pdfPapers: shell-script utilities for frequency-based multi-word phrase extraction from PDF documents

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Abstract: Biomedical research is intensive in processing information in the previously published papers. This motivated a lot of efforts to provide tools for text mining and information extraction from PDF documents over the past decade. The *nix (Unix/Linux) operating systems offer many tools for working with text files, however, very few such tools are available for processing the contents of PDF files. This paper reports our effort to develop shell script utilities for *nix systems with the core functionality focused on viewing and searching multiple PDF documents combining logical and regular expressions, and enabling more reliable text extraction from PDF documents with subsequent manipulation of the resulting blocks of text. Furthermore, a procedure for extracting the most frequently occurring multi-word phrases was devised and then demonstrated on several scientific papers in life sciences. Our experiments revealed that the procedure is surprisingly robust to deficiencies in text extraction and the actual scoring function used to rank the phrases in terms of their importance or relevance. The keyword relevance is strongly context dependent, the word stemming did not provide any recognizable advantage, and the stop-words should only be removed from the beginning and the end of phrases. In addition, the developed utilities were used to convert the list of acronyms and the index from a PDF e-book into a large list of biochemical terms which can be exploited in other text mining tasks. All shell scripts and data files are available in a public repository named pdfPapers on the Github. The key lesson learned in this work is that semi-automated methods combining the power of algorithms with the capabilities of research experience are the most promising for improving the research efficiency.

Keywords: Keyword extraction; portable document format; research automation; shell script; text mining

1. Introduction

There is a growing interest to automate the consumption of scientific knowledge to accelerate and automate research discoveries [1–3]. Semantic enrichment and effective representation models of research objects, their automated discovery and reuse can facilitate more effective collaboration between the humans and machines [4]. Scientific papers are used the primary means for storing and sharing the research findings and knowledge. The vast majority of scientific papers are available in portable document format (PDF). This format was developed in the early 90’s by Adobe to efficiently represent information contents on a page for the archival and presentation purposes. Unfortunately, the PDF does not support information extraction and subsequent information processing. For general scientific papers, the document elements of interest are metadata such as the paper title, authors and their affiliations, abstract, keywords, section titles and the corresponding full texts, figures, tables and their captions, and the list of references. For papers in chemistry, biology and medicine, the key elements also include names of chemical compounds, diseases, proteins, species, and genes. In engineering, mathematics and physics, mathematical expressions are often crucial for understanding the papers [5,6].
In this paper, we introduce several shell-script utilities newly developed for processing text contents of PDF documents. These utilities were bundled as pdfPapers in order to emphasize that they are aimed at processing the text contents in scientific papers. The shell scripts are commandline programs to be run in a terminal on a Unix or Linux operating system (OS). The implementation strategy was inspired by the popular pdfjam\(^1\) program which is a widely used shell script for manipulating pages of PDF files. The pdfjam provides a simplified interface to the \LaTeX\ package pdfpages\(^2\). More importantly, pdfjam has become available in the repositories of many common Linux distributions including Ubuntu, Debian, CentOS and Fedora.

The current development stage of pdfPapers did not reach the maturity required to be accepted by the Linux repositories. The initial source codes of pdfPapers was released on the Github\(^3\) under the GNU/GPL 2 license\(^4\) to support its future open source development. The main objective of pdfPapers utilities is to improve the processing workflow of information extraction from PDF files. The pdfPapers improves and adds new functionality to pdftotext which is likely the most reliable and the most commonly used tool for text extraction from PDF documents available on the Linux OS. The pdftotext program is distributed as one of the core utilities in the poppler\(^5\) library developed for PDF file conversion, manipulation and rendering. More specifically, the main functionality added to pdftotext by pdfPapers is handling special characters and non-typical encodings, joining words and sentences split across lines, columns, blocks and pages, searching the extracted text using case-insensitive regular expressions combined with logical operators, and generating the term-frequency (TF) statistics of multi-word phrases. The extracted text is partitioned into logical units referred to as blocks. The text blocks are defined by the internal structure of the PDF file, i.e., the blocks correspond to the layout of page elements defining the page content. The page layout is determined by the program which created the PDF file. For instance, a single paragraph of text may be spread over several blocks. The pdfPapers assigns each text block with a unique identifier, so the blocks can be copied, moved, deleted, concatenated, sorted, filtered, and eventually merged into a label-free text file as the input for subsequent text mining algorithms. For many PDF files, it is often the case that only a small number of blocks on every page is relevant while all other blocks can be discarded. The pdfPapers can visualize the block layout on every page to aid the decision which text blocks should be kept.

The text file produced by pdfPapers is more reliable for subsequent text mining than the raw text output produced by the standard pdftotext utility. The multi-word phrase identification problem assumed in this paper is one of many applications enabled by the reliable PDF to text conversion. Our experiments suggest that the TF analysis of key phrases is sufficient to provide good understanding of the contents and of the focus of the scientific paper even without considering a corpora of papers and with no regard to the prior domain knowledge represented as the controlled vocabulary, the list of domain terms or otherwise. This approach facilitates more efficient reading of scientific papers by individual researchers on their personal computers. Furthermore, our findings indicate that key phrases in scientific papers are context dependent, the stop-words should be removed after and not before the search for key phrases, and that the relevant multi-word phrases can be reliably detected by adding words to the previously found shorter phrases.

The rest of this paper is organized as follows. Section 2 surveys the existing text mining approaches and tools for keyword and knowledge extraction from biomedical papers. Section 3 outlines our

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1 https://github.com/rrthomas/pdfjam  
2 https://www.ctan.org/tex-archive/macros/latex/contrib/pdfpages  
3 https://github.com/ploskot/pdfPapers  
4 https://www.gnu.org/licenses/old-licenses/gpl-2.0.en.html  
5 https://pypi.org/project/poppler-utils
methodology for identifying important multi-word phrases in scientific papers. A necessary technical background to understand challenges of text extraction from PDF files is also given, and the pdfPapers utilities and their implementation are summarized. The results of identifying key phrases of up to 4 words in 5 selected biological papers, and an example of creating a list of biological terms from the e-book list of acronyms and the index are presented in Section 4. Our findings are discussed and evaluated in Section 5. The paper is concluded in Section 6.

2. Text Mining of Biomedical Documents

Keywords can direct researchers to important parts of the document. Keywords can be also utilized to produce document summary, perform topic classification, name entity recognition and other such tasks. The concept of keywords is intuitive, but it is difficult to define objectively [7]. The strategies how authors assign keywords to their papers is investigated in [8]. It has been found that the keywords selection is strongly biased by the authors’ background and expertise.

A recent very comprehensive survey of the keywords extraction methods and issues appeared in [9]. The survey attempts to define a ‘keyness’ of keyword, and how it can be related to different text features. The keywords or keyphrases are assumed to be lexical units which can best represent the document. The keyword selection can be made more objective by considering the exhaustivity, specificity, minimality, impartiality, representativity well-formedness, citationness, conformity, homogeneity and univocity of keywords.

It has been recognized early on that important keywords in scientific papers reflect their frequency of occurrence with respect to a domain-specific keyword distribution [10]. The domain distribution allows calculating the likelihood score for every word in the text. The fact that keywords are appearing statistically more often can overplay their differences rather than account for their lexical similarities and while neglecting their semantic differences [11]. In order to avoid over-interpretation or under-interpretation of keywords, it is recommended to study dispersion patterns, concordances and clusters of keywords, and to utilize annotated texts. The TF distribution across a corpus of documents for keywords identification is studied in [12]. Statistical approaches for keywords identification based on their frequency of occurrence are reviewed in [13].

