Subject Section

DTMiner: Identification of potential disease targets through biomedical literature mining

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Associate Editor: Dr. Jonathan Wren

Abstract

Motivation: Biomedical researchers often search through massive catalogues of literature to look for potential relationships between genes and diseases. Given the rapid growth of biomedical literature, automatic relation extraction, a crucial technology in biomedical literature mining, has shown great potential to support research of gene-related diseases. Existing work in this field has produced datasets that are limited both in scale and accuracy.
Results: In this study, we propose a reliable and efficient framework that takes large biomedical literature repositories as inputs, identifies credible relationships between diseases and genes, and presents possible genes related to a given disease and possible diseases related to a given gene. The framework incorporates name entity recognition (NER), which identifies occurrences of genes and diseases in texts, association detection whereby we extract and evaluate features from gene-disease pairs, and ranking algorithms that estimate how closely the pairs are related. The F1-score of the NER phase is 0.87, which is higher than existing studies. The association detection phase takes drastically less time than previous work while maintaining a comparable F1-score of 0.86. The end-to-end result achieves a 0.259 F1-score for the top 50 genes associated with a disease, which performs better than previous work. In addition, we released a web service for public use of the dataset.
Availability: The implementation of the proposed algorithms is publicly available at http://gdr-web.rwebox.com/public_html/index.php?page=download.php. The web service is available at http://gdr-web.rwebox.com/public_html/index.php
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Supplementary information: Supplementary data are available at *Bioinformatics* online.

1 Introduction

Recent scientific discoveries have revealed the molecular, cellular and genetic components of diseases. Researchers have gained many new insights into cellular signaling pathways, genetic alterations and their consequences. Combined with diagnostic breakthroughs, there have been increasing efforts and successes in identifying patient segments defined by biomarkers that are more susceptible to certain diseases or will maximally benefit from certain treatments. Traditionally, oncology was the disease area where the majority of such research was focused. However, in the last decades, there have been considerable advancements in other disease areas, such as respiratory diseases, infectious diseases and inflammatory diseases. All of these new findings are contained in the vast amount of biomedical literature. The effective extraction of gene-disease associations from biomedical literature will potentially enable the discovery and development of new therapeutic targets and patient segment

biomarkers. However, it has remained a daunting task because of the massive volume and the textual complexity of biomedical literature.

Given the strong demand for gene-disease relation extraction from the biomedical literature, over the years ample studies have attempted to tackle it or part of it. The task of gene-disease relation extraction can be broken down into three phases. The first is gene and disease recognition in free text, which can be categorized as a Named Entity Recognition (NER) problem. Machine learning-based methods are one of the approaches used to identify biomedical entities in free text. B Settles (Settles, 2004) proposed a conditional random field model ABNER to recognize biomedical named entities based on orthographic and semantic features. Z Ju et al (Ju *et al.*, 2011) used SVM to recognize biomedical named entities such as proteins and genes in biomedical literature. There are rule-based and pattern-based methods as well. Hanisch D et al (Hanisch *et al.*, 2005) developed a rule-based method to recognize genes and proteins in biomedical text. Singer and Collins (Singer and Collins, 1999) discussed the pattern-based method for name entity recognition in

their work. In this phase, we used search engines to enrich our disease/gene libraries. Previous efforts have been made to accomplish a similar task, including using the World Wide Web to enrich ontologies (Agirre *et al.*, 2000), using search engine query data to detect epidemics (Ginsberg *et al.*, 2009) and using Google data as a complement to co-occurrence frequency in the literature to identify disease-related genes (Kim *et al.*, 2015).

