previously as metadata into specific metadata classes: title (the title of the document), author (the names of the authors), affiliation (authors’ affiliations), editor (the names of the editors), correspondence (addresses and emails), type (the type specified in the document, such as “research article”, “editorial” or “case study”), abstract (document’s abstract), keywords (keywords listed in the document), bib_info (for zones containing various bibliographic information, such as journal name, volume, issue, DOI, etc.), dates (the dates related to the process of publishing the article).

Formally, the goal of metadata zone classification is to find a function

\[
\text{class}_M : Z_{DM} \rightarrow L_M
\]

where

\[
Z_{DM} = \{ z \in Z_D \mid \text{class}(z) = \text{metadata} \}
\]

\[
L_M = \{ \text{title, author, affiliation, editor, correspondence, type, abstract, keywords, bib_info, dates} \}
\]

Metadata classifier is based on Support Vector Machines and is implemented in a similar way as category classification. The classifiers differ in target zone labels, the features and SVM parameters used. The features, as well as SVM parameters were selected using the same procedure, described in Sections 4.3.1 and 4.3.2. The final classifier contains 53 features.
The decision of splitting zone classification into two separate classification steps, as opposed to implementing only one classification step, was based mostly on aspects related to the workflow architecture and maintenance. In fact both tasks have different characteristics and needs. The goal of the category classifier is to divide the article’s content into three general areas of interest, which can be then analysed independently in parallel, while metadata classifier focuses on far more detailed analysis of only a small subset of all zones.

The implementation of the category classifier is more stable: the target label set does not change, and once trained on a reasonably large and diverse dataset, the classifier performs well on other layouts as well. On the other hand, metadata zones have much more variable characteristics across different layouts, and from time to time there is a need to tune the classifier or retrain it using a wider document set. What is more, in the future the classifier might be extended to be able to capture new labels, not considered before (for example a special label for zones containing both author and affiliation, a separate label for categories or general terms).

For these reasons we decided to implement content classification in two separate steps. As a result the two tasks can be maintained independently, and for example adding another metadata label to the algorithm does not change the performance of recognizing the bibliography sections. It is also possible that in the future the metadata classifier will be reimplemented using a different technique, allowing to add new training cases incrementally, for example using a form of online machine learning.

As a result of metadata classification the zones labelled previously as metadata have specific metadata labels assigned, which gives the algorithm valuable hints where different metadata types are located in the document.

### 3.4.2 Affiliation-Author Relation Determination

As a result of classifying the document’s fragments, we usually obtain a few regions labelled as author or affiliation. In this step individual author names and affiliation strings are extracted and the relations between them are determined.

More formally, the goal of author-affiliation relation extraction is to determine for a given document $D$:

- $\text{aut}(D)$ — a list of document’s author full names,
- $\text{aff}(D)$ — a set of document’s affiliation strings,
- $\text{aa}(D)$ — a relation author-affiliation, where $(\text{aut}, \text{aff}) \in \text{aa}(D)$ if and only if the affiliation string represents the author’s affiliation.

In general the implementation is based on heuristics and regular expressions, and the details depend on article’s layout. There are two main styles used: (1) author names are grouped together in a form of a list, and affiliations are also placed together below the author’s list, at the bottom of the first page or even just before the bibliography section (an example is shown in Figure 3.10), and (2) each author is placed in a separate zone along with its affiliation and email address (an example is shown in Figure 3.11).
First step is to recognize the type of layout of a given document. If the document contains at least two zones labelled as affiliation placed approximately in the same horizontal line, the algorithm treats it as type (2), otherwise — as type (1).

![Figure 3.10: An example fragment of a page from a scientific publication with authors and affiliations zones. In this case the relations author-affiliation (coded with colors) can be determined with the use of upper indexes.](image1)

In the case of a layout of the first type (Figure 3.10), at the beginning authors’ lists are split using a predefined lists of separators. Then we detect affiliation indexes based on predefined lists of symbols and also geometric features, in particular y-position of the characters. Detected indexes are then used to split affiliation lists and assign affiliations to authors.

![Figure 3.11: An example fragment of a page from a scientific publication with authors and affiliations zones. In this case the relations author-affiliation can be determined using the distance and belonging to the same zone. The content of such a zone is split with the use of regular expressions.](image2)

In the case of a layout of the second type (Figure 3.11), each author is already assigned to its affiliation by being placed in the same zone. It is therefore enough to detect author name, affiliation and email address. We assume the first line of such a zone is the author name, email is detected based on regular expressions, and the rest is treated as the affiliation string.
3.4.3 Affiliation Parsing

Extracted affiliation strings are the input to affiliation parsing step [69], the goal of which is to recognize affiliation fragments related to *institution*, *address* and *country*. Additionally, country names are decorated with their ISO codes. Figure 3.12 shows an example of a parsed affiliation string.

![Interdisciplinary Centre for Mathematical and Computational Modelling, University of Warsaw, ul. Pawińskiego 5A blok D, 02-106 Warsaw, Poland](image)

Figure 3.12: An example of a parsed affiliation string. Colors mark fragments related to *institution*, *address* and *country*.

More formally, let $\Sigma_D$ be the alphabet used in the document $D$ and $s \in \Sigma_D^*$ — the non-empty affiliation string. Let’s also denote as $S$ a set of all (possibly empty) substrings of $s$:

$$S = \{w \in \Sigma_D^* \mid \exists_{w_1, w_2 \in \Sigma_D} w_1 w w_2 = s\}$$

The goal of affiliation parsing is to find:

- $\text{inst}(s) \in S$ — the name of the institution,
- $\text{addr}(s) \in S$ — the address of the institution,
- $\text{coun}(s) \in S$ — the name of the country,

such that $\text{inst}(s)$, $\text{addr}(s)$ and $\text{coun}(s)$ are pairwise non-overlapping substrings.

The first step of affiliation parsing is tokenization. The input string $s$ is divided into a list of tokens $t_1, ..., t_k$, such that $s = t_1 t_2 ... t_{k-1} t_k$, and each $t_i \in S$ is a maximum continuous substring containing only letters, only digits or a single other character.

After tokenization each token is classified as *institution*, *address*, *country* or *other*. The classification is done by a linear-chain Conditional Random Fields classifier, which is a state-of-the-art technique for sequence classification able to model sequential relationships and handle a lot of overlapping features.

The classifier uses the following binary features:

- **WORD** — every word (the token itself) corresponds to a feature.
- **RARE** — whether the word is rare, that is whether the training set contains less than a predefined threshold occurrences or it.
- **NUMBER** — whether the token is a number.
- **ALLUPPER** — whether it is all uppercase word.
• ALLLOWER — whether it is all lowercase word.
• STARTUPPER — whether it is a lowercase word that starts with an uppercase letter.
• COUNTRY — whether the token is contained in the dictionary of country words.
• INSTITUTION — whether the token is contained in the dictionary of institution words.
• ADDRESS — whether the token is contained in the dictionary of address words.

The dictionaries were compiled by hand using the resources from [34]. All the features exists in five versions: for the current token, for the two preceding tokens, and for the two following tokens.

After the classification the neighbouring tokens with the same label are concatenated. The resulting inst(s), addr(s) and coun(s) are the first occurrences of substrings labelled accordingly. Theoretically, the affiliation can contain multiple fragments of a certain label; in practice, however, as a result of the training data we used, one affiliation contains usually at most one substring of each kind: *institution*, *address* and *country*.

### 3.4.4 Metadata Cleaning

The purpose of the final step of metadata extraction stage is to gather the information from labelled zones, extracted author names, parsed affiliations and relations between them, clean the metadata and export the final record.

The cleaning is done with a set of heuristic-based rules. The algorithm performs the following operations:

• removing the ligatures from the text,
• concatenating zones labelled as *abstract*,
• removing hyphenation from the abstract based on regular expressions,
• as type is often placed just above the title, it is removed from the *title* zone if needed (based on a small dictionary of types),
• extracting email addresses from *correspondence* and *affiliation* zones using regular expressions,
• associating email addresses with authors based on author names,
• pages ranges placed directly in *bib_info* zones are parsed using regular expressions,
• if there is no pages range given explicitly in the document, we also try to retrieve it from the pages numbers on each page,
• parsing dates using regular expressions,
• journal, volume, issue and DOI are extracted from *bib_info* zones based on regular expressions.

Metadata cleaning is the final step of the metadata extraction stage. It results in the final metadata record of the document, containing the proper document metadata and exported as *front* section of the resulting NLM JATS file.

### 3.5 Bibliography Extraction

Bibliography extraction is next to metadata extraction another specialized extraction stage of the algorithm. During bibliography extraction, zones labelled previously as *references* are analyzed in order to extract parsed bibliographic references listed in the document.

The result of bibliography extraction is a list of bibliographic references, each of which is a tuple that can contain the following information:

- raw reference (string): raw text of the reference, as it was given in the input document,
- type (string): type of the referenced document; possible values are: *journal paper, conference paper, technical report*,
- title (string): the title of the referenced document,
- authors (a list of pairs of given name and surname): the full names of all the authors,
- source (string): the name of the journal in which the article was published or the name of the conference,
- volume (string): the volume in which the article was published,
- issue (string): the issue in which the article was published,
- year (string): the year of publication,
- pages (a pair of first and last page): the range of pages of the article,
- DOI (string): DOI identifier of the referenced document.

Each reference on the output contains the raw text and type; other information is optional. The output of bibliography extraction corresponds to the *back* section of the resulting NLM JATS record. Listing 3.2 shows an example of such a section.

Listing 3.2: Example document bibliography in NLM JATS format

```xml
<article>
  <back>
```

61
<ref-list>
  <ref>
    <mixed-citation>[1]
      <string-name>
        <given-names>E.</given-names> <surname>Braunwald</surname>
      </string-name>,
      <article-title>Shattuck lecture: cardiovascular medicine at the turn of the millennium: triumphs, concerns, and opportunities</article-title>,
      <source>New England Journal of Medicine</source>,
      vol. <volume>337</volume>,
      no. <issue>19</issue>,
      pp. <fpage>1360</fpage>-<lpage>1369</lpage>,
      <year>1997</year>.
    </mixed-citation>
  </ref>
  <ref>
    <mixed-citation>[2]
      <string-name>
        <given-names>R. L.</given-names> <surname>Campbell</surname>, <given-names>R.</given-names> <surname>Banner</surname>, <given-names>J. </given-names> <surname>Konick-McMahan</surname>, and <given-names>M. D. </given-names> <surname>Naylor</surname>
      </string-name>,
      <article-title>Discharge planning and home follow-up of the elderly patient with heart failure</article-title>,
      <source>The Nursing Clinics of North America</source>,
      vol. <volume>33</volume>,
      no. <issue>3</issue>,
      pp. <fpage>497</fpage>-<lpage>513</lpage>,
      <year>1998</year>.
    </mixed-citation>
  </ref>
  <ref>
    <mixed-citation>[3]
      <string-name>
        <given-names>S. A.</given-names> <surname>Murray</surname>
      </string-name>,
      <article-title></article-title>,
      <source></source>,
      vol. <volume></volume>,
      no. <issue></issue>,
      pp. <fpage></fpage>-<lpage></lpage>,
      <year></year>.
    </mixed-citation>
  </ref>
</ref-list>
<given-names>K.</given-names>
<surname>Boyd</surname>
</string-name>,
<string-name>
  <given-names>M.</given-names>
  <surname>Kendall</surname>
</string-name>,
<string-name>
  <given-names>A.</given-names>
  <surname>Worth</surname>
</string-name>, and
<string-name>
  <given-names>H.</given-names>
  <surname>Clausen</surname>
</string-name>,
<article-title>Dying of lung cancer or cardiac failure: prospective qualitative interview study of patients and their carers in the community</article-title>,
<source>British Medical Journal</source>,
vol. <volume>325</volume>,
no. <issue>7370</issue>,
pp. <fpage>929</fpage>-<lpage>932</lpage>,
<year>2002</year>.
</mixed-citation>
</ref>
</ref-list>
</back>
</article>

| Step                          | Goal                                      | Implementation        |
|-------------------------------|-------------------------------------------|-----------------------|
| 1. Reference strings extraction | Dividing the content of references zones into individual reference strings. | k-means clustering    |
| 2. Reference parsing          | Extracting metadata information from references strings. | CRF                   |
| 3. Reference cleaning         | Cleaning and exporting the final record. | heuristics            |

Table 3.3: The decomposition of bibliography extraction stage into independent steps.

Table 3.3 lists the steps executed during bibliography extraction stage. The detailed
descriptions are provided in the following sections: reference extraction (Section 3.5.1), reference parsing (Section 3.5.2) and reference cleaning (Section 3.5.3).

### 3.5.1 References Extraction

Zones labelled as references by category classifier contain a list of reference strings, each of which can span over one or more text lines. The goal of reference strings extraction is to split the content of those zones into individual reference strings.

Let’s denote as $Z_{DR}$ the set of all zones in the document labelled as references:

$$Z_{DR} = \{ z \in Z_D \mid \text{class}(z) = \text{references} \}$$

Let also $L_{ZR}$ be the set of all lines from the references zones:

$$L_{ZR} = \bigcup Z_{DR}$$

The goal of reference extraction is to find a partition $R = P(L_{ZR})$ such that each set $r \in R$ along with the order inherited from the set $L_{ZR}$ represents a single reference string. Let’s denote as $\text{ref}(l) \in R$ the reference of a given line $l \in L_{ZR}$, that is $r = \text{ref}(l) \iff l \in r$. The partition $R$ should respect the reading order in the line set, that is

$$\forall l_1,l_2,l_3 \in L_{ZR} \quad (l_1 \leq l_2 \leq l_3 \land \text{ref}(l_1) = \text{ref}(l_3) \Rightarrow \text{ref}(l_1) = \text{ref}(l_2))$$

Each line $l \in L_{ZR}$ belongs to exactly one reference string, some of them are first lines of their reference, others are inner or last ones. The sequence of all text lines belonging to bibliography section can be represented by the following regular expression:

```
( <first line of a reference>
  ( <inner line of a reference>*
    <last line of a reference>
  )?
) *
```

The task of grouping text lines into consecutive references can be solved by determining which lines are the first lines of their references. A set of such lines is shown in Figure 3.13. More formally, we are interested in finding a set $FL_{ZR} \subset L_{ZR}$, such that

$$|FL_{ZR}| = |R| \land \left( l \in FL_{ZR} \iff \left( \forall p \in L_{ZR} \quad (p < l \Rightarrow \text{ref}(p) \neq \text{ref}(l)) \right) \right)$$

Finding the set $FL_{ZR}$ is equivalent to finding the partition $R$, since every set $r \in R$ can be constructed by taking a first line $l \in FL_{ZR}$ and adding all the following lines until the next first line or the end of the line sequence is reached.
Figure 3.13: A fragment of the references section of an article. Marked lines are the first lines of their references. After detecting these lines, the references section content can be easily split to form consecutive references strings.

The pseudocode of the algorithm is presented in Algorithm 3.2. To find the set $FL_{ZR}$, we transform all lines to feature vectors and cluster them into two disjoint subsets. Ideally one of them is the set of all first lines ($FL_{ZR}$) and the other is equal to $L_{ZR} - FL_{ZR}$. The cluster containing the first line in $L_{ZR}$ (the smallest with respect to the order) is assumed to be equal to $FL_{ZR}$.

**Algorithm 3.2 Reference strings extraction algorithm**

1: function ExtractReferenceStrings(refLines)
2:     refLinesFV ← EXTRACTFEATURES(refLines) ▷ extract features for the lines
3:     clusters ← KMEANS(refLinesFV, 2) ▷ cluster lines into two subsets
4:     firstCluster ← clusters[0]
5:     refStrings ← () ▷ resulting reference strings list
6:     actString ← () ▷ current reference
7:     for i: 1 to LENGTH(refLines)-1 do
8:         if firstCluster = clusters[i] then ▷ current reference is completed
9:             ADD(refStrings, CONCATENATE(actString))
10:        actString ← ()
11:    end if
12:    ADD(actString, refLines[i])
13: end for
14: return refStrings
15: end function

For clustering lines we use k-means algorithm with Euclidean distance metric. In this case $k = 2$, since the line set is clustered into two subsets. As initial centroids we set the first line’s feature vector and the vector with the largest distance to the first one. We use the following features:
whether the line starts with an enumeration pattern — this feature activates only if there exists a preceding line with the same pattern, but labelled with the previous number, and if there exists a following line with the same pattern, but labelled with the next number,

• whether the previous line ends with a dot,

• the ratio of the length of the previous line to the width of the previous line’s zone,

• whether the indentation of the current line within its zone is above a certain threshold,

• whether the vertical distance between the line and the previous one is above a certain threshold (calculated based on the minimum distance between references lines in the document).

The result of the references extraction step is a list of bibliographic references in the form of raw strings, that undergo parsing in the next step.

3.5.2 References Parsing

Reference strings extracted previously contain important reference metadata. During parsing metadata is extracted from reference strings and the result is the list of document’s parsed bibliographic references. The information we extract from the strings include: author (including given name and surname), title, source, volume, issue, pages (including the first and last page number from a range) and year. An example of a parsed reference is shown in Figure 3.14.

[9] L. O’Gorman. The document spectrum for page layout analysis. IEEE Transactions on Pattern Analysis and Machine Intelligence, 15(11):1162–1173, 1993.

Figure 3.14: An example of a bibliographic reference with various metadata information highlighted using different colors, these are in order: author, title, journal, volume, issue, pages and year.

Formally, the task can be defined similarly as the task of affiliation parsing described in Section 4.4. The implementation is also similar: first a reference string is tokenized into a sequence of tokens. The tokens are then transformed into vectors of features and classified by a linear-chain CRF classifier. The classifiers differ in target labels and used features.

The token classifier uses the following token labels: first_name (author’s first name or initial), surname (author’s surname), title, source (journal or conference name), volume, issue, page_first (the lower bound of pages range), page_last (the upper bound of pages range), year and text (for separators and other tokens without a specific label).

The main feature is the token (the word) itself. This feature activates only if the number of its occurrences in the validation dataset exceeds a certain threshold. We also developed 34 additional binary features:
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- features checking whether all characters in the token are: digits, letters, letters or
digits, lowercase letters, uppercase letters, Roman numerals;
- whether the token starts with an uppercase letter;
- whether the token is: a single digit, a lowercase letter, an uppercase letter;
- whether the token is present in the dictionaries of: cities, publisher words, series
words, source words, number/issue words, pages words, volume words;
- whether the token is: an opening/closing parenthesis, an opening/closing square
bracket, a comma, a dash, a dot, a quotation mark, a slash;
- whether the token is equal to ”and” or ”&”;  
- whether the token is a dash placed between words;
- whether the token is a single quote placed between words;
- whether the token is a year.