The domain-independent scoring of words using so-called C/NC-values aims at enhancing the simple frequency of occurrence based identification [14]. The semantic similarity is combined with the word frequency in [15], and with a complete lexical database of English language in [16] to identify the document keywords. These approaches, however, require semantic labeling of words which significantly complicates the implementation.

The features which can be exploited for keyword extraction are enumerated in [17] including the frequency of occurrence, identification of nouns, the presence of upper-case letters, the use of specific font shapes and faces, the length of sentences they appear in, the presence of cue-words within the same sentence, a relative position of the keyword and its sentence within the paragraph, and the features based on conditional random-fields. The sets of predefined keywords can be used to calculate the importance weights of other words [18]. There have been also efforts to patent keyword extraction methods [19].

The multi-word phrases are distributed differently in different sections of scientific papers [20]. For instance, it was found that some key phrases may not be present in the abstract. Multi-word phrases within the text to extend the standard bag-of-words (BoW) approach are identified in [21] by generative probabilistic models. The multi-word phrases are then used to construct knowledge graphs representing the document. In [9], it is reported that single token keywords usually account for 17 – 20%, two-token keywords for 53 – 61% and three-token keywords for 21 – 18% of all keywords. However, other references report that the key phrases of more than 3 tokens can represent as many as 50%.
The emergence of open access publications has enabled more reliable keyword identification using full-text articles than assuming only the abstracts [22,23]. This has been confirmed by mining over 16 million full-text biomedical papers and automatically extracting protein-protein, disease-gene, and protein subcellular associations as the named entities in the papers [24]. Reference [25] suggests to identify useful terms by comparing the terms mentioned in abstract with their occurrences in the rest of the paper. Using the Medical Subject Headings\(^6\) (MeSH) thesaurus of biomedical terms and their frequency of occurrence, it was reported in [26] that the keyword density is the greatest in abstract followed by the results section whilst each section contains 30 – 40% of information unique to that section.

The automated extraction of topic keywords of biomedical documents and their classification according to MeSH is considered in [27]. The automated classification of research articles assuming their abstracts on PubMed\(^7\) is performed in [28]. The Jensen-Shannon divergence and cosine similarity are used to cluster keywords in [29]. Their performance is evaluated on categories of Wikipedia articles. The similarity of words can be also measured by the Jaccard coefficient as proposed in [30] to evaluate the document keywords against the index terms. It is shown in [31] that retrieval of relevant documents is improved by assigning MeSH terms also to the information queries. Different systems for automated assignment of MeSH terms to scientific texts were compared with the manual assignment in [31]. The keyword matching between the query and the documents has been described in [32] to aid biomedical research via integrative biology. The assignment of MeSH terms to biomedical articles is conceived as a ranking problem in [33].

More generally, text mining methods for system biology enable going beyond simple word searches [34,35]. The main tasks of biomedical text mining are reviewed in [7]. The surveys of text mining strategies for information extraction from scientific literature can be found in [36] and [37]. Reference [38] provides a comprehensive review of text mining methods for chemistry. Complete text mining workflows for cancer system biology are reviewed in [39]. Combining text mining with annotated experimental data for hypothesis generation and biological discovery is considered in [40] and [41]. Text mining for discovery of biological interactions and hypothesis generation is considered in [42]. Adverse drug reactions are inferred from the literature using the text mining methods in [43].

A corpus of 97 fully annotated biomedical articles is announced in [44] to serve as a benchmark for evaluating the performance of different text mining tools as demonstrated for sentence splitting, tokenization, syntactic parsing, and named entity recognition applications. More importantly, it was found that the performance of trainable machine learning methods may differ greatly if used on different data sets. Deep learning for text feature extraction including keyword identification has been considered in [18] and for the named entity recognition in [45–47]. A tool for chemical entity recognition in texts is presented in [48].

Automated classification of sentences into 11 core scientific concepts is performed in [49] using support vector machines and conditional random fields. It has been found that the most discriminatory features for this type of classification are grammatical dependencies between single word and two-word keywords. The conditional random-fields are used in [50] to perform the context-dependent classification of sentences in abstracts of scientific papers. The same problem was addressed in [51] using trained Bayesian classifiers.

The training data independent categorization of biomedical texts according to MeSH terms and the Gene Ontology is presented in [52]. The identification and subsequent classification of 10 distinct argumentative schemes typically used in genetic research papers have been implemented in [53]. The

\(^6\) https://www.nlm.nih.gov/mesh/index.html
\(^7\) https://pubmed.ncbi.nlm.nih.gov
4 types of binary argumentative relations between sentences were identified in [54] to obtain the graph structures of argument in scientific papers.

Automatic term recognition, document clustering, classification and summarization can improve the efficiency of performing systematic reviews of scientific literature [55–58]. A semi-automated screening of biomedical literature to identify relevant papers has been implemented in [59] using supervised machine learning. Reference [57] presents a text mining framework for bibliometric data to identify research trends and to design research.

There are online tools to define properly formed keywords for scientific papers, and to obtain the word lists of biomedical keywords and terms such as diseases, proteins, genes, chemicals, cell lines and species. The online DeCS/MeSH service allows to search the structured MeSH descriptors to index biomedical articles. The command-line keyword generator finds the most likely single-word keywords in a corpus of documents using either the TF or unsupervised latent Dirichlet allocation (LDA) machine learning model.

The PDFX online utility extracts logical units from a PDF file by first building a geometric model of every page containing textual and bitmap elements. The elements are merged into logical units using their location information on the page as well as using the font properties [60]. An open source layout-aware text extraction utility from PDF files was reported in [61]. The extraction is performed in blocks. The blocks are then classified into logical units, and reordered to create an appropriate reading flow. There are many other text extraction utilities from PDF files such as TextFromPDF, pdftxt, pdflines, and PDFBox.

TerMine is an online service for multi-word keywords identification. It can also utilize the dictionary of acronyms. BioText is a web-based application for searching abstracts, figure captions as well as full texts in over 300 open access biological journals [62]. BioReader is a web-based utility for automatically searching and classifying papers based on their abstract in PubMed database.

Textpresso is an online tool for full-text annotations via keyword queries and semantic categories. The SAPIENT software is a tool for automated annotations of sentences assuming the defined core scientific concepts. Tagcorpus is a C++ program to find the named entities of proteins, species, diseases, tissues, chemicals and drugs in a corpus of documents. LINNAEUS is a dictionary based utility for the name recognition of biological species.

sciBERT is a deep learning model trained on a large corpus of scientific papers which can be used for sentences annotations and classifications. CERMINE is a machine learning based system for automated

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8 http://ulib.iupui.edu/keywords
9 https://corposaurus.github.io/corpora
10 https://decs.bvsalud.org/en
11 https://lab.kb.nl/tool/keyword-generator
12 https://github.com/BMKEG/lapdftext
13 https://github.com/mihailsalari/TextFromPDF
14 https://pypi.org/project/pdftxt
15 https://github.com/proger/pdflines
16 https://pdfbox.apache.org
17 http://www.nactem.ac.uk/software/termine
18 http://biosearch.berkeley.edu
19 https://services.healthtech.dtu.dk/service.php?BioReader-1.2
20 https://textpressocentral.org/tpc
21 http://www.sapientaproject.com/software
22 https://github.com/larsjuhljensen/tagger
23 http://linnaeus.sourceforge.net
24 https://github.com/allenai/scibert
25 http://cermine.ceon.pl
extraction of metadata from scientific papers including authors names and affiliations, journal name, journal volume and number, and the list of references. In this regard, this utility appears to enhance the capabilities of PDFX.

