NegBERT: A Transfer Learning Approach for Negation Detection and Scope Resolution

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Abstract
Negation is an important characteristic of language, and a major component of information extraction from text. This subtask is of considerable importance to the biomedical domain. Over the years, multiple approaches have been explored to address this problem: simple rule-based systems, Machine Learning classifiers, Conditional Random Field Models, CNNs and more recently BiLSTMs. In this paper, we look at applying Transfer Learning to this problem. First, we extensively review previous literature addressing Negation Detection and Scope Resolution across the 3 datasets that have gained popularity over the years: BioScope Corpus, the Sherlock dataset, and the SFU Review Corpus. We then explore the decision choices involved with using BERT, a popular transfer learning model, for this task, and report a new state-of-the-art for scope resolution across all 3 datasets. Our model, referred to as NegBERT, achieves a token level F1 score on scope resolution of 92.36 on the Sherlock dataset, 94.53 on the BioScope Abstracts, 91.24 on the BioScope Full Papers, 89.94 on the SFU dataset, outperforming the previous state-of-the-art by a significant margin. We also analyze the model’s generalizability to datasets on which it is not trained.

Introduction
Negation Detection and Scope Resolution is an important subtask for tasks ranging from Sentiment Analysis, where the sentiment of a given sentence is dependent on negation, to query response systems like Chatbots, where negation entirely changes the meaning and hence the relevance of a certain body of text. A substantial portion of the research till date on this topic focused solely on data from the biomedical domain where use of negation cues is abundant, as in medical reports. While negation is intuitive for humans to spot, finding the exact words that indicate such negation and delineating the scope of such negation cues has proven to be a tricky problem for computer-based systems. One could imagine that finding negation cues and their scopes could be easily solved via rules and carefully designed heuristics, and this was the exact approach used by the initial few systems attempting this task. But given the complexities of human language, these approaches weren’t accurate enough. Thus, other methods were explored, and Deep Learning-based approaches have shown to be particularly promising.

A simple example of negation is as follows:

This is not [a negation].

We can observe that ‘not’ is the negation word (known as the negation cue) and the words whose meaning is altered by ‘not’ are ‘a’ and ‘negation’, which belong to what is known as the cue’s scope. Negation detection involves finding these negation cues, and scope resolution for each cue necessitates finding the words affected negatively by that cue (finding its scope).

Cues can come in a variety of ways:
1. An affix: (im)perfect, (a)typical, ca(n’t)
2. A single word: not, no, failed, lacks
3. A set of consecutive words or discontinuous words: neither…nor

The scope of a cue is also not constrained to be continuous. These facts, coupled with the relatively small dataset sizes compared to other NLP datasets, make this task particularly challenging to solve.

Transfer Learning, a method in which we train deep learning systems on huge corpora and then ‘transfer’ or tune these pretrained architectures on downstream tasks which have a dearth of data, has taken the NLP community by storm, achieving state-of-the-art results on almost every NLP task these models have been applied to. This method was originally used in Computer Vision, by training models on the ImageNet dataset which allowed them to capture important features in a picture, and then apply to other datasets by changing the output layer and training on the downstream task. Recently, a number of architectures including BERT (Devlin et. al. 2018) have applied this to NLP, contributing massively to the advancement of research in the field. Almost every NLP task benefitted from transfer learning, as training on massive corpora allowed these models to learn an understanding of language.
Motivated by the success of transfer learning, we apply BERT to negation detection and scope resolution. We explore the set of available datasets: the BioScope Corpus (Abstracts and Full Papers) (Vincze et al. 2008), the Sherlock Dataset (Morante and Blanco 2012) and the SFU Review Corpus (Konstantinova et al. 2012). We train NegBERT on one dataset and report the scores on testing all datasets, thus showing the generalizability of NegBERT. Since the BioScope dataset is primarily from the biomedical domain, while the Sherlock dataset is taken from stories by Sir Author Conan Doyle (literary work), and the SFU Review Corpus is a collection of product reviews (free text by human users), the 3 datasets belong to different domains.

This paper is organized as follows: In Section 2, we extensively review available literature on the subject. Section 3 contains the details of the methodology used for NegBERT, while 4 includes experimental details for our experimentation. In Section 5, we report the results and analyze them. Our conclusions and our perspective on the future scope for this problem is presented in Section 6.

