ABSTRACT

Claims are a fundamental unit of scientific discourse. The exponential growth in the number of scientific publications makes automatic claim extraction an important problem for researchers who are overwhelmed by this information overload. Such an automated claim extraction system is useful for both manual and programmatic exploration of scientific knowledge. In this paper, we introduce an online claim extraction system and a dataset of 1,500 scientific abstracts from the biomedical domain with expert annotations for each sentence indicating whether the sentence presents a scientific claim. We compare our proposed model with several baseline models including rule-based and deep learning techniques. Our transfer learning approach with a fine-tuning step allows us to bootstrap from a large discourse-annotated dataset (Pubmed-RCT) and obtains F1-score over 0.78 for claim detection while using a small annotated dataset of 750 papers. We show that using this pre-trained model based on the discourse prediction task improves F1-score by over 14 percent absolute points compared to a baseline model without discourse structure. We release a publicly accessible tool for discourse model, claim detection model, along with an annotation tool. We discuss further applications beyond Biomedical literature.

Keywords  Biomedical Claim · Scientific Claim Extraction · Recurrent Neural Network · Transfer Learning

1 Introduction

Claims are a fundamental unit of scientific discourse. However, the exponential growth of publications has made it challenging for researchers to keep track of research papers introducing new claims. Automatic extraction of claims from scientific articles promises to alleviate some of these problems, additionally supporting other scientific processes such as knowledge exploration, efficient reading [1], and automated text summarization [2]. DARPA’s recently launched Systematizing Confidence in Open Research and Evidence (SCORE) program to tackle automatic claim detection (with confidence measurement) underscores the importance of the task in wider contexts.

Recently, Thorne et. al. [3] released the FEVER dataset that consists of factual claims from Wikipedia validated by crowd-workers. Annotating scientific claims, on the other hand, requires significant domain expertise which makes it challenging to create a large dataset for training statistical models. Dernoncourt et. al. [1] released the PUBMEDRCT discourse-tagging dataset – a large-scale dataset of sentences from 200k structured abstracts from Pubmed, each
sentence is either from background, introduction, method, result, or conclusion sections. However, the annotated dataset related to scientific domain is still limited as presented in [4, 5, 6]. Since claim extraction and discourse tagging are related, it creates an opportunity for applying techniques that exploit weak supervision and transfer learning [7].

In this paper, we introduce a scientific claim detection task with a dataset of 1,500 scientific papers with expertly annotated claims. This is the largest claim-annotated dataset specifically aimed towards scientific documents. We build on a neural discourse tagging model based on a Bidirectional LSTM (Bi-LSTM) with Conditional Random Field (CRF) [8] and transfer the representations to train a claim extraction model. Our fine-tuned model achieves 47% higher F1-score compared to the rule-based method presented in the previous research [5]. We show that pre-training the model on the Pubmed-RCT dataset allows our model to achieve 14% higher F1-score than a model trained solely on the claim extraction dataset. We make the code for claim extraction, our dataset, and our annotation tool publicly available to the community.

2 Dataset: An expertly annotated dataset of biomedical claims

We introduce a novel dataset of expertly annotated claims in biomedical paper abstracts. While there are multiple definitions of scientific claims proposed in previous literature, we follow previous definitions (e.g., [5]) to characterize a claim as a statement that either (1) declares something is better, (2) proposes something new, or (3) describes a new finding or a new cause-effect relationship. One abstract can have multiple claims.

Three annotators with biomedical domain expertise and fluency in English are selected for the task. The annotators were presented with instructions and a few examples before starting to annotate. The full instructions provided to experts on the annotation tool are detailed in Appendix A. An example of an annotated claim from an abstract is shown in Figure 1. The abstracts are sampled from the top 110 biomedical venues by number of abstracts in the MEDLINE database from the year 2008 to 2018 parsed using the Pubmed Parser library [9]. The dataset consists of 1,500 abstracts containing 11,702 sentences. The pairwise inter-annotator agreement (IAA) scores between the three annotators (Cohen’s Kappa, \( \kappa \)) [10, 11] are 0.630, 0.575, and 0.678 respectively. The Fleiss’s Kappa between all annotators is 0.629. The final label for training the claim prediction model is computed as the majority vote between all three annotators, producing a total of 2,276 claim sentences. The low-IAA score is by nature of the task which is previously report in Lauscher et. al. [12]. The distribution of the relative position of the claims identified through this process are shown in Figure 6 in Appendix A. We compare IAA of the final label with crowdsourcing from annotators with no biomedical background and get \( \kappa \) of 0.096. This shows that a great deal of background knowledge is required for the annotation. Thus, annotating abstract could be expensive because of this specialization.

