Impact of Corpus Diversity and Complexity on NER Performance

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Abstract

We describe a cross-corpora evaluation of disease mention recognition for two annotated biomedical corpora: the Human Variome Project Corpus and the Arizona Disease Corpus. Our analysis of the performance of a state-of-the-art NER tool in terms of the characteristics and annotation schema of these corpora shows that these factors significantly affect performance.

1 Introduction

The recent growth of on-line biomedical literature has spawned an increasing number of NLP tools for content analysis that help researchers and practitioners access the latest developments in their fields. Examples of these tools include: BANNER – a Named Entity Recognizer (NER) for the biomedical domain (Leaman and Gonzalez, 2008); ABNER – a NER for molecular biology (Settles, 2004); and Whatizit – a Web service which provides functionality to perform text-mining tasks (Rebholz-Schuhmann et al., 2008). These tools in turn require the development of annotated training corpora, e.g., (Kim et al., 2003; Rosario and Hearst, 2004; Kulick et al., 2004; Pestian et al., 2007; Jimeno-Yepes et al., 2008; Bada et al., 2012).

Studies have been conducted to examine the performance of different NLP tools on a single corpus, e.g., (Jacob et al., 2013; Verspoor et al., 2012). However, experience shows that the characteristics of a corpus influence performance, e.g., (Cao and Zukerman, 2012) for sentiment analysis and (Pyysalo et al., 2008) in the biomedical space. In this paper, we analyze how the characteristics and annotation schemas of two corpora influence BANNER’s performance on the recognition of diseases (note that BANNER outperforms ABNER in the recognition of diseases (Leaman and Gonzalez, 2008)). The corpora in question are the Human Variome Project Corpus (HVPC) developed at NICTA (Verspoor et al., 2013), and the Arizona Disease Corpus (AZDC) – a popular medical resource developed at the University of Arizona (Leaman et al., 2009).

Our results show that BANNER’s performance on HVPC significantly exceeds its performance on AZDC. This is (at least partly) explained by differences in corpus characteristics, such as reduced disease mention diversity resulting from HVPC’s specific focus, and by some requirements of HVPC’s annotation schema. These observations suggest that corpus analysis should be conducted along with performance evaluation in order to appropriately assess the obtained results and the suitability of a corpus for training general NER tools.

2 Biomedical Corpora

AZDC is a biomedical textual resource focusing on disease annotation (Leaman et al., 2009). It was extracted from a corpus created by Craven and Kumlien (1999), which consists of sentences selected from MEDLINE® abstracts via queries for six proteins. All disease mentions in AZDC are annotated, with each disease annotation containing a Unified Medical Language System® (UMLS®) concept unique identifier (where possible).

HVPC is an annotated biomedical textual resource pertaining to human genetic variation and its relation to diseases (Verspoor et al., 2013). At present, the corpus comprises ten double-annotated plain-text full journal publications on inherited colorectal cancer, which were selected on the basis of their relevance to the genetics of the Lynch Syndrome. The annotation schema, which is tailored to the focus of the corpus, covers thirteen relations, such as “gene-has-mutation”, “mutation-has-size” and “disease-related-to-body-part”; and eleven entity types, such as genomic categories (e.g., “gene”, “mutation”), phenotypic categories (e.g., “disease”, “body-part”), categories

1 Of the above corpora, only Kulick et al.’s focuses on diseases at the same level of detail as the corpora considered in this paper, and may be investigated in the future.
related to the occurrence of mutations in a disease (e.g., “age”, “ethnicity”), and a “characteristic” category as a catch-all for information of interest that is otherwise uncategorized.

2.1 Comparison of Annotation Schemas

Both HVPC and AZDC annotate duplicate disease mentions in the same sentence, and abbreviations specific to the analyzed article (e.g., “Huntington disease (HD)”). In addition, they do not annotate stand-alone generic words (e.g., “disease”, “syndrome”), and disease names embedded into entities of other types (e.g., “Peter MacCallum Cancer Centre”). However, there are significant differences between these annotation schemas:

- **HVPC’s annotation guidelines** define the “disease” entity type as “an abnormal condition affecting the body of an organism”, and annotates modifiers such “healthy”, “unaffected” and “normal” as diseases of healthy individuals. In contrast, **AZDC** requires that disease mentions correspond to one of the several semantic types of the UMLS Semantic Group “disorders” (e.g., “disease or syndrome”, “injury or poisoning”, “mental dysfunction”, “sign or symptom”). As a result, disease effects are annotated as diseases in AZDC, but not in HVPC.

