Towards Fine-grained Citation Function Classification

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Abstract

We look into the problem of recognizing citation functions in scientific literature, trying to reveal authors’ rationale for citing a particular article. We introduce an annotation scheme to annotate citation functions in scientific papers with coarse-to-fine-grained categories, where the coarse-grained annotation roughly corresponds to citation sentiment and the fine-grained annotation reveals more about citation functions. We implement a Maximum Entropy-based system trained on annotated data under this scheme to automatically classify citation functions in scientific literature. Using combined lexical and syntactic features, our system achieves the F-measure of 67%.

1 Introduction

Citations in scientific papers serve different purposes, from comparing one work to another to acknowledging the inventor of certain concepts. Recognizing citation functions is important for understanding the structure of a single scientific document as well as mining citation graphs within a document collection. Therefore, this task has attracted researchers from the fields of discourse analysis, sociology of science, and information sciences for decades (Teufel et al., 2006a).

Most of the existing research in this area focused on the analysis of citation sentiment, which has achieved good accuracy (see, e.g., (Teufel et al., 2006a)). Citation sentiment analysis systems are usually able to identify positive, neutral, or negative opinions, but if we want to better understand the exact function of a citation, we need to know not only whether the authors like the citation, but also how the citation is used in a given context (Section 2).

In this paper, we try to reveal citation functions more accurately than simply classifying citation sentiment. We first create a two level coarse-to-fine grained annotation scheme (Section 3). The coarse-level annotation corresponds roughly to sentiment categories, including POSITIVE, NEGATIVE, and NEUTRAL. The fine-grained annotation scheme provides a more detailed description of citation functions, such as Significant, which asserts the importance of an article or a work, and Discover, which acknowledges the original discoverer/inventor of a method or material.

Using data annotated under this scheme, we train classifiers to determine citation functions, and experiment with features from lexical to syntactic levels (Section 4). We predict the fine-grained citation function at 67% in F-measure in our experiments, which is at the same level as the coarse-grained citation sentiment classification (Section 5).

2 Related Work

The background for our work is in citation analysis. Applications of citation analysis include evaluating the impact of a published literature through a measurable bibliometric (Garfield, 1972; Luukkonen, 1992; Borgman and Furner, 2002), analyzing bibliometric networks (Radev et al., 2009), summarizing scientific papers (Qazvinian and Radev, 2008; Abu-Jbara and Radev, 2011), generating surveys of scientific paradigms (Mohammad et al., 2009), among others. Correctly and accurately recognizing citation functions is a cornerstone for these tasks.
Researchers have introduced several annotation schemes for citation analysis. The work of Teufel et al. (2006b) is the most related to ours. They proposed an annotation scheme for citation functions based on why authors cite a particular paper, following Spiegel-Rüsing (1977). This scheme provides clear definition for some of the basic citation functions, such as Contrast, but mainly concerns the citations that authors compare to or build upon, ignoring the relationship between two cited works. Sometimes the relationship between two cited works is also meaningful and important, from which we can know more about the functions and influences of one cited work on other works. For example, the cited work may be utilized or applied by another cited work, which would be captured by Practical in our annotation scheme but considered as neutral under their scheme. In addition, their annotation scheme does not explicitly recognize milestone or standard work in a particular research field, while our annotation scheme does through the Significant function. We continue to use these basic functions, but try to expand their scheme by incorporating more functions, such as acknowledgement and corroboration, which reflects the attitude of the research community towards a citation.

Regarding the automatic recognition of citation functions or citation categories, Teufel et al. (2006a) presented a supervised learning framework to classify citation functions mainly utilizing features from cue phrases. Athar (2011) explored the effectiveness of sentence structure-based features to identify sentiment polarity of citations. Dong and Schäfer (2011) proposed a four-category definition of citation functions following Moravcsik and Murugesan (1975) and a self-training-based classification model. Different from previous work that mainly classified citations into sentiment categories or coarse-grained functions, our scheme, we believe, is more fine-grained. It is also worth noting that Teufel et al. (2006a), Athar (2011), and Dong and Schäfer (2011) all worked on citations in computational linguistics papers, but we investigate citations in biomedical articles.

3 Annotation

Our annotation scheme contains three general citation function categories: POSITIVE, NEUTRAL, and NEGATIVE: POSITIVE citations reflect agreement, usage, or compatibility with cited work; NEUTRAL citations refer to related knowledge or background in cited work; and NEGATIVE citations show weakness of cited work. These three general categories are often used as citation sentiments in previous citation sentiment analysis work. We extend these categories by sorting them into smaller subcategories that reflect the functions of citations. POSITIVE (see + in Table 1), for example, shows a general sentiment of agreement. We divide POSITIVE into Based_on, Corroboration, Discover, Positive, Practical, Significant, Standard, and Supply in order to more accurately describe how a citation is used. The details about each citation function are summarized in Table 1. We provide

| Citation Function | Description                                      |
|-------------------|--------------------------------------------------|
| Based_on+         | A work is based on the cited work                |
| Corroboration+    | Two works corroborate each other                 |
| Discover+         | Acknowledge the invention of a technique         |
| Positive+         | The cited work is successful                     |
| Practical+        | The cited work has a practical use               |
| Significant+      | The cited work is important                      |
| Standard+         | The cited work is a standard                     |
| Supply+           | Acknowledge the supplier of a material           |
| Contrast=         | Compares two works in a neutral way              |
| Co-citation=      | Citations that appear closely                     |
| Neutral=          | The cited work not belonging to other functions  |
| Negative−         | The weakness of the cited work is discussed      |