An open source software for comprehensive text analysis referred to as General Architecture for Text Engineering GATE has been under the development for nearly past 20 years. The usability of GATE was demonstrated in [63] for genomic-wide cancer mutation associations, medical records analysis, and for drug-related searches. It is concluded that text mining for life sciences and medical applications can be made to be well-defined and reproducible.

3. Methodology

Before describing our strategy for identifying multi-word phrases, and its implementation as a collection of shell script utilities, the main challenges of extracting text from PDF documents are reviewed. The extraction of text from PDF is a necessary step to enable processing the information contents of scientific papers.

3.1. Text extraction from PDF

The PDF file format has been developed in the 90’s by Adobe to describe page contents which can be flexibly and precisely rendered at appropriate resolution and scales on a variety of media. The PDF had replaced then prevailing postscript page description language. However, unlike postscript, PDF is missing many general features of programming languages as it focuses on its single main purpose, i.e., efficiently describing the page content. Moreover, unlike postscript, PDF files can directly render the selected page without requiring to rebuild the contents of all the preceding pages. The page contents are stored in a dictionary normally located at the end of the PDF file. The dictionary can be optimized, e.g., linearized and compressed for a better efficiency. The PDF documents can embed interactive forms, multimedia as well as fonts for the characters used in the document.

The page presentation focus of PDF is very suitable for archiving purposes and for consuming their information content by human readers. However, in the era of automated information processing, the PDF format is much less suitable. The content elements in a PDF document can be placed on pages in an arbitrary order with no regard to a logical structure of the document or the natural reading flow. For instances, a single paragraph of text may consist of multiple parts which are rendered in any order. Since the logical structure of a document is not available in the PDF file, it must be inferred. For example, the paragraphs and other text units can be inferred from the elements locations on the page, the inter-character spacing, and other font properties.

Another challenge in extracting text from PDF files is the use of special characters and different character encoding schemes. The special characters from different languages can be transliterated, or completely removed if they are isolated, e.g., used as mathematical symbols. However, converting the document characters from one encoding into another can be sometime problematic. It is recommended to use UTF-8 (Unicode Transformation Format 8-bit) encoding, since it can efficiently represent over 1.1 million of valid characters using 1 to 4 bytes (8-bit values).

The next challenge is joining the words which are split across lines or even pages. This is usually straightforward if the word is split across consecutive lines using a dash delimiter. However, the word can become permanently split if the delimiter has been replaced with a space during text extraction or character encoding changes. Such cases are very difficult to detect and rectify. Furthermore, it is often

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desirable to extract full sentences even if they are split across multiple lines or even pages. The beginnings 
and ends of sentences are usually detected by a set of delimiting characters such as dot, and exclamation 
and question marks which are preceded by a lower-case letter and followed by a space and an upper-case 
letter. Other separators such as comma, colon and semicolon can usually be removed unless they are 
utilized in semantic analysis of sentences. Our experiments suggest that it is best to remove all end-of-line 
characters within the paragraphs before joining the split words and sentences. It is also desirable to replace 
all repeated whitespace characters including spaces and tabs with a single space.

3.2. Identification of multi-word phrases

Our objective is to detect relevant or important multi-word phrases within the text extracted from 
a single PDF document. These phrases are deliberately not referred to as the most relevant or the most 
important, since the phrase relevance and importance is strongly dependent on the context and the task 
we are trying to accomplish. For instance, the same scientific paper may be added to one survey covering 
a certain topic based on one set of keywords, and then to another survey on a different topic assuming a 
different set of keywords. Both these sets of keywords which may best describe the paper can have little or 
even no overlap. However, if one set of keywords is the subset of another set of keywords, it is sensible to 
demand that the larger set is a better description of the paper than the smaller set. In this case, it may be 
possible to add more keywords to the set until they become a sufficiently good representation of the paper. 
This argument also implies that keywords can be assigned scores, so they can be sorted in terms of their 
relevance or importance.

An expert may assign synonymous terms to the paper that do not appear directly anywhere in the text. 
For example, these terms may be more appropriate terminology normally used within a given domain. 
Furthermore, similarly to uncertainty in determining how many keywords should be used to represent 
the paper, there is uncertainty in how many neighboring words should be assumed in identifying the 
relevant multi-word phrases. It is clear that a whole sentence is more accurate description of the paper 
than its part, provided that the efficiency of description may be ignored. However, unlike the problem of 
determining the sufficient number of keywords which likely depends on the paper length, its structure 
and its information content, the multi-word phrases of interest are likely to consist of only a small number 
words. Whether a shorter phrase is more relevant to better describe the paper than a longer phrase is again 
context dependent. Our experiments indicate that shorter phrases are preferred if more general scope of 
the paper is of interest whereas longer multi-word phrases tend to create a more narrow description of the 
paper.

In this paper, the keyword identification issues outlined above are addressed pragmatically by 
assuming the frequency of occurrence, i.e., the TF of individual keywords as well as of multi-word phrases 
as the main metric to enable their ranking. Since keywords with the largest TF are usually contained in 
the paper title, scoring the keywords by their TF can become easily biased due to many titles appearing 
in the list of references. Although it may be possible to detect and exclude the list of references when 
calculating the TF scores, we have investigated the strategy of calculating the spread of candidate keywords 
throughout the whole paper. In particular, if $s_i$ denotes the number of words between the keywords at 
word locations $l_i$ and $l_{i+1}$ in the paper, respectively, the spread of such keyword with its $N$ occurrences 
in the paper normalized by the mean value is computed as,

$$S = \frac{1}{N-2} \sum_{i=1}^{N-1} \left( s_i - \frac{1}{N-1} \sum_{i=1}^{N-1} s_i \right)^2 \left( \frac{1}{N-1} \sum_{i=1}^{N-1} s_i \right)^{-2}$$

(1)
where $s_i = l_{i+1} - l_i - 1$. The smaller the normalized spread $S$, the more evenly the keyword is distributed throughout the paper, and the more likely such keyword is sufficiently important, so it is mentioned in different parts of the paper. However, we did not observe major changes in the ordered lists of identified keywords by tweaking the scoring metric, although local changes in the list do appear if the scores are adjusted.

The word stemming and word normalizations have not been considered in our implementation, since they do not fundamentally affect our keyword search strategy. On the other hand, the case-insensitive search is assumed. It can be implemented by either converting all letters in the extracted text to lower-case, or by setting the case-insensitive options in calling the shell script commands. The stop-words should be removed, however, only under defined circumstances. The rules adopted for identifying multi-word keywords which were implemented in our shell scripts can be summarized as follows. It is assumed that the full-text extracted from a PDF file was already curated for special characters, split words and split sentences.