The second phase is to identify the relationships between genes and diseases. A relationship between a gene-disease pair can include but is not limited to therapeutic targets, prognostic factors etc. For example, in the sentence "Our prospective findings suggest that individuals carrying the HFE C282Y mutation may be at increased risk of CHD," a relationship between the gene "HFE" and the disease "CHD" is made clear. Kernel methods are widely used in relation extraction (Bunescu and Mooney, 2005; Zelenko *et al.*, 2003). Recently, several systems have been proposed to identify drug-gene relationships (Xu and Wang, 2012), drug-drug interactions (Percha et al., 2012; Segura-Bedmar *et al.*, 2011), and gene-disease relationships (Bravo *et al*., 2015; Pletscher-Frankild *et al*., 2015; Ozgur *et al.*, 2008). Kim S et al (Kim *et al.*, 2010) has successfully implemented dependency kernels to extract protein-protein interaction information. The Shallow Linguistic Kernel is also used to extract drug-drug interaction information (Segura-Bedmar *et al.*, 2011).

The third phase is to rank the gene-disease relations obtained from the previous phase in an intelligent manner. A frequency-based ranking system is commonly adopted in earlier works. BeFree (Bravo *et al.*, 2015) ranks the relationships according to the frequency of occurrence. Clematide et al (Clematide *et al*., 2012) uses a logistic regression-based method to optimize ranking of relations from curated abstracts.

There has been some work dedicated to the gene-disease relation extraction problem, which is the end-to-end problem that we try to solve in this paper. CoPub (Frijters *et al.*, 2008) provides a text mining tool that detects co-occuring biomedical concepts in abstracts from the MedLine literature database. BeFree (Bravo *et al.*, 2015) can be used in a text mining workflow aimed at extracting information on biological associations from scientific publications. But all current work is limited both in coverage and ranking precision.

Herein, we present a framework for extracting gene-disease relationships from biomedical literature that addresses all three phases. It takes large biomedical literature repositories and the name of a gene or a disease of interest as inputs and produces a meaningful ranked list of diseases or genes that are related to the input entity with supporting evidence. In the NER phase, we implemented an algorithm that combines dictionary-based fuzzy matching and conditional random fields (CRF) to recognize genes and diseases in free text. Next, we trained a SVM model combining lexical features and syntactic features to identify the relationships between genes and diseases. Finally, we proposed a ranking algorithm to rank the disease-related genes based on co-occurrence frequency, paper citations, and author information.

2   Materials and Methods

In this section, the data sources used in this work and the detailed algorithms and methods designed for this framework will be introduced.

2.1   Data Sources

The data used in this work mainly include the gene/disease term libraries, the biomedical literature database, the annotated data and the ground truth.

2.1.1   Gene Library

The gene library used in this study is a combination of three publicly available gene/protein databases, namely the NCBI-gene database (Brown *et al.*, 2015), the HGNC gene dataset (Gray *et al.*, 2015) and the UniProt knowledge base (Uniprot Consortium, 2015), with cross-references. NCBI-gene database contains almost all of the publicly available nucleotide sequences and their protein translations. By August, 2014, HGNC provided the names and symbols of 39,135 genes. UniProt is a comprehensive resource of protein sequence and functional information. Since genes are sometimes named after their protein names, UniProt is also used as a data source for gene recognition.

The combined gene library has 60,197 genes. Each gene and its synonyms were cross-referenced among all three data sources mentioned above.

2.1.2   Disease Term Library

Disease Ontology (Mitraka and Schriml, 2015), MedDRA(The Medical Dictionary for Regulatory Activities) (Brown *et al.*, 1999), UMLS (The Unified Medical Language System) (Bodenreider, O., 2004) and IDDB (Infectious Disease Database) were cross-referenced to yield the disease database used in this study. The disease term library is hierarchical. If disease A belongs to a parent class B, an attribute "is a" with the value being B will be attached to the disease A. In total, the disease library includes 22,831 diseases. For each disease, the library includes its unique identifier, disease name, disease synonyms, ID in each source disease database and its parent classes.

2.1.3   Biomedical Literature Database

The biomedical literature database used in this study is Medline (https://www.nlm.nih.gov/bsd/mms/medlineelements.html), the U.S. National Library of Medicine (NLM) journal citation database. It includes citations from more than 5,600 scholarly journals, over 25 million references to biomedical and life science journal articles from as early as 1946. The downloadable database contains 779 files in the XML format in chronological order. Every piece of data contains the PMID, the publication date, the author information, the citations etc. PubMed (http://www.ncbi.nlm.nih.gov/books/NBK25499/#chapter4.EFetch) provides retrieval APIs to Medline.