It is worth to notice that the token’s label depends not only on its feature vector,
but also on the features of the surrounding tokens. To reflect this in the classifier, the
token’s feature vector contains not only features of the token itself, but also features of two
preceding and two following tokens, similarly as in the case of the affiliation parser.

After token classification fragments labelled as first_name and surname are joined to-
gether based on their order to form consecutive authors, and similarly fragments labelled
as page_first and page_last are joined together to form pages range. Additionally, in the
case of title or source labels, the neighbouring tokens with the same label are concatenated.

As a result of reference parsing step, we have a list of the document’s bibliographic
references, each of which is a tuple containing the raw reference strings as well as the
metadata extracted from it.

3.5.3 References Cleaning

Similarly to metadata cleaning, references cleaning is the last step of the bibliography
extraction stage. Its purpose is to clean previously extracted data and export the final
record.

During references cleaning the following operations are performed:
- The ligatures are removed from the text.
- Hyphenation is removed from the strings based on regular expressions.
- DOI is recognized in the reference strings by a regular expression. The reference
parser is not responsible for extracting this information, because the dataset used for
training the token classifier does not contain enough references with DOI.
Finally, the type of the reference (journal paper, conference proceedings or technical report) is detected by searching for specific keywords in the reference string.

Reference cleaning is the last step of bibliography extraction. The entire stage results in a list of parsed bibliographic references, corresponding to the back section of the output NLM JATS record.

### 3.6 Structured Body Extraction

Structured body extraction is, next to metadata extraction and bibliography extraction, another specialized extraction stage of the algorithm. The purpose of structured body extraction is to obtain the main text of the document in the hierarchical form composed of sections, subsections and subsubsections by the analysis of the middle region of the document labelled previously as body.

Intuitively, the result of structured body extraction is the full text of the document represented by a list of sections, each of which might contain a list of subsections, each of which might contain a list of subsubsections. Each structure part (section, subsection and subsubsection) has the title and the text content.

More formally, for a given document $D$ we denote as $S_D$ the set of all structure parts. We have $S_D = S^1_D \cup S^2_D \cup S^3_D$, where $S^1_D \neq \emptyset$ is a set of the sections of the document, $S^2_D$ is a (possibly empty) set of subsections and $S^3_D$ is a (possibly empty) set of subsubsections.

The following statements are also true for the structured parts:

\[
\forall s_1, s_2 \in \{s^1_D, s^2_D, s^3_D\} \quad (s_1 \neq s_2 \Rightarrow s_1 \cap s_2 = \emptyset)
\]

\[
S^2_D = \emptyset \Rightarrow S^3_D = \emptyset
\]

The hierarchical structure of the document parts is defined by a parent function $\text{par} : S_D^2 \cup S_D^3 \to S_D^1 \cup S_D^2$, which maps the elements to their parents in the structure, in particular:

- $\forall s \in S_D^3 \quad \text{par}(s) \in S_D^1$
- $\forall s \in S_D^3 \quad \text{par}(s) \in S_D^2$

All the sets $S_D, S_D^1, S_D^2$ and $S_D^3$ are totally ordered sets, where the order corresponds to the natural reading order of the parts of the document. The order of the elements also respects the section hierarchy, in particular:

\[
\forall s_1, s_2 \in S_D^3 \quad \forall s_{1,2} \in S_D \quad (s_1 \leq s_2 \Rightarrow \text{par}(s_1) \leq \text{par}(s_2))
\]

Every structure part $s \in S_D$ has its title $\Gamma(s) \in \Sigma_D^*$ and the text content $C(s) \in \Sigma_D^*$. The text content is understood as the text associated directly with the given element, in particular the text contents of the children of a given element are not part of its text content; in order to obtain the full content of a given element one has to recursively iterate
over its descendants and concatenate their contents. The text content of every element precedes the text content of its descendants with respect to the document’s reading order.

The output of body extraction corresponds to the body section of the resulting NLM JATS record. Listing 3.3 shows an example of such a section. The paragraphs are shortened for conciseness.

Listing 3.3: Example document body in NLM JATS format

```xml
<article>
  <body>
    <sec>
      <title>Introduction</title>
      <sec>
        <title>Challenges</title>
        <p>In the West, carers of children with disabilities... </p>
        <p>Existing research has shown that carers of children... </p>
        <p>... </p>
      </sec>
      <sec>
        <title>Coping strategies</title>
        <p>Evidence suggests that... </p>
      </sec>
    </sec>
    <sec>
      <title>Design and methodology</title>
      <sec>
        <title>Study design</title>
        <p>We employed a qualitative phenomenological approach... </p>
      </sec>
      <sec>
        <title>Sample size determination and sampling procedure</title>
        <p>Children for the study were selected from 104 children... </p>
      </sec>
      <sec>
        <title>Development of research tools</title>
        <p>A checklist of questions was developed... </p>
      </sec>
      <sec>
        <title>Methods of data collection</title>
        <sec>
          <title>In-depth interviews</title>
          <p>In-depth interviews were conducted... </p>
        </sec>
      </sec>
      <sec>
        <title>Observations</title>
        <p>Passive observations consisted of systematic watching... </p>
      </sec>
    </sec>
  </body>
</article>
```
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Data analysis

Inductive analysis as described by...

Data triangulation from the interviews...

Ethical consideration

The study was approved by...

Table 3.4: The decomposition of body extraction stage into independent steps.

| Step                              | Goal                                                                 | Implementation   |
|-----------------------------------|----------------------------------------------------------------------|------------------|
| 1. Text content filtering         | Filtering out fragments related to the tables, images and equations from body parts of the document. | SVM              |
| 2. Section headers detection      | Detecting the body lines containing the titles of sections, subsections and subsubsections. | heuristics       |
| 3. Section hierarchy determination| Dividing the section headers into levels and building the section hierarchy. | heuristic clustering |
| 4. Structured body cleaning       | Cleaning and exporting the final structured body content.           | heuristics       |

Table 3.4 lists the steps executed during body extraction stage. The detailed descriptions are provided in the following sections: text content filtering (Section 3.6.1), section headers detection (Section 3.6.2), section hierarchy determination (Section 3.6.3) and structured body cleaning (Section 3.6.4).

3.6.1 Text Content Filtering

Text content filtering is the first step in the body extraction stage. The purpose of this step is to locate all the relevant (containing section titles and paragraphs) parts in the body of the document. The task is accomplished by classifying the body zones into one of the two classes: body_content (the parts we are interested in) and body_other (all non-relevant fragments, such as tables, table captions, the text belonging to images, image captions, equations, etc).

More formally, the goal of text filtering is to find a function

\[ \text{class}_B : Z_{DB} \rightarrow L_B \]
where

\[ Z_{DB} = \{ z \in Z_D \mid \text{class}(z) = \text{body} \} \]

\[ L_B = \{ \text{body}_\text{content}, \text{body}_\text{other} \} \]

The classifier is based on Support Vector Machines and is implemented in a similar way as category and metadata classifiers. It differs from them in target zone labels, the features and SVM parameters used. The features, as well as SVM parameters were selected using the same procedure as before, described in Sections [4.3.1] and [4.3.2]. The final body classifier contains 63 features capturing both the geometric and textual characteristics of classified zones.

As a result of text content filtering the set of zones labelled as body is split into two groups: the fragments containing section titles and paragraphs, which are further analyzed in the following steps, and the non-relevant fragments like tables and figures, which are ignored.

### 3.6.2 Section Headers Detection

The goal of section headers detection is to find all the headers in the body\_content zones, that is lines containing the titles of the sections, subsections and subsubsections of the document.

Let’s denote as \( Z_{DC} \) the set of all zones in the document \( D \) labelled as body\_content:

\[ Z_{DC} = \{ z \in Z_D \mid \text{class}(z) = \text{body} \land \text{class}_B(z) = \text{body}_\text{content} \} \]

Let also \( L_{ZC} \) be the set of all lines from the body\_content zones:

\[ L_{ZC} = \bigcup Z_{DC} \]

Every title of a section, subsection or subsubsection spans over one or more subsequent body content lines. In this step we are interested in finding a set of all headers \( H_D = \{ L_1, L_2, ..., L_{|S_D|} \} \) such that

- every header \( L_i \subset L_{ZC} \), \( L_i \neq \emptyset \) is a non-empty set of body\_content lines,
- the headers are pairwise disjoint:
  \[ \forall L_i, L_j \in H_D \quad (L_i \neq L_j \Rightarrow L_i \cap L_j = \emptyset) \]
- every header is a continuous sequence of lines:
  \[ \forall L_i \in H_D \quad \forall l_1, l_2, l_3 \in L_{ZC} \quad (l_1 \in L_i \land l_3 \in L_i \land l_1 \leq l_2 \leq l_3 \Rightarrow l_2 \in L_i) \]
Regardless of the document layout the header lines are always different in some way from much more numerous paragraph lines. In different layouts different ways to make header lines stand out are used; for example they can differ in the fonts, the size of the text, the enumeration patterns, the indentation or distance between lines, or any combination of these features. Some examples of header lines in different layouts are shown in Figure 3.15.

Since the header lines are always different in some way from the text used in the document’s paragraphs, and also far less common among the body_content lines, we are in fact looking for outliers in the set $L_{ZC}$. To make use of this observation, we analyze the entire populations of various feature values of the lines in $L_{ZC}$ for a given input document. For a single line and a specific feature calculated for the line we can obtain the standard score of this observation with respect to the entire population we are dealing with:

$$z = \frac{x - \mu}{\sigma}$$

where:

- $x$ is the value of the feature of interest calculated for the current line,
- $\mu$ is the mean of the feature values over the population of $L_{ZC}$,
- $\sigma$ is the standard deviation of the feature values in the population.

The closer $z$ is to 0, the more typical the line is with respect to the given feature. We use standard scores for the following features to detect the outliers in the populations:

- $z_h$ — line height,
- $z_l$ — line length,
- $z_x$ — the x-coordinate (the distance to the left edge of the page),
- $z_d$ — the distance from the previous line,
- $z_f$ — the font (fonts are encoded as subsequent natural numbers).

Unfortunately, although the standard scores proved to be very useful, they are not enough to detect the header lines with high precision. In practise we often have to deal with errors caused by the classification in the previous step, which results in small fragments of tables, images or captions still present in the set $L_{ZC}$. Since these fragments also visually differ from the paragraphs, they often appear as outliers as well. To counteract this we employed additional heuristics to filter out such lines.

In general the algorithm consists of two phases:

1. In the first phase we detect the first line of every header. More formally, we are interested in finding a set $FH_D = \{l_1, l_2, ..., l_{|S_D|}\}$, such that

$$\forall 1 \leq i \leq |S_D| \quad (l_i \in L_i \quad \land \quad \forall s \in L_i \quad l_i \leq s)$$
Figure 3.15: The examples of headers in different layouts. The header lines are always different from the paragraph lines in some way: (a) with the use of enumerations, (b) another type of enumeration, (c) the indentation, (d) the distance between lines, (e) and (f) the fonts.
2. In the second phase we find the remaining header lines, that is the set $\bigcup H_D - FH_D$.

The pseudocode of the first phase is presented in Algorithm 3.3. In the first phase we perform the following operations:

1. First, we iterate over all lines from the set $L_{ZC}$ and select the candidates for the first header lines. A line becomes a candidate if it is the first line in its zone and if it starts with an uppercase letter or a typical enumeration pattern (lines 3-7 in Algorithm 3.3).

2. Next, we remove candidates that do not meet certain criteria (lines 8-12 in Algorithm 3.3). A line is removed from the candidate set if at least one of the following conditions is true:
   - the line is too long (large $z_l$)
   - the text size is too small (small $z_h$)
   - the line is printed using a typical font, typical distance from the previous line and X coordinate ($z_f$, $z_d$ and $z_x$ all close to 0),
   - the text of the line contains a pattern characteristic for table or figure caption,
   - the text of the line contains characters typical for equations,
   - less than half of the characters in the line are letters,
   - the text of the line does not contain any 4-character continuous sequence of letters,
   - none of the five lines following the examined line starts with an uppercase letter.

3. Next, using the candidate set we identify a set of fonts typical for headers in a given document (lines 13-19 in Algorithm 3.3). A font is considered typical for headers if it appears in at least 3 candidate lines and its $|z_f|$ exceeds a certain threshold, which means it is an outlier with respect to the fonts. If headers are printed using the same font as the paragraphs, the font information cannot be safely used to extend the candidate set.

4. Next, we use the set of header fonts to extend the candidate set (lines 20-24 in Algorithm 3.3). We iterate again over all relevant lines and mark them as candidates if they use one of the header fonts and if they start with an uppercase letter or a typical enumeration pattern.

5. Finally, we delete candidate lines using similar criteria as in step 3, only this time the thresholds for normal scores are more tolerant (lines 25-29 in Algorithm 3.3).
Algorithm 3.3 First header lines extraction algorithm

1: function ExtractFirstHeaderLines(bodyLines)
2:     candidates ← ∅
3:     for line ∈ bodyLines do
4:         if IsFirstInZone(line) and MatchesHeaderRegexp(line) then
5:             Add(candidates, line)
6:         end if
7:     end for
8:     for candidate ∈ candidates do
9:         if VIOLATESHEADERCRITERIASTRICT(candidate) then
10:            DELETE(candidates, candidate)
11:        end if
12:     end for
13:     headerFonts ← ∅
14:     for candidate ∈ candidates do
15:         font ← FONT(candidate)
16:         if NumberOfLinesWithFont(font, candidates) ≥ 3 and ISOUTLIER(font) then
17:             Add(headerFonts, font)
18:         end if
19:     end for
20:     for line ∈ bodyLines do
21:         if CONTAINS(headerFonts, FONT(line)) and MatchesHeaderRegexp(line) then
22:             Add(candidates, line)
23:         end if
24:     end for
25:     for candidate ∈ candidates do
26:         if VIOLATESHEADERCRITERIASOFT(candidate) then
27:            DELETE(candidates, candidate)
28:        end if
29:     end for
30:     return candidates
31: end function

This approach allows to identify only the first line of each header, represented by the set $FH_D$, which corresponds to the target set $HD$. The sets might not be equal, as a header can span over more lines (an example is presented in Figure 3.16). In the last phase we examine each first line and select additional lines following it, if needed.

To detect additional header lines, we inspect the lines directly following every first header line found in the previous phase. The pseudocode of the algorithm is presented in Algorithm 3.4. For every first header line we execute the following steps:
(40°C). The obtained residue (crude ethanolic extract) was weighed and stored at -20°C at dark.

**Partial purification of the crude ethanolic extract of propolis by solvent partitioning with different polarity solvents**

The ethanolic extract of the propolis was dissolved in 80% (v/v) methanol until it was not sticky and then an equal volume of hexane was added, stirred (15 mins)

Figure 3.16: An example of a multi-line header consisting of three subsequent lines.

1. First we select the candidates for additional lines. We iterate over the lines directly following the main header line. A line is consider a candidate if its height is similar to the height of the main header line and if it is printed using the same font. We stop the iteration if we come across a line that does not meet these criteria, if we come across another first header line or if we already added three lines to the candidates list.

2. Selected candidates are added to the proper element in the set $H_D$ as additional lines if at least two of the following conditions are met:

   - the last candidate line is noticeably shorter than the main header line,
   - the last candidate is printed with a different indentation than the line following it,
   - the line following the last candidate starts with an uppercase,
   - the last candidate is written using a different font than the line following it.

The resulting set of headers $H_D$ corresponds to $S_D$ — the set of the sections, subsections and subsubsections of the document.

### 3.6.3 Section Hierarchy Determination

The purpose of section hierarchy determination is to reconstruct the hierarchy of sections from the set $H_D$. More precisely, our goal is to divide the set $H_D$ into disjoint subsets $H_D^1$, $H_D^2$ and $H_D^3$ corresponding to the sets of sections, subsections and subsubsections of the document, respectively. We are also interested in finding a parent function $\text{par}_H : H_D^2 \cup H_D^3 \to H_D^1 \cup H_D^2$, which maps subsections and subsubsections to their parents in the hierarchy and corresponds to the function par.

To find the sets $H_D^1$, $H_D^2$ and $H_D^3$, we make use of an observation that the headers of sections on the same hierarchy level are usually printed using a similar style. In the first step we cluster the set of headers $H_D$ with the use of the following simple clustering algorithm:
Algorithm 3.4 Header lines extraction algorithm

1: function EXTRACT_HEADERS(firstHeaderLines)
2:   headerLines ← ∅
3:   for line ∈ firstHeaderLines do
4:     header ← ∅
5:     ADD(header, line)
6:     candidates ← ∅
7:     actLine ← NEXT(line)
8:     while actLine ≠ null and SIZE(candidates) ≤ 3 do
9:       if FONT(actLine) ≠ FONT(line) then
10:          break
11:       if !ARESIMILAR(HEIGHT(actLine), HEIGHT(line)) then
12:          break
13:       end if
14:     end while
15:     ADD(candidates, actLine)
16:     actLine ← NEXT(actLine)
17:     if EVALUATE_CANDIDATES(candidates) then
18:       ADD_ALL(header, candidates)
19:     end if
20:   end for
21:   ADD(headersLines, header)
22: end function

1. We maintain a set of headers with no cluster assignment. At the beginning the set consists of all headers from $H_D$.

2. We randomly choose a header from the set. Then we compare the first line of selected header to the first lines of all the headers from the set and mark those which have the same font and similar height. All the selected headers form a new cluster and are removed from the set.

3. This step is repeated until the set is empty.

Let $CL_D = (c_{l_1}, c_{l_2}, ..., c_{l_{|S_D|}})$ be the sequence of clusters of the elements of the set $H_D = \{L_1, L_2, ..., L_{|S_D|}\}$ sorted with respect to the reading order of the headers. Since we are interested only in three section levels (scientific publications rarely contain more levels), we keep only the first three clusters appearing in the sequence $CL_D$. All the headers belonging to the remaining clusters are deleted from the header set.

Next we divide $H_D$ into the sets $H^1_D, H^2_D$ and $H^3_D$ and determine the final hierarchy:

1. The set $H^1_D$ is equal to $c_{l_1}$, the cluster of the first header $L_1$. 
2. We then divide the sequence of the headers into continuous subsequences, such that each subsequence starts with a header from $H^1_D$ and contains all the following headers until the next header of the first level (or the end of the sequence) is reached. These sequences represent the sections with their descendants and are then processed independently.

