

Comparison of keyword-extraction and word-vector generation methods for identifying related genomic datasets

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Abstract

Data-sharing requirements have led to wide availability of genomic datasets in public repositories. Researchers can reuse and combine these datasets to address novel hypotheses. However, after identifying one or more datasets that are relevant to a particular research question, a researcher may have difficulty identifying other datasets that are also relevant, due to the large quantity of available datasets and lack of structure with which they are described. In this study, we focus specifically on Gene Expression Omnibus, a repository that contains genomic data from hundreds of thousands of experiments that is commonly used in biomedical analyses. Notable efforts have been made to manually annotate these data but not been able to keep pace as new datasets are submitted. To address this problem, we use natural language processing (NLP). Under the assumption that a researcher has manually identified a subset of available datasets related to a particular research topic, we use NLP algorithms to extract keywords from the abstract associated with each dataset. Next we summarize the keywords using diverse embedding algorithms and compare the vectors generated to available datasets to identify potential related datasets.

In terms of word vector generation we test six different models. These models vary in training method, domain, and architecture. The six models are the following: BioWordVec - a FastText model trained on biomedical text, FastTextWiki - A FastText model trained on Wikipedia data, FastTextCBOW - a custom FastText model trained on only StarGEO data using the CBOW (continuous-bag-of-words) method, FastTextSkipGram - A custom FastText model trained on only StarGEO data using the SKIPGRAM technique, SciSpaCy - A SpaCy model trained on scientific literature, and SpaCy - A SpaCy model trained with the readily available large web corpus.

We also test nine keyword extraction methods. Three of the methods are statistical models while the other six are graphical methods. The statistical methods are TF-IDF, KP-Miner, and YAKE. TF-IDF works by comparing the frequency of each word found in the passage to its frequency in other passages that exist in the corpus. KP-Miner evaluates each word based on the context surrounding the words to identify keywords. YAKE combines elements of both TF-IDF and KP-Miner by using the context while also taking into account the frequency at which the word appears in the document. The first graphical approach we test is TextRank which is based off of a web technique called PageRank which is used for identifying related webpages through hyperlinks. TextRank performs a similar analysis with text by creating a graph where each word is represented as a node. Relationships between words are drawn as connected nodes. These relationships are used to identify keywords. TopicRank is a process similar to TextRank but the text is preprocessed to create n-grams of nouns and adjectives as keyphrase candidates before creating a graph with them to identify keywords. SingleRank is another extension of TextRank with each node having a weight value assigned to it. PositionRank is a more complicated extension of TextRank where the position of the word within the sentence is assigned a weight along with actual context as in TextRank. TopicalPageRank is another extension of TextRank that seeks to improve experience by weighting those words that appear more in the document. The last graphical approach is MultipartiteRank which uses a multipartite graph to construct the initial graph and calculate weights between nodes.

We found that different combinations of keyword extraction methods and word vector generation yield very different results. This variety was also reflected across the query domains. These results show that natural language processing is a powerful tool that can be harnessed for data collection and more research needs to be done in this area.

Introduction

Natural Language Processing is computational technique that allows computers to process human language [1]. In the past, Natural Language Processing has been used in several biomedical applications such as concept extraction, electronic health record analysis, and text mining. [2,3,4]. However there is a lack of research detailing natural language approaches to data collection, specifically the collection of relevant datasets for analysis. Recently an article was published that details an approach to dataset recommendation using a researchers interests and CV to identify datasets [5]. This paper also detailed some difficulties in dataset recommendation. Some of these challenges are a lack of widely-accepted metadata format, lack of available tools, and an exponential rise in available datasets [5]. In this paper we detail an alternative approach to address this problem using readily available natural language processing tools to identify related datasets from an initial set of related articles.

The major obstacle to data collection for a researcher is a lack of available tools. The aforementioned paper details an approach to help address this issue, but is not capable of using a user-generated query to identify related datasets. Another related tool is BioCaddie [6] which is an ongoing tool to index current datasets to make them easily searchable. However the advantage to our approach is that it requires no indexing and can be applied to any text-based data. Our methodology utilises two techniques widely used in natural language processing, namely keyword extraction and word vector generation [7,8]. Using these two tools, our approach can take several pre-identified datasets and identify other related datasets, no matter how niche the subject area. We test a variety of these different techniques to identify those that are most promising for future use.