Previous Work

In 2012, the *sem* Shared Task for the year was negation cue detection and scope resolution. The dataset used for this conference was the Sherlock dataset. The other 2 publicly available datasets are the Bioscope Corpus, and the SFU Review Corpus. In this section, we look at the previous literature addressing this task and summarize the results of those approaches at the end in a tabular format.

Rule-Based Approaches

The first approach that was explored in literature was a simple rule-based system. (Mutalik, Deshpande, and Nadkarni 2001). They tested the hypothesis that a lexical scanner that uses regular expressions to generate a finite state machine can detect negation cues in natural language. Their algorithm, NegFinder, was based on a manual inspection of 40 medical documents. They showed that it was possible to apply computational methods to detect negation cues in a sentence.

Chapman et al. (2001) proposed a simple regular expression algorithm (NegEx) to detect negation cues. They posited that medical language is lexically less ambiguous and hence a rule-based system can be applied, and that a simpler system than the one proposed by Mutalik et al. also performed well. NegEx is a very reliable algorithm in the medical domain, which has been extensively used in further research.

Sanchez-Graillet and Poesio (2007) looked at negation cue detection in the domain of Protein-Protein Interaction, proposing a heuristic-based system using a full dependency parser to extract negations tailored to that specific domain. They used the fact that rule-based systems had to be domain specific to perform well.

Huang and Lowe (2007) stated that previous research had shown that the scope of negation may be difficult to identify if the cues are more than a few words away, and hence focused on addressing this problem. They proposed combining regular expression matching with grammatical parsing, which allowed the rule-based systems to account for long-term dependencies.

For the *sem* 2012 Shared task, the team from UCM-1 (Albornoz et al. 2012) used a rule-based system to detect negation cues. Scopes were resolved using the syntax tree of the sentence in which the negation arises. Their system was initially intended for processing negation in opinionated texts and was adapted to fit the task requirements. The team from UCM-2 (Ballesteros et al. 2012) relied on a rule-based system engineered to the given dataset. Cue detection was performed via a static cue lexicon, scope was detected using rules based on a prior work by Ballesteros et al. for the BioScope Corpus, which was modified for the Sherlock Corpus. The team from UGroningen (Basile et al. 2012) also used a rule-based system based on NLP toolschain used to construct the Groningen Meaning Bank. Their system transformed the texts into logical formulas using the C&C tools and Boxer, another system. They concluded that it is not easy to transfer the information about negation from a formal, logical representation of scope to a theory-neutral surface-oriented approach.

These 3 methods showed how even rule-based systems with well-defined task-specific rules showed acceptable performance. The primary limitation, of course, were that these rules were not generalizable across domains or even datasets.

Sohn, Wu, and Chute (2012) looked to improve Mayo Clinic’s clinical Text Analysis and Knowledge Extraction System (cTAKES) negation annotator via dependency parsers and a rule-based system. They found that using dependency-based negation proved to be a superior alternative to the pre-existing cTAKES negation annotator.

Mehrabi et al. (2015) proposed DEEPEN as an improvement to NegEx which added dependency parsing to it. They looked at negation detection only and evaluated their system on the Mayo Clinical Dataset. They made NegEx, a very reliable system, much more accurate.

More recently, NegBio was introduced (Peng et al. 2017), which utilized Universal Dependency patterns for cue detection. They improved on NegEx and showed that for the medical domain, this performed extremely well. Thus, we observe that recent rule-based systems incorporate dependency parsing in their rules, showing how each word needs to be considered in the context of the words around it. The sequential order of words makes a big difference even in detecting negation.
Machine Learning Approaches

The use of Machine Learning techniques for negation detection was explored by Rokach, Romano, and Maimon (2007) who described an approach to automatically generate and heuristically evaluate Regular Expression patterns. They then fed the results of the pattern evaluations and a few other concept features to a decision tree classifier. They also looked at a cascade of classifiers to make decisions. The sentence was made to pass to the next level of the cascade if no negation was found. The cascade they proposed was 3 levels deep. They relied on the regular expression matching paradigm to generate features but allowed the ML model to use them to come up with better rules (decisions), thus improving on just rule-based systems.

