

EVIDENCEMINER: Textual Evidence Discovery for Life Sciences

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Abstract

Traditional search engines for life sciences (e.g., PubMed) are designed for document retrieval and do not allow direct retrieval of specific statements. Some of these statements may serve as textual evidence that is key to tasks such as hypothesis generation and new finding validation. We present EVIDENCEMINER, a web-based system that lets users query a natural language statement and automatically retrieves textual evidence from a background corpora for life sciences. EVIDENCEMINER is constructed in a completely automated way without any human effort for training data annotation. It is supported by novel data-driven methods for distantly supervised named entity recognition and open information extraction. The entities and patterns are pre-computed and indexed offline to support fast online evidence retrieval. The annotation results are also highlighted in the original document for better visualization. EVIDENCEMINER also includes analytic functionalities such as the most frequent entity and relation summarization. EVIDENCEMINER can help scientists uncover important research issues, leading to more effective research and more in-depth quantitative analysis. The system of EVIDENCEMINER is available at <https://evidenceminer.firebaseio.com/>¹.

1 Introduction

Search engines on scientific literature have been widely used by life scientists for discoveries based on past knowledge. Each day, millions of users query PubMed² and PubMed Central³ (PMC) for their information needs in biomedicine (Allot et al., 2019). However, traditional search engines for life sciences (e.g., PubMed) are designed for document

retrieval and do not allow direct retrieval of specific statements (Lu, 2011; Ren et al., 2017; Shen et al., 2018). With the results from those search engines, scientists still need to read a large number of retrieved documents to find specific statements as textual evidence to validate the input query. This textual evidence is key to tasks such as developing new hypotheses, designing informative experiments, or comparing and validating new findings against previous knowledge.

While the last several years have witnessed substantial growth in interests and efforts in evidence mining (Lippi and Torroni, 2016; Wachsmuth et al., 2017; Stab et al., 2018; Chen et al., 2019; Majithia et al., 2019; Chernodub et al., 2019; Allot et al., 2019), little work has been done for evidence mining system development in the scientific literature. A major difference between evidence in the scientific literature and evidence in other corpora (e.g., the online debate corpus) is that scientific evidence usually does not have a strong sentiment (i.e., positive, negative or neutral) in the opinion it holds. Most scientific evidence sentences are objective statements reflecting how strongly they support a query statement. Therefore, if scientists are interested in finding textual evidence for “*melanoma is treated with nivolumab*”, they may expect a ranked list of statements with the top ones like “bi-cytopenia in primary lung melanoma treated with nivolumab” as the textual evidence that supports the input query.

This paper presents EVIDENCEMINER, a web-based system for textual evidence discovery for life sciences (Figure 1). Given a query as a natural language statement, EVIDENCEMINER automatically retrieves sentence-level textual evidence from a background corpora of biomedical literature. EVIDENCEMINER is constructed in a completely automated way without any human effort for training data annotation. It is supported by

¹A brief demo of EVIDENCEMINER is available at <https://youtu.be/iYuQ6gsr--I>.

²<https://www.ncbi.nlm.nih.gov/pubmed/>

³<https://www.ncbi.nlm.nih.gov/pmc/>

novel data-driven methods for distantly supervised named entity recognition and open information extraction. EVIDENCEMINER relies on external knowledge bases to provide distant supervision for named entity recognition (NER) (Shang et al., 2018b; Wang et al., 2018b, 2019). Based on the entity annotation results, it automatically extracts informative meta-patterns (textual patterns containing entity types, e.g., CHEMICAL inhibit DISEASE) from sentences in the background corpora. (Jiang et al., 2017; Wang et al., 2018a; Li et al., 2018a,b). Sentences with meta-patterns that better match the query statement are more likely to be textual evidence. The entities and patterns are pre-computed and indexed offline to support fast on-line evidence retrieval. The annotation results are also highlighted in the original document for better visualization. EVIDENCEMINER also includes analytic functionalities such as the most frequent entity and relation summarization. The contributions and features of the EVIDENCEMINER system are summarized as follows.