3. If the header sequence contains more than one header, the cluster of the second element in the sequence is assumed to represent the second hierarchy level in this section. Thus we select all the headers in the sequence belonging to this cluster and form subsections.

4. All the remaining lines in the sequence form subsubsections.

5. For every subsection and subsubsection we set the parent section to be the last preceding section of the higher level.

The algorithm results in the division of the set $H_D$ into sets $H^1_D$, $H^2_D$ and $H^3_D$, which along with the reading order and parent function corresponds directly to the desired sections, subsections and subsubsections hierarchy of the document.

3.6.4 Structured Body Cleaning

Body cleaning is the final step in the structured body extraction path of the algorithm. Its purpose is to form the final section hierarchy along with the section titles and text content and clean the data.

The sections, subsections and subsubsections, and their hierarchy are formed based on the sets $H^1_D$, $H^2_D$ and $H^3_D$ and the parent function. The title of a content part is the concatenated text of all its header lines, in their reading order. Similarly, the text content of a content part is the concatenated text of the paragraph lines placed between its header and the header of the next content part.

The cleaning phase comprises removing the ligatures and end-of-line hyphenation based on regular expressions.

The result of the structured body extraction is a hierarchical structure of sections, subsections and subsubsections of the document along with all the content part titles and the text content. The extracted structured content corresponds to the body section of the resulting NLM JATS record.

3.7 Our Contributions

The proposed extraction algorithm is based to a great extend on a well-known supervised and unsupervised machine-learning techniques accompanied with heuristics. This section summarizes all the innovatory ideas and extensions we proposed.

One of the key contributions is the architecture of the entire extraction workflow and the decomposition of the problem into smaller, well-defined tasks. We designed four processing
paths: an initial path containing preprocessing, layout analysis and initial classification, and three specialized extraction paths analysing three separate document regions: metadata extraction, structured body extraction and bibliography extraction path. Each path consists of several steps executed in a sequence. Each step solves a single, well defined problem and its implementation is independent of other workflow parts.

For the first workflow step, character extraction, iText library was used. Based on the observations related to various rare cases and problems with PDF files, we added an additional cleaning step (Section 3.2.1), the goal of which is to reduce the number of extracted characters by removing duplicates, characters not visible in the resulting file, or characters used for objects other than the text of the document.

The page segmentation algorithm, Docstrum, was enhanced with a few modifications related to identifying words, merging lines, scaling the thresholds relatively to line heights, etc. (Section 4.2). The evaluation we performed showed our modifications increased the accuracy of recognizing lines and zones in the document (Section 4.2).

We developed a large set of 103 numeric features for document’s text zones capturing all aspects of the content and appearance of the text and allowing to classify fragments with high accuracy (Sections 3.3, 3.4.1 and 3.6.1). The features were subjected to semi-automatic selection process separately for every classifier, which reduced the dimensionality of the feature vectors and resulted in only the most useful features being included in the models.

We also developed a set of features for citation and affiliation tokens, which allow to parse affiliations and citations with high accuracy (Sections 4.4 and 3.5.2). These features are based purely on the text of the tokens and are accompanied with dictionaries of words commonly appearing as particular metadata fields.

A clustering-based approach was proposed for extracting reference strings from the document. This method does not require expensive training set preparation and parameter learning, while still achieving very good results (Section 3.5.1).

We also proposed an algorithm based on normal scores of various statistics for selecting section header lines from the text content of the document (Section 3.6.3). This is based on a simple observation that within one document numerous text paragraph lines have similar values of certain features, and thus the farther the line’s feature value is from the document’s mean, the higher probability that as an outlier it is not a paragraph line.

Finally, we designed a clustering-based algorithm for retrieving the hierarchy of sections (Section 3.6.3). The approach is based on an observation, that section titles of the same hierarchy level are printed using similar style. As an unsupervised algorithm, it does not require gathering training data and performing the training.

3.8 Limitations

The extraction algorithm described in this chapter has a number of limitations.

Currently the algorithm does not include any optical character recognition phase, it analyses only the PDF text stream found in the input document. As a result, PDF docu-
ments containing scanned pages in the form of images are not properly processed.

There is also another problem related to analysing the underlying PDF text stream rather than the visible shapes printed on the document’s pages. In some cases the underlying text might not be the same as the visible one, for example due to objects covering other objects, or custom mappings between the characters and printed glyphs used in a given PDF. In such rare cases the information extracted by the algorithm might not match the text visible to the document readers.

The extraction algorithm analyses only the content of a single PDF file, and only the information explicitly given in the document has a chance to be extracted. The algorithm does not infer any new information based on the content, in particular it does not extract the language the document is written in based on n-grams, compile the document summary by selecting the most important sentences and phrases or extract the keywords from the text using statistical methods.

Finally, the extraction algorithm does not analyse some regions typically present in scientific articles, such as: tables, acknowledgments, conflict statements or authors’ contributions.
Chapter 4

Experiments and Evaluation

This chapter contains all the details related to the experiments we performed on the algorithm and its individual steps, as well as the methodology and results of the evaluation used to assess the quality of the extraction process and to compare it to other existing methods.

The data used for the experiments is based on the following resources: PubMed Central Open Access Subset\(^1\), Directory of Open Access Journals\(^2\), Elsevier\(^3\), and Cora Citation Matching dataset\(^4\). All the datasets used in the experiments were prepared semi-automatically.

The experiments we performed comprise the adjustment of the Support Vector Machine-based classifiers, including semi-automatic feature selection and automatic best SVM parameters choosing with the use of a validation dataset.

The most important part of the chapter is the methodology and the results of the evaluation of the entire extraction algorithm. We evaluated the performance of the algorithm with respect to its entire functionality: extracting the basic document metadata, bibliography and structured text content. The scores achieved by our algorithm were also compared to the performance of four similar solutions.

We also performed the evaluation of the following individual steps of the algorithm: page segmentation, category classification, metadata classification, body classification, affiliation parsing and reference parsing. Other steps were not directly evaluated, mainly due to the fact, that creating ground truth datasets for them would be very time-consuming. Since all the steps affect the final extraction results, they were all evaluated indirectly by the assessment of the performance of the entire algorithm.

The chapter is organized as follows. Section 4.1 contains all the details related to the datasets used for experiments as well as the procedures used for creating them. The following sections provide the information related to the methodology and the results of the evaluation of the individual steps of the algorithm: page segmentation (Section 4.2),

\(^1\)http://www.ncbi.nlm.nih.gov/pubmed
\(^2\)https://doaj.org/
\(^3\)http://www.elsevier.com/
\(^4\)http://people.cs.umass.edu/~mccallum/data.html
content, metadata and body classification (Section 4.3), affiliation parsing (Section 4.4) and reference parsing (Section 4.5). In Section 4.6 we report the results of the evaluation of the entire extraction algorithm and the comparison with other similar tools. Finally Section 4.7 covers the time performance issues of the extraction algorithm.

4.1 Datasets Overview

The following resources were used as a basis for the datasets used in all the experiments: PubMed Central Open Access Subset, Directory of Open Access Journals, Elsevier and Cora Citation Matching.

Directory of Open Access Journals (DOAJ) is an online directory providing access to open access, peer-reviewed journals. DOAJ contains nearly 2 million articles in the form of PDF files and the corresponding metadata in Dublin Core format.

Elsevier is a publisher publishing over 250,000 articles a year in over 3,000 journals. Unfortunately, its resources are not open access and were available for our experiments based on a dedicated license.

PubMed Central Open Access Subset (PMC) contains over 1 million life sciences publications in PDF format, and their corresponding metadata in the form of NLM JATS files. NLM JATS files contain a rich set of document’s metadata (title, authors, affiliations, abstract, journal name, etc.), structured full text (sections, section titles, paragraphs, tables, equations), and also document’s parsed bibliography.

Cora Citation Matching dataset, commonly referred to as Cora-ref dataset, is a widely used set of parsed bibliographic citations useful for evaluating citation parsing and matching solutions.

In case of most experiments these datasets could not be used directly, due to missing or fragmentary information and the differences in the formats or labelling. We employed these resources as a basis to construct our own datasets, which were then used in the experiments.

Table 4.1 summarizes all the dataset types used for the experiments. Structure datasets contain the documents in the form of serialized geometric models of their content along with the zone labels. Metadata datasets contain the pairs of the source PDF files and their corresponding metadata records. The affiliation dataset contains the affiliation strings with tagged metadata and similarly, the citation dataset contains the citation strings with tagged metadata. The following sections provide more details related to the contents of the datasets, their purpose and the process of creating them.

4.1.1 Structure Sets

A structure set contains the documents in the form of serialized geometric models of their content along with the zone labels. We use TrueViz [46] as a serialization format. Structure sets were used for the evaluation of the page segmenter, and also for training and evaluation of the zone classifiers. We use two structure datasets: GROTOAP [73, 74] and
| Type                | Contents                | Format              | Sources            | Purposes                                                                 |
|---------------------|-------------------------|---------------------|--------------------|--------------------------------------------------------------------------|
| structure set       | geometric models of the documents | TrueViz             | DOAJ, PMC          | the evaluation of the page segmentation, the training and the evaluation of the zone classifiers |
| metadata set        | pairs of PDF files and corresponding metadata records | PDF + NLM JATS     | PMC, Elsevier      | the evaluation of the entire algorithm, the comparison with other similar tools |
| affiliation set     | affiliation strings with tagged metadata | NLM JATS            | PMC                | the evaluation of the affiliation parser                                 |
| citation set        | citation strings with tagged metadata | NLM JATS            | Cora-ref, PMC      | the evaluation of the citation parser                                     |

Table 4.1: The summary of all the dataset types used for the experiments.

GROTOAP2 [66, 67], which were built in a different way and are used for slightly different purposes.

**GROTOAP**

GROTOAP (GROund Truth for Open Access Publications) [73, 74] is a structure set built semi-automatically upon a group of scientific articles from DOAJ database. GROTOAP consists of:

- 113 scientific publications in PDF format,
- corresponding ground truth files in TrueViz format containing the geometric hierarchical structure of the input documents along with their zone labels.

The process of creating GROTOAP dataset was semi-automatic and consisted of the following phases:

1. selecting and downloading a set of publications based on metadata from DOAJ database,
2. automatic extraction of hierarchical structure using our extraction tools,
3. manual correction of the results of automatic structure extraction with the use of a visual editing tool.
All the publications in the dataset were taken from journals distinguished with SPARC Europe Seal for Open Access Journals. We harvested Directory of Open Access Journals for basic metadata of all articles from these journals, including links to full texts. Next, we randomly selected articles to be downloaded. The selected group contains one article from each four journals published by the same publisher, 113 articles in total. Articles published by the same publisher have usually very similar layout, and as a result the layout distribution in the group is similar to the layout distribution in the entire DOAJ database.

To minimize the time needed for manual correction, first we processed selected publications using tools implemented in our metadata extraction process in order to automatically extract their structure. First, individual characters and their bounding boxes were extracted, then we segmented pages. Finally, zone classifiers assigned labels to all zones in the documents.

During the last phase TrueViz files created automatically were corrected by a group of people with the use of a visualization and editing tool. The correction phase included verifying words, lines and zones generated by metadata extraction tools, splitting incorrectly merged objects and merging incorrectly split ones, verifying and correcting labels assigned to zones. To minimize human errors we performed an additional checking phase, which included an inspection and approval by an independent judge.

The last two phases were executed twice. In the first round we used the default version of the extraction tools on a very small subset of GROTOAP. This resulted in a substantial number of errors, since the tools were not trained or adjusted in any way to perform well on the layouts present in the dataset. After the manual correction of these files, they were used to retrain and adjust the classification algorithms. The new versions were then used in the second round on the remaining documents, which resulted in much less errors and less time spent on the manual correction.

Since GROTOAP’s creation process required a manual correction of every document, it does not scale well. The resulting dataset is relatively small and every attempt to expand it is time-consuming and expensive. The layout distribution in the dataset resembles the distribution in the DOAJ database, but its small size resulted in a lot of journals and layouts missing. Due to the small size and lack of diversity, the algorithms trained on GROTOAP did not generalize well enough and performed worse on diverse sets. To solve this problem, we decided to use a different, scalable approach to create much larger dataset, which resulted in GROTOAP2.

GROTOAP2

GROTOAP2 [66,67] is a successor of GROTOAP. GROTOAP2 is also a structure set, and can be used for the same purposes. The dataset is based on born-digital PDF documents from PubMed Central Open Access Subset. In contrast to GROTOAP, the method used to construct GROTOAP2 is scalable and efficient, which allowed to construct much larger and diverse dataset. Table 4.2 compares the basic size-related parameters of GROTOAP and GROTOAP2.
The comparison of the parameters of GROTOAP and GROTOAP2 datasets.
The table shows the numbers of different publishers and journals included in both datasets, as well as the numbers of documents, pages, zones and zone labels.

GROTOAP2 contains 13,210 scientific publications in the form of the geometric model of their content serialized using TrueViz format. The final list of zone labels in GROTOAP2 includes: abstract, acknowledgment, affiliation, author, bib_info, body, conflict_statement, copyright, correspondence, dates, editor, equation, figure, glossary, keywords, page_number, references, table, title, title_author, type, unknown.

GROTOAP2 was created semi-automatically from PMC resources (Figure 4.1). Since the ground truth files in PMC (the metadata records in NLM JATS format) contain only the annotated text of documents, and do not preserve any geometric features related to the way the text is displayed in the PDF files, they could not be directly used as a structure set. Instead we used the text annotations from the ground truth files to assign labels to zones automatically, while the zones, lines and words themselves were constructed using our extraction and segmentation tools. More precisely, GROTOAP2 was created in the following steps:

1. First, a large group of files were randomly selected from PMC resources. We obtained both the input PDF files and the corresponding metadata records.

2. The PDF files were processed automatically by our algorithms in order to extract the hierarchical geometric structure and the reading order. More precisely, character extraction, page segmentation and reading order resolving steps were executed.

3. The text content of every zone was then compared to labelled text from NLM JATS files with the use of Smith-Watermann sequence alignment algorithm [63]. By selecting the annotated text fragment the most similar to the zone’s text we were able to assign labels to the zones in the structure.

4. Files with a lot of zones labelled as ”unknown”, that is zones, for which the labelling process was unable to find a label, were filtered out.

5. A small random sample of the remaining files was inspected manually. This resulted in identifying a number of repeated problems and errors in the dataset.

| Number of | GROTOAP | GROTOAP2 |
|-----------|---------|----------|
| publishers| 12      | 208      |
| journals  | 113     | 1,170    |
| documents | 113     | 13,210   |
| pages     | 1,031   | 119,334  |
| zones     | 20,121  | 1,640,973|
| zone labels| 20     | 22       |

Table 4.2: The comparison of the parameters of GROTOAP and GROTOAP2 datasets.
Figure 4.1: Semi-automatic method of creating GROTOAP2 dataset. First, automatic tools extracted the hierarchical geometric structure and the reading order of a document. Next, we automatically assigned labels to zones by matching their text to labelled fragments from NLM JATS files. Finally, additional rules were developed manually and applied to the dataset in order to increase the labelling accuracy.

6. Based on the results of the analysis, we developed a set of heuristic-based rules and applied them to the entire dataset in order to increase the labelling accuracy.

In the first phase of ground truth generation process we used our automatic algorithms. First, the characters were extracted from PDF files. Then, the characters were grouped into words, words into lines and finally lines into zones by the page segmenter. After that reading order analysis was performed resulting in elements at each hierarchy level being stored in the order reflecting how people read manuscripts.

In the second phase the text content of each zone extracted previously was matched against the labelled text fragments extracted from corresponding NLM JATS files. We used Smith-Watermann sequence alignment algorithm \[63\] to measure the similarity of two text strings. For every zone, a string with the highest similarity score above a certain threshold was chosen from all the strings extracted from the ground truth file. The label of the chosen string was then used to assign a functional label to the zone. If this approach failed, the process tried to use ”accumulated” distance, which makes it possible to assign a label to these zones that form together one ground truth entry, but in the geometric structure were segmented into several parts. If again none of the similarity scores exceeded the threshold value, the zone was labelled as unknown. After processing the entire page, an additional attempt to assign a label to every unknown zone based on the labels of its
neighbouring zones was made.

Data in NLM JATS files in PMC vary greatly in quality from perfectly labelled down to containing no valuable information. Poor quality NLMs result in sparsely labelled zones in generated TrueViz files, as the labelling process has no data to compare the zone text content to. Hence, it was necessary to filter documents whose zones are labelled in satisfying measure, that is the documents containing only a small number of zones labelled as *unknown*. Figure 4.2 shows the histogram of the label coverage among the processed documents defined as the percentage of zones labeled with a specific class other than *unknown*. There are many documents (43%) having more than 90% of zones labelled, and only those documents were selected for further processing steps.

![Figure 4.2: Histogram of documents in the dataset having given percentage of zones with an assigned specific (not unknown) class value.](image)

We also wanted to be sure that the layout distributions in the entire processed set and the filtered subset are similar. The layout distribution in a certain document set can be approximated by the publisher or journal distribution. If poor quality metadata was associated with particular publishers or journals, choosing only highly covered documents could result in eliminating particular layouts entirely, which was to be avoided. We calculated the similarity of publisher distributions of two sets using the following formula:

\[
\text{sim}(A, B) = \sum_{p \in P} \min(d_A(p), d_B(p))
\]
where $P$ is the set of all publishers in the dataset and $d_A(p)$ and $d_B(p)$ are the percentage share of a given publisher in sets $A$ and $B$, respectively. The formula yields 1.0 for identical distributions, and 0.0 in the case of two sets, which do not share any publishers. The same formula can be used to calculate the similarity with respect to journal distribution. In our case the similarity of publisher distributions of the originally processed set and the subset of documents with at least 90% labelled zones is 0.78, and the similarity of journal distributions 0.70, thus the distributions are indeed similar.

After filtering the files we randomly chose a sample of 50 documents, which were subjected to a manual inspection done by a human expert. The sample was big enough to show common problems occurring in the dataset, and small enough to be manually analyzed within a reasonable time. The inspection revealed a number of repeated errors made by the automatic annotation process. Based on the results we developed a few simple heuristic-based rules, which would reduce the error rate in the final dataset. Some examples of the rules are:

- In some cases the zone labelled as *title* contained not only the title as such, but also a list of document’s authors. We decided to introduce a new label *title_author* for such cases. We detect those zones based on the similarity measures and assign the new label to them.