In 2008, Morante and Daelemans (2008) proposed a system to both detect negation and find its scope in biomedical texts. This paper focused on the scope detection task, which hadn’t been previously explored. They proposed a memory-based scope finder that works in 2 phases, cue detection and scope resolution. They used a k-Nearest Neighbors Classifier with features extracted from the sentence and modified to the task at hand. This was a novel approach to negation detection at the time and was performed on the BioScope Corpus.

In 2009, Morante and Daelemans (2009) used IGTREE, which is a memory-based learning algorithm, as implemented in TiMBL, to detect cues. For scope resolution, they used a metalearner that used the predictions by 3 classifiers which predicted whether a given token was the beginning of a scope, end of the scope of neither. They used a memory-based algorithm, SVM and CRF as the 3 classifiers. This was also done on the Bioscope Corpus and achieved the state-of-the-art results in cue detection on the Bioscope Corpus. This algorithm was majorly rule based for detecting cues, as the algorithm only ran for words that were not a part of a predefined lexicon of words.

For the *sem 2012 Shared Task, the team from UAB-CoRAL: (Gyawali and Solorio 2012) found the cue using a lexicon and classified each word as in-scope or out-of-scope by extracting features from a 2-tuple of words (the negation cue and the word under consideration) and passing through a classifier. The team from UiO1: (Read et. al. 2012) detected cues in a similar way to Lapponi et. al. (Lapponi et. al. 2012). They used an SVM as the classifier. For scope resolution, they looked at the syntactic units and developed heuristics to improve the system and incorporated a data-driven approach which involved a ranking approach over syntactic constituents. At the time, this outperformed all other algorithms, majority of which were rule-based for the *sem 2012 Shared Task.

In 2014, Packard et. al. (2014) looked at negation scope resolution as a semantic problem, and their approach worked over explicit and formal representations of propositional semantics. They proposed an MRS Crawler, and a maximum entropy model for parse ranking, trained on a different dataset of encyclopedia articles and tourist brochures. They achieved the maximum F1 score and outperformed all systems from *sem 2012 Shared Task on the Sherlock dataset.

In 2015, Cruz, Taboada, and Mitkov (2015) looked at the Simon Fraser University (SFU) Review Corpus. They classified words as per the BIO representation schema. Another classifier attempted to tell if tokens in a sentence are in the scope of a negation cue. They used an SVM classifier with an RBF kernel and used Cost Sensitive Learning to deal with the imbalanced classification.

Ou and Patrick (2015) looked at negation cue detection and experimented with 3 methods: lexicon-based, syntax-based (both rule-based) and an SVM classifier. The SVM classifier delivered the best results. They collected their own dataset which had data from the biomedical domain. This showed that the most promise was not in furthering rule-based systems, but in exploring ML techniques for negation detection.

Conditional Random Field Approaches

A third approach to this task used the inherent sequential order to a sentence, by using Conditional Random Fields (CRFs). Agarwal and Yu (2010) used this approach for scope detection. Their system was robust and could identify scope in both biomedical and clinical domains. Morante and Daelemans had in contrast looked at the task as classification of word pairs, the negation word and the word to be labelled.

Council, McDonald, and Velikovich (2010) looked at negation in the context of improved sentiment analysis. They detected cues using a lexicon of explicit negation cues, and scopes using a CRF model as an annotator in a larger system. While they evaluated their system on the BioScope Corpus, they constructed a corpus called Product Reviews for their task. They showed that training on the biomedical domain and testing on the Product Reviews or vice versa led to poor results. This suggested that the corpuses constructed were too small and thus approaches too task-specific to be generalized to natural language.

For the *sem 2012 Shared task, the team from UMICHIGAN (Abu-Jbara and Radev 2012) trained a CRF on the lexical, structural and syntactic features of the data for both cue detection and scope resolution. They expanded the set of features given to the CRF. The team from FBK (Chowdhury 2012) trained CRF classifiers, trained on only features provided by the dataset. A different set of features was considered for the CRF which exploited phrasal and contextual clues along with token specific features. The team from UiO2: (Lapponi et. al. 2012) detected cues by maintaining a corpus and classifying known cue words as
cue or non-cue. Scope was detected using CRFs trained on lexical and syntactic features, together with a fine-grained set of labels that captured the scopal behavior of certain tokens. The team from UW - Washington (White 2012) detected cues using regular expression rules from the training data. Scope tokens were detected using a CRF sequence tagger and custom defined features fed to the CRF. Li and Lu (2018) used models based on CRFs, semi-Markov CRF and latent-variable CRF, and achieved better results than previously reported on the Sherlock dataset, beating out all deep learning-based systems as well. Their key observation was that certain useful information such as features related to negation cue, long distance dependencies as well as some latent structural information could be exploited for such a task.