1. We build EVIDENCEMINER, a web-based system for textual evidence discovery for life sciences. EVIDENCEMINER is supported by novel methods for distantly supervised named entity recognition and pattern-based open information extraction.
2. The retrieved evidence sentences can be easily located in the original text. The entity and relation annotation results are also highlighted in the original document for better visualization.
3. Analytic functionalities are included such as finding the most frequent entities/relations for given entity/relation types, and finding the most frequent entities given a relation type with another entity.

2 Related Work

Search engines performing sentence-level retrieval have been developed in the biomedical domain. For example, Textpresso (Müller et al., 2004) highlights the query-related sentences in the retrieved documents. However, the sentence highlighting is only based on query word matching, which does not necessarily find sentences semantically related to the input query. Another example is LitSense (Allot et al., 2019), which retrieves semantically similar sentences in biomedical literature given

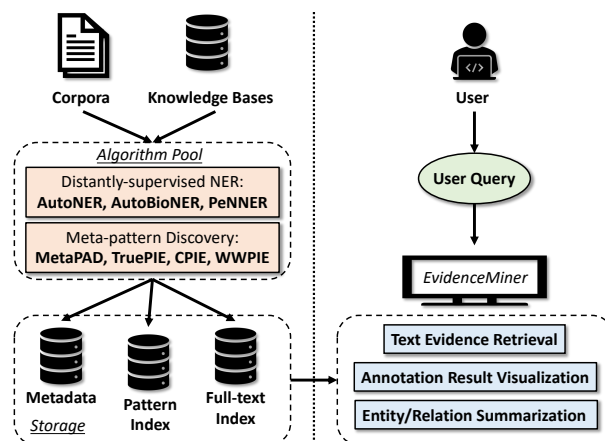


Figure 1: System architecture of EVIDENCEMINER.

a query sentence. It returns best-matching sentences using a combined approach of traditional word matching and neural embedding. However, their neural embeddings are noisy and thus negatively impact the effectiveness in retrieving query-specific evidence sentences. EVIDENCEMINER is more effective compared with LitSense for textual evidence retrieval in biomedical literature.

Similar tools are also developed for other domains, such as claim mining and argument mining tools on Twitter or news articles. PerspectroScope (Chen et al., 2019) allows users to query a natural language claim and extracts textual evidence in support or against the claim. ClaimPortal (Majithia et al., 2019) is an integrated infrastructure for searching and checking factual claims on Twitter. TARGER (Chernodub et al., 2019) is an argument mining framework for tagging arguments in the free input text and keyword-based retrieval of arguments from the argument-tagged corpus. Most of these tools rely on fully supervised methods that require human-annotated training data. It is difficult to directly apply these systems to other domains, such as life sciences, since it is non-trivial to retrieve the set of human-annotated articles and the annotations are prone to errors (Levy et al., 2017).

3 System Description

EVIDENCEMINER consists of two major components: an open information extraction pipeline and a textual evidence retrieval and analysis pipeline. The open information extraction pipeline includes two functional modules: (1) distantly supervised NER, and (2) meta-pattern-based open information extraction; whereas the textual evidence retrieval and analysis pipeline includes three functional mod-

Background corpora	Cancers	Heart Diseases
#PubMed abstracts	48,201	11,766
#PMC full-text papers	7,130	1,151
#Sentences in total	1,466,091	246,106
#Entity instances	3,315,092	400,327
#Relation instances	29,160	9,576

Table 1: Basic statistics of background corpora. It includes PubMed abstracts and PMC full-text papers related to cancers and heart diseases published in 2019.

ules: (1) textual evidence search, (2) annotation result visualization in the original document, and (3) the most frequent entity and relation summarization. Figure 1 shows the system architecture of EVIDENCEMINER. The functional modules are introduced in the following sections.

3.1 Open Information Extraction

The open information extraction pipeline extracts entities with distant supervision from knowledge bases and relations with automatic meta-pattern discovery methods. In particular, to extract high-quality entities and relations, we design noise-robust neural models for distantly supervised named entity recognition (Shang et al., 2018b; Wang et al., 2019) and wide-window meta-pattern discovery methods to deal with the long and complex sentences in biomedical literature (Wang et al., 2018a; Li et al., 2018b).