- Pages numbers included in NLM files are usually page ranges from the entire journal volume or conference proceedings book. In PDF file, on the other hand, pages are sometimes simply numbered starting from 1. In such cases the zones containing page numbers could not be correctly labelled using text content matching. We detect those zones based on their text content and the distance to the top or bottom of the page and label them as *page_number*.

- Figures’ captions were often mislabelled as *body_content*, especially when the caption contains very similar text to one of the paragraphs. We used a regexp to detect such zones and label them as *figure*.

- Similarly, tables’ captions mislabelled as *body_content* are recognized by a regexp and labelled as *table*.

- A table placed in the document often contains many small zones, especially if every cell forms a separate zone. The text content of such a small zone can often be found in document’s paragraphs as well, therefore those zones are sometimes mislabelled as *body_content*. To correct this, we detect small zones lying in the close neighbourhood of table zones and label them as *table*.

- Due to the lack of data in NLM files, zones containing information related to document’s editors, copyright, acknowledgments or conflict statement are sometimes not labelled or mislabelled. Since those zones are relatively easy to detect based on section titles and characteristic terms, we use regexps to find them and label them correctly.
Zones that occur on every page or every odd/even page and are placed close to the top or bottom of the page were often not labelled, in such cases we assigned `bib_info` label to them.

The inspection also revealed segmentation problems in a small fraction of pages. The most common issue were incorrectly constructed zones, for example when the segmentation process put every line in a separate zone. Those errors were also corrected automatically by joining the zones that are close vertically and have the same label.

**GROTOAP and GROTOAP2 evaluation**

Every ground truth file in GROTOAP dataset was corrected by a human expert, and thus we can assume the quality of GROTOAP is close to perfect. The process of creating GROTOAP2, however, did not include manual inspection of every document by a human expert, which allowed us to create a large dataset, but also caused the following problems:

- segmentation errors resulting in incorrectly recognized zones and lines and their bounding boxes,
- labeling errors resulting in incorrect zone labels in the dataset.

We evaluated GROTOAP2 dataset in order to estimate how accurate the labelling in the ground truth files is. We did not perform the evaluation of the segmentation quality. Two kinds of evaluation were performed:

- direct evaluation involved the manual inspection of a small subset of ground truth files from GROTOAP2,
- indirect evaluation included comparing the performance of our metadata extraction algorithm trained on GROTOAP and GROTOAP2 datasets.

For the direct manual evaluation we chose a random sample of 50 documents (disjoint with the sample used before to construct the rules). We evaluated two document sets: files obtained before applying the rules and the same documents from the final dataset. The groups contain 6,228 and 5,813 zones in total, respectively (the difference is related to the zone merging step which reduces the overall number of zones). In both groups the errors were corrected by a human expert, and the original files were then compared to the corrected ones, which gave the precision and recall values of the annotation process for each zone label for two stages of the process. The overall accuracy of the annotation process increased from 0.78 to 0.93 after applying heuristic rules. More details about the results of the evaluation can be found in Table 4.3.

For the indirect evaluation we compared the overall performance of our metadata extraction algorithm trained on the entire GROTOAP dataset and randomly chosen 1000 documents from GROTOAP2 dataset in two versions: before applying correction rules and after. The evaluation was done with the use a PMC-based dataset (more details about the
Table 4.3: The results of manual evaluation of GROTOAP2. The table shows the precision, recall and F-score values for every zone label for the annotation process without and with heuristic-based rules. The correct labels for zones were provided by a human expert. No values appear for labels that were not present in the automatically annotated dataset.
### Table 4.4

|                | GROTOAP | GROTOAP2 |
|----------------|---------|----------|
| Precision      | 77.13%  | 81.88%   | 82.22%   |
| Recall         | 55.99%  | 70.94%   | 76.96%   |
| F-score        | 62.41%  | 75.38%   | 79.34%   |

Table 4.4: The comparison of the performance of the metadata extraction algorithm trained on GROTOAP, GROTOAP2 before applying improvement rules and final GROTOAP2. The table shows the mean precision, recall and F-score values calculated as an average of the values for individual metadata classes.

The table shows the mean precision, recall and F-score values calculated as an average of the values for individual metadata classes. The evaluation methodology can be found in Section 4.6. The system achieved the average F-score (calculated as an average over all metadata categories) 62.41% when trained on GROTOAP, 75.38% when trained on GROTOAP2 before applying rules and 79.34% when trained on the final version of GROTOAP2. The detailed results are shown in Table 4.4.

GROTOAP and GROTOAP2 datasets are similar in the structure, they both contain the documents in the form of hierarchical geometric model serialized using TrueViz format. However, due to the different nature of their creation procedures resulting in different characteristics, we use them for different purposes.

In GROTOAP every document was inspected and corrected by a human expert, and thus we can assume the structure and labelling in the dataset are close to 100% correct. GROTOAP was used to evaluate the performance of the page segmenter, but the dataset was too small and not diverse enough to be useful for the zone classifiers.

In GROTOAP2 we omit the manual correction of every file, which resulted in a large and diverse dataset, but with the zone labelling only 93% accurate. Since the page segmenter was directly used for creating of the dataset, GROTOAP2 could not be used for its evaluation. The zone classifiers, on the other hand, were not involved in the process of assigning labels, and thus GROTOAP2 could be used for the experiments with zone classification: feature selection and SVM parameters adjustment, final zone classifiers evaluation and training.

### 4.1.2 Metadata Sets

Metadata sets are used to assess the quality of the entire extraction algorithm in all its aspects: basic metadata extraction, bibliography extraction and structured content extraction. Metadata sets contain documents in the form of pairs: a source PDF document and the corresponding ground truth metadata in NLM JATS format. Metadata sets were built using the resources from PubMed Central Open Access Subset and Elsevier.

The main dataset we used to assess the performance of the extraction algorithm and to compare it with similar solutions is a subset of PMC containing 1,943 documents from...
1,943 different journals compiled by Alexandru Constantin\footnote{http://pdfx.cs.man.ac.uk/serve/PMC-sample_1943.zip}.

We also used Elsevier resources to compile an additional metadata set of 2,508 documents. The dataset was created by randomly selecting a group of articles and filtering those with a references section present in the metadata record. Elsevier dataset was not used to assess the performance of the section hierarchy extraction, since Elsevier’s ground truth metadata records we had access to lack this part.

The content classification models in our algorithm were trained on GROTOAP2, which was built from documents from PMC. Even though we made sure the training, validation and testing subsets were pairwise disjoint, our algorithm might have a slight advantage on the PMC dataset over other similar solutions, depending on what documents and layouts their default versions were trained.

### 4.1.3 Citation Set

Citation set \cite{64} contains parsed bibliographic references and is used to evaluate and train the reference parser. Citation set was built using the data from Cora-ref \cite{53} and PMC resources.

Cora-ref already contains parsed references. Unfortunately, due to some differences in the labels used, labels mapping had to be performed. Labels from original datasets were mapped in the following way: \textit{title} and \textit{year} remained the same; \textit{journal}, \textit{booktitle}, \textit{tech} and \textit{type} were mapped to \textit{source}; \textit{date} was mapped to \textit{year}. Labels \textit{author} and \textit{pages} were split respectively into \textit{givenname} and \textit{surname}, \textit{page\_first} and \textit{page\_last} using regular expressions. All remaining tokens were labelled as \textit{text}.

The ground truth files from PMC also contain parsed references. Unfortunately, in most cases they do not preserve the entire reference strings from the original PDF file, separators and punctuation are often omitted. For this reason the reference set was built using a similar technique as in the case of GROTOAP2. We extracted reference strings from PDF files using our extraction algorithm and labelled them using annotated reference data from NLM files. Only the references with high labelling coverage (the percentage of the tokens labelled with a specific label) were selected for the final set.

The final citation dataset contains parsed citation from both sources combined into a single dataset of 6,858 parsed citations in total.

### 4.1.4 Affiliation Set

Affiliation set \cite{68} contains parsed affiliations and was used to evaluate and train the affiliation parser. The dataset is based on PMC resources.

The ground truth files in PMC contain parsed affiliations, but the quality of the labelling varies a lot from file to file, and the entire raw affiliation strings from the original article are rarely preserved. To overcome these issues, once again we used a technique similar as in the case of GROTOAP2 and the citation dataset. We built the affiliation
dataset automatically by matching labelled metadata from the ground truth files against affiliation strings extracted from PDFs by the extraction algorithm. We also filtered out the affiliations poorly covered by specific labels, which was typically caused by poor quality ground truth labelling or extraction errors.

The final affiliation dataset used for parser evaluation contains 8,267 parsed affiliations.

4.2 Page Segmentation

Page segmentation was evaluated using the entire GROTOAP dataset containing 113 documents. During the evaluation the ground truth geometric hierarchical structure of the test document was compared to the corresponding structure built from scratch by the page segmenter.

The goal of the evaluation was to assess how well on average the algorithm reconstructs the words, lines and zones of a document. Let $D^G$ be the ground truth document from GROTOAP dataset and $D^T$ the corresponding document with words, lines and zones rebuilt from the characters by the segmentation algorithm. For every pair $(D^G, D^T)$ we calculated the following scores:

- the percentage of correctly constructed words:
  $$\text{score}_{D,W} = \frac{|CW_D|}{|W_{DG}|}$$
  where $CW_D$ is the set of words correctly built by the segmenter and $W_{DG}$ is the set of words in the ground truth document;

- the percentage of correctly constructed lines:
  $$\text{score}_{D,L} = \frac{|CL_D|}{|L_{DG}|}$$
  where $CL_D$ is the set of lines correctly built by the segmenter and $L_{DG}$ is the set of lines in the ground truth document;

- the percentage of correctly constructed zones:
  $$\text{score}_{D,Z} = \frac{|CZ_D|}{|Z_{DG}|}$$
  where $CZ_D$ is the set of zones correctly built by the segmenter and $Z_{DG}$ is the set of zones in the ground truth document.
A word is considered correctly constructed if the corresponding word in the ground truth document contains the same set of characters (the order of the elements is not taken into account):

\[ CW_D = W_{DT} \cap W_{DG} = \{ w_t \in W_{DT} \mid \exists w_g \in W_{DG} \ par^{-1}(w_t) = par^{-1}(w_g) \} \]

where \( par \) is a function mapping elements to their parents, in particular characters to their words.

Similarly, a line is considered correctly constructed if the corresponding line in the ground truth document contains the same set of characters (the inner division into words or the order of elements are not taken into account):

\[ CL_D = \{ l_t \in L_{DT} \mid \exists l_g \in L_{DG} \ anc^{-1}(l_t) = anc^{-1}(l_g) \} \]

where \( anc = par \circ par \) is a function mapping elements to the parents of their parents, in particular characters to their lines.

Finally, a zone is considered correctly constructed if the corresponding zone in the ground truth document contains the same set of characters (the inner division into words and lines or the order of elements are not taken into account):

\[ CZ_D = \{ z_t \in Z_{DT} \mid \exists z_g \in Z_{DG} \ anc^{-1}(z_t) = anc^{-1}(z_g) \} \]

where \( anc = par \circ par \circ par \) is a function mapping elements to the parents of the parents of their parents, in particular characters to their zones.

The overall scores for the entire test set were obtained by calculating the average values over all tested documents.

Using this methodology we performed the evaluation of two versions of the segmentation algorithm: the original Docstrum (only the scores for lines and zones were calculated, as the original algorithm does not determine words) and the algorithm enhanced with the modifications listed in Section 4.2. The results are shown in Figure 4.3. The modifications resulted in increased scores in case of both lines and zones.

There are two main document regions contributing to the low scores in the case of zones: metadata regions and table/figure regions. When metadata fragments play different roles in the document, but are displayed close to each other (for example title and authors, authors and affiliations), in GROTOAP they are split into separate zones with different labels. The page segmenter, on the other hand, analyses only the geometric traits and often will merge such fragments into one zone. What is more, as a result of an arbitrary decision in GROTOAP every table and figure is placed in one separate zone. From the segmentation point of view, however, such areas usually are sparse and contain more geometrically separated zones, which is usually the segmenter’s output. Since the typical document contains much more table/figure zones than metadata zones, they are the main cause of the errors.

To illustrate this, we recalculated the scores for the subsets of the documents with the tables and figures regions filtered out. The results are shown in Figure 4.4. Filtering out
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Figure 4.3: The results of page segmentation evaluation. The plot shows the accuracy of extracting zones, lines and words for the original Docstrum algorithm and Docstrum enhanced with our modifications. Since the original algorithm does not determine words, only the score for the enhanced version is given in this case.

The tables/figures regions resulted in all scores increase, the largest increase appears in the case of the zones.

4.3 Content Classification

The following experiments were performed in the context of content classification: selecting the best features for the classifiers (Section 4.3.1), finding the best classification parameters (Section 4.3.2) and the evaluation of the classifiers (Section 4.3.3). The experiments were performed for every SVM classifier used in the algorithm: category classifier (Section 3.3), metadata classifier (Section 3.4.1) and body classifier (Section 3.6.1).

4.3.1 Feature Selection

Feature selection was performed with the use of the validation set, which is a subset of GROTOAP2 containing 100 documents with 14,000 labelled zones in total. For each classifier a total of 103 features were analyzed.

In general feature selection is based on the analysis of the correlations between the features and between features and expected zone labels. For simplicity we treat all the features as numerical variables; the values of binary features are decoded as 0 or 1. The labels, on the other hand, are an unordered categorical variable.
Figure 4.4: The results of page segmentation evaluation. The plot shows the accuracy of extracting zones, lines and words for the original Docstrum algorithm and Docstrum enhanced with our modifications. The scores are calculated for the subset of the documents’ zones, with tables and figures regions filtered out. Since the original algorithm does not determine words, only the score for the enhanced version is given in this case.
Let \( L \) be a set of zone labels of a given classifier, \( n \) the number of the observations (zones) in the validation dataset and \( k = 103 \) the initial number of analysed features. For \( i \)th feature, where \( 0 \leq i < k \), we can define \( f_i \in R^n \), a vector of the values of the \( i \)th feature for subsequent observations. Let also \( l \in L^n \) be the corresponding vector of zone labels.

In the first step we removed redundant features, highly correlated with other features. For each pair of feature vectors we calculated the Pearson correlation score and identified all the pairs \( f_i, f_j \in R^n \), such that

\[
|\text{cor}(f_i, f_j)| > 0.9
\]

Next, for every feature from highly correlated pairs we calculated the mean absolute correlation:

\[
\text{cor}_m(f_i) = \frac{1}{k(k-1)} \sum_{j=0}^{k-1} \text{cor}(f_i, f_j)
\]

and from each highly correlated pair the feature with higher \( \text{cor}_m \) was eliminated. Let’s denote the number of remaining features as \( k' \).

After eliminating features using correlations between them, we analysed the features using their associations with the expected zone labels vector \( l \). To calculate the correlation between a single feature vector \( f_i \) (numeric) and label vector \( l \) (unordered categorical) we employed Goodman and Kruskal’s \( \tau \) (tau) measure [24].

In order to calculate \( \tau \) measure, we treat both feature vector \( f_i \) and label vector \( l \) as random variables. Let’s denote as \( \{\pi_{st}\} \) the joint distribution of \( f_i \) and \( l \); \( \pi_{st} \) is the probability that an observation has a label \( t \) and the value of its \( i \)th feature is \( s \). Let’s also denote as \( \{\pi_t\} \) the marginal distribution of labels, and \( \{\pi_s\} \) the marginal distribution of all observed values of the feature \( f_i \). Goodman and Kruskal’s \( \tau \) measure is calculated as

\[
\tau(f_i, l) = \frac{V(l) - E(V(l|f_i))}{V(l)}
\]

where

- \( V(l) \) is a measure of variation for the marginal distribution \( \{\pi_t\} \) calculated as

\[
V(l) = 1 - \sum \pi_t^2
\]

- \( V(l|f_i) \) is a measure of variation for the distribution of labels for a fixed value of \( i \)th feature calculated in the same way

- \( E(V(l|f_i)) \) is the expected value of the conditional variation \( V(l|f_i) \) calculated as

\[
E(V(l|f_i)) = \sum s \pi_s V(l|s)
\]
Let \( f_0, f_1, \ldots, f_{k'} - 1 \) be the sequence of the feature vectors ordered by non-decreasing \( \tau \) measure, that is

\[
\tau(f_0, l) \leq \tau(f_1, l) \leq \ldots \leq \tau(f_{k' - 1}, l)
\]

The features were then added to the classifier one by one, starting from the best one (the mostly correlated with the labels vector, \( f_{k' - 1} \)), and at the end the classifier contained the entire feature set. At each step we performed a 5-fold cross-validation on the validation dataset and calculated the overall F-score as an average over the scores of individual labels. We used feature scaling and classes weights based on the number of their training samples to set larger penalty for less represented classes. SVM classifier was trained using RBF kernel.

For \( i, j \in L \) let’s denote as \( C(i, j) \) the number of observations with true label \( i \) classified as \( j \) by the classifier. We calculate the overall F-score as

\[
F = \frac{1}{|L|} \sum_{i \in L} 2(P(i)^{-1} + R(i)^{-1})^{-1}
\]

where

- \( P(i) \) is the precision for a specific label \( i \) calculated as

\[
P(i) = \frac{C(i, i)}{\sum_{j \in L} C(j, i)}
\]

- \( R(i) \) is the recall for a specific label \( i \) calculated as

\[
R(i) = \frac{C(i, i)}{\sum_{j \in L} C(i, j)}
\]

For completeness, we also repeated the same procedure with reversed order of the features, starting with less useful features.

Using the results, we eliminated a number of the least useful features \( f_0, f_1, \ldots, f_t \), such that the performance of the classifier with the remaining features was similar to the performance of the classifier using the entire feature set.

For the category classifier the entire zone set from the validation set was used, and the specific labels were mapped to their general categories: metadata, body, references and other. The set contains 14,000 zones represented by features and zone labels. 20 features were removed based on between-feature correlation analysis. The remaining 83 features were analyzed using the \( \tau \) measure. The results are shown in Figure 4.5. The final feature set for this classifier contains 54 features with the best \( \tau \) measure.

For analyzing the metadata classifier we used only the zones of the category metadata, which left us with 2,743 zones represented by features and zone labels. At the beginning 4 features were eliminated because there was no variation in their values in the metadata.
Figure 4.5: Average F-score for category classifier for 5-fold cross-validation for various numbers of features. Darker line shows the change in F-score, while adding features from the most to the least useful one, and the lighter line shows the increase with the reversed order. The vertical line marks the feature set chosen for the final classifier.

zone subset. 22 features were removed based on between-feature correlation analysis. The remaining 77 features were analyzed using the \( \tau \) measure. The results are shown in Figure 4.6. The final feature set for the metadata classifier contains 53 features with the best \( \tau \) measure.