1. The objective is to identify the multi-word phrases having the largest frequency of occurrence.
2. The phrases are searched hierarchically at multiple levels. Starting at level 1, the one-word keywords are obtained, then at level 2, the two-word keywords are identified and so on.
3. The candidate keywords in the next level can be enumerated by appending or prepending single words to the phrases in the current level.
4. The number of phrases considered at a given level should be larger than at the previous level.
5. The phrases can contain stop-words provided that the stop-words are neither their first nor the last word. However, the phrases can contain stop-words anywhere, provided that these phrases are used to generate new extended candidate phrases at the next level, and not used as the phrases identified at the current level.
6. It is desirable to manually prune the phrases generated at every level in order to prevent the unlikely phrases to propagate to the next level.

The selection of important multi-word phrases at each level is depicted in Figure 1. At each level, the phrases consisting of one or more words are ranked by their frequency of occurrence. The blue cells represent the phrases which are selected at each level. However, the search for phrases at the next level requires that many other phrases in pink cells are considered too. The ratio of the number of blue cells to the number of pink cells can be 1 : 10 or even smaller. Although the overall number of candidate phrases (blue and pink cells) growth rapidly at each next level, the number of meaningful phrases in blue cells is quickly reduced after level 2. The crossed phrases (words) can be excluded automatically (e.g., they do
not satisfy the stop-word constraint), or they can be excluded manually by inspection (e.g., they may be outside the intended scope or context).

![Diagram](image)

**Figure 1.** The proposed hierarchical iterative procedure for generating the relevant multi-word phrases.

Any scoring system to sort the candidate keywords is an attempt to estimate the likelihood that the considered keywords are relevant or important in a given context and a given application. Provided that the number of phrases considered from the previous level is sufficiently large, the actual choice of the scoring metric appears to be less important. The number of candidate phrases grows significantly at each level. On the other hand, the number of meaningful phrases having some minimum number of occurrence decreases rapidly at each level. These two opposing phenomena usually yields the maximum number of meaningful keywords for two-word phrases.

Some frequent words can have a common prefix. There are cases where it makes sense to merge such words. However, this affects the generation of longer phrases using the proposed procedure, so the word stemming has not been considered. Nevertheless, manually pruning the generated lists of phrases proved to be a very robust strategy to obtain the satisfactory results. For instance, the two-word phrase, ‘in vivo’, would normally be discarded, since the first word is a stop-word, however, manual pruning can keep this term in the list of candidate two-word phrases.

### 3.3. Implementation as shell-scripts

Our implementation was inspired by pdfjam. It is a shell script for manipulating pages of PDF files which is available in most Linux distributions. In general, the Linux shell has been designed from the very beginning to be strongly oriented on text processing. There are many standard tools available in every Linux shell that are specialized for such processing. The most commonly used are these utilities:

1. **tr**: a utility to translate and delete characters in text files
2. **grep**: a utility to select lines in a text file that match given pattern
3. **sed**: a streaming editor for filtering and transforming text streams
4. awk: a text processor implementing a full programming language for patterns matching and text processing.

It should be noted that text processing in the Linux shell is line oriented, i.e., a text file is processed line by line. This may create problems when the textual information to be processed is spread over multiple lines, and e.g. paragraph by paragraph processing instead of the default line by line processing is required. There are strategies for implementing multiline processing of text, and it has been done in our scripts, but it makes the scripts more complicated.

The shell scripts reported in this paper were developed and tested in BASH (Bourne Again Shell) version 5.0.17 on Fedora Linux Workstation version 33. These scripts are developed and distributed under the name pdfPapers. In addition to the above mentioned standard Linux shell programs, our implementation utilizes the following shell script programs which may not be installed by default:

1. poppler-utils: a collection of Python utilities for manipulating and converting PDF files which are based on the open-source Poppler PDF library
2. convert: a powerful image converter which can transform many different file formats; it is included in ImageMagick collection of tools
3. gnuplot: an interactive plotting program supporting many different output devices and formats
4. gawk: a GNU implementation of awk with some extensions
5. pdftotext: probably the most reliable open-source utility in Linux for extracting text from PDF files
6. iconv: a utility for converting text between different encoding formats
7. aspell: an interactive spell checker supporting different languages and file formats

The pdfPapers program consists of 6 shell scripts offering different complimentary functions. The basic functionality of pdfls and pdfsearch utilities is sketched in Figure 2. These two scripts are typically used for batch processing and viewing of multiple PDF files. The other 4 shell scripts, i.e., pdfastext, textblocks, texttoinfo and texttodict are intended to process a single input file. The basic functionality of these 4 other scripts is shown in Figure 3. All scripts can be invoked to display more detailed usage instructions. The latest version of pdfPapers software is freely available for download and testing from the Github public repository27. The content of the repository is briefly described in the appendix. The examples from the repository are described in the next section.

![Diagram](https://github.com/ploskot/pdfPapers)
Figure 3. The basic functionality of pdfastext, textblocks, and texttodict and texttoinfo shell scripts.

pdfastext is a shell script wrapper for the standard pdftotext utility. It tries to remedy some deficiencies of pdftotext and also add some new features. In particular, the text file generated by pdftotext is curated for
non-printable characters which can be deleted or transcribed, and the words and sentences split across lines can be merged together. An additional file containing meta-information such as the number of pages in the input PDF file, the author and the producer of the PDF file, the number of words and characters on each page, and the location of bounding boxes can be produced. By default, the extracted text is composed of logical units referred to as blocks. The blocks reflect how the text contents were laid out on the page by the PDF creation software. Consequently, the blocks of text can differ vastly from the natural logical flow of the textual contents as desired by a human reader. The blocks are labeled as the decimal numbers, \( N.M \), where \( N \) is the page number and \( M \) is the block counter within the page. Furthermore, in order to visualize the block labels and their locations on the page, pdfastext can also generate a graphical image of every page with the text blocks overlayed on the original PDF page in the background.

**textblocks** is a shell script for manipulating blocks of text which were produced by pdfastext. The changes can be done on the input file, or a new file can be produced. Due to the complexity of processing, this script also provides extensive logging of all operations carried out and other informative messages into a log file or to the standard terminal output. This is useful for debugging and to understand unexpected outcomes of the processing. The script textblocks can provide information on the blocks contained in the input file, and check if the blocks are complete (i.e., having both opening and closing tags and an assigned unique label) and sorted by their label. A sophisticated block addressing scheme utilizing ranges allows to perform the operations on given combinations of blocks, pages or on the whole file. The non-printable characters can be transliterated, or the characters in selected blocks can be changed to lower-case or upper-case. Any character can be replaced or appended with a specified string, and the selected strings can be replaced with other strings. For example, it is possible to break the text in selected blocks into words or sentences, replace multiple spaces with a single space, delete leading or trailing spaces from lines, and delete empty lines. Another option can produce statistics for the selected blocks about their number of words, the number of words not in a spelling dictionary, and the number of non-printable characters. The textblocks script can insert new blocks at a given location (e.g., before or after the existing block). The new blocks can be empty or contain a given string. The blocks can be copied or moved to a new location within the input file, or to the output file. The block labels can be changed, or orderly renumbered. The blocks can be sorted by their label. The selected blocks can be deleted, or merged into one of the existing blocks. Finally, the text inside selected blocks can be filtered with a given function or another shell script.