2.1.4   Annotated Data

In order to train and evaluate the methods and tools used in this work, we gathered annotated texts containing a total of 2340 positive disease-gene relationship labels and 1437 negative relationship labels. 2113 of the positive labels and 1010 of the negative labels are from Genetic Association Databases (GAD) (Becker *et al.*, 2004), a database of genetic association data from complex diseases and disorders. Since GAD didn't label all gene/disease entities contained within a sentence, which will bias our NER training, many of the data from GAD are re-annotated manually by domain experts for gene entities, disease entities, positions of genes and positions of diseases at the sentence level. The remaining training data are sentences randomly selected from the biomedical abstracts in Medline. Gene entities, disease entities, positions of genes, positions of diseases and the relationships between genes and diseases are manually labeled in each sentence.

2.1.5   Ground Truth

Human annotated gene-disease associations for 10 randomly selected diseases obtained from DisGeNET (http://www.disgenet.org/) serve as

our ground truth data set. The diseases include Retinitis Pigmentosa, Adrenal Gland Chromaffinoma, Bipolar I Disorder, Hyperlipidemia, Papilloma, Thrombocytopenia, Glioblastoma, Hernia Diaphragmatic, Brain Ischemia, and Cerebrovascular Accident. The ground truth is used to evaluate the end-to-end results of a system.

2.2 Extraction Workflow

To extract gene-disease associations from biomedical literature, we aim to extract from Medline triples of the format (disease; gene; score). "Disease" and "gene" denote the unique identifiers of diseases and genes respectively in our disease library and gene library. "Score" refers to the plausibility of gene-disease associations. When the user queries the relevant genes of a particular disease, the framework will return the results based on "score".

Fig. 1. Work Flow of Extracting Gene-Disease Associations from Medline.

Specifically, to accomplish the goal, we first pre-process the data from Medline and obtain three kinds of information: 1) Title and abstract of articles, 2) author information, and 3) article reference information. Then, the gene/disease recognition module processes the titles and abstracts using both a Stanford NER tool (Finkel et al., 2005) trained on 2000 annotated sentences (1000 from GAD and 1000 from our manually labeled data library) and a dictionary-based longest match strategy using the gene and disease libraries. Recognition results of the two methods are combined. In case of discrepancies, heuristic rules are applied to resolve them. Next, in the association detection phase, all recognized gene-disease pairs that co-occur within the same sentence are considered as candidate evidence. A binary SVM classifier, which extracts two types of features, namely local lexical features and global syntactic features, is used to determine the plausibility of the candidate pairs. Finally, positive pairs are ranked by three methods. The basic method is counting the co-occurrence frequency. The second method is to weigh each co-occurrence by the PageRank of the paper from which the evidence was extracted, in a paper citation network constructed from PubMed. The last and most advanced method considers the duplicated evidence published by the same author, and thus suppresses the contribution of such evidence. Details of each part of the workflow will be presented in the sections below.

2.3 Gene/Disease Recognition

The gene/disease recognition task is an NER task where the entities being recognized are genes and diseases. We brought up a hybrid recognition method in this study. A CRF-based NER tool, namely the Stanford NER tool (Finkel *et al.*, 2005), is combined with a dictionary-based longest match strategy.

The Stanford NER tool provides a general implementation of (arbitrary order) linear chain CRF sequence models. It was trained on 2,000 annotated sentences from Medline before being used to recognize genes and diseases names in the titles and abstracts of articles from Medline. Recognized genes and diseases are then mapped to the unique identifiers in the gene and disease libraries. The Stanford NER is further enhanced in the following fashion. If a gene or a disease recognized by the Stanford NER tool can't be found in the libraries, a web crawler will automatically query Bing (https://www.bing.com/) to search for information

that can relate the gene/disease name to one of the unique identifiers. A gene/disease is added to the results only when it can be related to a unique identifier. If a gene/disease that can be related to a unique identifier is currently not in its synonym set, it will be added as a synonym.