Similarly, for analyzing the body classifier we used only the zones of the category body, which left us with 9,394 zones represented by features and zone labels. At the beginning 3 features were eliminated because there was no variation in their values in the zone subset. 21 features were removed based on between-feature correlation analysis. The remaining 79 features were analyzed using the \( \tau \) measure. The results are shown in Figure 4.7. The final feature set for the body classifier contains 63 features with the best \( \tau \) measure.

34 features are common for all classifiers, although they often differ a lot in their \( \tau \) correlation measure. The features present in the case of metadata classifier and missing in other classifiers are mostly related to the presence of the keywords characteristic for zones like affiliation, keywords, addresses, license, etc. The features present in the case of category classifier and missing in others are related to the page numbers, references regions and the last pages of the document in general. The features present in the case of body classifier and missing in others are related to the keywords and characters characteristic for zones like figure or table captions or equations.
Figure 4.6: Average F-score for metadata classifier for 5-fold cross-validation for various numbers of features. Darker line shows the change in F-score, while adding features from the most to the least useful one, and the lighter line shows the increase with the reversed order. The vertical line marks the feature set chosen for the final classifier.

Figure 4.7: Average F-score for body classifier for 5-fold cross-validation for various numbers of features. Darker line shows the change in F-score, while adding features from the most to the least useful one, and the lighter line shows the increase with the reversed order. The vertical line marks the feature set chosen for the final classifier.
4.3.2 Parameters Adjustment

The best SVM parameters were also found using the same validation dataset containing 14,000 zones in the case of category classifier, 2,743 zones in the case of metadata classifier and 9,394 zones in the case of body classifier. For performance reasons, the dataset used for category classifier was reduced to a smaller set of 10,478 zones randomly chosen from the original set. As a result of the feature selection procedure, each classifier used a different set of features. We performed a grid search over all combinations of the parameter values within some ranges and chose the parameters which resulted in the highest scores obtained during the cross-validation.

First, the feature vectors were scaled linearly to interval [0, 1] according to the bounds found in the learning samples. In order to find the best parameters for the classifiers we performed a grid-search over the parameter space for four different kernels (linear, polynomial, radial-basis and sigmoid). For every combination of the kernel and its parameters we performed a 5-fold cross-validation. We also used classes weights based on the number of their training samples to set larger penalty for less represented classes. Finally, we chose those parameters, for which we obtained the highest mean F-score calculated as an average over the scores for individual classes (the same way as in the case of feature selection).

We test several ranges of the following parameters:

- \( C = \{2^i | i \in [-5, 15]\} \) — a set of possible values of the penalty parameter,
- \( D = \{2, 3, 4\} \) — a set of degrees for polynomial kernels,
- \( \Gamma = \{2^i | i \in [-15, 3]\} \) — a set of possible values of the kernel coefficient \( \gamma \),
- \( R = \{-100, -10, -1, 0, 1, 10, 100\} \) — a set of possible values of the kernel coefficient \( r \),

The following parameter spaces were used:

- linear kernel: 1-dimensional space \(< C >\),
- polynomial kernel: 4-dimensional space \(< D, \Gamma, R, C >\),
- RBF kernel: 2-dimensional space \(< \Gamma, C >\),
- sigmoid kernel: 3-dimensional space \(< \Gamma, R, C >\).

Chosen parameters for all the classifiers are shown in Table 4.5. The detailed results, including the best mean F-score values for all classifiers and all kernel function types obtained during 5-fold cross-validation, as well as related values of the parameters, can be found in appendix A in Section A.1.
### 4.3.3 Zone Classification

The final versions of the zone classifiers (with selected features and the best SVM parameters found) were evaluated by a 5-fold cross-validation using zone test set, which is a subset of GROTOAP2 (disjoint with the zone validation set). Zone test set consists of 2,551 documents containing 355,779 zones in total, 68,557 of which are metadata zones and 235,126 of which are body zones.

During the cross-validation each zone from the test set was classified and tested once. Based on these pairs (ground truth label, classifier’s label) we constructed the confusion matrix for the classification and calculated the precision, recall and F-score measures for individual zone labels.

The confusion matrix is indexed by the set of labels of a given classifier. The value in the row \( i \) and column \( j \) is equal to the total number of zones with true label \( i \) labelled as \( j \) by the classifier during the cross-validation. The values on the matrix diagonal represent the number of correctly classified zones of respective types and the sum of all cells equals to the size of the zone test set. The precision, recall and F-score values for individual labels are calculated in the same way as before.

The exact confusion matrices for all the zone classifiers can be found in appendix A in Section A.1. In this chapter we present the visualizations of the matrices, generated in the following way: the values in the original matrix were scaled relatively to the sum of the rows (the number of zones of respective classes in the ground truth test set) and logarithmic function was applied to the resulting fractions. As a result, the value in the cell in row \( i \) and column \( j \) corresponds to the fraction of the zones with true label \( i \) that were classified by the classifier as \( j \).

Table 4.5 shows the precision, recall and F-score values for individual classes for category classification. Figure 4.8 presents the visualization of the confusion matrix for this classifier.

The results of the category classifier are very good. The lowest scores were achieved in the case of the label *other*, which is a special label for all the zones that do not fit into the three main categories, and thus is the least consistent in the feature values.

Table 4.6 shows the precision, recall and F-score values for individual classes for metadata classification. Figure 4.9 presents the visualization of the confusion matrix for this classifier.

The results of the metadata classifier are also good. *bib_info* zones seem to be often confused with other zones, but the precision and recall for this class is one of the highest. This is caused by the fact that there are a few times more *bib_info* zones in the test set.
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|                | precision (%) | recall (%) | F-score (%) |
|----------------|---------------|------------|-------------|
| metadata       | 97.03         | 96.88      | 96.96       |
| body           | 98.12         | 98.98      | 98.55       |
| references     | 98.15         | 95.63      | 96.88       |
| other          | 96.26         | 91.96      | 94.06       |
| average        | 97.39         | 95.86      | 96.61       |

Table 4.6: Precision, recall and F-score values for individual classes for category classification.

Figure 4.8: The visualization of the confusion matrix of the category classification. The value in the cell in row $i$ and column $j$ corresponds to the fraction of the zones with true label $i$ that were classified by the classifier as $j$. The lighter the cell color, the higher the fraction and the more confusion between the two classes.
Figure 4.9: The visualization of the confusion matrix of metadata classification. The value in the cell in row $i$ and column $j$ corresponds to the fraction of the zones with true label $i$ that were classified by the classifier as $j$. The lighter the cell color, the higher the fraction and the more confusion between the two classes.
Table 4.7: Precision, recall and F-score values for individual classes for metadata classification.

| Class       | Precision (%) | Recall (%) | F-score (%) |
|-------------|---------------|------------|-------------|
| abstract    | 97.19         | 98.00      | 97.59       |
| affiliation | 94.40         | 94.38      | 94.39       |
| author      | 96.13         | 96.41      | 96.27       |
| bib_info    | 98.11         | 98.68      | 98.40       |
| corresp.    | 91.38         | 88.32      | 89.82       |
| dates       | 94.75         | 93.20      | 93.97       |
| editor      | 95.67         | 97.48      | 96.57       |
| keywords    | 92.39         | 79.12      | 85.24       |
| title       | 98.51         | 98.14      | 98.33       |
| type        | 89.42         | 87.14      | 88.27       |
| copyright   | 95.41         | 95.15      | 95.28       |
| average     | 94.85         | 93.27      | 94.01       |

Table 4.8: Precision, recall and F-score values for individual classes for body classification.

| Class         | Precision (%) | Recall (%) | F-score (%) |
|---------------|---------------|------------|-------------|
| body_content  | 96.84         | 96.47      | 96.65       |
| body_other    | 96.55         | 97.91      | 96.73       |
| average       | 96.70         | 96.69      | 96.69       |

than any other zone class. The classes pairs often confused with each other are: affiliation and correspondence, which is related to the fact that affiliation strings sometimes contain postal or email addresses, and abstract and keywords, which is a results of the fact that these regions are often placed close to each other, sometimes even in the same geometric zone, and are often printed using the same font and formatting style.

Table 4.8 shows the precision, recall and F-score values for individual classes for body classification. Figure 4.10 shows the visualization of the confusion matrix for this classifier.

4.4 Affiliation Parsing

Affiliation parser was evaluated by a 5-fold cross-validation with the use of the entire set of 8,267 parsed affiliations from the affiliation dataset.

The affiliation set was randomly divided into 5 disjoint subsets and each subset was
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Figure 4.10: The visualization of the confusion matrix of body classification. The value in the cell in row \( i \) and column \( j \) corresponds to the fraction of the zones with true label \( i \) that were classified by the classifier as \( j \). The lighter the cell color, the higher the fraction and the more confusion between the two classes.

processed by the affiliation parser trained on the labelled tokens from the remaining 4/5 of the affiliations. The parsing results in each fold were then compared to the gold standard.

First, we compared the token labelling obtained from the parser to the labelling in the test set. The confusion matrix for token classification was constructed in the same way as confusion matrices for zone classifiers. The exact values can be found in appendix A in Section A.1. The precision and recall values for the individual labels were also calculated the same way and are presented in Table 4.9. Figure 4.11 shows the visualization of the confusion matrix for this classifier, generated the same way as before.

In addition to evaluating individual token classification, we also checked for how many affiliations the entire fragments (institution, address or country) were labelled correctly.

|        | precision (%) | recall (%) | F-score (%) |
|--------|---------------|------------|-------------|
| address| 96.74         | 97.25      | 97.00       |
| country| 99.63         | 99.22      | 99.42       |
| institution | 98.66      | 98.45      | 98.55       |
| average | 98.34         | 98.31      | 98.32       |

Table 4.9: Precision, recall and F-score values for individual classes for affiliation token classification.
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Figure 4.11: The visualization of the confusion matrix of affiliation token classification. The value in the cell in row $i$ and column $j$ corresponds to the fraction of the tokens with true label $i$ that were classified by the parser as $j$. The lighter the cell color, the higher the fraction and the more confusion between the two classes.

We considered a fragment labelled correctly if it was equal to the gold standard data. The following results were obtained:

- institution was correctly recognized in 92.39% of affiliations,
- address was correctly recognized in 92.12% of affiliations,
- country was correctly recognized in 99.44% of affiliations,
- 92.05% of affiliations were entirely correctly parsed.

As can be clearly seen from the results, the country is relatively easy to locate in the affiliation string, as it usually uses a very limited number of words from an easy to compile dictionary. The institution and address are more difficult and more often confused with each other.

4.5 Reference Parsing

Bibliographic reference parser was evaluated with the use of a 5-fold cross-validation on the subset of the citation test set containing 2,000 parsed citations.

The test set was randomly divided into 5 disjoint subsets and each subset was processed by the parser trained on the labelled tokens from the remaining 4/5 of the test set. After
Table 4.10: Precision, recall and F-score values for individual classes for citation token classification.

|                | precision (%) | recall (%) | F-score (%) |
|----------------|---------------|------------|-------------|
| given_name     | 94.66         | 96.12      | 95.38       |
| surname        | 94.05         | 95.49      | 94.76       |
| title          | 97.93         | 97.76      | 97.85       |
| source         | 93.41         | 93.93      | 93.67       |
| volume         | 96.53         | 95.73      | 96.13       |
| issue          | 78.62         | 86.81      | 82.51       |
| year           | 98.53         | 97.64      | 98.08       |
| page_first     | 98.02         | 97.58      | 97.80       |
| page_last      | 98.16         | 99.38      | 98.77       |
| text           | 96.75         | 95.77      | 96.26       |
| average        | 94.66         | 95.62      | 95.12       |

parsing the citation strings we compared the token labelling to the gold standard labelling from the dataset.

The confusion matrix for token classification was constructed in the same way as confusion matrices for zone classification and can be found in appendix A in Section A.1. The precision and recall values for the individual labels were also calculated the same way and are presented in Table 4.10. Figure 4.12 shows the visualization of the confusion matrix for this classifier.

The worst precision and recall were achieved in the case of the label issue, which is the least common label in the test set. The label text seems to be the most confused with the other labels, which is caused by the fact that it is the most common label, and also some regions in the automatically constructed test set might be mislabelled as text. The mostly confused label pairs are: givenname and surname (these tokens are almost always close to each other) and title and source (which are also close to each other, and sometimes it is not a trivial task to find the border between the two).

We also evaluated the precision and recall of entire task of extracting metadata from citation strings. A citation consists of a raw string and a set of substrings labelled with metadata classes. Let \( R^G \) be a parsed citation from the test set and \( R^T \) — the corresponding citation processed by the parser during the evaluation. Let also \( C_{R^G} \) be the set of substrings of the class \( C \) in the citation \( R^G \), and similarly \( C_{R^T} \) — the set of substrings of the class \( C \) in the citation \( R^T \).

We calculate the precision, recall and F-score for citation \( R \) and class \( C \) as:
Figure 4.12: The visualization of the confusion matrix of citation token classification. The value in the cell in row $i$ and column $j$ corresponds to the fraction of the tokens with true label $i$ that were classified by the classifier as $j$. The lighter the cell color, the higher the fraction and the more confusion between the two classes.
Figure 4.13: Bibliographic reference parser evaluation. The figure shows the average precision and recall values for extracting reference fragments belonging to individual metadata classes. A given fragment is considered correctly extracted, if it is identical to the ground truth data.

\[
P(R, C) = \frac{|C_{RG} \cap C_{RT}|}{|C_{RT}|}
\]

\[
R(R, C) = \frac{|C_{RG} \cap C_{RT}|}{|C_{RG}|}
\]

\[
F(R, C) = 2 \cdot (P(R, C)^{-1} + R(R, C)^{-1})^{-1}
\]

The average precision, recall and F-score are calculated as mean values over all citations in the dataset. Figure 4.13 shows the average precision and recall values for individual metadata classes.

The highest scores were obtained in the case of the labels \textit{volume}, \textit{year} and \textit{pages}. This is related to the fact, that these fragments are comparatively easy to locate, because they are numerical and usually formatted in the same way. The lowest scores were achieved in the case of \textit{issue}, which is most likely caused by the fact that the test set contains only few cases of citations with the issue tagged, as this information is often missing in the reference string.

4.6 Extraction Evaluation

This sections reports the methodology and results of the evaluation of the entire extraction process in all its aspects: metadata extraction, bibliography extraction and structured body
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extraction. The results are also compared with the results achieved by similar tools on the same datasets.

Two datasets are used for these experiments: a subset of PMC containing 1,943 documents and a subset of Elsevier dataset with 2,508 documents in total. The PMC dataset is disjoint with both the validation and training sets used before.

We used the test sets to assess the quality of our algorithm and to compare it to other, similar systems. The following systems were evaluated: GROBID\(^6\) PDFX\(^7\) ParsCit\(^8\) and pdf-extract\(^9\). Each system extracts a slightly different range of metadata information. Table 4.11 summarizes the scope of the information extracted by various metadata extraction approaches.

4.6.1 Evaluation Methodology

The PDF files from each test set were processed by each system, including our algorithm. The extraction results were then compared to the gold standard XML data from the test sets, resulting in the scores for each metadata category. The only exception was ParsCit, which is not able to directly process PDF files. In this case we generated text versions of the input files using pdftotext tool, which were then used as the input for ParsCit.

None of the systems processed successfully all the test files. The analysis resulted in an error in some cases. We also set up a timeout of 20 minutes for processing one files, which was exceeded in a number of cases. Table 4.12 shows the number and percentage of successfully processed files for each system.

We evaluated how well the systems extract the following metadata categories:

- title (a single string),
- authors (a list of authors’ full names),
- affiliations (understood as raw strings, the affiliations’ metadata was not evaluated in these experiments),
- relations author–affiliation (a list of pairs author full name – affiliation raw string),
- email addresses (a list of strings),
- relations author–email (a list of pairs author full name – email string),
- abstract (a single string),
- keywords (a list of strings),
- journal (a single string),

\(^6\)https://github.com/kermitt2/grobid
\(^7\)http://pdfx.cs.man.ac.uk/
\(^8\)http://aye.comp.nus.edu.sg/parsCit/
\(^9\)https://github.com/CrossRef/pdfextract
Table 4.11: The comparison of the scope of the information extracted by various metadata extraction systems. The table shows simple metadata types (eg. title, author, abstract or bibliographic references), relations between them (author — affiliation, author — email address), and also metadata in the structured form (references and affiliations along with their metadata).
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| system      | PMC           | Elsevier      |
|-------------|---------------|---------------|
| our algorithm | 1940 (99.8%)  | 2508 (100%)   |
| GROBID      | 1941 (99.9%)  | 2506 (99.9%)  |
| PDFX        | 1907 (98.1%)  | 2439 (97.2%)  |
| ParsCit     | 1924 (99.0%)  | 2505 (99.9%)  |
| pdf-extract | 1912 (98.4%)  | 2352 (93.8%)  |

Table 4.12: The number and percentage of successfully processed files from each dataset for each system.

- volume (a single string),
- issue (a single string),
- pages range (a single relation first page – last page),
- year (a single string),
- DOI identifier (a single string),
- bibliographic references (understood as raw strings, the references’ metadata was not evaluated in these experiments),
- section headers (a list of strings),
- section headers hierarchy (a list of pairs section level – section header).

Each metadata category was evaluated separately. For each category we report the overall performance scores (precision, recall and F-score) on each dataset for each system that is able to extract the given category. We also performed statistical analysis to find out which differences in performance are statistically significant.

In general we deal with two types of metadata categories: those that appear at most once per document (”single” types: title, abstract, journal, volume, issue, pages range, year and DOI) and those present as lists (”list” types: authors, affiliations, email addresses, all relations, keywords, bibliographic references and section headers). Once again ParsCit is an exception to this rule. Since the system returns labelled document text instead of outputting the extraction results in the form of a structured metadata record, all metadata categories may appear more than once per document, along with the confidence scores. In the case of single metadata types we decided to choose for testing the information with the highest confidence returned by ParsCit.
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Performance Scores

We calculated the overall performance scores (precision, recall and F-score) for each combination of extraction system, dataset and metadata category, provided that a given system is able to extract the information of a given category.

The overall performance scores are calculated based on the scores for the individual files. Let \(D^G\) be the ground truth document from the test set and \(D^T\) — the corresponding metadata document created by the evaluated system. For a metadata class \(C\) we denote as \(C_{DG}\) the list of metadata instances of class \(C\) associated with the document \(D^G\), and similarly, \(C_{DT}\) is the list of metadata instances of class \(C\) associated with the document \(D^T\). Both lists can be empty, if a certain metadata category is missing in the record. In the case of ”single" metadata types the lists contain at most one element.