**Reinforcement Learning Approaches**

A distinctive and unique approach to negation scope resolution was the application of reinforcement learning. Prolloch, Feuerriegel, and Neumann (2016) looked at negation detection in the context of a decision support system for sentiment analysis. Their system thus represented the state by the encoding of the position in a sentence, and the set of actions as setting the state to negated or not negated. Thus, each token was labelled by the system by taking an action given the current state. This approach did not work as well as one would have hoped.

**Deep Learning Approaches**

More recent approaches have looked to apply Deep Learning architectures to the task. Qian et al. (2016) were the first to apply deep learning to negation scope detection. They used Convolutional Neural Networks to path features to generate embeddings, which they concatenated with position features and fed to a softmax layer to compute confidence scores of its location labels. They used this system on the BioScope Corpus and outperformed all existing systems on the BioScope Abstracts.

Fancellu, Lopez, and Webber (2016) looked at neural networks for scope detection. They rightly point out that most systems were highly engineered and only tested on the same genre they were trained on. They experimented with a one-hidden layer feed forward neural network and a bidirectional LSTM (BiLSTM) on the Sherlock Dataset, and found that the BiLSTM performed the best. Lazib et al. (2016) at around the same time looked to Recurrent Neural Network variants for scope resolution. They experimented with RNN, LSTM, BiLSTM, GRU and CRF on the SFU Review Corpus Dataset. The BiLSTM, again, gave the best performance. Thus, we see different datasets benefiting from the use of BiLSTMs, indicating the potential in DL-based methods.

Fancellu et al. (2017) performed an analysis of the available datasets and showed that there existed a problem which enabled systems to gain high accuracy, namely that negation scopes were frequently annotated as a single span of text delimited by punctuation. They pointed out that the Bioscope and SFU Review corpus suffer from this problem, while the Sherlock Corpus does not. They also improved upon their previous model published in 2016 (BiLSTM) by making joint predictions for all words. Their earlier approach would model the prediction of scope as independent predictions for each word. They added a dependence on the previous prediction for the next. By doing so, they managed to improve the best system for the task.

Fancellu, Lopez, and Webber (2018) showed that BiLSTMs were the state of the art, and that models suffer from genre (domain) effects. They also looked at cross-lingual scope detection, finding negation scope in languages where annotations aren’t available, which is a common problem for low-resource languages.

Gautam et al. (2018) looked at handling negation in tutorial dialogues. They too looked at LSTMs to solve a sequence labelling problem and got promising results on a custom dataset. Both cue detection and scope resolution were done using LSTMs.

Taylor and Harabagiu (2018) used a combined BiLSTM to label cue and scope simultaneously. They wanted to look to augment patient cohort identification from electroencephalography reports. They preprocessed the text first, and then used the Gensim implementation of word2vec to generate embeddings for the text. Word embeddings were the first attempt at using Transfer Learning in NLP.

More recently, Bhatia et al. (2019) used a shared encoder and 2 separate decoders to get the entities and negations respectively. They performed evaluation over the i2b2/VA dataset and a proprietary medical condition dataset and showed that the joint model outperforms all standard models. They used a BiLSTM to encode the sequence at the word level, and an LSTM decoder. This method showed the power of using a joint encoding for both tasks.

Chen (2019) used attention based BiLSTM networks and word embeddings to detect assertions and negations. This method applied attention, one of the more promising components of architectures addressing other NLP problems, to scope resolution.

| Authors         | Approach           | Precision | Recall | F1-Score |
|-----------------|--------------------|-----------|--------|----------|
| NegFinder       | Rule-Based         | NA        | 95.7   | NA       |
| NegEx           | Rule-Based         | 84.49     | 77.84  | 81.03    |
| Rokach et. al.  | ML Classifier Cascade | 87.8     | 80.99  | 84.47    |
| Sanchez et. al. | Rule-Based         | 89.15     | 67.27  | 76.68    |
| Huang et. al.   | Rule-Based         | 99.8      | 92.6   | NA       |