3 The Discourse Prediction and Claim Extraction tasks

In this section, we introduce the discourse prediction task and the claim extraction task. Formally, an abstract is represented as a sequence of sentences \( S = \{S_1, ..., S_n\} \). In PUBMEDRCT dataset, each sentence is associated with a discourse type \( \{D_1, ..., D_k\} \), where \( D_i \in \{Objective, Introduction, Methods, Results, or Conclusions\} \). The discourse prediction task is to predict the discourse types for a sequence of sentences from a new abstract. The claim extraction task is to predict whether a sentence \( S_i \) is a claim or not (0 / 1 classification) for a given sequence of sentences \( S \).
Figure 2: **Schematic of Transfer Learning with fine-tuning technique.** The last layer of the discourse classification model is replaced by the claim extraction model. Transfer learning and fine-tuning is applied to adapt from the learned discourse classification structure.

### 4 Discourse Prediction Model based on Structured Abstracts

To train a discourse prediction model, we use the P**UBLMEDRCT** dataset [1] which contains discourse types associated with each sentence in 200,000 abstracts. We experiment with two main neural architectures – (i) vanilla Bi-LSTM model and (ii) Bi-LSTM with CRF layer (Bi-LSTM CRF) presented by [8]. The CRF layer takes the outputs at each timestep of the Bi-LSTM layer and uses them to jointly infer the most probable discourse type for all sentences in a given sequence of sentences. Transfer learning and fine tuning are applied to pre-trained discourse models to train the claim extraction model later on.

### 5 Claim Extraction Model

We experiment with the following three models for claim extraction.

#### 5.1 Rule-based claim extraction

We implement a baseline model using the rule-based claim extraction algorithm presented by Sateli et. al. [5]. It processes part-of-speech patterns and pre-defined set of keywords that signals claim statements. We re-implement the algorithm in Python with the `spacy` library [13] which achieves a similar F1-score to that reported in the original paper (Table 1).

#### 5.2 Sentence embedding with discourse probability

We implement another baseline model using the sentence classification technique presented by Arora et. al. [14]. The sentence embedding is calculated by a weighted combination of the inverse word frequency in MEDLINE abstracts and word embeddings. Then, first principal component of the embedding is subtracted to capture second order information. Then, we concatenate a sentence embedding with discourse probability calculated by the discourse prediction model. We then apply regularized logistic regression to predict the probability of a claim.

#### 5.3 Transfer Learning with fine-tuning from discourse prediction model

First, the discourse Bi-LSTM and Bi-LSTM CRF models are trained based on PubMedRCT dataset using pre-trained word embeddings selecting from Glove word vector [15] with 300 dimensions or PubMed pre-trained word vector with 200 dimensions [16]. We train the discourse model with batch size of 64 with a reduce-on-plateau learning rate
scheduler with factor of 0.5 and Adam optimizer \[17\] with the learning rate of 0.001 for all experiments. All models are implemented using the AllenNLP library \[18\]. Then, we apply transfer learning technique and fine tuning to train the models on our expertly annotated dataset. The schematic of the training process can be found in figure 2.