Next, a dictionary-based longest match algorithm is implemented using the gene and disease libraries as dictionaries. The longest match strategy uses a sliding window. A fixed-length window slides within the sentence and the words within the window are fuzzy matched to the items included in the gene and disease libraries. The "fuzzy match" strategy picks up both terms that are exact matches and terms with small discrepancies in some punctuation or singular/plural form. (For example, "lung type-i cell membrane-associated glycoprotein" is considered a match to "lung type i cell membrane-associated glycoprotein", and "benign gastric tumours" is considered a match to "benign gastric tumour".) If the words covered by the window are matched to a gene or a disease, they will be marked to make sure that other matched words will not overlap with them. When the window reaches the end of the sentence, the window length is reduced by one, and the window resumes sliding from the start of the sentence, until the length is zero.

The results of the two methods are combined and a number of heuristic rules are applied to resolve possible discrepancies: 1) If a term's length is less than four characters, it is likely to be either an acronym or an incorrect recognition. It will be treated as an acronym if its longer synonym (complete form) occurs in the former context. 2) If a term with less than four characters does not have a longer synonym occurring in the text before it, but it is recognized by the enhanced Stanford NER, then it will be added to the final results. 3) If a term is recognized by both the dictionary-based method and the enhanced Stanford NER, the result of the enhanced Stanford NER is used. The rationale is that the enhanced Stanford NER takes advantage of web search engines, which encompasses more knowledge and therefore is potentially more accurate in recognizing named entities.

Genes and diseases may sometimes share the same synonyms. Thus, a term may be mapped to several unique identifiers. However, if a synonym of the term occurs in the previous context and the synonym can be mapped to a specific unique identifier, the term will be considered as belonging to the same unique identifier. Otherwise, the term is mapped to each of the unique identifiers once. Considering the hierarchies among genes and diseases, a term will be mapped not only to its unique identifier, but also its parent class's unique identifier.

Gene-disease pairs recognized in this phase are considered candidate evidences for association between the gene and the disease.

2.4 Association Detection

In this step, a binary SVM classifier is implemented to determine the plausibility of association between a gene and a disease based on the gene-disease pairs extracted from the previous step. Given a sentence $S=w_1,…,g,…,w_i,…,d,…,w_n$, the classifier decides whether there is a gene-disease relation between entities g and d.

The classifier utilizes two types of features, namely local lexical and global syntactic features. The local lexical feature contains words surrounding the gene or the disease terms in the original text. The global syntactic feature, which contains unigrams, bigrams and trigrams drawn from 1) the shortest path between the gene and the disease terms in the dependency tree, and 2) the path between the least common ancestor (LCA) of the two terms and the root of the dependency tree. The features are detailed in Table 1. Feature 1 is the local lexical feature and contains the context information of the gene and the disease terms, while features

2 and 3 are the global syntactic features and contain rich syntactic information from the dependency tree. The lemmas and the dependency tree are generated by the Stanford CoreNLP tool (Manning *et al.*, 2014).

Table 1. Features Extracted for Association Detection

Feature	Type	Description
1	Local lexical feature	Lemmas of the two words in front of the gene term and the two words behind the gene term, and lemmas of the two words in front of the disease term and the two words behind the disease term.
2	Global syntactic feature	Unigram, bigram, and trigram of lemmas on the shortest path between the gene and the disease terms in the dependency tree.
3	Global syntactic feature	Unigram, bigram, and trigram of lemmas on the path between the LCA of the gene and the disease terms and the root of the dependency tree.

The effect of words with the part-of-speech (POS) tag "neg" or "advmod" that modify verbs is taken into account in feature extraction. (For example, the word "not" in "does not relate with" or the word "rarely" in "rarely indicates the association" strongly implies the negative association of a candidate pair.). Words with POS tag "neg" or "advmod" that modify verbs are included in the paths used by global features. Besides, the gene and the disease terms in the paths are replaced with the general names "GENE" and "DISEASE", because specific gene/disease names do not contain information concerning association detection.