Table 1. Previous Work on custom datasets.
### Table 2. Previous Work on BioScope Corpus (Abstracts)

| Authors                      | Approach         | Precision | Recall  | F1-Score |
|------------------------------|------------------|-----------|---------|----------|
| Morante et. al. (2008)       | ML Classifier    | 100       | 95.72   | 97.81    |
| Agarwal et. al.              | CRF              | 97.31     | 95.74   | 96.5     |
| Peng et. al.                 | Rule-Based       | 96.1      | 95.7    | 95.9     |

### Table 3. Previous Work on BioScope Corpus (Full Papers)

| Authors                      | Approach         | Precision | Recall  | F1-Score |
|------------------------------|------------------|-----------|---------|----------|
| UMichigan                    | CRF              | 94.31     | 87.88   | 90.98    |
| UCM-1                        | Rule-Based       | 89.26     | 91.29   | 90.26    |
| UCM-2                        | Lexicon          | 81.34     | 64.39   | 71.88    |
| UGroningen                   | Rule-Based       | 88.89     | 84.85   | 86.82    |
| UABCoRAL                     | CRF              | 93.41     | 91.29   | 92.34    |
| UABCoRAL                     | Lexicon          | 85.93     | 85.61   | 85.77    |
| UI/O2                        | Lexicon          | 89.17     | 93.56   | 91.31    |
| UI/O1                        | ML Classifier    | 91.42     | 92.8    | 92.1     |
| UWashington                  | Rule-Based       | 88.04     | 92.05   | 90.0     |

### Table 4. Previous Work on the Sherlock Dataset

| Authors                      | Approach         | Precision | Recall  | F1-Score |
|------------------------------|------------------|-----------|---------|----------|
| UMichigan                    | CRF              | 84.85     | 80.66   | 82.7     |
| UCM-1                        | Rule-Based       | 85.37     | 68.53   | 76.03    |
| UCM-2                        | Rule-Based       | 58.3      | 67.7    | 62.65    |
| UGroningen                   | Rule-Based       | 69.2      | 82.87   | 75.17    |
| FBK                          | CRF              | 81.53     | 82.44   | 81.98    |
| UABCoRAL                     | ML Classifier    | 85.37     | 68.86   | 76.23    |
| UI/O2                        | CRF              | 86.03     | 81.55   | 83.73    |
| UI/O1                        | Data Driven Ranking | 81.99   | 88.81   | 85.26    |
| UWashington                  | CRF              | 83.26     | 83.77   | 83.51    |
| Packard et. al.              | ML Classifier    | 86.1      | 90.4    | 88.2     |
| Fancellu et. al. (2016)      | BILSTM           | 92.62     | 85.13   | 88.72    |
| Fancellu et. al. (2017)      | BILSTM-Joint     | NA        | NA      | 87.93    |
| Li et. al.                   | CRF              | 94        | 85.3    | 89.4     |

### Table 5. Previous Work on SFU Review Corpus

| Authors                      | Approach         | Precision | Recall  | F1-Score |
|------------------------------|------------------|-----------|---------|----------|
| Cruz et. al.                 | ML Classifier    | 82.44     | 93.22   | 89.64    |
| Fancellu et. al. (2016)      | BILSTM           | NA        | NA      | 89.93    |
| Fancellu et. al. (2017)      | BILSTM-Joint     | NA        | NA      | 88.34    |

### Methodology

We approach the task in the typical 2-stage fashion: negation cue detection performed before scope resolution. For both stages, we use Google’s Bidirectional Encoder Representation for Transformers (Devlin et. al. 2018) (BERT-base) with a classification layer on top of it. We use huggingface’s PyTorch implementation of BERT, and finetune the bert-base uncased model (110 million parameters) to the training sets.

For negation detection, we use the following annotation schema:
- 0 – Affix
- 1 – Normal Cue
- 2 – Part of a multword cue
- 3 – Not a Cue

This scheme is useful for the Sherlock dataset which has annotations for affixes, but the BioScope Corpus and SFU Review Dataset do not have annotations for affixes. Hence, when we test inter-dataset performance, we consider cues that are affixes as normal cues, and predictions of affixes as predictions of normal cues. (i.e. 0 and 1 are considered as the same label for the purpose of evaluation). We also use a 5th label for the padded tokens and set the class weights for that token category to 0 to avoid training on it.