**texttoinfo** is a shell script to perform text mining tasks. In the current version of pdfPapers, only the BoW with the frequency of occurrence and the multi-word phrase extraction of a given length surrounding the keyword defined by a regular expression have been implemented. It is recommended that a clean text file is passed as the input to this script. Since the text mining tasks are usually the most time consuming, in future versions of pdfPapers, it may be better to implement text mining algorithms in other programming languages which are faster such as Java, Python or C/C++.

**texttodict** is a shell script for creating dictionaries for aspell or for creating simple lists of words. The list of words can be obtained from the input text file as a BoW or as a dump of the existing aspell dictionary.

**Typical workflow** starts from exploring the contents of collected PDF files using the pdfsl and pdfsearch utilities. Both utilities are straightforward to use. Their command-line calls are intuitive, and their implementation is fast. They enable to narrow down the focus on a relatively small number of PDF documents which may be worth exploring more deeply. The information contents of the selected PDF documents should be explored one by one. In the first step, the PDF file is converted to a text file using the pdfastext utility. Many text blocks on the page often contain supporting information which can be safely discarded prior to text mining. It is recommended to first copy the relevant blocks into a new text file using the textblocks utility. The page previews showing text block layouts for every page can be obtained in the
first step with pdfastext utility. The text can be further cleaned as required using textblocks. In the last step, the frequency of occurrence statistics of multi-word phrases are obtained by running the texttoinfo command.

4. Results

The pdfPapers shell script utilities were used to extract the most frequently occurring phrases or 1 to 4 words in 5 selected papers in biology and life sciences. The keyword extraction from the papers is presented in subsections 4.1 to 4.5. In addition, the list of biological terms was created by extracting all words and phrases from the index and a table of acronyms in a PDF e-book. It is described in subsection 4.6. The shell scripts as well as data files for all examples considered can be found in the public Github repository (cf. Appendix).

4.1. Example 1

The extraction of the most frequent multi-word phrases was performed for the paper [64]. It is a relatively short paper consisting of 6 pages. The paper contains mathematical symbols and equations, 5 figures, but no tables. In addition to the standard content elements such as the paper and section titles, authors names and affiliations, the paper contains 4 author suggested keywords (“synthetic circuits, optimal filtering, noise cancellation, adaptive design”), the statement about the author contributions, acknowledgment, and a box summarizing the paper significance. A summary of the process of generating the multi-word phrases of 1 to 4 words is given in Table 1. The whole process was completed in 62s.

| Level | Phrases | Count | Run time | Output file   |
|-------|---------|-------|----------|---------------|
| 1     | single word | 200   | 1s       | ex5-sample1.w1|
| 2     | 2-words   | 200   | 1s       | ex5-sample1.w2|
| 3     | 3-words   | 1863  | 25s      | ex5-sample1.w3|
| 4     | 4-words   | 2703  | 35s      | ex5-sample1.w4|

Table 2. The multi-word phrases and their counts identified in paper [64]

| Level 1 | Level 2 | Level 3 | Level 4 |
|---------|---------|---------|---------|
| 67      | 1.817 filter | 26 poisson filter | 10 ensemble poisson filter |
| 37      | 2.760 circuit | 20 death process | 6 signal of interest |
| 36      | 1.424 noise | 16 optimal filter | 6 number of plasmid |
| 35      | 2.518 appendix | 16 birth rate | 6 dna strand displacement |
| 33      | 1.804 rate | 14 system identification | 6 constitutive promoter pmc |
| 29      | 1.471 sensor | 14 noise cancellation | 4 vitro using dna |
| 24      | 1.636 section | 13 sensor reaction | 4 using dna strand |
| 23      | 0.977 time | 13 differential equation | 4 strand displacement cascades |
| 22      | 2.246 birth | 12 optimal filters | 4 stochastic simulations of |
| 21      | 1.587 estimator | 10 synthetic circuits | 4 sensor time points |
| 21      | 0.930 filtering | 10 strand displacement | 4 sensor rate c |
| 20      | 1.712 filters | 10 kalman filter | 4 remarkably high precision |
| 19      | 2.426 optimal | 10 in vitro | 4 number of plasmids |
| 19      | 1.086 process | 10 ensemble poisson | 4 information about z |
| 18      | 2.560 ensemble | 10 cell cycle | 4 birth and death |
| 18      | 1.226 biochemical | 8 transcription rate | 4 degree of model mismatch |
| 18      | 1.128 dynamics | 8 time points | 4 death process z 2 |
| 17      | 4.191 circuits | 8 optogenetic circuit | 4 circuit in escherichia coli |
| 17      | 1.169 signal | 8 mmse estimator | 4 birth and death rates |
|         |          |          | 3 used an optogenetic |
|         |          |          | 4 approach in vitro using |

Table 1. Generation of multi-word phrases for paper [64]
Table 2 shows the multi-word phrases of 1 to 4 keywords and their frequency of occurrence which were identified in paper [64]. The number of phrases shown in Table 2 is 20 for each level. The total number of phrases generated at each level is shown in Table 1. Note that all words in Table 2 have been converted to lower-case letters. For the first level, the second column gives the normalized spreads of given single word keywords within the paper which were calculated using eq. (1). Note that there is a striking difference between having only 4 keywords which were provided by the authors, and having over 80 phrases across 4 levels given in Table 2 to describe and understand the paper. The authors provided keywords are likely sufficient for reliably indexing the paper in the paper databases. However, in order to understand the scientific and information contents of the paper clearly requires to consider many more phrases which are not restricted by their length.

The scripts and the input and output files used in this example can be obtained from the sub-directory example01/ located in the pdfPapers Github repository (cf. Appendix).

4.2. Example 2

The extraction of the most frequent multi-word phrases was performed for the paper [65]. This is a longer paper having 11 pages, but only 3 displayed mathematical equations and 2 displayed chemical reaction equations. The paper structure is otherwise standard with several statements given at the end of the paper just before the references. There are only 3 figures with captions, and no tables. The authors specify 7 key phrases (“Mathematical model, Predictive model, Fundamental physical laws, Phenomenology, Membrane-bounded compartment, T-cell receptor, Somitogenesis clock”). A summary of the process of generating the multi-word phrases of 1 to 4 words is given in Table 3. The whole process was completed in 84s.

| Level 1 | Level 2 | Level 3 | Level 4 |
|---------|---------|---------|---------|
| 35  | 3.165 model | 19 mathematical model | 12 model is correct |
| 34  | 2.905 biology | 16 systems biology | 8 her1 and her7 |
| 32  | 3.407 models | 14 negative feedback | 8 fundamental physical laws |
| 30  | 4.700 assumptions | 14 mass action | 8 based on fundamental |
| 26  | 3.530 cell | 12 reverse modeling | 6 heinrich and rapoport |
| 22  | 1.491 mathematical | 12 cell receptor | 6 forward and reverse |
| 22  | 1.035 molecular | 10 somitogenesis clock | 6 factor attachment protein |
| 19  | 2.182 protein | 10 identical compartments | 5 attachment protein receptor |
| 17  | 4.074 modeling | 8 time delays | 4 protein tyrosine kinase |
| 16  | 5.581 conclusions | 8 rapoport model | 4 physics or even |
| 15  | 4.217 physics | 8 physical laws | 4 negative feedback loop |
| 15  | 2.422 figure | 8 molecular biology | 4 molecular dynamics models |
| 14  | 6.837 clock | 8 mathematical models | 4 models in biology |
| 14  | 2.111 time | 8 lewis model | 4 kinetic proofreading scheme |
| 14  | 2.111 time | 8 fundamental physical | 4 guarantee of logical |
| 14  | 2.039 data | 7 feedback loop | 4 guarantee that a model |
| 13  | 4.922 snares | 6 time delay | 4 fit what you want |
| 13  | 4.666 compartments | 6 somite formation | 4 bind better to coat |
| 13  | 4.283 negative | 6 sensitive factor | 4 guarantee of logical |
| 13  | 0.457 biological | 6 reverse model | 4 based on fundamental physical |