Take the following sentence as an example:

> All three complementary approaches employed (family-based, case-control and quantitative trait design) suggest a role for the MAO A promoter-region polymorphism in confering risk for ADHD in our patient population.

In this sentence, "MAO A" is a gene term and "ADHD" is a disease name. A part of the dependency tree of the sentence is drawn in Figure 2. "for", "the", "promoter-region", "polymorphism", "risk", "for", "in" and "our" are extracted for feature 1. From the shortest dependency path between the gene and the disease terms, n-grams like "risk for DISEASE" and "in risk for" are extracted for feature 2. The LCA of the gene and the disease terms in the dependency tree is "suggest". N-grams including "suggest role for" and "role for polymorphism" are extracted for feature 3.
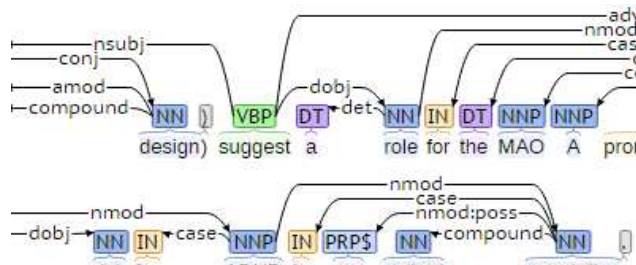

Fig. 2. Part of the Dependency Tree of sentence "All three complementary approaches employed (family-based, case-control and quantitative trait design) suggests a role for the MAO A promoter-region polymorphism in confering risk for ADHD in our patient population."

After the features are extracted, libsvm (Chang and Lin, 2011) is used to train the binary SVM classifier. The kernel function of SVM grades the local lexical feature (i.e. feature 1) and the global syntactic features (i.e. feature 2 and 3) and combines the scores linearly. The features are treated as a bag of words. Every possible word or n-gram is considered a dimension in a vector. If the feature contains a particular word/n-gram, the value of the corresponding dimension is set to one; otherwise, it is zero. The similarity between two instances of features is quantified by the cosine value between vectors.

A set of positive gene-disease pairs along with the unique identifiers of journal articles in which they co-occur are generated and passed on to the next step.

2.5 Ranking

For a given disease, hundreds of positive gene-disease pairs are generated from the previous steps, and vice versa. The ranking of genes for a particular disease and the ranking of diseases for a particular gene is done using the following three ranking methods.

The basic ranking method uses the co-occurrence frequency. Different pairs with the same disease are ranked by the number of distinct journal article in which they co-occur.

The second method is to grant a weight to each co-occurrence according to the PageRank of the journal article, in a paper citation network constructed from PubMed. PageRank was proposed by Larry Page and Sergey Brin (Page *et al.*, 1999). It is used by Google for website ranking. PageRank operates on the idea that the more important a website is, the more websites will link to it. So it utilizes the number and importance of websites that link to a given website to assess the importance of this website, or the PageRank of the website. In this study, we apply the principle of PageRank to the task of publication citation. If a journal article is cited by more articles and the articles that cite it are more influential, the article itself is more influential and its PageRank is higher.

According to the reference information obtained from Medline, we first built a paper citation network, as shown in Figure 3. Nodes in the network denote the journal articles, and the edge from node A to node B means that Paper A cites Paper B. Based on the paper citation network, the PageRank of each node (i.e. each article) is calculated.
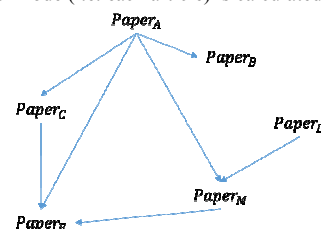

Fig. 3. Simplified Paper Citation Network

When we get the PageRank of the articles, the following formula is used to calculate the score of the gene-disease pair, where g denotes the gene, d denotes the disease, $C_{(g,d)}$ denotes the set of all the articles that contain the (g,d) pair and pr(a) denotes the PageRank of paper a.

$$Score(g, d) = \sum_{a \in C_{(g,d)}} pr(a) \qquad (1)$$

The third ranking method takes the authors into consideration. Biomedical researchers, who focus on specific diseases or genes, may write

about the same gene-disease pair in multiple publications. For instance, Mark J Sarnak mentioned the association between Kidney Failure and Cystatin C in up to twelve distinct papers. They should not be considered as twelve independent evidences. In the third method, if a gene-disease pair is repeatedly mentioned by the same author, the contribution of the duplicated evidence will be suppressed.