Table 1: Annotation Scheme for Citation Function: + represents POSITIVE sentiment, = represents NEUTRAL sentiment, and − represents negative sentiment

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Based on Results based on the Comparative Toxicogenomics Database (CTD) [14], we constructed a human P-PAN.

Corroboration This observation is in accordance with previously published data [39].

Discover The core of our procedure is derived from the “target hopping” concept defined previously [3].

Positive Therefore, a systems biology approach, such as the one that was successfully employed by Chen and colleagues [1], is an effective alternative for analyzing complex diseases.

Practical Molecular Modeling and Docking Genetic algorithm GOLD (Genetic Optimization for Ligand Docking), a docking program based on genetic algorithm [39][42] was used to dock the ligands to the protein active sites.

Significant In addition to nanomaterial composition, size and concentration, the influence of cell type is of paramount importance in nanomaterial toxicity as highlighted in other recent investigations in cell vs. cell comparisons [49].

Standard A standard genetic algorithm [31] was used to select the final physicochemical properties of Pafig with population size of 10, crossover probability of 0.8, mutation probability of 0.01 and predetermined number of 200 generations.

Supply The rate constants obtained directly from the ultrafast, time-resolved optical spectroscopic experiments carried out (Polivka et al. 2005) are shown in Table.

Contrast In contrast to Rodgers et al., [34] who targeted planktonic species in AMD solutions and sediments, Bond et al. [37] primarily sampled biofilms.

Co-Citation They bear specific regulatory properties and mechanisms (Babu et al, 2004; Wang and Purisima, 2005).

Neutral Lage and collaborators [12] predicted 113 new disease-candidate genes by comparing their protein-interaction neighborhood with associated phenotypes.

Negative A range of methods have been applied to S. mutans typing, one of the earliest of which was based on susceptibility to bacteriocins [14], [15] but was found to lack reproducibility and was not readily transferred between laboratories.

Table 2: Citation Function Examples

| Citation Function | Example |
|-------------------|---------|
| Based on† | Results based on the Comparative Toxicogenomics Database (CTD) [14], we constructed a human P-PAN. |
| Corroboration† | This observation is in accordance with previously published data [39]. |
| Discover† | The core of our procedure is derived from the “target hopping” concept defined previously [3]. |
| Positive† | Therefore, a systems biology approach, such as the one that was successfully employed by Chen and colleagues [1], is an effective alternative for analyzing complex diseases. |
| Practical† | Molecular Modeling and Docking Genetic algorithm GOLD (Genetic Optimization for Ligand Docking), a docking program based on genetic algorithm [39][42] was used to dock the ligands to the protein active sites. |
| Significant† | In addition to nanomaterial composition, size and concentration, the influence of cell type is of paramount importance in nanomaterial toxicity as highlighted in other recent investigations in cell vs. cell comparisons [49]. |
| Standard† | A standard genetic algorithm [31] was used to select the final physicochemical properties of Pafig with population size of 10, crossover probability of 0.8, mutation probability of 0.01 and predetermined number of 200 generations. |
| Supply† | The rate constants obtained directly from the ultrafast, time-resolved optical spectroscopic experiments carried out (Polivka et al. 2005) are shown in Table. |
| Contrast¬ | In contrast to Rodgers et al., [34] who targeted planktonic species in AMD solutions and sediments, Bond et al. [37] primarily sampled biofilms. |
| Co-Citation¬ | They bear specific regulatory properties and mechanisms (Babu et al, 2004; Wang and Purisima, 2005). |
| Neutral¬ | Lage and collaborators [12] predicted 113 new disease-candidate genes by comparing their protein-interaction neighborhood with associated phenotypes. |
| Negative¬ | A range of methods have been applied to S. mutans typing, one of the earliest of which was based on susceptibility to bacteriocins [14], [15] but was found to lack reproducibility and was not readily transferred between laboratories. |

4 Recognizing Citation Functions

We use the Maximum Entropy (MaxEnt) model to classify all citations into the above citation function categories. We experiment with both surface and syntactic features. When parsing the context sentence, we replace each citation content with a <CITATION> symbol, in order to remove the contextual bias.

4.1 Surface Features

We capture n-grams, signal words collected by system developers, pronouns, negation words, and words related to formulae, graphs, or tables in the context sentence as surface level features.

- **N-Gram Features** use both uni-grams of the context sentence and the tri-gram context window that contains the citation.