Precision, recall and F-score for a document \(D\) and metadata category \(C\) are then calculated in the following way:

\[
P(D, C) = \begin{cases} \text{null} & \text{if } C_{DT} = \emptyset \\ \frac{|C_{DG} \cap C_{DT}|}{|C_{DT}|} & \text{otherwise} \end{cases}
\]

\[
R(D, C) = \begin{cases} \text{null} & \text{if } C_{DG} = \emptyset \\ \frac{|C_{DG} \cap C_{DT}|}{|C_{DG}|} & \text{otherwise} \end{cases}
\]

\[
F(D, C) = \begin{cases} \text{null} & \text{if } P(D, C) = \text{null} \text{ and } R(D, C) = \text{null} \\ 0 & \text{if } P(D, C) = \text{null} \text{ or } R(D, C) = \text{null} \\ 0 & \text{if } P(D, C) \cdot R(D, C) = 0 \\ 2(P(C)^{-1} + R(C)^{-1})^{-1} & \text{otherwise} \end{cases}
\]

The intersection \(C_{DG} \cap C_{DT}\) is a set of elements present in both lists, with respect to the comparison method, which differs between metadata categories.

The overall precision, recall and F-score for the entire test set are computed as averages over all non-null values. As a result, in general the overall F-score is not equal to the harmonic mean of the overall precision and recall scores.

Statistical Analysis

For each metadata category and each dataset we compared the performances of every pair of relevant systems in order to test the following null hypothesis: the performances of the two systems are on average the same. In all tests we compare two lists of F-scores obtained for individual documents, with all records containing null values removed prior to the test. The lists contained only the results for the documents successfully processed by the two systems of interest.
In the case of single metadata categories, the F-score for a given document is always equal to 1 (the metadata information was extracted correctly) or 0 (the metadata information was extracted incorrectly). Since we were interested in a difference between two paired proportions, we used McNemar’s test \[55\].

In the case of list metadata categories, we were interested in analysing paired differences between F-scores for individual documents and we used Wilcoxon signed-rank test \[78\], a paired difference test in which we do not have to assume normal distribution in the population, in contrast to more popular paired Student’s t-test.

To make sure we do not obtain significant results simply by chance, as a result of performing many statistical tests, we used the Bonferroni correction \[19\] and compared the p-values to the significance level of 5% divided by the number of tests performed within each category.

In every test we compute the p-value and compare it to the significance level adjusted accordingly to the number of executed tests. Based on this we decide whether we accept the null hypothesis or not, and thus whether the difference in performance between the two tested approaches is statistically significant.

### Comparison Details

The metadata information extracted from the documents are compared in various manners, depending on the metadata category.

The titles and abstracts are compared in a way that takes into account some minor differences related to encoding, character case, the presence of spaces, the representation of accents, etc. The strings are considered equal if at least one of the following two conditions is met: if normalized strings (with all non-alphanumerical characters removed) are identical, or if the similarity calculated using the Smith-Watermann sequence alignment algorithm exceeds a predefined threshold. To calculate the Smith-Watermann similarity we use the following formula:

$$
\text{sim}(s_1, s_2) = \frac{2 \cdot \text{sw}(s_1, s_2)}{l(s_1) + l(s_2)}
$$

where \(s_1\) and \(s_2\) are the sequences of tokens of the compared strings, \(l(s)\) is the size of the sequence \(s\) and \(\text{sw}(s_1, s_2)\) is the Smith-Watermann distance of the two sequences \(s_1\) and \(s_2\).

Two keyword strings are considered equal if they are identical after a basic (default in all our experiments) normalization, which includes converting to lower case an trimming. Since ParsCit system only marks the entire keywords section, but does not extract the list of individual keywords, it was excluded from the keywords evaluation.

The author names are considered equal if their normalized forms (with all non-letters removed) are identical. This allows to take into account some minor differences like the presence or absence of spaces or dots following the initials. However, in case of the problems with the encoding or when one name is given in the full form and the other using initials, the names will not match.
The affiliations are tokenized and compared using cosine distance with a threshold. Cosine distance allows not to take into account the order of words, which helps in the case of systems which do not preserve the original affiliation string and the order of its tokens, but rather output only the structured affiliation metadata. In the case of extracting the affiliations only the raw affiliation strings are evaluated, the affiliation metadata is omitted.

Emails are compared after normalization, which includes removing all characters that are not alphanumerical or '@'. We also remove prefixes like "E-mail:" and similar from the email strings, as some systems, in particular GROBID and ParsCit, leave it in the output.

A relation (author-email or author-affiliation) is considered correct if both elements match their respective elements in compared pair. Individual elements are compared in the same way as described above.

As journal name is often abbreviated in the input PDF document and given in the full form in the ground truth metadata record, we consider it extracted correctly if its normalized version (with all non-letters removed) is a non-empty subsequence of the ground truth journal name.

The pages range is correct if both first and the last page number is identical to the ground truth data. Similarly, the volume, issue, year and DOI are correct only if identical to the ground truth data.

The references are compared similarly as affiliations: using a cosine distance with a threshold. As a result we do not take into account the order of the tokens, and we can reliably evaluate the systems which return the references in a highly structured form without preserving the original references strings.

The section headers are compared similarly as the title and abstract: with a use of Smith-Watermann similarity with a threshold. In addition to comparing the lists of section headers, we also assess the performance of extracting the section hierarchy by comparing the relations of the form section level – section title. The levels are equal only if identical, and section titles are compared as before.

4.6.2 Evaluation Results

This section contains the summary of the results of the evaluation described above. The detailed precision, recall and F-score values, as well as the p-values obtained in all statistical tests can be found in the appendix A.

Document Metadata

In this section we report the evaluation results related to the document metadata. We divided the metadata categories into three groups: basic document metadata (the title, abstract and keywords), authorship metadata (author names, affiliations, relations author–affiliation, email addresses, relations author–email) and bibliographic metadata (journal name, volume, issue, pages range, year of publication and DOI identifier).

Figure 4.14 shows the average F-score for the basic metadata categories for all tested systems on the PMC test set. In this set our algorithm achieved the best scores in all
Figure 4.14: The results of the evaluation of five different extraction systems with respect to the basic document metadata. The figure shows the average F-score over all documents from PMC test set.

categories.

Figure 4.15 shows the average F-score for the basic metadata categories for all tested systems on the Elsevier test set. In this set every category has a different winner, and there are small differences between our algorithm, GROBID and PDFX in the case of title, and between our algorithm and GROBID in the case of keywords.

Figure 4.16 shows the average F-score for the authorship metadata categories for all tested systems in the PMC test set. Our algorithm achieved the best scores in all categories except for the email address, where it was outperformed by PDFX. In the case of authors there is only a small difference between our solution and GROBID.

Figure 4.17 shows the average F-score for the authorship metadata categories for all tested systems for the Elsevier-based test set. Once again PDFX proved to be the best in extracting email addresses. In the first three categories GROBID achieved the best results and our algorithm was the second best, with small differences between the two approaches. Our algorithm performed the best in extracting author-email relations.

Figure 4.18 shows the average F-score for the bibliographic metadata categories for all tested systems for the PMC-based test set. Our algorithm achieved the best scores in all categories except for DOI, where the differences in F-score for the three systems are relatively small.

Figure 4.19 shows the average F-score for the bibliographic metadata categories for all tested systems for the Elsevier-based test set. Similarly as before, our algorithm achieved
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Figure 4.15: The results of the evaluation of five different extraction systems with respect to the basic document metadata. The figure shows the average F-score over all documents from Elsevier test set.

Figure 4.16: The results of the evaluation of four different extraction systems with respect to the authorship-related metadata. The figure shows the average F-score over all documents in PMC test set.
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Figure 4.17: The results of the evaluation of four different extraction systems with respect to the authorship-related metadata. The figure shows the average F-score over all documents from Elsevier test set.

Figure 4.18: The results of the evaluation of three different extraction systems with respect to the bibliographic metadata. The figure shows the average F-score over all documents from PMC test set.
Figure 4.19: The results of the evaluation of three different extraction systems with respect to the bibliographic metadata. The figure shows the average F-score over all document from Elsevier test set.

the best results in all categories except for DOI. In the case of DOI our algorithm performed the worst, and the differences between the scores achieved by PDFX and GROBID are relatively small.

Bibliographic References

In this section we report the evaluation results with respect to extracting references from the bibliography section.

The results are shown in Figure 4.20. In both datasets our algorithm performed the best, although the differences between the algorithms are not large.

Section Hierarchy

This section contains the results of the evaluation of extracting the hierarchy of section headers.

The results are shown in Figure 4.21. We only used PMC test set for this experiment, as Elsevier data does not contain any information related to the section hierarchy. In both tasks (extracting the section headers and extracting their hierarchy) our algorithm performed the best, although the differences between algorithms are not large.
Figure 4.20: The results of the evaluation of various extraction systems with respect to bibliographic references extraction. The figure shows the average F-score over all documents from both PMC and Elsevier test sets.

Figure 4.21: The results of the evaluation of various extraction systems with respect to section headers extraction. The figure shows the average F-score over all documents from PMC test set for two tasks: extracting the header titles and extracting the header hierarchy.
Summary

We evaluated five different extraction systems (our algorithm, GROBID, PDFX, ParsCit and pdf-extract) on two test sets (PMC and Elsevier). The systems processed the input PDF files and the resulting metadata records were compared to the ground truth metadata records in order to assess how well various metadata categories are extracted. The evaluation comprised seventeen extraction tasks: extracting title of the document, abstract, keywords, authors' full names, authors' affiliation strings, relations author–affiliation, authors' email addresses, relations author–email, journal name, volume and issue numbers, pages range, year of publication, DOI identifier, reference strings placed in the document, the titles of the sections and relations section level–section title.

Table 4.13 presents the winner for each test set and each metadata category. In some cases the difference between the winner and other systems were small, but in almost all statistical tests we performed the differences between the winner and other systems proved to be statistically significant, the only exception being GROBID's win in extracting affiliations on Elsevier dataset. More detailed results related to the p-values obtained can be found in the appendix A.

In the case of PMC dataset our algorithm was the winner in all categories except for email addresses and DOI. In the case of Elsevier the results are worse, our algorithm was the winner in eight out of fifteen categories. PDFX achieved the best scores in the case of email addresses and DOI identifier in both test sets. GROBID performed the best in extracting abstract, authors and affiliations in Elsevier test set. ParsCit and pdf-extract systems did not win in any category. Table 4.14 shows for every system the number of categories the system was the best in, either in both datasets or one of them.

4.6.3 Error Analysis

The extraction errors made by our algorithm can be divided into two groups: metadata was not extracted or the extracted information is incorrect. The majority of errors happen in the following situations:

- When two (or more) zones with different roles in the document are placed close to each other, they are often merged together by the segmenter. In this case the classification is more difficult and by design only one label is assigned to such a hybrid zone. A potential solution would be to introduce additional labels for pairs of labels that often appear close to each other, for example title_author or author_affiliation, and split the content of such zones later in the workflow.

- The segmenter introduces other errors as well, such as incorrectly attaching an upper index to the line above the current line, or merging text written in two columns. These errors can be corrected by further improvement of the page segmenter.

- Zone classification errors are also responsible for a lot of extraction errors. These errors can be improved by adding training instances to the training set and improving the labelling accuracy in GROTOAP2.
Table 4.13: The winner of extracting each metadata category in each test sets. In almost every case the difference between the winner and other approaches was statistically significant. The only exception is extracting affiliations on Elsevier dataset won by GROBID (marked with a star), where the difference between GROBID and our algorithm was not statistically significant.
Table 4.14: The summary of the systems comparison. The table shows the number of categories won by every extraction system in (1) both test sets, and (2) one of the test sets. In 8 categories our algorithm was the best in both test sets, and in 7 categories — in one test set.

- Sometimes the metadata, usually keywords, volume, issue or pages, is not explicitly given in the input PDF file. Since our algorithm analyses the PDF file only, such information cannot be extracted. This is in fact not an extraction error. Unfortunately, since ground truth NLM data in PMC usually contains such information, whether it is written in the PDF or not, these situations also contribute to the overall error rates (equally for all evaluated systems).

The most common extraction errors include:

- Title merged with other parts of the document, when title zone is placed close to another region.

- Title not recognized, for example when it appears on the second page of the PDF file.

- Title zone split by the segmenter into a few zones, and only a subset of them is correctly classified.

- Authors zone not labelled, in that case the authors are missing.

- Authors zone merged with other fragments, such as affiliations or research group name, in such cases additional fragments appear in the authors list.

- Affiliation zone not properly recognized by the classifier, for example when it is not visually separated from other zones, or placed at the end of the document. Affiliations are missing in that case.

- The entire abstract or a part of it recognized as body by the classifier, as a result the abstract or a part of it is missing.
The first body paragraph recognized incorrectly as abstract, as a result the extracted abstract contains a fragment of the document’s proper text.

Bibliographic information missing from a PDF file or not recognized by the classifiers, as a result journal name, volume, issue and/or pages range are not extracted.

Keywords missing because the zone was not recognized or not included in the PDF file.

A few of the references zones classified as body, in such cases some or all of the references are missing.

When header titles are too similar to paragraph lines, the algorithm might not recognize them properly, and as a result they will be missing in the section hierarchy.

If some parts of the document’s body, such as table/figure fragments, are not filtered out during the text content filtering, they are sometimes treated incorrectly as header lines.

### 4.7 Time Performance

In addition to evaluating the performance of the algorithm, we also measured the time required to process a scientific article. For these experiments we used a sample of 200 articles from PMC, selected randomly from the subset successfully process by all the tested algorithms.

Figure 4.22 shows the histogram of our algorithm’s processing time for this subset. The mean processing time was 16.74 seconds.

In our algorithm the processing time of a document depends linearly on its number of pages. The Pearson correlation between these variables on the tested subset was 0.70. Figure 4.23 shows the processing time as a function of the number of the document’s pages.

The most time-consuming phases of the algorithm are: structure extraction (which inspects the entire input document analyzing the individual characters and their mutual positions), body extraction (which processes a large, middle region of the publication) and category classification (which processes all the zones in the document sequentially). Figure 4.24 shows the boxplots of the percentage of time spent on each phase.

The most time consuming steps of the algorithm are the following: category classification (which processes all the zones in the document sequentially), page segmentation (which processes all the pages and depends quadratically on the number of the characters on the page), header extraction (which iterates over all lines of the text of the document) and content filtering (which classifies all the zones of the text of the document). Figure 4.25 shows the percentage of time spent on each algorithm step.

There are also large differences in processing time between all five tested tools. Figure 4.26 compares the average processing time of all tested algorithms. GROBID and
Figure 4.22: The histogram of our algorithm’s processing time for a random subset of 200 documents from PMC.

Figure 4.23: The processing time as a function of the number of pages of a document.
Figure 4.24: The boxplots of the percentage of time spent on each phase. Character extraction, category classification and body extraction are the most time-consuming phases of the algorithm.
Figure 4.25: The percentage of time spent on each algorithm step (the cleaning steps are omitted).
Figure 4.26: The comparison of the average processing time of all tested extraction algorithms on a random subset of 200 documents from PMC.

ParsCit proved to be the fastest. The slowest is PDFX, which is a result of the system being available only as a web service and thus suffering from network transmission overhead.
Chapter 5

Summary and Future Work

In this chapter we conclude the thesis by summarizing the research, listing the most important achievements of our work and discussing the potential improvements and extensions for the future.

5.1 Summary

The background of the research described in the thesis is closely related to the problems of scholarly communication in the digital era. With huge and still growing volume of scientific literature, keeping track with the latest scientific achievements becomes a major challenge for the researchers. Scientific information overload problem contributes to slowing down the scholarly communication and knowledge propagation across the academia.

The main objective of our work was to tackle the problem of scientific information overload. This goal is accomplished by equipping digital libraries and research infrastructures with means allowing them to support the process of consuming the growing volume of scientific literature by interested readers. This in turn will boost the communication among the scientists and facilitate the knowledge propagation in the scientific world.

We proposed an automatic, novel method for extracting machine-readable, structured metadata from unstructured scientific publications in born-digital PDF format. Our approach can be used within a digital library whenever it has to deal with resources with missing, erroneous or fragmentary document metadata. The algorithm can be used both for assisting the users in the process of providing the rich metadata for the documents they submit and also automatically processing large volumes of already existing resources.

Based on the metadata extraction results, a digital library can provide reliable services such as intelligent search tools, proposing similar and related documents, building and visualizing interactive citation and author networks, providing various citations-based statistics, and so on. This in turn enables the users to effectively explore the map of science, quickly get familiar with the current state of the art of a given problem and reduce the volume of articles to read by retrieving only the most relevant and interesting positions.
5.2 Conclusions

We designed and implemented an accurate automatic algorithm for extracting rich metadata directly from a scientific publication in PDF format. Proposed algorithm takes a single publication on the input, performs a thorough analysis of the document and outputs a structured machine-readable metadata record containing:

- a rich set of document’s metadata, such as title, abstract, keywords, authors’ full names, their affiliations and email addresses, journal name, volume, issue, pages range, year of publication, etc.,
- a list of references to other documents given in the article in a structured form along with their metadata,
- structured full text with sections and subsections hierarchy.

Designed as a universal solution, the algorithm is able to handle a vast variety of scientific publications reasonably well, instead of being perfect in processing a limited number of document layouts only. We achieved this by employing supervised and unsupervised machine-learning algorithms trained on large diverse datasets, which also resulted in increased maintainability of the system, as well as its ability to adapt to new, previously unseen document layouts.

Since our main objective was to provide a useful, accurate solution to a practical problem, machine learning-based solutions are accompanied with a number of heuristics. This approach proved to achieve good results in practice, although perhaps lacks the simplicity and elegance of algorithms based purely on machine learning.

The evaluation we conducted showed good performance of the proposed metadata extraction algorithm. The comparison to other similar systems also proved our algorithm performs better than competition for most metadata types, winning 23 out of 32 evaluation tasks.

The proposed extraction algorithm is based to a great extent on a well-known supervised and unsupervised machine-learning techniques accompanied with heuristics. Nevertheless, the research contains a number of innovatory ideas and extensions:

1. One of the key contributions is the architecture of the extraction workflow and the decomposition of the entire extraction problem into smaller tasks.
2. We enhanced the Docstrum-based implementation of page segmentation with a few modifications listed in Section 4.2, resulting in increased algorithm accuracy.
3. We developed a large set of 103 zone features capturing all aspects of the zone content and appearance, which allows to classify zones with high accuracy (Sections 3.3, 3.4.1 and 3.6.1).
4. We developed a set of features for affiliation tokens allowing to parse affiliations with high accuracy (Section 4.4).
5. We proposed a clustering-based algorithm for extracting reference strings (Section 3.5.1).