We assume that the sum of weights an author can grant to different evidences of the same pair is one. If an author mentions the same pair in multiple publications, the weights of the evidence from each of the publications is equal and sums to one. The weight of each paper where the evidence of (g,d) is extracted is

$$w_a(g,d) = \frac{\sum_{x \in l} \frac{1}{|c_x|}}{|l|} \qquad (2)$$

where l denotes the author list of paper a, $|c_x|$ denotes the number of papers author x wrote about (g,d). Then we can modify the score function of gene-disease pairs proposed in the formula (1).

$$Score(g,d) = \sum_{a \in C_{(g,d)}} w_a(g,d) \times pr(a) \qquad (3)$$

The fourth method uses a PageRank function that is adjusted by a time factor. This is based on the observation that recently published papers may have "less exposure" for citation than those published before them. The time-weighted PageRank is defined as below.

$$pr(u) = d \sum_{v \in B(u)} \frac{pr(v)}{N_v} + (1 - d) \times T_u \qquad (4)$$

where T_u denotes a smoothed time factor related to each paper's year of publication. Disease gene pairs mentioned by the same author is also be suppressed in this method.

2.6   Significance Testing

The micro sign test (Yang et al., 1999) is used to examine whether the improvements in F1-scores are statistically significant. A one-sided p-value that is less than 0.05 is considered as statistically significant.

3   Results

The number of associations extracted by our method is shown in Table 2. The number of associations extracted by our method is significantly larger than Befree (Bravo et al., 2015). At the meantime, the precision of our extraction is better than Befree, which is detailed in Section 3.3.

Table 2 Results of Extracted Associations Compared to BeFree

	Associations	Genes	Diseases
DTMiner	**1,728,535**	**16,893**	**9,950**
BeFree	131,012	2,803	2,751

3.1 Gene/Disease Recognition

First, we evaluated the Gene/Disease recognition module on 800 annotated sentences. In these 800 sentences, 592 diseases and 525 genes were labeled. The recognition results are shown in Table 3. We found that Stanford NER tool has high precision but poor recall. By combining it with dictionaries, our hybrid recognition method has about a 0.125 enhancement on the F-score than the dictionary-only method, which is

similar to the method used by BeFree (Bravo et al., 2015) and CoPub (Frijters et al., 2008). The F-score improved about 0.014 (p < 0.01) after we enriched our gene and disease dictionary using Bing. Our method also performs much better than ABNER (Settles, 2004) on these sentences.

Table 3.   Results of Gene/Disease Recognition

	Precision	Recall	F-score
ABNER	0.593	0.549	0.57
Only Dictionary	0.839	0.659	0.738
Stanford NER tool	**0.954**	0.524	0.673
Before enriched by Bing	0.851	0.875	0.863
After enriched by Bing	0.87	**0.885**	**0.877**

3.2 Relation Extraction

We evaluated the performance of the SVM classifier through 10-fold cross validation on a training set with 2,080 positive samples and 1,277 negative samples. The result is shown in Table 4. We found that the F-score can only reach 0.755 if we use the local lexical features alone. However, if we use both the local features and the global features, the SVM classifier achieves the best performance.

Table 4.   Results of Gene/Disease Relation Extraction

Feature	Precision	Recall	F-score
Local Lexical Feathers	0.761	0.748	0.755
Global Syntactic Features	0.827	0.853	0.839
Local+Global features	**0.846**	**0.88**	**0.863**

Due to the large volume of biomedical literature, computation time becomes an important issue in the relationship extraction task. A comparison between the state-of-art system BeFree and our work is shown in Table 5. Although the F-score of our work is slightly lower than that of BeFree, the training speed of the classifier and the testing speed on 420 randomly selected instances of our work are significantly (more than 10x) faster.