Methods

Data collection

As a reference standard, we used annotations from Search Tag Analyze Resource for GEO (STARGEO) [9]. In STARGEO, biomedical graduate students manually curate sample metadata and assign tags to GEO series. We used these annotations to identify series that had been associated with a given phenotype. To represent different types of queries that researchers might perform in GEO, we searched for human phenotypes that would result in a small, medium, or large number of GEO series. We also sought to represent diverse phenotypic categories. On XX[TODO: Please indicate exact or approximate date], we identified two phenotypes with ~100 series, two with ~20 series, and two with fewer than 10 series[Table 1]. (Because STARGEO is an ongoing project, it is likely that additional articles will be associated with these tags over time.) For each GEO series, we used the STAR application programming interface[10] to download the associated abstract, title, and accession number.

Table 1: Caption for this example table.

<i>STARGEO tag(s)</i>	<i>Number of GEO series</i>
Family History + Breast Cancer	6
Liver Damage + Hepatitis	9
Monozygotic Twins	25
Kidney + Tumor + Cell Line	16
Diabetes + Type 1	97
Osteosarcoma	112

Keyphrase extraction

[TODO: Please move the following sentence to the Introduction if these papers are not already mentioned there. Also, make sure we are describing how these models were used and briefly what the authors found.] A variety of natural language processing models are effective on biomedical literature [11,12].

For each abstract, we sought to identify n keyphrases that would most effectively characterize the semantic meaning of the abstract. In our benchmark comparisons, we used n values of 10, 20, and 30 and applied nine unsupervised, keyphrase-extraction techniques to each abstract. To ensure consistency across the techniques, we used the pke Python module[https://aclanthology.org/C16-2015/] for all nine techniques, which were TFIDF[13,14], KP-Miner[15], YAKE[16], TextRank[17], SingleRank[18], TopicRank[19], TopicalPageRank[20], PositionRank[21] and MultipartiteRank[https://arxiv.org/abs/1803.08721]. These techniques uses different algorithmic approaches. [TODO: Will you please clarify what the following sentence is referring to. Is there a specific data file?]An example of the diversity of returned keywords is available in the appendix.

Word-vector models

Using keyphrases from each abstract, we generated word vectors—numeric representations of the text—based on models that had previously been trained on large amounts of unlabeled text. We generated the word vectors using the *fastText* (version X.XX[TODO: specify version]) and *spaCy*

(version Y.Y[TODO: specify version]) open-source libraries [22,23,24], which both have been used widely in biomedical applications [11,25,26] and differ in their methodologies. fastText provides two approaches for generating word vectors: Skip-gram and Continuous-Bag-Of-Words (CBOW). Given a particular word (or subword), the Skip-gram method trains a neural network to predict surrounding (sub)words; the weights of the network's hidden layer are used in the word vector. The CBOW method uses a similar approach but attempts to predict a (sub)word of interest, given a fixed-size window of surrounding (sub)words. For spaCy, we used named-entity recognition models with tokenized, hashed representations constructed from word features[27].[TODO: Please check this wording against what you understand.] We generated a word vector for each keyphrase, summed the vectors for a given abstract, and then divided by the number of keywords in the abstract (as a form of standardization). This technique has been shown to be a simple and accurate way to combine multiple embeddings into a single vector and is often used to generate document-level embeddings [28].
%https://towardsdatascience.com/word2vec-skip-gram-model-part-1-intuition-78614e4d6e0b

“FastText [8] expresses a word by the sum of the N-gram vector of the character level. The embedding method at the subword level solves the disadvantages that involve difficulty in application to languages with varying morphological changes or low frequency. This method was strong at solving the OOV problem, and accuracy was high for rare words in the word set. BioWordVec [9] learns clinical record data from PubMed and MIMIC-III clinical databases using fastText. Based on 28,714,373 PubMed documents and 2,083,180 MIMIC-III clinical database documents, the entire corpus was built. The Medical Subject Headings (MeSH) term graph was organized to create a heading sequence and to carry out word embedding based on a sequence combining MeSH and PubMed. BioWordVec provided a 200-dimensional pretrained word embedding matrix”

[TODO: Please move this to the Introduction.] Both of these algorithms have been shown effective on biomedical natural language processing, but [TODO: this wording is vague. Please add some details to make it concrete.]small differences have been shown between the word vectors generated from either algorithm [29].