- **Signal Word Features** check whether the text signals for a citation function (151 words/phrases in total, collected by system developers from dictionaries) appear in the context sentence.

- **Pronoun Features** look for third-person pronouns and their positions in the context sentence.
CITATION identified the promoters of 52 A. thaliana microRNA genes, and showed …

- **Negation Features** fire if negation words (135 words in total) appear in the context sentence with its scope.

- **FGT Features** fire if words or structures like formula, graph, or table appear in the context sentence.

4.2 **Syntactic Features**

We capture more generalized or long-distance information by taking advantages of syntactic features.

**The Part-of-Speech Features** use Part-of-Speech (POS) tags adds generalizability to surface level signals, e.g., “VERB with” covers signals like “experiment with” and “solve with”, which might indicate a practical function. We use a combination of POS tags and words in a two-word context window around the <CITATION> as features. In Figure 1, “VBD_DT”, “identified_DT”, and “VBD_the” would be extracted.

**The Dependency Features** use the dependency structure of the context sentence to capture grammatical relationships between a citation and its signal words regardless of the distance between them. We extract both dependency triples and dependency labels as features. In Figure 1, if we extract dependency relations and labels attached to a <CITATION>, we would obtain “NSUBJ_identified_CITATION”, “NSUBJ”, and “NSUBJ_showed_CITATION” as dependency features. “NSUBJ_showed_CITATION” captures the long-distance relation between <CITATION> and a signal word “showed”, which other features miss.

5 **Experiments**

From 91 annotated articles with total 6,355 citation instances, we train our model and test the performance through a 10-fold cross-validation procedure, so that each fold randomly contains 9 (or 10) articles with their associated citation instances.

| Features          | P    | R    | F1  |
|-------------------|------|------|-----|
| baseline          | 0.67 | 0.44 | 0.53|
| baseline + fgt    | 0.67 | 0.44 | 0.53|
| baseline + sig    | 0.67 | 0.44 | 0.53|
| baseline + neg    | 0.68 | 0.44 | 0.54|
| baseline + pron   | 0.68 | 0.44 | 0.54|
| baseline + dep    | 0.72 | 0.54 | 0.62|
| baseline + pos    | 0.75 | 0.58 | 0.65|
| baseline + pos + dep | 0.74 | 0.61 | 0.67|

Table 3: Overall Performance Using Different Features: n-gram features (baseline), FGT features (fgt), signal word features (sig), negation features (neg), pronoun features (pron), dependency structure features (dep), and Part-of-Speech features (pos).

Table 3 shows the overall performance in Precision (P), Recall (R), and F-measure (F1) by incorporating different feature sets, at a 99.8% confidence level according to the Wilcoxon Matched-Pairs Signed-Ranks Significance Test. If we randomly assign one of the citation function classes to each citation instance, the performance is only 3.8% in F-measure. In addition, a simple majority classifier assigns each citation with whichever class that is in the majority in the training set, also only obtaining F-measure of 42.2%. Our results clearly show that our MaxEnt system easily outperforms these two simple baseline classifiers.

We compare F-measure of coarse-grained sentiment classification and fine-grained citation func-
| Function Class | P    | R    | F1   | Distribution |
|----------------|------|------|------|--------------|
| Based_on⁺      | 0.250| 0.029| 0.051| 0.028        |
| Corroboration⁺ | 1.000| 0.022| 0.043| 0.036        |
| Discover⁺      | 0.861| 0.750| 0.802| 0.123        |
| Positive⁺      | N/A  | 0.000| N/A  | 0.001        |
| Practical⁺     | N/A  | 0.000| N/A  | 0.010        |
| Significant⁺   | N/A  | 0.000| N/A  | 0.006        |
| Standard⁺      | 0.500| 0.333| 0.400| 0.002        |
| Supply⁺        | 0.000| 0.000| N/A  | 0.012        |
| Contrast⁻      | 0.667| 0.250| 0.364| 0.006        |
| Co-Citation⁻   | 0.721| 0.792| 0.755| 0.333        |

Table 4: Performance and Distribution of Citation Function Classes

| Citation Sentiment | P    | R    | F1   |
|--------------------|------|------|------|
| coarse-grained POSITIVE | 0.93 | 0.45 | 0.60 |
| fine-grained POSITIVE   | 0.82 | 0.43 | 0.57 |

Table 5: Comparison of Coarse- and Fine-grained Citation Function Classification on POSITIVE

6 Conclusion

In this paper, we introduced the task of citation sentiment analysis and citation function classification, which aims to analyze the fine-grained utility of citations in scientific documents. We described an annotation scheme to annotate citation functions in scientific papers into fine-grained categories. We presented our Maximum Entropy-based system to automatically classify the citation functions, explored the advantages of different feature sets, and confirmed the necessity of using syntactic features in our task, obtaining 67% of final F-measure score.

For future work, we plan to explore more features and perform more citation function-specific annotation for scarce functions in the current annotated corpus. Furthermore, we will also apply our annotation scheme and classification method in scientific literature from different domains, as well as investigate more elaborate machine learning models and techniques.

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