Table 5.   Comparison of Relation Extraction Performance

Framework	F-score	Training Time (s)	Testing Time (s)
DTMiner	0.863	**24**	**241**
BeFree	**0.898**	384	4393

3.3 Ranking

The ground truth is obtained from DisGeNET. We selected 10 diseases and computed the mean reciprocal rank (MRR) of ranks obtained by the three methods mentioned above. The result is shown in Table 6. For most diseases, the suppressed PageRank achieves the best performance. Overall, compared with the frequency-based method, the MRR increased 10.6% if we weighted the paper with PageRank score. And, after suppressing the contribution of the same author, the MRR increased by 8.4% .

Table 6. MRR Results of Different Ranking Methods

Disease	Frequency-Based	PageRank-Based	Suppressed PageRank	Weighted PageRank
retinitis pigmentosa	0.111	0.141	0.146	0.156
adrenal gland chromaffinoma	0.161	0.194	0.212	0.207
bipolar i disorder	0.26	0.268	0.273	0.26
hyperlipidemia	0.267	0.279	0.325	0.325
papilloma	0.183	0.24	0.321	0.226
thrombocytopenia	0.089	0.072	0.063	0.063
glioblastoma	0.278	0.3	0.346	0.274
hernia diaphragmatic	0.026	0.028	0.029	0.027
brain ischemia	0.052	0.076	0.067	0.06
cerebrovascular accident	0.178	0.178	0.147	0.175
overall	0.161	0.178	0.193	0.177

Then, we randomly chose five different diseases (cerebrovascular accident, brain ischemia, hernia diaphragmatic, thrombocytopenia and retinitis pigmentosa) and evaluated the top K ranking of our results. The result is shown in Table 7. If we select the top-50 genes, the Suppressed PageRank method achieves the better result compared with other methods. While K increases, the performance of these four methods' is similar. This is because when K increases, most of the known disease-related genes are ranked on top. The numbers of true positives, false positives, and false negatives for the Suppressed PageRank method are listed in the supplementary material, as well as some examples.

Table 7. F-score of top-K of the Rankings

Top K	Freq-Based	PR-Based	Weighted PR	Sup-PR	BeFree	CoPub
K = 50	0.221	0.228	0.237	**0.241**	0.213	0.212
K=100	0.236	0.235	0.230	**0.238**	0.214	0.211
K=150	0.22	**0.221**	0.216	0.216	0.186	0.192
K=200	0.196	0.196	**0.201**	0.197	0.167	0.175

We also compared our results with BeFree (Bravo *et al.*, 2015) and Copub (Frijters *et al.*, 2008). The results are shown in Figure 4. In most cases, Suppressed PageRank results are about 0.03 higher than CoPub and BeFree. In addition, our system extracts many more genes associated with a specific disease. (cerebrovascular accident: 1238 associated genes; brain ischemia: 1588; hernia diaphragmatic: 266; thrombocytope-

nia: 1049; retinitis pigmentosa: 818) For example, we extracted 818 genes associated with *retinitis pigmentosa*, while BeFree only extracts 193 genes (of which 142 are in our results) and Copub extracts 179 genes (of which 124 are in our results). Manual inspection of 40 of the 818 genes reveals that 34 of these associations are correct. This shows that our approach not only achieves much better coverage, but also competitive accuracy.
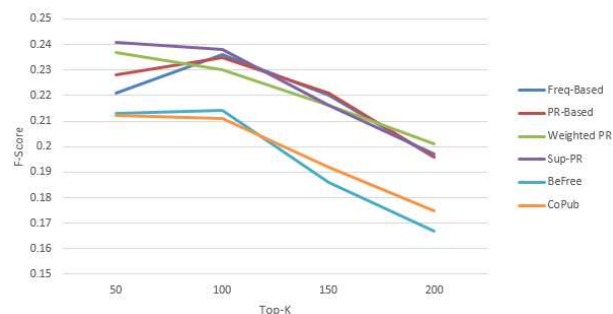
Fig. 4. F-score of Top-K Rankings