Training corpora

[TODO: Please move these ideas to the Introduction or Discussion.] The source of the training data is an important aspect of generating word vectors. Recent literature supports using training data from a research domain that matches the domain of the testing data [11]. However, the benefits of using domain-specific training data remain under question [12].

We used models that had been pre-trained on text from diverse sources. The BioWordVec model[30] was trained on PubMed abstracts and clinical notes from the MIMIC-III database[31] (downloaded from <https://ftp.ncbi.nlm.nih.gov/pub/lu/Suppl/BioSentVec/>). It uses fastText to encode and summarize n-gram representations of words in 200-dimensional word-embedding matrix.

To test this effect we trained models on biomedical literature as well as general sources such as blogs, news articles, and Wikipedia entries [32].

Depending on the model, the word vectors differed in length between 100 and 300. [TODO: Please indicate the vector length for each model and a brief explanation of why we used different lengths.]

Emphasize that we used English corpora.

This training data has several possible algorithms for processing and generating word vectors. There are a total of 6 models tested in this paper. fastText and Spacy are compared head to head, as well as different algorithms and training data. A summary of each model and brief details are shown below.

A spaCy NER model trained on the BC5CDR corpus.

Model	Summary
BioWordVec	fastText Model trained on generic biomedical data with Skip-gram
FastTextWiki	fastText model trained on Wikipedia data with CBOW
FastTextSKIPGRAM	fastText model trained on GEO data using Skip-gram
FastTextCBOW	fastText model trained on GEO data using CBOW
SciSpacy	A Spacy model trained on biomedical data
SpacyWebLG	A Spacy model trained on general Web text ((blogs, news, comments))

Model Evaluation

We tested each combination of keyword extraction and word-vector generation method...

All model evaluation is performed in a Docker container to allow other researchers to perform the same analysis described in this section [33]. The Docker image used to build the container is the python:3.8.5 image available on the Docker website [34]. Running the docker container as pulled from github will run a bash script that performs the following steps. 1. STARGEO is queried to prepare the six queries. The prepareQueryData.py script takes two arguments. The first is a list of GEO identifiers and the second is the query number that these identifiers should belong to. PrepareQueryData.py creates a file system that contains all the abstract and titles of the series that correspond to each identifier. The file system will put each text file into the directory for the corresponding query. This script also randomly selects half of the data to be used as the training data. 2. GetGeoQueries.py is run. This script uses text files generated by GEO to evaluate the performance of GEO. A detailed explanation of this is found below in the manual comparison section. 3. A do loop iterates over the numbers 10, 20, and 30. These numbers are the number of keywords that each model should try to identify from the text. Each iteration performs the following analysis. i. Six scripts that correspond to SciSpaCy, BioWordVec, FastTextWiki, SpaCy, FastTextSkipGram, and FastTextCBOW are run. Each of these scripts takes the following three arguments: number of keywords, vector size, and number of STARGEO articles. Each script performs the following steps: a. All candidate articles from STARGEO are queried b. The specific word vector model is loaded (SciSpaCy, BioWordVec, ...) c. For each query and keyword combination findSimilarity() is run in Helper.py and added to a multiprocessing thread. This script prints to an output file the calculated similarity of each article using each combination d. The top 1, 10 and 100 articles are returned to compare against the articles that STARGEO previously identified as related.

Reduced Set Testing

The results contained within this paper are from a reduced set of all STARGEO articles (266) plus an additional 1000 randomly queried articles from GEO. The purpose for performing the reduced set was the full 41,823 article corpus from STARGEO ran for over one month and we were not able to complete the full testing. A reduced corpus of 1000 articles allowed us to compare the various methods head to head without the need for extensively long wait times. However the analysis is set up in such a way as to allow the researcher to easily change the amount of articles used in the analysis.