| Model                           | Validation |        |        | Test  |        |        |
|---------------------------------|------------|-------|-------|-------|-------|-------|
|                                 | Precision  | Recall| F1-score | Precision | Recall | F1-score |
| Rule-based (Sateli et. al.)     | 0.349      | 0.364| 0.356  | 0.315      | 0.322 | 0.319  |
| Last sentence as a claim        | 0.845      | 0.542| 0.660  | 0.835      | 0.548 | 0.662  |
| Sent Embedding                  | 0.605      | 0.641| 0.623  | 0.624      | 0.674 | 0.648  |
| Sent Embedding + Discourse      | 0.709      | 0.723| 0.716  | 0.715      | 0.711 | 0.713  |
| Bi-LSTM CRF only annotation data| 0.778      | 0.521| 0.624  | 0.701      | 0.609 | 0.652  |
| Bi-LSTM CRF Conclusion as Claim | 0.616      | 0.773| 0.685  | 0.582      | 0.792 | 0.671  |
| Transfer Learning (Pubmed)      | 0.735      | 0.723| 0.729  | 0.723      | 0.730 | 0.727  |
| Transfer Learning (Glove)       | 0.738      | 0.765| 0.751  | 0.762      | 0.729 | 0.745  |
| Transfer Learning CRF (Pubmed)  | 0.840      | 0.764| 0.800  | 0.887      | 0.685 | 0.773  |
| Transfer Learning CRF (Glove)   | 0.859      | 0.750| 0.801  | 0.866      | 0.727 | 0.790  |

Table 1: **Model Evaluation on claim annotation dataset.** Transfer Learning model is done by taking pre-trained discourse model for sentence prediction. Transfer Learning with CRF is done by taking pre-trained discourse model with CRF layer.

6 Evaluation and Results

We perform experiments using 50% of the corpus for training (750 articles), 25% for validation (375 articles), and 25% for testing (375 articles). We use precision, recall, and F1-score to evaluate the performance of the models (Table 1). We compare the performance of rule-based model, predicting last sentence as a claim, sentence embedding model, sentence embedding with a concatenation of discourse probabilities (Sentence Embedding + Discourse), Bi-LSTM with CRF layer trained only using the claim extraction dataset, Bi-LSTM with CRF layer where we use the conclusion class as a true label for claim, transfer learning of vanilla Bi-LSTM of discourse prediction, and transfer learning from Bi-LSTM with CRF layers.

The rule-based model presented by Sateli et. al. \[5\] achieves F1-score of 0.35 and it is overall significantly lower than all other models. This shows that the rule-based approach built for the CS domain does not transfer well to the biomedical domain. Predicting last sentence as a claim gives a high precision but relatively low recall since claim can occur outside the last sentence. We observe that the transfer learning with fine-tuning of pretrained Bi-LSTM CRF model from discourse task achieves the best F1-score in claim extraction task in the biomedical domain. The GloVe pre-trained word vector gives a slightly better performance compared to the Pubmed vectors. These results suggest that overall discourse information is very relevant and improves performance substantially. The difference between F1-score of the best model without discourse and model with pre-trained discourse is 14%.

Error Analysis The best model correctly predicts all claims in abstracts for 60 percent of test articles. 31 percent of the articles has only one missclassified sentence. We now examine the rest of the cases where we misclassified more than one sentence. We found two types of errors. In one type of error, the model is unusually confident that the last sentence contains a claim. For example, for the article PMID: \[25717311\] the model wrongly predicts the sentence "Results are discussed in the context of developmental theories of visual processing and brain-based research on the role of visual skills in learning to read." as a claim when in reality is just a result statement. In another type of error, the model predicts with low probability that claims are in the middle of the abstract. For example, for the abstract PMID: \[24806295\] it misses predicting the following sentence as a claim "... Our results also show that aMCI forms a boundary between normal aging and AD and represents a functional continuum between healthy aging and the earliest signs of dementia." even though it predicts the previous sentence as a claim correctly. Investigating the cause of this pattern and making modifications to address these issues are an area of future work.