- **AZDC** requires mention boundaries to be set to a minimum span of text necessary to describe the most specific form of a disease. In contrast, **HVPC** seems to be more restrictive with respect to disease mention boundaries. Specifically, many of the modifiers describing the type of a disease (which are included in disease mentions in AZDC) are attributed to the “characteristic” entity type (Section 1). For example, “classical galactosemia” and “unilateral retinoblastoma” are disease mentions according to AZDC, while only the head noun is a disease mention according to HVPC.

- **HVPC** annotates only the last and most complete part of a disease coordination\(^2\) (e.g., in “breast and ovarian cancer”, “breast” is annotated as a body part\(^3\)), while **AZDC** annotates a coordination as separate but overlapping mentions of a disease (e.g., “breast and ovarian cancer” and “ovarian cancer”).

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\(^2\)This was originally done in response to the BRAT annotation tool (Stenetorp et al., 2012) not allowing annotation of discontinuous entities (since rectified).

\(^3\)A refinement is to consider (body-part, disease) related pairs as multi-word disease names, which would boost the mention-length counts for HVPC in Figure 2.

These aspects account for the simplicity, brevity and higher structural regularity of HVPC disease mentions compared to those in AZDC (Section 2.2).

2.2 Comparison of Corpora Parameters

We have analyzed HVPC and AZDC with respect to the following parameters: size of the corpora in terms of number of sentences and tokens; number of disease mentions and unique disease mentions; and distribution of sentence length, disease mention length and disease mention frequency. The results, which appear in Tables 1 and 2, and Figures 1 and 2, reveal the following differences between HVPC and AZDC, which explain why AZDC is more difficult to analyze automatically than HVPC:

- **Unique disease mentions** – The ratio of unique disease mentions to total disease mentions in HVPC (8.4%) is much lower than in AZDC (37.2%) (Table 1). In addition, in HVPC a small set of unique mentions has very high frequency compared to AZDC (Table 2). These properties of HVPC may be attributed to its narrow focus on the Lynch Syndrome.

- **Sentence length and complexity** – In general, sentence length is significantly higher in AZDC (Figure 1). This may be attributed in part to the way in which HVPC and AZDC were constructed: AZDC contains only sentences extracted from biomedical paper abstracts, while HVPC consists of full papers, which in addition to sentences, contain section headings and table and figure captions.

- **Disease mention length** – Most disease mentions in HVPC consist of 1 or 2 terms, while AZDC contains a large number of multi-word complex disease mentions (Figure 2).

3 NER Performance

In this section, we describe the experiments we performed to evaluate the performance achieved for HVPC and AZDC by a state-of-the-art NER tool, viz BANNER (Leaman and Gonzalez, 2008) (Section 1). We also analyze the types of errors made by BANNER on each corpus, and discuss their connection to the annotation guidelines.

**BANNER** is a NER system developed for use in the biomedical domain. It uses a mechanism based on Conditional Random Fields (CRF) (Lafferty et al., 2001) to assign labels to input tokens, and considers the following features: (1) lemma for a token; (2) part of speech; (3) orthographic features, such as capitalization, presence of digits, prefixes and suffixes, and 2 and 3-character n-grams.
Table 1: Various quantitative parameters of HVPC and AZDC. Unique mentions refer to all (case-sensitive) textually identical disease mentions.

| Parameter               | HVPC   | AZDC   |
|-------------------------|--------|--------|
| # of sentences          | 2116   | 2783   |
| # of tokens             | 52454  | 79950  |
| Total # of disease mentions | 1552   | 3228   |
| # of unique disease mentions | 130    | 1202   |

Table 2: Frequencies of disease mentions.

| Parameter                      | HVPC   | AZDC   |
|--------------------------------|--------|--------|
| Frequency mean                 | 11.94  | 2.73   |
| Frequency standard deviation   | 22.39  | 5.65   |
| Ratio of top N frequent mentions to all mentions | 0.51 0.14 | 0.73 0.22 | 0.85 0.28 |

3.1 Experimental Set-Up

**BANNER configuration:** We used the 19th SVN revision of BANNER (sourceforge.net/p/banner/code/HEAD/tree/) with the following parameters: (1) parenthesis post-processing, post processing of abbreviations specific to an article, and numeric normalization switched “on”; (2) IOB (Inside, Outside, Begin) label model with second order CRF model; and (3) no dictionary.

**Matching schemes:** BANNER’s performance was assessed using the following matching schemes: (1) exact, (2) left border, (3) right border, (4) left or right border, (5) entity inclusion (one entity is a subset of another), and (6) entity overlap. The first scheme provides the most stringent measure of performance, while the other schemes provide different types of fuzzy matches.

**Dataset preparation:** BANNER contains a dataset loader specifically created for AZDC, while HVPC had to be segmented into sentences. This was done by training the OpenNLP sentence splitter (opennlp.apache.org/) on 70% of HVPC, and manually fixing the nine errors that remained after automatic sentence splitting.