Manual Gene Expression Omnibus Evaluation

Gene Expression Omnibus (GEO) is the parent corpus from which STARGEO is derived [35]. To compare our technique directly to GEO we use a manual evaluation. We first use the advanced search option on GEO to input the exact queries we used from STARGEO. To maintain consistency with STARGEO, the results are limited to series and human genomic data. A summary file of all the results is downloaded and analyzed. To ensure equal comparison the results are filtered to only include those datasets that exist in STARGEO's corpus while excluding SuperSeries. Using the same technique for the STARGEO evaluation the top 1,10, and 100 articles are identified and compared against the relevant articles from STARGEO.

Results

The two main techniques in this paper are keyword identification and word vector generation. Both of these methods are described below.

Keyword Identification

Keyword extraction is a vital part of the analysis. There are a variety of techniques to achieve this, and we test the most common 9 techniques in this paper. Each technique performs the analysis slightly differently and this leads to variation in the keywords identified. An example of the variation is shown below.

Sample Abstract -> "BRCA1 and BRCA2 are the genes related with breast and ovarian cancer. They have function in DNA repair processes and thus they are tumor suppressor genes. There are hundreds of mutations identified in these genes. Functional deficiencies due to these mutations impair DNA repair and cause irregularities in the DNA synthesis. The standard method for the laboratory assessment of these BRCA genes includes comprehensive sequencing and testing of broad genomic rearrangements. Members of the families with BRCA mutations have an increased risk for early onset of breast cancer and ovarian cancer occurring at any age."

Keyword Extraction Technique	Top 3 Keywords returned
TopicRank	'mutations', 'breast', 'dna repair processes'
TextRank	'dna repair processes', 'tumor suppressor genes', 'serum ca-125 levels'
SingleRank	'brca mutations', 'brca genes', 'breast cancer'
TopicalPageRank	'brca genes', 'brca mutations', 'tumor suppressor genes'
MultipartiteRank	'mutations', 'genes', 'dna repair processes'

Word Vector Generation

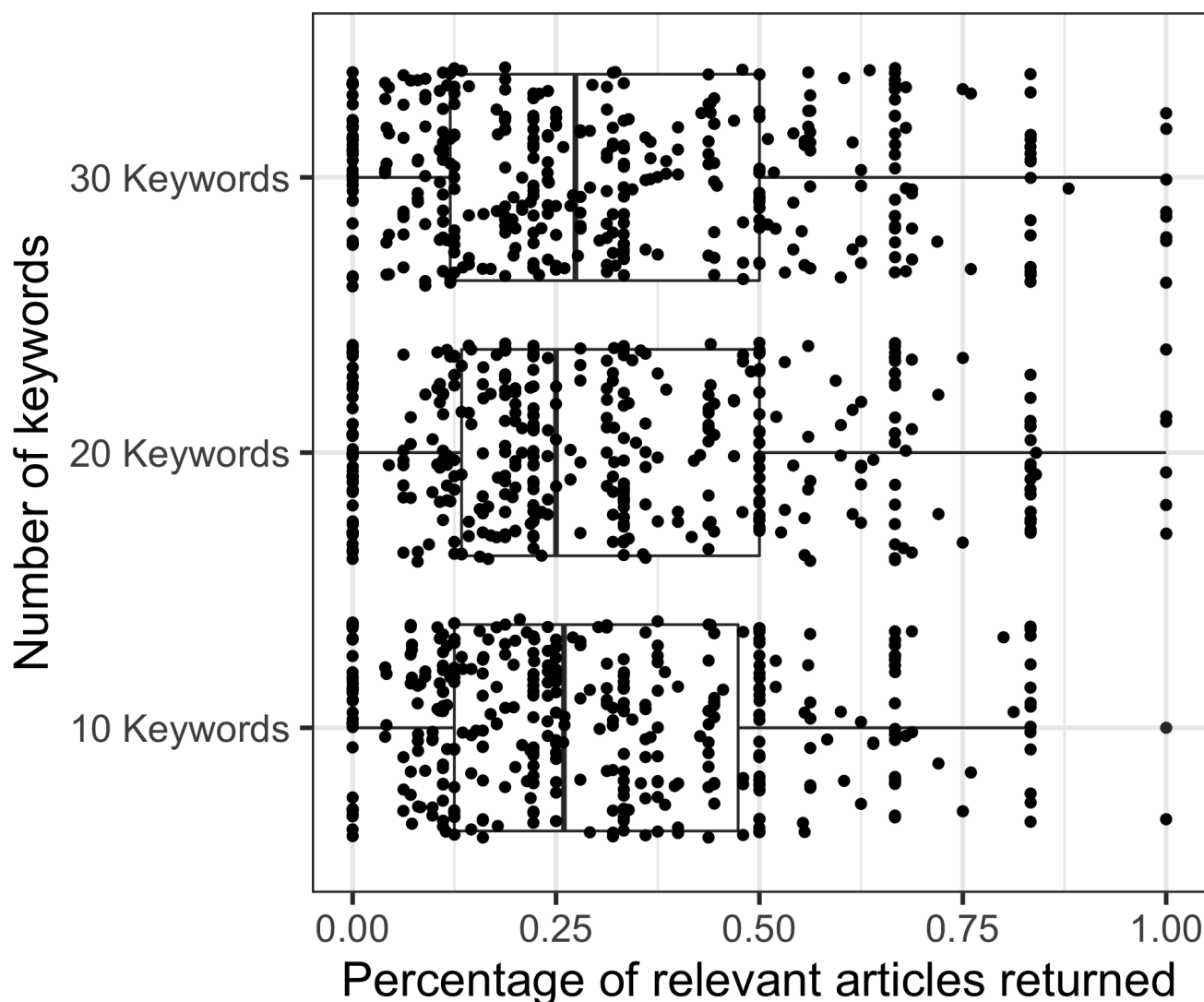
Vector generation is how similarities between articles are calculated. This allows us to give a numerical percentage to quantify the relationship between two datasets. In our analysis we test 6 models that can generate vectors. Each model is trained on unique text and will yield slightly different word vectors. This in turn will generate slightly different cosine similarities. An example of vector generation is shown below:

Word	Vector
Database	[1.3863622 1.0939984 -2.1352 -1.9841313 -0.31141075 1.3959851 ...]
Gene	[1.4969006 2.7855976 -4.313326 -2.5572329 -0.9275282 0.43499815 ...]
Mutation	[2.7130241e+00 2.5561374e-01 -2.1098554e+00 -2.1719341e+00 ...]
Disease	[1.9606729e+00 3.5872436e-01 -2.9315462e+00 -2.3048987e+00 ...]

Evaluation Results


Effect of Number of Keywords Returned on the Percentage of Relevant Articles Returned at 100 Articles

Number of Keywords Extracted vs Percentage of Relevant Articles Returned



This summary graph shows the relationship between the number of keywords queried and percentage of relevant articles returned at 100 articles. Between the three groups a wilcoxon test found no significant difference.

30 keywords

This graph is an example of a graph generated by the AllGraphs script in /images/. All other models are contained in the appendix. This graph is 30 keywords using the SciSpaCy model.  SciSpaCy.

GEO Results

This graph contains the manual Gene Expression Omnibus results.  GEO_Results

Discussion

Overview

The purpose of this project was to illustrate the usage of Natural Language Processing in the data collection phase of any project and to identify techniques to use in future projects. NLP has already been shown to be useful to find related articles of scientific nature [36,37,38]. However to our knowledge no project has been done comparing word vector generation and keyword extraction techniques for usage in data collection. This is addressed in our paper in the head to head comparison of these techniques. We hope this will further our knowledge as to how natural language processing might help researchers in future studies.

Motivation

This project was motivated through our personal experiences attempting to find datasets. Often as researchers a project will began as a big picture idea and the first step is the collection of related datasets to further narrow the project idea. This step can be time-consuming and frustrating due to the lack of tools available and the massive amount of data that exists. Existing tools are limited by user-provided queries that may not be precise. Existing tools such as the search function of Gene Expression Omnibus that take user generated queries are often limited by the exact phrasing of the query. For example the query “mohs” returns 100 results but “moh’s” returns 33 different results. Experiences like this motivated us to look for a technique that could use a dataset to identify related datasets free of human-generated queries.

Observations

The results show a wide variety of accuracy across the queries. This pattern of the same natural language processing technique giving disparate results on intrinsic evaluations is one commonly seen in natural language processing evaluations [8,29,39]. However the results do show a pattern that the best performing results are when the model and data are similar. Another interesting observation is the varying results between queries. The best performing queries are consistently queries one and two which are the smallest queries with six and nine results respectively. This would imply that the more narrowly defined a query, the better this technique can perform.