7 Related Work

Previous research has analyzed news \[19, 20\], social media \[21\], persuasive essays and scientific articles \[22\], and Wikipedia \[23, 3\] to extract claims and premises, a task called Argumentation Mining. However, in the biomedical domain, the emphasis and data availability have been substantially less compared to these other domains. In particular, claim extraction in Biomedical domain has been dominated by rule-based techniques \[5\] and classic machine learning techniques \[6, 24\] whereas modern Argumentation Mining relies on deep learning techniques such as in \[25, 26, 27\] which show that learning from weak supervision can help improve several text prediction tasks.
Current datasets for claim extraction in scientific domain are relatively small. Moreover, they are in constrained fields such as computer science, computational linguistic, and chemistry. [6] produced a CoreSC dataset containing 265 articles in physical chemistry and biochemistry. [28] produced the Dr. Inventor dataset which contains annotations of 40 computer graphics articles. [4] introduced a dataset of 75 articles for predicting discourse using articles from Pubmed. [5] presented a dataset with annotations for claims and contributions using full text of 30 articles from computer science domains. Biomedical literature may benefit from previous development, but it is unclear how well we can translate such domains into it.

8 Conclusion and Future work

Automatically extracting claims made in scientific articles is becoming increasingly important for information retrieval task. In this paper, we present a novel annotated dataset for claim extraction from the biomedical domain and several claim extraction models drawing from recent developments in weak supervision and transfer learning. We show that transfer learning helps with the claim extraction task. We also release the data, the code, and a web service demo of our work so that the community can improve upon it. Claim extraction is an important task to automate, and our work helps in this direction.

There are several improvements that we foresee being addressed in the future. Due to idiosyncrasies of the dataset, one of the problems is that our best model is slightly biased towards predicting the last few sentences of an abstract as claims. While this is mostly correct for biomedical papers, it might not be the structure of other fields, such as Computer Science or Social Science. Also, we are not certain about why the word vectors learned from PubMed are no better than the GloVe vectors. Perhaps, specializing the distributed representation of vectors to the domains should help more. In the future, we will collect and annotate data for other domains including Social Science and Computer Science, and improve our word vector representations.

Overall, with the substantial improvement we show here, we believe these models could be used in information extraction systems to support scholarly search engines such as Semantic Scholar or Pubmed. By making the dataset and code available to the community, we hope to invite other researchers in the quest of analyzing scientific publications at scale.

9 Acknowledgement

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A Appendix

We show example screenshots of the output from claim prediction tool in figure [3]. The first page of the annotation tool contains the description of the task. The second page contains title and abstract of the sample publications to be annotated. The abstract is pre-splitted into sentences which allows annotators to tag each sentence in the abstract. A screenshot of the annotation tool instruction and annotation example are shown in figures [4] and [5] respectively.

We report distribution of the relative position of the final label claims in figure [6]. Around 55.3 percent of the claims are located in the last sentence and the rest are elsewhere in the abstract.
Multiplex genome engineering using CRISPR/Cas systems.

Functional elucidation of causal genetic variants and elements requires precise genome editing technologies. The type II prokaryotic CRISPR (clustered regularly interspaced short palindromic repeats)/Cas adaptive immune system has been shown to facilitate RNA-guided site-specific DNA cleavage. We engineered two different type II CRISPR/Cas systems and demonstrate that Cas9 nucleases can be directed by short RNAs to induce precise cleavage at endogenous genomic loci in human and mouse cells. Cas9 can also be converted into a nicking enzyme to facilitate homology-directed repair with minimal mutagenic activity. Lastly, multiple guide sequences can be encoded into a single CRISPR array to enable simultaneous editing of several sites within the mammalian genome, demonstrating easy programmability and wide applicability of the RNA-guided nuclease technology.

Prediction

Functional elucidation of causal genetic variants and elements requires precise genome editing technologies. **BACKGROUND**

The type II prokaryotic CRISPR (clustered regularly interspaced short palindromic repeats)/Cas adaptive immune system has been shown to facilitate RNA-guided site-specific DNA cleavage. **BACKGROUND**

We engineered two different type II CRISPR/Cas systems and demonstrate that Cas9 nucleases can be directed by short RNAs to induce precise cleavage at endogenous genomic loci in human and mouse cells. **RESULTS**

Cas9 can also be converted into a nicking enzyme to facilitate homology-directed repair with minimal mutagenic activity. **CONCLUSIONS**

Lastly, multiple guide sequences can be encoded into a single CRISPR array to enable simultaneous editing of several sites within the mammalian genome, demonstrating easy programmability and wide applicability of the RNA-guided nuclease technology. **CONCLUSIONS**

**CLAIM**

Figure 3: Screenshot of the output from Discourse and Claim Prediction tool. A sample discourse and claim prediction from CRISPR/Cas article published in Science (PMID: 23287718) using transfer learning of Bi-LSTM CRF model with fine-tuning.