For scope resolution, we use a binary labelling scheme, 0 as not a token and 1 as a token. We feed sentences which we know have cues to the model, and to encode that information into the input, we consider 2 methods:
1. Replace: We replace the token which is the cue with another special token which represents the kind of token it is according the cue detection labelling scheme. Thus, ‘[im]polite’ becomes ‘token[0]’, ‘not’ becomes ‘token[1]’, and ‘neither’ and ‘nor’ both become ‘token[2]’.
2. Augment: We keep the original word and add the special token according to the scheme above immediately before the word. Thus, ‘[im]polite’ becomes ‘token[0] polite’, ‘not’ becomes ‘token[1] not’, and ‘neither’ becomes ‘token[2] neither’.

We need to preprocess the input to the model, as the tokenization performed by BERT’s BytePairEncoding creates a labelling issue. For instance:

I am not impolite. -> I, am, not, im, #polite.
While we only have 3 labels for the sentence, BERT has to be fed 4 (1 label per token). Hence, we replicate the label for all tokens created from that word.

Postprocessing is also needed for converting the token-level predictions to word-level predictions. Hence, we consider the output for each token as a probability distribution over the classes possible and average them out for all tokens in a word, giving us a probability distribution for a word over all classes of tokens. A simple argmax gives us our required token type.

**Experimentation**

We use Google’s BERT (Devlin et al. 2018) (bert-base-uncased variant) as the base model to generate contextual embeddings for the sentence. The input to the BERT model is a sequence of tokenized and encoded tokens of a sentence. We then use a vector of dimension \( R_H \times N_L \) to compute scores per token, for the classification task at hand. BERT outputs a vector of size \( R_H \) per token of the input, which we feed to a common classification layer of dimension \( R_H \times 5 \) for cue detection and \( R_H \times 2 \) for scope resolution. We use early stopping on dev data for 6 epochs as tolerance and F1 score as the early stopping metric, use the Adam optimizer with an initial learning rate of 3e-5, and the Categorical Cross Entropy Loss with class weights as described above to avoid training on the padded label outputs.

We perform cue detection and scope resolution for all 3 datasets, and train on 1 and test on all datasets. For the Sherlock dataset, the training data is the Sherlock Train data used in *sem 2012 Shared Task available in cd-sco. The dev data is the dev data provided in the Sherlock Corpus, and the test data is the Sherlock Cardboard and Circle data used as test data for *sem 2012. For all other corpuses, we use a default 70 – 15 – 15 split for the train-dev-test data. We trained the models on free GPUs available via Google Colaboratory, the training scripts are publicly available.

**Results**

The results are tabulated in tables 6-9 below.

For cue detection, on the Sherlock dataset test data, we see that we outperform the best system [FBK Chowdhury] by 0.6 F1 measure. On the BioScope Abstracts, we perform reasonably well. Unlike Morante and Daelemans, we do so without using a word lexicon taken from the data itself, thus allowing the model to generalize, as seen in its performance on BioScope Full Papers (F1: 92.42). On the BioScope Full papers, we are able to achieve 90.43 F1 when training on the same data, but we do note that the amount of training data available is significantly lower than for the other datasets, and while general Deep Learning based approaches cannot perform well in such situations, we still manage to perform well. On the SFU Review Corpus, we achieve an F1 of 87.08.

For the inter-dataset comparison, we note that the model generalizes well across different domains, except the SFU corpus. We think this is due to annotation differences in both datasets, and that SFU corpus has cues that the other corpuses do not have.

| Dataset                | Sherlock (Dev Set) | BioScope (Abstracts) | BioScope (Full Papers) | SFU |
|------------------------|-------------------|----------------------|------------------------|-----|
| Sherlock (Dev Set)     | 93.68             | 73.51                | 72.03                  | 69.04 |
| Sherlock (Test Set)    | 92.94             | 73.62                | 69.63                  | 70.51 |
| Bioscope (Abstracts)   | 76.71             | 95.65                | 92.37                  | 83.86 |
| Bioscope (Full Papers) | 73.2              | 92.42                | 90.23                  | 79.68 |
| SFU Review Corpus      | 36.92             | 17.44                | 59.24                  | 87.08 |

Table 6. F1 Scores. A row represents the test dataset, a column represents the train dataset.