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Table 4. The multi-word phrases and their counts identified in paper [65]

| Level 1 | Level 2 | Level 3 | Level 4 |
|---------|---------|---------|---------|
| 35  | 3.165 model | 19 mathematical model | 12 model is correct |
| 34  | 2.905 biology | 16 systems biology | 8 her1 and her7 |
| 32  | 3.407 models | 14 negative feedback | 8 fundamental physical laws |
| 30  | 4.700 assumptions | 14 mass action | 8 based on fundamental |
| 26  | 3.530 cell | 12 reverse modeling | 6 heinrich and rapoport |
| 22  | 1.491 mathematical | 12 cell receptor | 6 forward and reverse |
| 22  | 1.035 molecular | 10 somitogenesis clock | 6 factor attachment protein |
| 19  | 2.182 protein | 10 identical compartments | 5 attachment protein receptor |
| 17  | 4.074 modeling | 8 time delays | 4 protein tyrosine kinase |
| 16  | 5.581 conclusions | 8 rapoport model | 4 physics or even |
| 15  | 4.217 physics | 8 physical laws | 4 negative feedback loop |
| 15  | 2.422 figure | 8 molecular biology | 4 molecular dynamics models |
| 14  | 6.837 clock | 8 mathematical models | 4 models in biology |
| 14  | 2.111 time | 8 lewis model | 4 kinetic proofreading scheme |
| 14  | 2.111 time | 8 fundamental physical | 4 guarantee of logical |
| 14  | 2.039 data | 7 feedback loop | 4 guarantee that a model |
| 13  | 4.922 snares | 6 time delay | 4 fit what you want |
| 13  | 4.666 compartments | 6 somite formation | 4 bind better to coat |
| 13  | 4.283 negative | 6 sensitive factor | 4 guarantee of logical |
| 13  | 0.457 biological | 6 reverse model | 4 based on fundamental physical |

The scripts and the input and output files used in this example can be obtained from the sub-directory example01/ located in the pdfPapers Github repository (cf. Appendix).
Table 4 shows the multi-word phrases of 1 to 4 keywords and their frequency of occurrence which were identified in paper [65]. The number of phrases shown in Table 4 is 20 for each level. The total number of phrases generated at each level is shown in Table 3. Note that all words in Table 4 have been converted to lower-case letters. For the first level, the second column gives the normalized spreads of given single word keywords within the paper which were calculated using eq. (1). As for the previous example, the number of generated key phrases is significantly larger than the number of authors nominated keywords.

The scripts and the input and output files used in this example can be obtained from the sub-directory example02/ located in the pdfPapers Github repository (cf. Appendix).

4.3. Example 3

The extraction of the most frequent multi-word phrases was performed for the paper [66]. This paper is different from all other example papers considered in that it was published more than 30 years ago. Then, sometime later, the paper was made available as a PDF document. Although a visual presentation of the paper is appealing, the extraction of text from the PDF file turned out to be problematic. In addition to many special characters in non-standard fonts, the text blocks occasionally mix text lines from neighbouring columns indicating that pdftotext had failed to recognize the locations and properly group some lines of the text. Consequently, the text file generated by pdfastext had to be checked and several blocks of text manually corrected. This suggests that the process of making the older scientific papers available as PDF documents could be improved, otherwise their conversion to text is less reliable than for more recently published papers.

The paper [66] does not contain any authors specified keywords, statements and even no references. There are 9 figures, some of them very large, and no tables. A summary of the process of generating the multi-word phrases of 1 to 4 words is given in Table 5. The whole process was completed in 69s.

Table 5. Generation of multi-word phrases for paper [66]

| Level | Phrases | Count | Run time | Output file |
|-------|---------|-------|----------|-------------|
| 1     | single word | 200   | 1s       | ex5-sample3.w1 |
| 2     | 2-words  | 200   | 2s       | ex5-sample3.w2 |
| 3     | 3-words  | 1980  | 25s      | ex5-sample3.w3 |
| 4     | 4-words  | 3060  | 41s      | ex5-sample3.w4 |

Table 6. The multi-word phrases and their counts identified in paper [66]

| Level 1 | Level 2 | Level 3 | Level 4 |
|---------|---------|---------|---------|
| 33 | 1.562 energy | 40 | turing machine | 28 | amount of energy | 14 | minimum amount of energy |
| 40 | 4.307 machine | 21 | logic gate | 12 | random thermal motion | 10 | absence of a ball |
| 40 | 3.515 ball | 19 | fredkin gate | 8 | left or right | 6 | segment to the left |
| 33 | 2.738 computer | 17 | ball computer | 6 | segment of pipe | 6 | presence of a ball |
| 31 | 6.548 head | 16 | minimum amount | 6 | order to perform | 6 | in order to perform |
| 31 | 1.555 computation | 14 | thermal motion | 6 | movement of bits | 6 | expend as little energy |
| 28 | 3.095 information | 14 | logic gates | 6 | held in place | 6 | energy as we wish |
| 26 | 1.467 state | 12 | random thermal | 6 | frictionless billiard balls | 6 | bit onto the tape |
| 25 | 3.898 forward | 12 | billiard balls | 6 | expended in order | 6 | ball in a particular |
| 24 | 4.930 input | 11 | head molecule | 6 | expend as little | 6 | at a logic gate |
| 23 | 5.110 turing | 10 | transition rules | 6 | enzymatic turing machine | 6 | as little energy as |
| 22 | 2.832 gate | 10 | master camshaft | 6 | clockwork turing machine | 4 | two balls arrive simultaneously |
| 21 | 4.034 balls | 10 | fredkin gates | 6 | bits of information | 4 | together with tommaso toffoli |
| 21 | 3.929 segment | 10 | billiard ball | 5 | expenditure of energy | 4 | taking a long time |
| 21 | 3.482 logic | 8 | uncertainty principle | 4 | without any friction | 4 | split segment of pipe |
| 20 | 8.331 base | 8 | static friction | 4 | uncertainty principle does | 4 | sometimes the enzyme takes |
| 20 | 0.981 amount | 8 | small amount | 4 | two balls arrive | 4 | as we wish |
| 19 | 7.191 molecule | 8 | reversible turing | 4 | state to state | 4 | small amount of energy |
| 19 | 4.075 tape | 8 | input lines | 4 | right or left | 4 | set of transition rules |
| 19 | 2.656 motion | 8 | driving force | 4 | represent the output | 4 | rna strand and releases |
Table 6 shows the multi-word phrases of 1 to 4 keywords and their frequency of occurrence which were identified in paper [66]. The number of phrases shown in Table 6 is 20 for each level. The total number of phrases generated at each level is shown in Table 5. Note that all words in Table 6 have been converted to lower-case letters. For the first level, the second column gives the normalized spreads of given single word keywords within the paper which were calculated using eq. (1).