6. We developed a set of features for reference tokens allowing to parse references with high accuracy (Section 3.5.2).

7. We proposed an algorithm based on normal scores for selecting section header lines from the text content of the document (Section 3.6.2).

8. We proposed a simple clustering approach for building the section hierarchy (Section 3.6.3).

9. We proposed a scalable, efficient method for constructing gold standard publication datasets (Section 4.1.1).

5.3 Outlook

There are several areas where the extraction algorithm can still be improved to extract higher quality metadata or extended to capture more information hidden in unstructured documents.

The algorithm currently processes only born-digital document, in which the text is present as PDF stream rather than the images of scanned pages. The documents containing scanned pages are not properly processed, which concerns older resources in particular. We plan to improve this by extending the workflow and adding an optical character recognition step to the algorithm.

Some algorithm steps, such as parsing authors’ zones, associating authors with affiliations, detecting header titles, are currently performed using heuristics. In the future we plan to experiment with machine learning-based approaches as well, which might make the algorithm generalize better and increase its flexibility.

We would also like to experiment with an unsupervised approach to assist the citation parsing. This would be based on an observation that the citations usually share the same format within a document, which could provide useful information in the cases of citations more problematic to parse the default way.

Currently the algorithm ignores certain document’s regions, in particular tables, which contain useful information present in the documents in an unstructured form. In the future we plan to extend the workflow so that it is able to extract tables from the documents and present their content in a machine-readable, structured form.

Apart from the tables, the algorithm currently ignores other useful information that might be present in the analyzed document, such as document’s categories listed in the first page, the funding information or the roles of the authors described in a separate section. In the future we plan to successfully extend the range of information the algorithm is able to extract.

Last but not least, in documents of various domains there are a lot of useful and important information present in the text of the document, but not expressed directly,
such as the reasons the document cites other documents, the methods used in the paper, the problem the paper addresses, or the experiment results. In the future we would like to experiment with machine learning and natural language processing techniques in order to acquire a deeper understanding of the text of the input scientific publication.
Appendix A

Detailed Evaluation Results

The appendix contains detailed results of the performed experiments (the best SVM parameters and average F-scores for all kernels and all zone classifiers, the confusion matrices for the evaluation of all zone and token classifiers), the systems evaluation and comparison results (the precision, recall and F-scores for all tested systems, all test sets and all metadata categories, as well as the p-values for all statistical tests).

A.1 Content Classification Parameters

The best SVM parameters for the zone classifiers were chosen by a grid-search with the use of the zone validation dataset. For various SVM kernels and parameters combinations we performed a 5-fold cross-validation on the validation dataset and calculated the overall F-score as an average over F-scores for individual class labels. For the final classifiers the kernel and parameters that gave the best score were chosen.

Tables A.1-A.3 present the best SVM parameters for all the SVM kernels for all zone classifiers (category, metadata and body classifier) as well as the F-scores obtained during the parameter searching.

A.2 Content Classification Evaluation

All the classifiers used in the extraction algorithm were evaluated by a 5-fold cross-validation on a respective test set. In every case we generated a confusion matrix and calculated the precision, recall and F-score for individual class labels.

The confusion matrix $CM$ for a given classifier is indexed by the set of the classifier’s labels $L$. The value $CM(i, j)$, where $i, j \in L$ is equal to the total number of instances with true label $i$ labelled as $j$ by the classifier during the validation. The values on the matrix diagonal represent the number of correctly classified instances of respective types and the sum of all cells equals to the size of the test set.

The precision for a given class label $l \in L$ is calculated as the fraction of the number of instances labelled as $l$ by the classifier that were correctly labelled. Similarly, the recall
## APPENDIX A. DETAILED EVALUATION RESULTS

### Category classification

| kernel   | linear | polynomial | RBF | sigmoid |
|----------|--------|------------|-----|---------|
| $log_2(c)$ | 10     | -2         | 5   | 10      |
| $d$       | -      | 3          | -   | -       |
| $log_2(\gamma)$ | -     | 0          | -2  | -4      |
| $r$       | -      | 1          | -   | -1      |
| mean F-score (%) | 91.55 | 94.90      | **94.99** | 94.50 |

Table A.1: The results of SVM parameters searching for category classification. The table shows the best mean F-score values for all kernel function types obtained during 5-fold cross-validation, as well as related values of the parameters. The best parameters are bolded.

### Metadata classification

| kernel   | linear | polynomial | RBF | sigmoid |
|----------|--------|------------|-----|---------|
| $log_2(c)$ | 5      | -4         | 5   | 8       |
| $d$       | -      | 3          | -   | -       |
| $log_2(\gamma)$ | -     | 0          | -3  | -4      |
| $r$       | -      | 0          | -   | -1      |
| mean F-score (%) | 86.02 | **88.61** | 88.01 | 87.80 |

Table A.2: The results of SVM parameters searching for metadata classification. The table shows the best mean F-score values for all kernel function types obtained during 5-fold cross-validation, as well as related values of the parameters. The best parameters are bolded.

### Body classification

| kernel   | linear | polynomial | RBF | sigmoid |
|----------|--------|------------|-----|---------|
| $log_2(c)$ | 7      | 3          | 4   | 14      |
| $d$       | -      | 4          | -   | -       |
| $log_2(\gamma)$ | -     | -3         | -2  | -7      |
| $r$       | -      | 1          | -   | -1      |
| mean F-score (%) | 94.49 | **96.03** | 95.98 | 95.74 |

Table A.3: The results of SVM parameters searching for body classification. The table shows the mean F-score values for all kernel function types obtained during 5-fold cross-validation, as well as related values of the parameters. The best parameters are bolded.
APPENDIX A. DETAILED EVALUATION RESULTS

| Category classification          | metadata | body    | references | other | precision (%) | recall (%) |
|---------------------------------|----------|---------|------------|-------|---------------|------------|
| metadata                        | 66,421   | 1,819   | 76         | 241   | 97.03         | 96.88      |
| body                            | 1,324    | 232,739 | 173        | 890   | 98.12         | 98.98      |
| references                      | 39       | 692     | 17,605     | 73    | 98.15         | 95.63      |
| other                           | 668      | 1,960   | 82         | 30,977| 96.26         | 91.96      |

Table A.4: Confusion matrix for category classification for 5-fold cross-validation. Rows and columns represent the desired and obtained classification result, respectively. Bold values on the main matrix diagonal represent correctly classified zones of respective classes.

for the label \( l \) is calculated as the fraction of the number of instances with true label \( l \) that were correctly labelled.

Tables A.4 - A.6 present the confusion matrices, as well as precision, recall and F-score values for individual class labels obtained from the evaluation of the zone classifiers (category, metadata and body classifier).

Tables A.7 - A.8 presents the confusion matrices, as well as the precision, recall and F-score values for individual class labels for affiliation and citation token classification, respectively.

A.3 Performance Scores

We performed the evaluation of five different extraction systems (our algorithm, GROBID, PDFX, ParsCit and Pdf-extract) with respect to extracting various metadata types on two different test sets (PMC and Elsevier).

Tables A.9 - A.13 show the precision, recall and F-scores for all metadata categories for the tested systems.

A.4 Statistical Analysis

We performed statistical tests for both test sets, for every metadata category and every pair of systems that are able to extract the category. The aim of a single test is to establish whether the difference in the systems’ performance is statistically significant. This is done by comparing the obtained p-value to the significance level adjusted using the Bonferroni correction.

Tables A.14 - A.30 show the p-values for all performed statistical tests.
## APPENDIX A. DETAILED EVALUATION RESULTS

### Metadata classification

|                | abstract | affiliation | author | bib_info | correspondence | dates | editor | keywords | title | type | copyright | precision (%) | recall (%) |
|----------------|----------|-------------|--------|----------|---------------|-------|--------|----------|-------|------|-----------|----------------|------------|
| abstract       | 6,858    | 8           | 6      | 68       | 10            | 3     | 2      | 21       | 5     | 11   | 6         | 97.19          | 98.00      |
| affiliation    | 21       | 3,474       | 24     | 45       | 88            | 6     | 10     | 4        | 0     | 3    | 6         | 94.40          | 94.38      |
| author         | 8        | 16          | 2,682  | 40       | 17            | 0     | 3      | 0        | 5     | 10   | 1         | 96.13          | 96.41      |
| bib_info       | 83       | 24          | 30     | 40,964   | 23            | 110   | 1      | 27       | 16    | 127  | 105       | 98.11          | 98.68      |
| correspond.    | 5        | 135         | 16     | 45       | 1,580         | 2     | 1      | 1        | 0     | 1    | 3         | 91.38          | 88.32      |
| dates          | 3        | 0           | 2      | 183      | 2,796         | 0     | 0      | 1        | 0     | 13   | 13        | 94.75          | 93.20      |
| editor         | 0        | 7           | 5      | 0        | 0              | 0     | 0      | 0        | 0     | 0    | 0         | 95.67          | 97.48      |
| keywords       | 38       | 10          | 4      | 154      | 0              | 1     | 2      | 826      | 4     | 3    | 2         | 92.39          | 79.12      |
| title          | 10       | 1           | 10     | 20       | 0              | 1     | 0      | 2        | 5     | 0    | 5         | 98.51          | 98.14      |
| type           | 13       | 0           | 4      | 169      | 0              | 1     | 1      | 11       | 5     | 4    | 3         | 89.42          | 87.14      |
| copyright      | 17       | 5           | 7      | 66       | 9              | 31    | 1      | 2        | 3     | 6    | 3         | 95.41          | 95.15      |

Table A.5: Confusion matrix for metadata classification for 5-fold cross-validation. Rows and columns represent the desired and obtained classification result, respectively. Bold values on the main matrix diagonal represent correctly classified zones of respective classes.

### Body classification

|                | body_content | body_other | precision (%) | recall (%) |
|----------------|--------------|------------|---------------|------------|
| body_content   | 112,315      | 4,112      | 96.84         | 96.47      |
| body_other     | 3,662        | 115,037    | 96.55         | 97.91      |

Table A.6: Confusion matrix for body content classification for 5-fold cross-validation. Rows and columns represent the desired and obtained classification result, respectively. Bold values on the main matrix diagonal represent correctly classified zones of respective classes.
## APPENDIX A. DETAILED EVALUATION RESULTS

### Affiliation token classification

|          | address | country | institution | precision (%) | recall (%) |
|----------|---------|---------|-------------|---------------|------------|
| address  | 44,463  | 12      | 1243        | 96.74         | 97.25      |
| country  | 55      | 8,102   | 9           | 99.63         | 99.22      |
| institution | 1442    | 18      | 92,449      | 98.66         | 98.45      |

Table A.7: Confusion matrix for affiliation token classification for 5-fold cross-validation. Rows and columns represent the desired and obtained classification result, respectively. Bold values on the main matrix diagonal represent correctly classified tokens of respective classes.

### Citation token classification

|          | given_name | surname | title | source | volume | issue | year | page_first | page_last | text | precision (%) | recall (%) |
|----------|------------|---------|-------|--------|--------|-------|------|------------|-----------|------|---------------|------------|
| given_name | 9,529      | 172     | 20    | 3      | 0      | 0     | 2    | 0          | 0         | 188  | 94.66         | 96.12      |
| surname   | 163        | 6,858   | 30    | 6      | 0      | 0     | 0    | 0          | 0         | 125  | 94.05         | 95.49      |
| title     | 23         | 55      | 20,761| 168    | 1      | 1     | 5    | 0          | 0         | 222  | 97.93         | 97.76      |
| source    | 21         | 30      | 165   | 8,544  | 12     | 2     | 4    | 6          | 1         | 311  | 93.41         | 93.93      |
| volume    | 1          | 1       | 2     | 21     | 1,279  | 3     | 1    | 7          | 1         | 20   | 96.53         | 95.73      |
| issue     | 1          | 0       | 2     | 7      | 1      | 250   | 1    | 4          | 5         | 17   | 78.62         | 86.81      |
| year      | 0          | 1       | 8     | 7      | 0      | 3     | 1,945| 1          | 0         | 27   | 98.53         | 97.64      |
| page_first| 0          | 0       | 0     | 3      | 14     | 2     | 4    | 1,533      | 2         | 13   | 98.02         | 97.58      |
| page_last | 0          | 0       | 0     | 1      | 1      | 1     | 1    | 2          | 1,440     | 3    | 98.16         | 99.38      |
| text      | 329        | 175     | 212   | 387    | 17     | 56    | 17   | 11         | 11        | 18   | 27,547        | 96.75      |

Table A.8: Confusion matrix for citation token classification for 5-fold cross-validation. Rows and columns represent the desired and obtained classification result, respectively. Bold values on the main matrix diagonal represent correctly classified tokens of respective classes.
# APPENDIX A. DETAILED EVALUATION RESULTS

|                  | our algorithm | PDFX  | GROBID | ParsCit | Pdf-extract |
|------------------|---------------|-------|--------|---------|-------------|
| **PMC**          |               |       |        |         |             |
| title            | 95.84         | 86.25 | 89.88  | 38.31   | 49.48       |
|                  | 93.87         | 86.16 | 85.11  | 33.89   | 49.48       |
|                  | 93.87         | 86.16 | 85.11  | 33.89   | 49.48       |
| abstract         | 83.19         | 67.63 | 77.61  | 56.42   | —           |
|                  | 80.40         | 60.85 | 70.82  | 56.18   | —           |
|                  | 79.61         | 60.53 | 70.53  | 55.45   | —           |
| keywords         | 91.61         | —     | 87.34  | —       | —           |
|                  | 60.42         | —     | 54.79  | —       | —           |
|                  | 60.80         | —     | 54.80  | —       | —           |
| **Elsevier**     |               |       |        |         |             |
| title            | 92.04         | 93.68 | 88.36  | 31.32   | 39.75       |
|                  | 86.42         | 91.91 | 81.93  | 24.12   | 39.82       |
|                  | 86.35         | 91.76 | 81.86  | 24.08   | 39.75       |
| abstract         | 64.40         | 66.68 | 84.35  | 50.39   | —           |
|                  | 64.98         | 62.83 | 75.94  | 55.72   | —           |
|                  | 59.46         | 60.70 | 73.98  | 49.92   | —           |
| keywords         | 89.58         | —     | 91.53  | —       | —           |
|                  | 78.58         | —     | 74.75  | —       | —           |
|                  | 77.44         | —     | 74.09  | —       | —           |

Table A.9: The results of the evaluation of five different extraction systems with respect to the basic document metadata. Each cell shows the average precision, recall and F-score. In every category the best score is bolded.
### APPENDIX A. DETAILED EVALUATION RESULTS

#### Authorship Metadata

|                      | our algorithm | PDFX | GROBID | ParsCit |
|----------------------|---------------|------|--------|---------|
| **PMC**              |               |      |        |         |
| authors              | **89.98**     | 86.45| **87.75**| 52.31   |
|                      | 88.09         | —    | **84.04**| 72.34   |
| affiliations         | 83.97         | 84.41| 80.84  |         |
|                      | **84.41**     | 61.50| 44.44  |         |
| author-affiliation   | 55.86         | 54.23|        |         |
|                      | **71.71**     | 45.70|        |         |
|                      | **54.23**     | 38.28|        |         |
| emails               | 52.11         | 54.55| 82.22  | 46.73   |
|                      | 43.58         | **41.48**| 5.61  | 34.42   |
|                      | 30.35         | **41.48**| 5.44  |         |
| author-email         | **50.63**     | 46.63|        |         |
|                      | 42.12         | 5.48 |        |         |
|                      | **29.36**     | 5.32 |        |         |
| **Elsevier**         |               |      |        |         |
| authors              | **85.27**     | 88.63| 84.66  | 41.62   |
|                      | 81.43         | —    | **82.24**| 32.17   |
| affiliations         | 81.67         | **85.58**| 66.21|         |
|                      | 80.36         | **81.83**| 30.82|         |
|                      | 76.05         | **77.25**| 32.17|         |
| author-affiliation   | 46.71         | 50.39|        |         |
|                      | 70.34         | **72.99**|       |         |
|                      | 43.51         | **46.38**|       |         |
| emails               | **84.66**     | 79.79| 80.43  | 65.81   |
|                      | 61.26         | **97.41**| 3.74  | 48.53   |
|                      | 55.85         | **78.92**| 3.79  | 37.76   |
| author-email         | **78.52**     | 76.09|        |         |
|                      | **56.74**     | 3.55 |        |         |
|                      | **51.76**     | 3.59 |        |         |

Table A.10: The results of comparing the performance of various metadata extraction systems with respect to the authorship-related metadata. In every cell the precision, recall and F-score values are shown. The best results in every category are bolded.
### APPENDIX A. DETAILED EVALUATION RESULTS

#### Bibliographic Metadata

|   | our algorithm | PDFX  | GROBID |
|---|--------------|-------|--------|
|   |              | 79.80 | 74.09  |
| journal | 73.51 | 73.51 | 20.92  |
| volume | 93.13 | 83.14 | 32.07  |
| issue | 52.65 | 28.02 | 21.17  |
| pages | 87.10 | 80.46 | 25.67  |
| year | 96.86 | 95.52 | 93.20  |
| DOI | 98.13 | 75.93 | 99.29  |

#### Elsevier

|   | our algorithm | PDFX  | GROBID |
|---|--------------|-------|--------|
|   | 81.63        | 84.41 |        |
| journal | 70.18 | 70.18 | 25.06  |
| volume | 87.53 | 79.54 | 31.46  |
| issue | 17.99 | 14.70 | 11.89  |
| pages | 93.18 | 86.64 | 27.94  |
| year | 67.64 | 65.83 | 82.87  |
| DOI | 96.21 | 84.75 | 97.52  |

Table A.11: The results of comparing the performance of various metadata extraction systems with respect to the bibliographic metadata. In every cell the precision, recall and F-score values are shown. The best results in every category are bolded.
### References

|                | our algorithm | PDFX | GROBID | ParsCit | Pdf-extract |
|----------------|---------------|------|--------|---------|-------------|
| **PMC**        |               |      |        |         |             |
| *references*   | **96.17**     | 89.68| 86.31  | 81.21   | 80.40       |
| **90.45**      | 84.78         | 87.81| 71.81  | 57.48   |
| **90.29**      | 84.93         | 86.11| 72.64  | 58.44   |
| **Elsevier**   |               |      |        |         |             |
| *references*   | **85.98**     | 81.91| 77.92  | 81.71   | 68.58       |
| **84.16**      | 72.55         | 78.35| 74.57  | 51.39   |
| **84.09**      | 72.99         | 76.39| 74.56  | 52.27   |

Table A.12: The results of comparing the performance of various metadata extraction systems with respect to the bibliographic references extraction. In every cell the precision, recall and F-score values are shown. The best results in every category are bolded.