Data Collection. To obtain the background corpora for EVIDENCEMINER, we collect the titles and abstracts of 26M papers from the entire PubMed⁴ dump, and the full-text contents of 2.2M papers from PubMed Central⁵ (PMC). For the demonstration purpose, we select a subset of documents published in 2019 that are specifically related to two important diseases (cancers and heart diseases) to form the background corpora. The subset of documents are selected by concept matching on MeSH⁶, a biomedical concept ontology with the concepts related to cancers (Neoplasms) and heart diseases (Cardiovascular Diseases). Table 1 summarizes the statistics of the background corpora.

Distantly Supervised Named Entity Recognition. EVIDENCEMINER relies on UMLS⁷, a comprehensive biomedical knowledge base to provide distant supervision for named entity recognition. We select 5 major biomedical entity types

(Organism, Fully Formed Anatomical Structure, Chemical, Physiologic Function, and Pathologic Function) including 17 fine-grained entity types (Archaeon, Bacterium, Eukaryote, Virus, Body Part/Organ/Organ Component, Tissue, Cell, Cell Component, Gene or Genome, Chemical, Organism Function, Organ or Tissue Function, Cell Function, Molecular Function, Disease or Syndrome, Cell or Molecular Dysfunction, Experimental Model of Disease, and Pathological Function) from UMLS as the entity types to be annotated. To tackle the problem of limited coverage of the input dictionary, we first apply a data-driven phrase mining algorithm, AutoPhrase (Shang et al., 2018a), to extract high-quality phrases as additional entity candidates. Then we automatically expand the dictionary with a novel dictionary expansion method (Wang et al., 2019). The expanded dictionary is used to label the input corpora with the 17 fine-grained entity types to train a neural model. We apply AutoNER (Shang et al., 2018b), a state-of-the-art distantly supervised NER method that effectively deals with noisy distant supervision. Comparing with PubTator (Wei et al., 2013), a state-of-the-art BioNER system trained with massive human annotation on 5 biomedical entity types, EVIDENCEMINER can automatically annotate 17 fine-grained entity types with high quality without any human effort for training data annotation.

Meta-pattern Discovery. Based on the entity annotation results above, meta-patterns can be automatically discovered from the corpora to support textual evidence discovery. Meta-patterns are defined as sub-sequences in an entity-type-replaced corpus with at least one entity type token in it. For example, “PPAR gamma agonist” and “caspase 1 agonist” are two word-sequences in the raw corpus. If we replace all the entities (i.e., “PPAR gamma” and “caspase 1”) with their corresponding entity types (i.e., \$GENE) in the raw corpus, “PPAR gamma agonist” and “caspase 1 agonist” will be represented as one meta-pattern “\$GENE agonist” in the entity-type-replaced corpus. Meta-patterns containing at least two entity types (e.g., “\$CHEMICAL induce \$DISEASE”) are relational meta-patterns. Quality relational meta-patterns can serve as informative textual patterns that guide textual evidence discovery. We apply two state-of-the-art meta-pattern discovery methods, CPIE (Wang et al., 2018a) and WW-PIE (Li et al., 2018b), to extract high-quality meta-patterns from the NER-

⁴<https://pubmed.gov/pubmed>

⁵<https://pubmed.gov/pmc>

⁶<https://www.nlm.nih.gov/mesh/>

⁷<https://www.nlm.nih.gov/research/umls/index.html>

tagged corpora. Both methods are specifically designed to better deal with the long and complex sentence structures in the biomedical literature. In EVIDENCEMINER, we combine the meta-pattern extraction results from CPIE and WW-PIE as our informative meta-patterns to guide textual evidence retrieval. We use Elasticsearch⁸ to create the index for each sentence for fast online retrieval. In addition to indexing the keywords, we also index each sentence with the meta-patterns it matches and the corresponding entities extracted by the meta-patterns in the sentence.

3.2 Textual Evidence Retrieval and Analysis

The textual evidence retrieval and analysis pipeline retrieves textual evidence given a user-input query statement and the indexed corpora. The retrieved evidence sentence can be easily located in the original text. The entity and relation annotation results are also highlighted in the text for better visualization. EVIDENCEMINER also includes analytic functionalities such as finding the most frequent entities and relations as summarization.