3.4 Web-based Service

The DTMiner web server is a gene-disease association discovery platform using the U.S. National Library of Medicine (NLM) journal citation database, MEDLINE, as a data source. It is accessible from the website: http://gdr-web.rwebox.com/public_html/index.php. DTMiner allows user-friendly access to a gene-disease relationship database. The associations between genes and diseases are represented in a bipartite graph and it permits both queries of genes and diseases. For a disease (or gene) query, DTMiner will provide multiple disease (or gene) choices ranked by the string similarity of the users' input. Next, the website displays all the genes (or diseases) related to the users' selection according to their relative weighted PageRank. Further, a user can find the evidence of each disease-gene pair (the papers where they co-occur) for further details. See Fig. 5., Fig. 6. and Fig.7. for example.

Fig. 5. Search for lung disease

Fig. 6. Select the First Choice

Fig. 7. Click Evidence for More Details

We also provide a URL for users to submit a query directly from a program and return Json-encoded results to the program, which is http://gdr-web.rwebox.com/public_html/get-disease.php for disease and http://gdr-web.rwebox.com/public_html/get-gene.php for gene. Please see http://gdr-web.rwebox.com/public_html/index.php?page=help.php for more details.

4   Discussion

In the named entity recognition phase, the dictionary-only method, which is similar to the method BeFree (Bravo *et al.*, 2015) and CoPub (Frijters *et al.*, 2008) used, shows an F-score of 0.738. We achieved a 0.125 improvement on the F-score by combining the Stanford NER tool with the dictionary-based method. The CRF model behind the Stanford NER tool takes advantage of the distribution information of words and thus compensates the dictionary-only method. Incorporating the Internet search engine further improved the F-score by 0.014, for that information from the Internet enriched our gene/disease libraries.

In the relation extraction phase, we achieved an F-score of 0.863 using both the local lexical features and global syntactic features. Using the local lexical features or the global syntactic features alone gives a lower F-score, which indicates that, both the local and the global features are effective and necessary. While the F-score of our method is nearly as good as that of BeFree (Bravo *et al.*, 2015), our speed is more than 10 times faster. It is because we utilized fewer but more representative features than BeFree so that we can achieve this advantage in speed while maintaining the F-score.

In terms of the MRR results, the suppressed PageRank method achieved the best overall performance. The PageRank-based method increased the overall MRR by 10.6%. This is because our PageRank-based method weighted the trustworthiness of each paper according to the citation information. The suppressed PageRank method further improved the overall MRR by 8.4%. This supports our assumption that some authors wrote multiple papers about the same gene-disease association and such behavior will falsely boost the ranking of the aforementioned association in the PageRank-based method. The same judgement

on the performance of the four ranking methods is given by the F-score results. Adding a time factor in the PageRank function does not seem to improve the MRR. This may suggest that cutting edge research get cited frequently despite the short amount of time since publication.

Furthermore, our end-to-end results showed that our system extracted much more genes related to a given disease than BeFree (Bravo *et al.*, 2015) and CoPub (Frijters *et al.*, 2008) did. This is due to the large scale of our input and the good performance of our NER method and relationship extraction method.

5   Conclusion

In this paper, we proposed a framework for the automatic extraction of gene-disease relation from biomedical literature. For the gene and disease recognition, we built large gene and disease libraries by combining and cross referencing existing biomedical knowledge bases. We enriched our dictionary by identifying new synonyms using search engines. For association detection, we designated effective features and built an efficient SVM classifier. For the ranking, we considered the weight of papers and the other contributions by the same authors and proposed three different algorithms for ranking. In addition, we launched a web service for public access to our results. Overall, our system created a disease-gene association dataset that is several times larger than any previously reported dataset of similar nature, achieved a good balance between accuracy and computation time, and outperformed existing state-of-the-art systems on similar tasks. The system has been made available online for free public access, which will potentially enable the discovery and development of new therapeutics and breakthrough in diagnostics.

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