### Section Hierarchy Metadata

|                | our algorithm | PDFX | GROBID | ParsCit |
|----------------|---------------|------|--------|---------|
| **PMC**        |               |      |        |         |
| *header titles*| **75.82**     | 71.34| 72.20  | 41.41   |
| **70.95**      | 61.29         | 67.28| 30.36  |
| **70.70**      | 62.34         | 67.28| 31.62  |
| *level-header title* | 66.56 | **68.96** | — | 24.28 |
| **61.72**      | 59.28         | —    | 18.11  |
| **61.93**      | 60.35         | —    | 19.32  |

Table A.13: The results of comparing the performance of various metadata extraction systems with respect to the section hierarchy-related metadata. In every cell the precision, recall and F-score values are shown. The best results in every category are bolded.
### APPENDIX A. DETAILED EVALUATION RESULTS

#### Table A.14: P-values obtained in pairwise statistical tests comparing the performance of extracting the title by various systems. Significance level for these tests was 0.0025. All the statistically significant results are bolded.

|          | our algorithm | GROBID   | PDFX    | ParsCit | Pdf-extract |
|----------|---------------|----------|---------|---------|-------------|
| **PMC**  |               |          |         |         |             |
| our algorithm | -            | 3.89e-22 | 9.43e-17| 1.12e-241| 9.21e-175  |
| GROBID    | 3.89e-22      | -        | 0.35    | 7.01e-194| 1.04e-118  |
| PDFX      | 9.43e-17      | 0.35     | -       | 9.32e-189| 4.65e-135  |
| ParsCit   | 1.12e-241     | 7.01e-194| 9.32e-189 | -     | 8.05e-28  |
| Pdf-extract | 9.21e-175   | 1.04e-118| 4.65e-135| 8.05e-28 | -          |

#### Table A.15: P-values obtained in pairwise statistical tests comparing the performance of extracting the abstract by various systems. Significance level for these tests were 0.0042. All the statistically significant results are bolded.

|          | our algorithm | GROBID   | PDFX    | ParsCit |
|----------|---------------|----------|---------|---------|
| **PMC**  |               |          |         |         |
| our algorithm | -            | 4.64e-14 | 3.13e-54| 5.04e-67|
| GROBID    | 4.64e-14      | -        | 8.48e-12| 5.26e-28|
| PDFX      | 3.13e-54      | 8.48e-12 | -       | 0.0028  |
| ParsCit   | 5.04e-67      | 5.26e-28 | 0.0028  | -       |

|          | our algorithm | GROBID   | PDFX    | ParsCit |
|----------|---------------|----------|---------|---------|
| **Elsevier** |              |          |         |         |
| our algorithm | -            | 8.95e-22 | 0.042   | 4.80e-14|
| GROBID    | 8.95e-22      | -        | 1.66e-27| 1.06e-60|
| PDFX      | 0.042         | 1.66e-27 | -       | 7.76e-09|
| ParsCit   | 4.80e-14      | 1.06e-60 | 7.76e-09 | -       |
### Keywords

|          | our algorithm | GROBID | PMC       |
|----------|---------------|--------|-----------|
| our algorithm | -             | 0.0031 |           |
| GROBID   | 0.0031        | -      |           |

### Elsevier

|          | our algorithm | GROBID | PMC       |
|----------|---------------|--------|-----------|
| our algorithm | -             | 4.61e-05 |           |
| GROBID   | 4.61e-05      | -      |           |

Table A.16: P-values obtained in pairwise statistical tests comparing the performance of extracting the keywords by various systems. Significance level for these tests were 0.025. All the statistically significant results are bolded.

### Authors

|          | our algorithm | GROBID | ParsCit |
|----------|---------------|--------|---------|
|          | GROBID        | ParsCit|         |
| PMC      |               |        |         |
| our algorithm | -             | 2.02e-06 | 3.05e-192 |
| GROBID   | 2.02e-06      | -      | 6.95e-191 |
| ParsCit  | 3.05e-192     | 6.95e-191 | -       |

### Elsevier

|          | our algorithm | GROBID | ParsCit |
|----------|---------------|--------|---------|
|          | GROBID        | ParsCit|         |
| our algorithm | -             | 1.61e-05 | 5.43e-244 |
| GROBID   | 1.61e-05      | -      | 1.20e-268 |
| ParsCit  | 5.43e-244     | 1.20e-268 | -       |

Table A.17: P-values obtained in pairwise statistical tests comparing the performance of extracting the authors by various systems. Significance level for these tests were 0.0083. All the statistically significant results are bolded.
### APPENDIX A. DETAILED EVALUATION RESULTS

#### Affiliations

|          | our algorithm | GROBID   | ParsCit  |
|----------|---------------|----------|----------|
| PMC      |               | 3.24e-76 | 5.57e-144|
| GROBID   | 3.24e-76      | -        | 1.34e-17 |
| ParsCit  | 5.57e-144     | 1.34e-17 | -        |

#### Elsevier

|          | our algorithm | GROBID   | ParsCit  |
|----------|---------------|----------|----------|
| our algorithm | -             | 0.030    | 5.41e-231|
| GROBID   | 0.030         | -        | 4.58e-227|
| ParsCit  | 5.41e-231     | 4.58e-227| -        |

Table A.18: P-values obtained in pairwise statistical tests comparing the performance of extracting the affiliations by various systems. Significance level for these tests were 0.0083. All the statistically significant results are bolded.

#### Author-affiliation

|          | our algorithm | GROBID |
|----------|---------------|--------|
| PMC      |               | 1.77e-49|
| GROBID   | 1.77e-49      | -      |

#### Elsevier

|          | our algorithm | GROBID |
|----------|---------------|--------|
| our algorithm | -             | 0.0042 |
| GROBID   | 0.0042        | -      |

Table A.19: P-values obtained in pairwise statistical tests comparing the performance of extracting the relations author-affiliation by various systems. Significance level for these tests were 0.025. All the statistically significant results are bolded.
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|       | Emails |       |       |       |
|-------|--------|-------|-------|-------|
|       | **our algorithm** | GROBID | PDFX | ParsCit |
| **PMC** |       |       |       |       |
| **our algorithm** | - | 1.15e-82 | 1.53e-88 | 0.011 |
| GROBID | 1.15e-82 | - | 2.80e-175 | 2.41e-90 |
| PDFX | 1.53e-88 | 2.80e-175 | - | 2.43e-90 |
| ParsCit | 0.011 | 2.41e-90 | 2.43e-90 | - |
| **Elsevier** |       |       |       |       |
| **our algorithm** | - | 5.71e-218 | 6.31e-128 | 8.30e-36 |
| GROBID | 5.71e-218 | - | 0 | 2.76e-142 |
| PDFX | 6.31e-128 | 0 | - | 1.87e-205 |
| ParsCit | 8.30e-36 | 2.76e-142 | 1.87e-205 | - |

Table A.20: P-values obtained in pairwise statistical tests comparing the performance of extracting the email addresses by various systems. Significance level for these tests were 0.0042. All the statistically significant results are bolded.

|       | Author-email |       |       |
|-------|--------------|-------|-------|
|       | **our algorithm** | GROBID |       |
| **PMC** |       |       |       |
| **our algorithm** | - | 6.13e-80 |       |
| GROBID | 6.13e-80 | - |       |
| **Elsevier** |       |       |       |
| **our algorithm** | - | 1.41e-201 |       |
| GROBID | 1.41e-201 | - |       |

Table A.21: P-values obtained in pairwise statistical tests comparing the performance of extracting the relations author-email by various systems. Significance level for these tests were 0.025. All the statistically significant results are bolded.
### Table A.22: P-values obtained in pairwise statistical tests comparing the performance of extracting the journal by various systems. Significance level for these tests were 0.025. All the statistically significant results are bolded.

|        | Our Algorithm | GROBID       |
|--------|---------------|--------------|
| PMC    |               | 4.32e-190    |
| Elsevier| 4.32e-190    | 3.81e-205    |

### Table A.23: P-values obtained in pairwise statistical tests comparing the performance of extracting the volume by various systems. Significance level for these tests were 0.025. All the statistically significant results are bolded.

|        | Our Algorithm | GROBID       |
|--------|---------------|--------------|
| PMC    |               | 4.45e-177    |
| Elsevier| 4.45e-177    | 2.73e-222    |
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| Issue | our algorithm | GROBID |
|-------|---------------|--------|
| PMC   |
| our algorithm | - | 8.01e-15 |
| GROBID   | 8.01e-15 | - |
| Elsevier |
| our algorithm | - | 2.57e-26 |
| GROBID   | 2.57e-26 | - |

Table A.24: P-values obtained in pairwise statistical tests comparing the performance of extracting the issue by various systems. Significance level for these tests were 0.025. All the statistically significant results are bolded.

| Pages | our algorithm | GROBID |
|-------|---------------|--------|
| PMC   |
| our algorithm | - | 5.52e-194 |
| GROBID   | 5.52e-194 | - |
| Elsevier |
| our algorithm | - | 2.47e-315 |
| GROBID   | 2.47e-315 | - |

Table A.25: P-values obtained in pairwise statistical tests comparing the performance of extracting the pages by various systems. Significance level for these tests were 0.025. All the statistically significant results are bolded.
### Table A.26: P-values obtained in pairwise statistical tests comparing the performance of extracting the year by various systems. Significance level for these tests were 0.025. All the statistically significant results are bolded.

| Year | our algorithm | GROBID |
|------|---------------|--------|
| PMC  |               |        |
| our algorithm |     | 2.44e-228 |
| GROBID | 2.44e-228 |    |

| Elsevier | our algorithm | GROBID |
|----------|---------------|--------|
| our algorithm |     | 2.13e-47 |
| GROBID | 2.13e-47 |    |

### Table A.27: P-values obtained in pairwise statistical tests comparing the performance of extracting the DOI identifier by various systems. Significance level for these tests were 0.0083. All the statistically significant results are bolded.

| DOI | our algorithm | GROBID | PDFX |
|-----|---------------|--------|------|
| PMC |               |        |      |
| our algorithm |     | 1.79e-18 | 3.40e-07 |
| GROBID | 1.79e-18 |    | 8.30e-36 |
| PDFX | 3.40e-07 | 8.30e-36 |    |

| Elsevier | our algorithm | GROBID | PDFX |
|----------|---------------|--------|------|
| our algorithm |     | 6.84e-52 | 3.61e-65 |
| GROBID | 6.84e-52 |    | 2.45e-13 |
| PDFX | 3.61e-65 | 2.45e-13 |    |
## APPENDIX A. DETAILED EVALUATION RESULTS

### Table A.28: P-values obtained in pairwise statistical tests comparing the performance of extracting the references by various systems. Significance level for these tests were 0.0025. All the statistically significant results are bolded.

|                | our algorithm | GROBID     | PDFX   | ParsCit | Pdf-extract |
|----------------|---------------|------------|--------|---------|-------------|
| our algorithm  | -             | 1.79e-118  | 1.06e-14 | 3.13e-160 | 1.60e-169   |
| GROBID         | 1.79e-118     | -          | 1.37e-44 | 3.15e-56 | 5.60e-73    |
| PDFX           | 1.06e-14      | 1.37e-44   | -       | 7.04e-78 | 4.04e-120   |
| ParsCit        | 3.13e-160     | 3.15e-56   | 7.04e-78 | -       | 5.07e-19    |
| Pdf-extract    | 1.60e-169     | 5.60e-73   | 4.04e-120 | 5.07e-19 | -          |

### Table A.29: P-values obtained in pairwise statistical tests comparing the performance of extracting the section titles by various systems. Significance level for these tests were 0.0042. All the statistically significant results are bolded.

|                | our algorithm | GROBID     | PDFX   | ParsCit |
|----------------|---------------|------------|--------|---------|
| our algorithm  | -             | 1.61e-138  | 1.52e-77 | 5.00e-78 |
| GROBID         | 1.61e-138     | -          | 0.0037 | 0.058   |
| PDFX           | 1.52e-77      | 0.0037     | -      | 0.18    |
| ParsCit        | 5.00e-78      | 0.058      | 0.18   | -       |
| Pdf-extract    | 2.33e-198     | 4.88e-95   | 5.01e-92 | 7.38e-92 |

Table A.28: P-values obtained in pairwise statistical tests comparing the performance of extracting the references by various systems. Significance level for these tests were 0.0025. All the statistically significant results are bolded.

Table A.29: P-values obtained in pairwise statistical tests comparing the performance of extracting the section titles by various systems. Significance level for these tests were 0.0042. All the statistically significant results are bolded.
|                  | our algorithm | PDFX   | ParsCit |
|------------------|---------------|--------|---------|
| **Level-header** |               |        |         |
| **PMC**          |               |        |         |
| our algorithm    | -             | 0.0030 | 3.00e-199 |
| PDFX             | 0.0030        | -      | 1.37e-255 |
| ParsCit          | 3.00e-199     | 1.37e-255 | -       |

Table A.30: P-values obtained in pairwise statistical tests comparing the performance of extracting the relations level-header by various systems. Significance level for these tests were 0.0083. All the statistically significant results are bolded.
Appendix B

System Architecture

This chapter provides all the details related to the implementation of the metadata extraction algorithm, which is available as an open-source CERMINE system (Content ExtRactor and MINEr).

CERMINE provides the entire functionality of the described extraction algorithm. The system is available as a web service$^1$ and open-source library written in Java$^2$. CERMINE is licensed under GNU Affero General Public License version 3.

B.1 System Usage

![CERMINE demonstrator service. It allows to extract metadata, structured full text and bibliography from a PDF document.](image)

The system allows the user to perform the following tasks:

- Extracting metadata, structured full text and bibliography from a PDF document. The output format is NLM JATS.

---

$^1$[http://cermine.ceon.pl](http://cermine.ceon.pl)

$^2$[https://github.com/CeON/CERMINE](https://github.com/CeON/CERMINE)
APPENDIX B. SYSTEM ARCHITECTURE

- Extracting metadata from a citation string. The output format is NLM JATS or BibTeX.

- Extracting metadata from an affiliation string. The output format in NLM JATS.

The demonstrator of the system is available at http://cermine.ceon.pl (Figure B.1). Currently it allows to perform only the first task.

There are three ways of using CERMINE system: RESTful services, Java API and executable JAR file.

CERMINE provides three RESTful services, which can be accessed for example using cURL tool. Listing B.1 shows how to access the services in order to process entire PDF file, parse a citation or parse an affiliation.

Listing B.1: The usage of CERMINE RESTful services.

```
$ curl -X POST --data-binary @article.pdf \
   --header "Content-Type: application/binary" \
   http://cermine.ceon.pl/extract.do

$ curl -X POST --data "reference=the text of the reference" \
   http://cermine.ceon.pl/parse.do

$ curl -X POST --data "affiliation=the text of the affiliation" \
   http://cermine.ceon.pl/parse.do
```

CERMINE can also be used directly in Java projects by adding a dependency and repository to the project’s pom.xml file. Listing B.2 shows the relevant fragment of the pom.xml file and listing B.3 shows example code snippets using CERMINE’s Java API.

Listing B.2: CERMINE’s dependency and repository

```
<dependency>
   <groupId>pl.edu.icm.cermine</groupId>
   <artifactId>cermine-impl</artifactId>
   <version>1.6</version>
</dependency>

<repository>
   <id>icm</id>
   <name>ICM repository</name>
   <url>http://maven.icm.edu.pl/artifactory/repo</url>
</repository>
```
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Listing B.3: Example code using CERMINE API.

```java
PdfNLMContentExtractor extractor = new PdfNLMContentExtractor();
InputStream inputStream = new FileInputStream("path/to/pdf/file");
Element result = extractor.extractContent(inputStream);

CRFBibReferenceParser parser = CRFBibReferenceParser.getInstance();
BibEntry reference = parser.parseBibReference(referenceText);

CRFAffiliationParser parser = new CRFAffiliationParser();
Element affiliation = parser.parse(affiliationText);
```

Lastly, CERMINE can be used as an executable JAR file that can be downloaded from the Maven repository. Listing B.4 shows example commands that can be used for processing a PDF file, parsing citations or affiliations.

Listing B.4: Example commands using executable JAR file

```bash
$ java -cp cermine-impl-1.7-SNAPSHOT-jar-with-dependencies.jar \
   pl.edu.icm.cermine.PdfNLMContentExtractor \
   -path path/to/directory/with/pdfs/or/a/single/pdf

$ java -cp cermine-impl-1.7-SNAPSHOT-jar-with-dependencies.jar \
   pl.edu.icm.cermine.bibref.CRFBibReferenceParser \
   -reference "the text of the reference"

$ java -cp cermine-impl-1.7-SNAPSHOT-jar-with-dependencies.jar \
   pl.edu.icm.cermine.metadata.affiliation.CRFAffiliationParser \
   -affiliation "the text of the affiliation"
```

B.2 System Components

The source code of the system and all the components is available on GitHub. The project contains the following subprojects:

- **cermine-impl** — the entire extraction workflow,
- **cermine-tools** — tools that are not part of the main workflow, for example SVM best parameters searching, models building, datasets creation,
- **cermine-web** — the demonstrator and RESTful services.

3http://maven.ceon.pl/artifactory/simple/kdd-shapshots/pl/edu/icm/cermine/cermine-impl/
4https://github.com/CeON/CERMINE
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The code structure reflects the decomposition of the workflow into paths and steps. The most important packages are:

- pl.edu.icm.cermine — main extraction classes,
- pl.edu.icm.cermine.structure — preprocessing, layout analysis and category classification,
- pl.edu.icm.cermine.metadata — basic metadata extraction,
- pl.edu.icm.cermine.content — structured full text extraction,
- pl.edu.icm.cermine.bibref — bibliography extraction,
- pl.edu.icm.cermine.tools — utility classes, related mainly to various machine learning algorithms used.

CERMINE uses the following external libraries: iText for parsing PDF stream\(^5\), LibSVM \(^1\) for Support Vector Machines classifiers and GRMM and MALLET \(^54\) for linear-chain Conditional Random Fields.

\(^5\)http://itextpdf.com/
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