Textual Evidence Search. Given a user-input query statement and the indexed corpora, EVIDENCEMINER retrieves and ranks the candidate sentences with a combined approach of keyword weighting and meta-pattern weighting. Sentences with meta-patterns that better match the query statement are ranked higher as textual evidence. This ranking mechanism is more effective compared with existing methods (e.g., LitSense) for textual evidence retrieval in biomedical literature (see Section 4). We use Elasticsearch to support keyword and meta-pattern search over the indexed corpora.

In Figure 2, we show an example of our search interface. For example, if scientists are interested in finding the textual evidence for “*melanoma is treated with nivolumab*”, they can search it in EVIDENCEMINER and see the top results such as “*bi-cytopenia in primary lung melanoma treated with nivolumab*” (Figure 2a). If they click one of the top results, the retrieved sentence will be highlighted in the original article (Figure 3) on the annotation interface. Moreover, EVIDENCEMINER allows more flexible queries such as a mixture of keywords and relational patterns. For example, if scientists are interested in finding the diseases that can be treated with the chemical “nivolumab”, but are not sure which disease to search, they may input a query like

“*nivolumab, DISEASEORSYNDROME treat with CHEMICAL*”. EVIDENCEMINER automatically finds all the textual evidence indicating a “treatment” relationship with the chemical “nivolumab” (Figure 2b).

Annotation Result Visualization. The annotation interface shows all the annotated entities and relations for better visualization. For example, in Figure 3, we color all the annotated entities with different colors for different types. We use five different colors for the five major biomedical entity types and two additional colors for two specific fine-grained types, “Gene or Genome” and “Disease or Syndrome”, since those two are the most frequent biomedical entity types. In Figure 3, we see that the “melanoma” is colored as a “Disease or Syndrome” and “nivolumab” is colored as a “Chemical”. We also list all the meta-pattern instances and meta-patterns that match the sentences in the article. If the user clicks the meta-pattern instances, the corresponding sentences will also be highlighted in the article. In Figure 3, a meta-pattern “DISEASEORSYNDROME patient treat with CHEMICAL” captures the entity pair “melanoma” and “nivolumab” in the article.

Entity and Relation Summarization. To make our system more user-friendly and interesting, we add analytic functionalities for the most frequent entity and relation summarization. For example, in Figure 4, if scientists are interested in finding the most frequent diseases, they can search “entity_type=DISEASEORSYNDROME” in our analytic interface and see the top entities such as *tumor* and *breast cancer*. Similarly, if scientists are interested in finding the most frequent chemical-disease pairs with a treatment relation, they can search “pattern=DISEASEORSYNDROME treat with CHEMICAL” in our analytic interface and see the top entity pairs such as *HCC&sorafenib*. More interestingly, if researchers are interested in finding the most frequent diseases that can be treated by a specific chemical (e.g., nivolumab), they can search “entity=nivolumab&pattern=DISEASEORSYNDROME treat with CHEMICAL” in our analytic interface and see the most frequent diseases, such as *melanoma* and *NSCLC*, that can be treated with nivolumab. With these analytic functionalities, EVIDENCEMINER can help scientists uncover important research issues, leading to more effective research and more in-depth quantitative analysis.

⁸<https://www.elastic.co/>

melanoma is treated with nivolumab

Example : NSCLC is treated with nivolumab, HCC is treated with sorafenib, prostate cancer is treated with androgen

Sentence Analytics

"melanoma is treated with nivolumab" (Total: 7000, Took: 134ms)
-- At most 10 results are shown per page --

Bicytopenia in Primary Lung Melanoma Treated with Nivolumab. [Title]
Evidence Score: 26.57 | 2019 | Internal medicine (Tokyo, Japan) | PMID30449777 | Ayuma, Takahashi

Predicting marker for early progression in unresectable melanoma treated with nivolumab. [Title]
Evidence Score: 25.82 | 2019 | International journal of clinical oncology | PMID30168088 | Tomohiro, Kondo

METHODS: A retrospective review was performed on 39 consecutive patients with unresectable melanoma treated with nivolumab. [Context]
Evidence Score: 24.87 | 2019 | International journal of clinical oncology | PMID30168088 | Tomohiro, Kondo
Title: Predicting marker for early progression in unresectable melanoma treated with nivolumab.