The amount of keywords does not impact the percentage of relevant articles returned. This is likely due to the fact that 10 keywords is sufficient to capture the meaning of the query. Adding more keywords only adds irrelevant noise to the model.

Practical Utility

Our results show a practical utility for this technique to a researcher who is interested in a very specific knowledge base. If a researcher has previously identified several articles that deal with a narrowly defined subject area, using this technique to query a larger database (not StarGEO) would result in the discovery of potentially all the related datasets that exist in that database. Using this technique, the researcher can bypass the arduous process of collecting datasets and trying to determine which are useful. This technique can also be used to look at multiple datasets within in a broad context. While not useful for potentially finding a niche dataset from a broad query, the ability of this technique to find even distantly related dataset could be used to facilitate a broad understanding of the datasets related to a concept.

It is important to note that this is not a well-polished tool free of bugs. This is a proof of concept that can be applied in various situations to yield useful results. Any customization would require the manual editing of the code to fit the use case.

Limitations

There are several limitations to our approach. Most obvious is a lack of methods to compare it against. There exists no other tool for gathering related datasets from an initial cohort of datasets. This means that the only external evaluation possible is to compare it to hand curation of datasets by other researchers. We did consider this option but rejected it due to the subjective nature of human curation and the time it would require of the participants. There are also other keyword extraction and word vector generation techniques. Our keyword extraction techniques were limited to those available in the PKR Python package to ensure consistency. Word vectors were limited to the those that were most commonly tested and available in other NLP related papers [[12](#),[40](#)]. Further testing is warranted on less known models and techniques.

All analysis were performed on a Dell PowerEdge R730xd server with two Intel Xeon E5-2640 v4 2.4GHz CPUs that each support 10 cores with two threads apiece with a total of 256gb of RAM. All analyses were run using the Multiprocessing package that allowed each combination of keyword extraction and word vector to each be run as a separate task. This hardware was not capable of running the full analysis even using the multiprocessing package. We hypothesis this is due to the relatively long time it takes to generate a word vector.

Appendix

Comparison of Keywords Techniques

Test Abstract from PubMed. [41] Text = "OBJECTIVE: Novel biomarkers of disease progression after type 1 diabetes onset are needed. RESEARCH DESIGN AND METHODS: We profiled peripheral blood (PB) monocyte gene expression in 6 healthy subjects and 16 children with type 1 diabetes diagnosed ~3 months previously, and analyzed clinical features from diagnosis to 1 year. RESULTS: Monocyte expression profiles clustered into two distinct subgroups, representing mild and severe deviation from healthy controls, along the same continuum. Patients with strongly divergent monocyte gene expression had significantly higher insulin dose-adjusted HbA1c levels during the first year, compared to patients with mild deviation. The diabetes-associated expression signature identified multiple perturbations in pathways controlling cellular metabolism and survival, including endoplasmic reticulum and oxidative stress (e.g. induction of HIF1A, DDIT3, DDIT4 and GRP78). qPCR quantitation of a 9-gene panel correlated with glycaemic control in 12 additional recent-onset patients. The qPCR signature was also detected in PB from healthy first-degree relatives. CONCLUSIONS: A PB gene expression signature correlates with glycaemic control in the first year after diabetes diagnosis, and is present in at-risk subjects. These findings implicate monocyte phenotype as a candidate biomarker for disease progression pre- and post-onset, and systemic stresses as contributors to innate immune function in type 1 diabetes."

Keyword Extraction Technique	Keywords Returned
TopicRank	"monocyte gene expression", "diabetes onset", "year"
TextRank	"divergent monocyte gene expression", "monocyte gene expression", "pb gene expression signature"
SingleRank	"pb gene expression signature", "divergent monocyte gene expression", "monocyte gene expression"
TopicalPageRank	"pb gene expression signature", "divergent monocyte gene expression", "monocyte gene expression"
MultipartiteRank	"monocyte gene expression", "diabetes onset", "type"

30 Keywords

SpaCy_30. FastText CBOW_30. FastText Skipgram_30. FastText Wiki_30. SpaCy_30.

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