The scripts and the input and output files used in this example can be obtained from the sub-directory example03/ located in the pdfPapers Github repository (cf. Appendix).

4.4. Example 4

The extraction of the most frequent multi-word phrases was performed for the paper [67]. The paper contains 4 figures and 1 large table. Fortunately, the text automatically detected in the table was properly extracted into separate blocks, so they can be excluded from the main text or merged into one large block for the subsequent text mining. There are no author defined keywords and no other statements. The references are included at the end of the paper. A summary of the process of generating the multi-word phrases of 1 to 4 words is given in Table 7. The whole process was completed in 92s.

Table 7. Generation of multi-word phrases for paper [67]

| Level | Phrases | Count | Run time | Output file |
|-------|---------|-------|----------|-------------|
| 1     | single word | 200   | 1s       | ex5-sample4.w1 |
| 2     | 2-words   | 200   | 2s       | ex5-sample4.w2 |
| 3     | 3-words   | 2423  | 36s      | ex5-sample4.w3 |
| 4     | 4-words   | 3079  | 53s      | ex5-sample4.w4 |

Table 8. The multi-word phrases and their counts identified in paper [67]

| Level 1 | Level 2 | Level 3 | Level 4 |
|---------|---------|---------|---------|
| 85      | 1.692 limits | 35 integrated circuit | 12 limits to computation | 4 two or three dimensions |
| 39      | 1.115 integrated | 42 integrated circuits | 10 integrated circuit design | 4 transfer between carriers device |
| 36      | 2.843 power | 22 emerging technologies | 6 ten years ago | 4 size and delay variation |
| 33      | 1.613 circuit | 20 fundamental limits | 6 speed of light | 4 scale to large sizes |
| 32      | 2.881 energy | 19 time limits | 6 modern integrated circuits | 4 permission from gold standard |
| 31      | 1.738 circuits | 14 power consumption | 6 limits to computing | 4 nonphysical limits to computing |
| 27      | 3.242 quantum | 12 technology node | 6 improvements in computer | 4 limits on fundamental limits |
| 25      | 1.023 technologies | 12 quantum computers | 5 modern integrated circuit | 4 information transfer between carriers |
| 24      | 3.636 design | 12 gate dielectric | 4 voltage scaling 56 | 4 image redrawn from figure |
| 24      | 1.914 computing | 12 engineering obstacles | 4 universality circuit delay | 4 fundamental limits to computation |
| 24      | 1.903 computation | 10 supply voltage | 4 transfer between carriers | 4 carriers device gate dielectric |
| 24      | 1.180 scaling | 10 moore’s law | 4 size and delay | 4 between carriers device gate |
| 21      | 4.418 computers | 10 logic gates | 4 semiconductor integrated circuits | 2 years and 600 years |
| 19      | 1.020 time | 10 fundamental limit | 4 scale to large | 2 works around engineering obstacles |
| 18      | 1.644 technology | 10 circuit design | 4 redrawn from figure | 2 wires in several square |
| 17      | 0.801 performance | 9 time limit | 4 reasonably tight limits | 2 wires get slower relative |
| 16      | 1.319 interconnect | 8 universal computers | 4 reasonably tight limit | 2 wires stacks from 1997 |
| 15      | 3.654 transistors | 8 sequential algorithm | 4 quantum information processing | 2 wider gate dielectric layer |
| 14      | 2.396 manufacturing | 8 power density | 4 permission from gold | 2 wider dielectric layers 26 |

Table 8 shows the multi-word phrases of 1 to 4 keywords and their frequency of occurrence which were identified in paper [67]. The number of phrases shown in Table 8 is 20 for each level. The total number of phrases generated at each level is shown in Table 7. Note that all words in Table 8 have been converted to lower-case letters. For the first level, the second column gives the normalized spreads of given single word keywords within the paper which were calculated using eq. (1).

The scripts and the input and output files used in this example can be obtained from the sub-directory example04/ located in the pdfPapers Github repository (cf. Appendix).
4.5. Example 5

The extraction of the most frequent multi-word phrases was performed for the paper [68]. This is a long paper with 21 pages and relatively complicated structure. There are 16 figures and 2 tables. There are several statements including the author contributions, acknowledgment, the support information summaries, and an inset with the authors summary. There are several displayed mathematical and chemical equations, and some inline mathematical symbols and expressions. However, the conversion of PDF to a text file was straightforward, since only a small number of text blocks containing meaningful information had to be collected for the subsequent text mining. A summary of the process of generating the multi-word phrases of 1 to 4 words is given in Table 9. The whole process was completed in 244s, more than double in comparison to all previous papers considered. Likewise, the number of candidate 3-word and 4-word phrases is nearly doubled in comparison with the previous papers.

| Level | Phrases | Count | Run time | Output file |
|-------|---------|-------|----------|-------------|
| 1     | single word | 200   | 1s       | ex5-sample5.w1 |
| 2     | 2-words | 200   | 3s       | ex5-sample5.w2 |
| 3     | 3-words | 4019  | 85s      | ex5-sample5.w3 |
| 4     | 4-words | 6946  | 155s     | ex5-sample5.w4 |

Table 9. Generation of multi-word phrases for paper [68]

Table 10. The multi-word phrases and their counts identified in paper [68]

| Level 1 | Level 2 | Level 3 | Level 4 |
|---------|---------|---------|---------|
| 128     | 2.318   | inducer | 10      | transcription and translation |
| 128     | 1.494   | model   | 58      | inducer concentration |
| 106     | 2.201   | cell    | 44      | rate constants |
| 88      | 3.140   | repressor | 43    | in vivo |
| 71      | 6.637   | burst   | 42      | positive feedback |
| 69      | 2.096   | operator | 42      | inducer concentrations |
| 67      | 2.157   | state   | 41      | burst size |
| 59      | 4.218   | noise   | 38      | rate constant |
| 59      | 3.104   | cells   | 33      | induced state |
| 59      | 1.834   | simulations | 32 | state model |
| 56      | 2.399   | concentration | 28 | stochastic simulations |
| 55      | 1.693   | distributions | 28 | population distributions |
| 53      | 2.182   | expression | 28 | cell cycle |
| 53      | 1.997   | rate    | 24      | operator complex |
| 52      | 1.817   | using   | 24      | free operator |
| 51      | 2.730   | lacy    | 24      | burst frequency |
| 51      | 1.854   | figure  | 22      | protein lifetime |
| 50      | 2.779   | mean    | 22      | inducer molecules |
| 49      | 2.412   | gene    | 22      | genetic switch |
| 49      | 2.382   | protein | 21      | coli cell |

Table 10 shows the multi-word phrases of 1 to 4 keywords and their frequency of occurrence which were identified in paper [68]. The number of phrases shown in Table 10 is 20 for each level. The total number of phrases generated at each level is shown in Table 9. Note that all words in Table 10 have been converted to lower-case letters. For the first level, the second column gives the normalized spreads of given single word keywords within the paper which were calculated using eq. (1).