A 49-year-old patient with metastatic melanoma was treated with nivolumab (Opdivo). [Context]
Evidence Score: 24.33 | 2019 | Clinical nuclear medicine | PMID31306191 | Micheline, Razzouk-Cadet
Title: Nivolumab-Induced Pneumonitis in Patient With Metastatic Melanoma Showing Complete Remission on 18F-FDG PET/CT.

Response to imatinib in vaginal melanoma with KIT p.Val559Gly mutation previously treated with nivolumab, pembrolizumab and ipilimumab. [Title]
Evidence Score: 23.99 | 2019 | The Journal of dermatology | PMID30614559 | Takayoshi, Komatsu-Fuji

No dose response relation has been observed in melanoma patients treated with intravenous nivolumab dosed from 0.1 to 10 mg/kg.

Label Coloring & Frequent Associated Entities

- Organism
 - Eukaryote
 - Virus
- Fully Formed Anatomical Structure
 - Body Part, Organ, or Organ Component
 - Tissue
 - Cell
 - Cell Component
 - Gene or Genome
- Chemical
- Physiologic Function
 - Organism Function
 - Organ or Tissue Function
 - Cell Function
 - Molecular Function
- Pathologic Function
 - Disease or Syndrome
 - Cell or Molecular Dysfunction

(a) Query: *melanoma is treated with nivolumab*

nivolumab, DISEASEORSYNDROME treat with CHEMICAL

Example : NSCLC is treated with nivolumab, HCC is treated with sorafenib, prostate cancer is treated with androgen

Sentence Analytics

"nivolumab, DISEASEORSYNDROME treat with CHEMICAL" (Total: 7000, Took: 140ms)
-- At most 10 results are shown per page --

METHODS: A retrospective review was performed on 39 consecutive patients with unresectable melanoma treated with nivolumab. [Context]
Evidence Score: 30.20 | 2019 | International journal of clinical oncology | PMID30168088 | Tomohiro, Kondo
Title: Predicting marker for early progression in unresectable melanoma treated with nivolumab.

studied gut microbiome in NSCLC patients treated with nivolumab and in healthy people [78]. [Context]
Evidence Score: 30.04 | 2019 | International journal of molecular sciences | PMID31003463 | Kamila, Wojas-Krawczyk

A 49-year-old patient with metastatic melanoma was treated with nivolumab (Opdivo). [Context]
Evidence Score: 29.57 | 2019 | Clinical nuclear medicine | PMID31306191 | Micheline, Razzouk-Cadet
Title: Nivolumab-Induced Pneumonitis in Patient With Metastatic Melanoma Showing Complete Remission on 18F-FDG PET/CT.

OBJECTIVE: To comprehensively evaluate the clinical presentation of endocrine irAEs in patients with lung cancer treated with nivolumab. [Context]
Evidence Score: 30.04 | 2019 | Endocrinologia, diabetes y nutricion | PMID29910159 | Ana M, Ramos-Leví
Title: Nivolumab-induced thyroid dysfunction in patients with lung cancer.

We report four cases of advanced renal cell carcinoma with peritoneal metastases treated with nivolumab. [Context]
Evidence Score: 28.95 | 2019 | Hinyokika kyo. Acta urologica Japonica | PMID31697887 | Takuya, Hida
Title: [Clinical Effect of Nivolumab on Advanced Renal Cell Carcinoma with Peritoneal Metastasis].

Label Coloring & Frequent Associated Entities

- Organism
 - Eukaryote
 - Virus
- Fully Formed Anatomical Structure
 - Body Part, Organ, or Organ Component
 - Tissue
 - Cell
 - Cell Component
 - Gene or Genome
- Chemical
- Physiologic Function
 - Organism Function
 - Organ or Tissue Function
 - Cell Function
 - Molecular Function
- Pathologic Function
 - Disease or Syndrome
 - Cell or Molecular Dysfunction

(b) Query: *(nivolumab, DISEASEORSYNDROME treat with CHEMICAL)*

Figure 2: The search interface with the textual evidence retrieved. The evidence score indicates the confidence of each retrieved sentence being a supporting evidence of the input query.