For scope resolution: On the Sherlock dataset, we achieve an F1 of 92.36, outperforming the previous State of the Art by a significant margin (almost 3.0 F1). On the BioScope Abstracts, we achieve an F1 of 92.36, outperforming the best architecture by 1.25 F1. On the Bioscope Full Papers, we outperform the best architecture by almost 3.0 F1 when training on the same dataset. On the SFU Review Corpus, we achieve an F1 score equal to the state-of-the-art architecture by Fancellu et al.
Augment

| Dataset            | Author        | Previous SOTA | NegBERT | Gain |
|--------------------|---------------|---------------|---------|------|
| Sherlock (Dev Set) | Chowdhury (FBK) | 92.34         | 92.94   | 0.6  |
| Sherlock (Test Set)| Chowdhury (FBK) | 92.34         | 92.94   | 0.6  |
| BioScope (Abstracts)| Morante et. al. (2009) | 98.68         | 95.65   | -3.03|
| BioScope (Full Papers) | Morante et. al. (2009) | 97.81         | 92.42   | -5.39|
| SFU Review         | Cruz et. al.  | 89.64         | 87.08   | -2.56|

Table 7. Token Level F1 Scores. A row represents the test dataset, a column represents the train dataset.

For negation cue detection, we observe a significant gap between our model, NegBERT, and the current state-of-the-art systems, while we outperform the baseline systems. We believe this is so as these datasets are fairly limited in size and scope, and for a such a task, bigger models like BERT need a lot more examples to train on to master the finer points of negation detection, while this is straightforward to handle for rule-based approaches and smaller datasets. This model does outperform other Deep Learning based systems applied to negation cue detection.

Table 8. Negation Cue Detection Results (F1 Score): Summary

| Dataset                  | Author               | Previous SOTA | NegBERT | Gain |
|--------------------------|----------------------|---------------|---------|------|
| Sherlock (Abstracts)     | Li et. al. (2017)    | 89.4          | 92.36   | 2.94 |
| BioScope (Abstracts)     | Fancellu et. al. (2017) | 92.11         | 94.53   | 2.42 |
| BioScope (Full Papers)   | Morante et. al. (2009) | 84.71         | 91.24   | 6.53 |
| SFU Review               | Fancellu et. al. (2016) | 89.93         | 89.94   | 0.01 |

Table 9. Scope Resolution Results (Token Level F1): Summary

NegBERT’s gain in accuracy on Scope Resolution is because it allows contextual embeddings and knowledge transfer across millions of documents to downstream tasks.

When we trained on BioScope Abstracts and tested on the BioScope BioMedical Corpus, we surprisingly observed a state-of-the-art result of 91.24 (a gain of 3.89 F1 points over training on BioScope Full Papers), which is far beyond the achievable results on training and evaluating on the BioMedical sub corpora. This is only possible because of BERT’s pretraining, and the similarity of the sub corpora of the BioScope Corpus.

We also notice that in general, though the cross-dataset generalizability is acceptable, it is far from what one would desire. We believe that the combination of these 2 results indicate that the datasets are highly disjoint in their representations of negations and are fairly limited in size, both of which contribute to the system’s inability to perform well on unseen data from a different domain, but perform well on data from within the same domain.

Conclusion and Future Scope

Negation Cue Detection and Scope Resolution is a very well researched problem. We reviewed all existing papers and identified the research trends moving towards Deep Learning approaches. Following the general trend in the NLP community, we looked to the new generation of transfer learning models (BERT) to solve both tasks. We explored the set of design choices and reported a significant improvement in scope detection systems using BERT-base uncased model. We also analyzed the inter-domain generalization of the models, and noted that the use of our proposed architecture, NegBERT, as the underlying model allows for really good performance on scope resolution for unseen datasets from different domains. We reported a new state-of-the-art model on every publicly available dataset using the same architecture with no task-specific tuning and the same set of hyperparameters for scope resolution. Thus, we clearly establish the usefulness of pretrained models and the usage of transfer learning to the task of negation scope resolution.

We envision that the future progress in this task should focus on the use of ever-changing state-of-the-art models in the transfer learning domain which have significant potential to improve the accuracy of the system. We feel that a bigger dataset is needed to extract the maximum generalizability from such architectures.

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