The scripts and the input and output files used in this example can be obtained from the sub-directory example05/ located in the pdfPapers Github repository (cf. Appendix).
4.6. Example 6

In the last example, a table of acronyms and the index from a biochemistry e-book in the PDF format were used to create the lists of biochemical phrases. Such list can be utilized for keyword extraction and other text mining tasks assuming biochemical literate. The PDF to text conversion was achieved using the pdfastext utility. A small number of irrelevant text blocks was then deleted, for example, those containing page numbers. The non-printable characters were deleted, and multiple space and empty lines were also removed. There are 93 one-word, 124 two-word, 79 three-word, 14 four-word, 9 five word and only 3 six-word acronyms among 322 acronyms in total. This acronym distribution approximately reflects the distributions of keywords identified in the previous five examples. Note also that only the acronym definitions were considered whereas the actual acronyms were removed from the output file. Utilizing the shell scripts was particularly useful for processing the 53 page index file, and creating the list of over 11,000 biochemical terms. The scripts and the input and output files used in this example can be again obtained from the sub-directory example10/ located in the pdfPapers Github repository (cf. Appendix).

5. Discussion

Most publishers require that the authors add a certain minimum number of keywords to their paper. These keywords are a subjective choice as they reflect how the authors would like their paper to be perceived and indexed. For indexing, the keywords with broader coverage are preferred. However, such general coverage is unsatisfactory when trying to understand information contents of papers. Since the paper title and abstract are usually made available even in paid-for journal repositories, it is sometime recommended to select the keywords covering the rest of the paper and which are not contained in the paper title and abstract. This improves the efficiency of keywords use, and subsequently also the paper visibility in searches. The coverage efficiency can be also improved if there is little information overlap among the keywords. The keywords could be assigned the level or a category of importance. For example, having the primary and secondary keywords can enable more robust information processing applications beyond information retrieval and indexing.

In our experiments, we observed that having about 10’s of phrases consisting of up to 4 words and having the largest frequency of occurrence gives a reasonably good idea about the unique focus of the paper. The number of 2-word phrases considered can be as large as 30 or 40, since there usually exist many such plausible phrases in most papers. The shorter phrases of 1 or 2 words provide more general view on the paper whereas longer phrases of more than 3 words give increasingly specialized view on the paper. Even if only 20 single word keywords with the largest frequency of occurrence can be considered to a be a sufficiently good description of the paper key topics, it is important to assume at least 200 such single word keywords to construct the most frequently occurring 2-word phrases. Instead of simply enumerating the important phrases as was done in the previous section, the word clouds and word clusters and other visualization methods may be preferred in some applications.

The following strategies were ignored in our current implementation of the pdfPapers utilities, but they could improve the reliability of keyword identification:

1. The words and their counts can be merged if they have a common prefix. The phrases containing words with common prefix can be clustered.
2. The location of candidate keywords or phrases within the paper appears to be important. For example, since the keywords tend to occur in the paper title, there are often many candidate keywords detected in the list of references which can easily bias their frequency counts.
3. Synonymous, similar and otherwise related words can be identified and treated as a group instead of individual words.
4. There should be specific rules for acronyms to be counted as keywords.
5. The text left over from displayed mathematical equations and figure labels can be detected and removed, since it rarely contains any meaningful information.

6. Merging of split words, sentences and paragraphs could be further improved to be more reliable in most situations encountered.

7. It would be useful to specify which features to use for detecting keywords and key phrases as one of the script parameters. Then different search strategies can be checked for any paper considered, and the human observer decides which feature is the most suitable in a given context.

Our experiments showed that the keyword extraction process is surprisingly robust to the selection of scoring metric. Despite imperfections in PDF to text conversions, and using a simple frequency of occurrence metric, satisfactory sets of multi-word phrases can be identified. Using more complex strategies and their more reliable implementation appear to change the ordering of phrases locally rather than globally. Consequently, it is important to generate a sufficient number of phrases using any scoring function to reliably obtain the most important phrases among the first, say, 20 having the highest scores.

Having a fully automated system for the keywords identification would be certainly very desirable. However, the complexity of implementing such system can grow rapidly, and it may never reach the level of experience of a human researcher in evaluating scientific papers. The human brain seems to be extremely good in solving complex problems where the efficiency is not an issue. On the other hand, the human brain is very inefficient in solving simpler tasks, particularly if they are of large scale; this is where the automated systems can serve the researchers very well. As indicated in Figure 4, our target is the yellow area where we can combine efficient automated systems with the capability of the human brain. In this paper, the semi-automated system generates the lists of 1 to 4 word phrases which can be quickly evaluated by the human researcher to correct for deficiencies in the algorithm, and to decide which phrases can be discarded despite having large scores.

The text mining algorithms are time consuming which calls for more efficient implementation in other languages such as Java, Python or C/C++. Nevertheless, the core functionality of searching, viewing and extracting text from PDF files can be provided as shell scripts as long as it is reliable. The ultimate goal is to develop standard tools for working with PDF documents on *nix systems which can be accepted to the program repositories for these operating systems.
6. Conclusions

The paper reported implementation of shell script utilities to extract the most frequently occurring multi-word phrases from PDF documents. The utilities are available for download from the public Github repository named pdfPapers. The core functionality provided by pdfPapers includes a sequential viewing of collections of PDF files, producing the frequency of occurrence of combined logical and regular expressions for a group of PDF files, and performing more reliable conversions of PDF to text. The identification of the most frequent multi-word phrases was chosen as an example of text mining application. The development of pdfPapers was motivated by the availability of many tools for working with the contents of text files on *nix (Unix/Linux) systems whereas such tools are very scarce for PDF documents. Our literature survey showed that there were a lot of efforts to develop software for working with the contents of PDF files over the past decade. Many of these programs are either offered online as web applications, and not as commandline utilities to run locally, or they do not support group processing of multiple PDF files.

Our strategy for extracting the multi-word phrases is to find longer phrases by prepending and appending candidate words to the sufficient number of the most frequently occurring shorter phrases. The word stemming is not consider, and the word search is made to be case insensitive. Unlike the methods described in the literature, our experiments suggest that stop-words should only be removed if they are the first or the last word in a phrase. The automatically identified frequent phrases can be manually pruned to remove the phrases which are likely to have small relevance in a given context. This is akin to combining the power of human brain to solve complex tasks with the efficiency of computer algorithms to address computing problems at scale.

The developed utilities were demonstrated on finding the most frequently occurring phrases of 1 to 4 words in 5 selected papers in biology and life sciences. The text extraction from more recently published papers appear to be significantly easier than from the older papers. Another example case demonstrated how to convert the list of acronyms and the index from a PDF e-book into the list of biological terms which can be used to aid keyword identification and other text mining tasks. The scripts and data files for all examples are available in the pdfPapers Github public repository.
Appendix

The pdfPapers repository on Github contains the following directories and files.

- example01/ directory with scripts and outputs for processing the paper
- example02/ directory with scripts and outputs for processing the paper
- example03/ directory with scripts and outputs for processing the paper
- example04/ directory with scripts and outputs for processing the paper
- example05/ directory with scripts to create the list of biological terms from an e-book index
- en-dat a dump of aspell US-English dictionary
- en-stopwords a list of common stop words
- pdfastext a shell script
- pdfls a shell script
- pdfsearch a shell script
- README.md a readme file
- textblocks a shell script
- textblocks.1 a help file for the shell script
- textblocks.t examples of function calls for the shell script
- texttoinfo a shell script
- texttoinfo.1 a help file for the shell script
- texttodict a shell script
- texttodict.1 a help file for the shell script

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