EvidenceMiner

Label Coloring & Entity Counts

Sorted By: None

- Organism
 - Eukaryote
- Fully Formed Anatomical Structure
 - Body Part, Organ, or Organ Component
 - Cell
 - Cell Component
 - Gene or Genome
- Chemical
- Physiologic Function
 - Organism Function
 - Organ or Tissue Function
 - Cell Function
 - Molecular Function
- Pathologic Function
 - Disease or Syndrome
 - Cell or Molecular Dysfunction
 - Experimental Model of Disease

objective response of 55% (95% CI 45–66). The median duration of intracranial response has not been reached. Ipilimumab monotherapy has been studied in a phase II study in 72 patients with melanoma and brain metastases [22]. Patients received four doses of 10 mg/kg intravenous ipilimumab once every 3 weeks. Patients who were clinically stable at week 24 were eligible to receive 10 mg/kg ipilimumab every 12 weeks. Patients in cohort A were neurologically asymptomatic and were not receiving corticosteroids at inclusion. Patients in cohort B were symptomatic and received a stable dose of corticosteroids. The primary endpoint was the proportion of patients with disease control, defined as complete response, partial response or stable disease after 12 weeks, assessed with modified WHO criteria. The above mentioned clinical trials clearly demonstrated intracranial responses of patients with melanoma brain metastases treated intravenously with immune checkpoint inhibitors. Four other clinical trials with nivolumab and ipilimumab in patients with melanoma brain metastases are ongoing [23]. In a phase II trial nivolumab and ipilimumab is combined with radiotherapy (NCT03340129). In a phase III trial nivolumab and ipilimumab are combined with fotemustine (NCT02460068). Recently, a phase I/II trial (NCT03025256) of concurrent intravenous and intrathecal nivolumab for patients with leptomeningeal metastases has started. IgG4 antibodies can undergo Fab (Fragment antigen binding)-arm exchange [24, 25]. Fab-exchange can be prevented by introducing a mutation in the hinge region of the antibody, as has been done for nivolumab [25, 26]. The constant region fragment (Fc) of the antibody determines the effector functions and kinetics [27]. Antibodies with neonatal Fc receptor (FcRn) binding can enter cells via endocytosis and are prevented from degradation by the FcRn, resulting in a prolonged elimination half-life [27–29]. Nivolumab is an IgG4 antibody with FcRn binding [30]. IgG4 antibodies like nivolumab have a low potential to induce antibody dependent cell mediated cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC) [27, 30]. This prevents toxic effects of nivolumab on the lymphocytes themselves and thereby preserves T cell function. Nivolumab binds to native PD-1 molecules expressed on activated T cells with an EC50 of 0.64 nM [30].

Q. No dose response relation has been observed in melanoma patients treated with intravenous nivolumab dosed from 0.1 to 10 mg/kg.

The receptor occupancy of nivolumab has been investigated at a dose range from 0.1–10 mg/kg. The median PD-1 receptor occupancy by nivolumab was 64–70% across all dose levels. These results demonstrate that the majority of PD-1 receptors are bound by nivolumab at the lowest dose level tested (0.1 mg/kg). No effect between dose and receptor occupancy was observed within the studied dose range. A sustained receptor occupancy above 70% of nivolumab on PD-1 on circulating T cells has been observed for more than 2 months after nivolumab infusion despite a serum half-life of nivolumab of 12 to 20 days regardless of dose [26]. Nivolumab pharmacokinetics Nivolumab is dosed intravenously and has linear pharmacokinetics within the studied dose range of 0.1–10 mg/kg [2]. Based on population pharmacokinetic analysis at steady state at dose level 3 mg/kg every 2 weeks, the clearance, terminal half-life and

Meta-pattern Extractions

Instances	Meta Pattern
• melanoma • nivolumab	DISEASEORSYNDROME patient treat with CHEMICAL
• melanoma • brain metastases	DISEASEORSYNDROME patient with DISEASEORSYNDROME
• Tumor • lymphocytes	DISEASEORSYNDROME infiltrating CELL
• brain metastases • inhibitors	DISEASEORSYNDROME treat with CHEMICAL
• melanoma • nivolumab	DISEASEORSYNDROME patient treat with CHEMICAL

Figure 3: The annotation interface with all the entity and relation annotation results.