The Task

In this task, you will identify whether a given sentence contains a claim. If the given sentence contains claim, you can check the checkbox.

Overview

A claim is a statement of belief that can be argued against. This statement is a claim because someone can argue against it. In a research article, scientists make a claim and present evidence supporting their claim.

What is a claim statement?

A sentence can be marked as a claim, if any one of the following is true:

- It declares something is better -- for example: "Our method outperforms existing techniques"
- It proposes something new -- for example: "We propose a novel medicine"
- It describes a new finding or a new cause-effect relationship -- for example: "We find that Bedaquiline has anti-cancer activity"

All of the above can be argued against, based on evidence.

Examples

Here are some examples of claim tagging from 3 sample papers from PubMed

**PUBMED:** 12136955
**NOT CLAIM:** Several recent studies of aging and cognition have attributed decreases in the efficiency of working memory processes to possible declines in attentional control, the mechanism(s) by which the brain attempts to limit its processing to that of task-relevant information.

**NOT CLAIM:** Here we used fMRI measures of neural activity during performance of the color-word Stroop task to compare the neural substrates of attentional control in younger (ages: 21-27 years old) and older participants (ages: 60-75 years old) during conditions of both increased competition (incongruent and congruent neutral) and increased conflict (incongruent and congruent neutral).

**CLAIM:** We found evidence of age-related decreases in the responsiveness of structures thought to support attentional control (e.g., dorsolateral prefrontal and parietal cortices), suggesting possible impairments in the implementation of attentional control in older participants.

Figure 4: Screenshot of the instruction of annotation tool. The annotators are presented by the task instruction, definition of a claim, and examples of annotated documents before the task.
A Morphological Hessian Based Approach for Retinal Blood Vessels Segmentation and Denoising Using Region Based Otsu Thresholding.

Diabetic Retinopathy (DR) harm retinal blood vessels in the eye causing visual deficiency. The appearance and structure of blood vessels in retinal images play an essential part in the diagnoses of an eye sicknesses. We proposed a less computational unsupervised automated technique with promising results for detection of retinal vasculature by using morphological hessian based approach and region based Otsu thresholding. Contrast Limited Adaptive Histogram Equalization (CLAHE) and morphological filters have been used for enhancement and to remove low frequency noise or geometrical objects, respectively. The hessian matrix and eigenvalues approach used has been in a modified form at two different scales to extract wide and thin vessel enhanced images separately. Otsu thresholding has been further applied in a novel way to classify vessel and non-vessel pixels from both enhanced images. Finally, postprocessing steps has been used to eliminate the unwanted region/segment, non-vessel pixels, disease abnormalities and noise, to obtain a final segmented image. The proposed technique has been analyzed on the openly accessible DRIVE (Digital Retinal Images for Vessel Extraction) and STARE (STructured Analysis of the REtina) databases along with the ground truth data that has been precisely marked by the experts.

Diabetic Retinopathy (DR) harm retinal blood vessels in the eye causing visual deficiency.

The appearance and structure of blood vessels in retinal images play an essential part in the diagnoses of an eye sicknesses.

We proposed a less computational unsupervised automated technique with promising results for detection of retinal vasculature by using morphological hessian based approach and region based Otsu thresholding. CLAIM

Figure 5: Screenshot of the annotation tool. The abstracts are sampled from MEDLINE database, sentences are pre-split, and annotators can select which sentences are claims.

Figure 6: Distribution of relative position of annotated claims in the dataset. Around 55.3 percent of the claims are located in the last sentence and the rest are elsewhere in the abstract.