3.2 Performance Evaluation

We performed 10-fold cross validation over both corpora, and employed the standard performance metrics of *Precision, Recall* and *F-score*.

The results in Table 3 show that BANNER achieves excellent performance (*F-score*=0.9164) for HVPC on exact matches, which cannot be substantially improved by relaxing the matching scheme. In contrast, AZDC’s *F-score*=0.7365 for the exact matching scheme increases by up to 15% with matching-scheme relaxation.4

The good performance of BANNER on HVPC may be attributed to the single-disease focus of the corpus, its sentence brevity, and its disease-mention properties, which in turn are influenced by the annotation schema (Section 2). The latter may also explain the relative insensitivity of BANNER to the matching scheme relaxation: BANNER tends to have NE boundary detection problems mostly for long disease mentions, which are under-represented in HVPC.

With regard to AZDC, the results in Table 3 indicate that the main cause of the relatively low performance of BANNER is its inaccurate left boundary detection, which affects performance for both the exact and left-border schemes.

4In another set of experiments, BANNER trained on AZDC and tested on HVPC exhibited inferior performance (*F-score*=0.4453 for the exact matching scheme and *F-score*=0.6166 for overlap matching), thus confirming the large difference and non-interchangeability of these two datasets and their annotation schemas.
### 3.3 NER Errors

Below we consider the errors identified in (Leaman et al., 2009) for AZDC (items 1-3), and add another type of error (item 4):

1. Improper handling of coordinations (AZDC), which occurs quite often, despite the addition of a coordination-handling post-processing step. **BANNER** tends to combine separate mentions of the form “disease1 and disease2” (false positives), while sometimes missing annotated coordinations (false negatives).

2. Inability to correctly detect boundaries of disease mentions (AZDC and HVPC). This problem is exacerbated in AZDC when diseases are referred to by their effects rather than their names (e.g., “premature periodontal destruction”), or disease names contain attributes (e.g., “high myopia”).

3. Incorrect identification of acronyms and abbreviations specific to the analyzed article (AZDC and HVPC).

4. Overlooking (false negatives) or mistaken annotation (false positives) of disease names (AZDC and HVPC). In particular, this happens for words characterizing a health condition, e.g., “affected”, “normal” or “healthy” (HVPC only), and diseases referred to by their effects (AZDC only).

This analysis confirms that the difference in **BANNER**’s performance on HVPC and AZDC is partly caused by differences in the annotation guidelines for these two corpora:

- **AZDC** contains many coordinations, while HVPC’s annotation guidelines circumvent the “coordination problem” (Section 2).
- Disease effects and characteristics are not annotated as disease names in HVPC. In contrast, the number of such mentions in AZDC is high, and its disease mentions in general are usually longer and more diverse than disease mentions in HVPC.

These factors explain the increased difficulty of disease-mention identification and mention-boundary detection in AZDC compared to HVPC.

### 3.4 Baseline Performance on HVPC

The simplicity of HVPC is further demonstrated by evaluating the performance of a very simple baseline algorithm that extracts disease mentions from HVPC. This algorithm applies the Unix string-matching utility `grep` to each word in a small (42 word) dictionary that was quickly constructed. The dictionary was created by collecting all the disease mentions and their morphological variations from the Wikipedia article about the Lynch Syndrome, and adding six terms (“healthy”, “normal”, “unaffected”, “polyp”, “polyps” and “polyposis”). The results obtained by this baseline for the exact matching scheme (Precision = 0.8777, Recall = 0.7352 and F-score=0.8001) are significantly better than the **BANNER** scores for AZDC.

### 4 Conclusion

In this paper, we presented a case study of two corpora with disease annotations. Our results show that the domain and construction method of a corpus, the restrictions imposed on disease definitions, and other annotation schema requirements are likely to have a high impact on NER performance. In particular, HVPC is an easy corpus for NER in comparison with AZDC due to its low lexical variability, the brevity and high regularity of its disease names, and the requirements of the HVPC annotation schema.

We conclude that corpus features identified in this paper are predictive of NER performance, and possibly of performance in other tasks, and should be taken into account during corpus selection. In particular, we note that HVPC is not very suitable for the development of NER tools for disease name recognition in general. However, this corpus may be useful for the development and assessment of (disease) relation extraction (RE) tools, as it minimizes the noise introduced by incorrect NER. In addition, it may be suitable for training NER and RE tools for applications focused on particular diseases.

Future research directions include studying other biomedical corpora and specializing high-diversity corpora (e.g., AZDC) to determine characteristics that most affect NER performance.
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