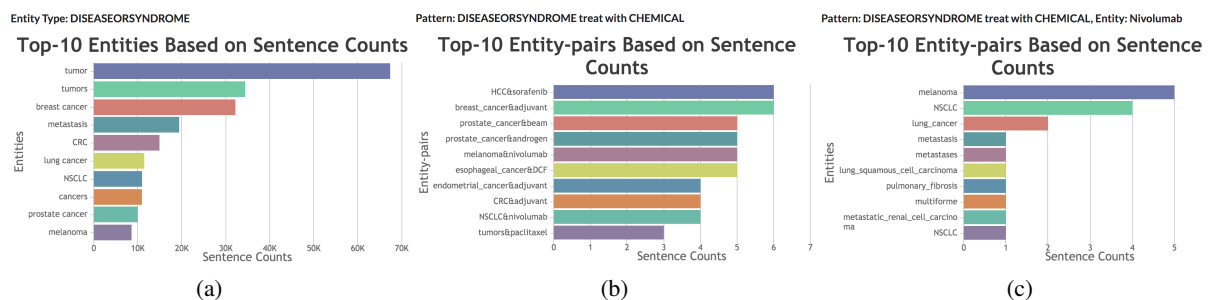


Figure 4: The analytic interface with the entity and relation summarization results. The queries used are (a) `entity_type=DISEASEORSYNDROME`, (b) `pattern=DISEASEORSYNDROME treat with CHEMICAL`, and (c) `entity=nivolumab&pattern=DISEASEORSYNDROME treat with CHEMICAL`.

Method / nDCG	@1	@5	@10
BM25	0.714	0.720	0.746
LitSense	0.599	0.624	0.658
EVIDENCEMINER	0.855	0.861	0.889

Table 2: Performance comparison of the textual evidence retrieval systems with nDCG@1,5,10.

4 Evaluation

To demonstrate the effectiveness of EVIDENCEMINER in textual evidence retrieval, we compare its performance with the traditional BM25 (Robertson et al., 2009) and a recent sentence-level search engine, LitSense (Allot et al., 2019). The background corpus is the same PubMed subset for all the compared methods. We first ask domain experts to generate 50 query statements based on the relationships between three biomedical entity types (gene, chemical, and disease) in the Comparative Toxicogenomics Database⁹. Then we ask domain experts to manually label the top-10 retrieved evidence sentences by each method with three grades indicating the confidence of the evidence. We use the average normalized Discounted Cumulative Gain (nDCG) score to evaluate the textual evidence retrieval performance. In Table 2, we observe that EVIDENCEMINER always achieves the best performance compared with other methods. This method for text evidence retrieval has been accepted by the International Conference on Intelligent Systems for Molecular Biology (ISMB) 2019 for a presentation at the special session on Text Mining for Biology and Healthcare.

5 Further Development

There are many directions in which we hope to develop EVIDENCEMINER further.

⁹<http://ctdbase.org>

Extended Search Functions. In some cases, a strict query matching may not find sufficiently high-quality answers due to the stringent search requirements or limited available entities that match the search queries. In this case, a smart query processor should automatically kick-in to do an approximate match. Such a match could be a graph-based approximate match (e.g., match the most critical subcomponent of document graphs) or an embedding-based semantic match (e.g., matching similar entities based on the approximate semantics computed by text embedding).

Comparative and Timeline Summarization. For a comparative summary, a user may query a set of entities (e.g., genes or diseases). We need to conduct a summary of the major differences among the set of genes or diseases to be compared by analyzing massive text on the fly (using our precomputed index and preprocessing mechanisms). For a timeline summary, a user may query certain entities and we will show its most frequent, closely associated entities/relations over time. With such facilities, scientists will be able to recognize the differences among comparative classes and know the trend of research related to particular entities.

6 Conclusion

We build EVIDENCEMINER, a web-based system for textual evidence discovery for life sciences. The retrieved evidence sentences can be easily located in the background corpora for better visualization. EVIDENCEMINER also includes analytic functionalities such as the most frequent entity and relation summarization. Biomedical scientists have found EVIDENCEMINER to be useful in their research. We will continue developing EVIDENCEMINER to be a more intelligent system that can assist in more efficient and in-depth scientific discoveries.

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