Extracting Concepts for Precision Oncology from the Biomedical Literature

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Abstract

This paper describes an initial dataset and automatic natural language processing (NLP) method for extracting concepts related to precision oncology from biomedical research articles. We extract five concept types: CANCER, MUTATION, POPULATION, TREATMENT, OUTCOME. A corpus of 250 biomedical abstracts were annotated with these concepts following standard double-annotation procedures. We then experiment with BERT-based models for concept extraction. The best-performing model achieved a precision of 63.8%, a recall of 71.9%, and an F1 of 67.1. Finally, we propose additional directions for research for improving extraction performance and utilizing the NLP system in downstream precision oncology applications.

1 Introduction

Precision medicine is a paradigm in which treatment decisions are based not just on a patient’s disease status, but on a variety of other factors including specific genetic, environmental, and other factors. The preeminent use case for precision medicine thus far has been cancer, i.e. precision oncology. Precision oncology is a rapidly-developing field, with a growing number of treatments, trials, and genomic markers. Since drugs can be targeted to relatively rare mutations, the number of studied treatments is greatly expanded and these can be referred to by a variety of names (e.g., the name used in pre-clinical trials is often different than the final drug name). Since the gene mutations can be relatively rare, clinical trial structures have had to be altered to better fit the precision medicine paradigm. And, critically, there are thousands of known genetic mutations from hundreds of cancer-related genes. Sizable effort is thus required to curate all of these types of information to make them available in a usable form to both researchers and clinicians.

Our prior work has focused on this problem from an information retrieval (IR) perspective: how does one find patient-specific information (given a type of cancer, mutation, etc.) from the vast trove of precision medicine-related publications. IR systems were evaluated for this task in the TREC Precision Medicine tracks. We also developed PRIMROSE, a search engine that implements many of the best aspects of precision oncology search. A consistent weakness in these IR approaches, however, was difficulty dealing with the complex semantics of precision oncology articles: identifying the exact treatments studied in an article, which types of cancer the treatment applies to, etc. This task is more consistent with a natural language processing (NLP) information extraction (IE) approach. Therefore, in this work we report the initial development of an NLP system for extracting five key elements of biomedical articles for precision oncology: the type(s) of cancer studied, the mutations that were targeted, the specific population it is limited to, the treatment evaluated, and any available outcome information summarized in the abstract. Because of the fast-moving nature of the field, we focus on biomedical abstracts instead of full-text articles. Not only are the abstracts publicly available well before the full text, but many of the latest-breaking developments in precision oncology are presented at talks in major oncology conferences and only the abstracts for these talks are provided.

To gauge the complexity of this NLP task, we collected a pilot corpus of 250 biomedical abstracts drawn from the TREC Precision Medicine dataset. The five concept types—CANCER, MUTATION, POPULATION, TREATMENT, and OUTCOME—were double-annotated and reconciled. Two models based on BERT, and specifically the BioBERT model pre-trained on biomedical text, were evaluated: BioBERTBASE and BioBERTLARGE. The difference between these models is the number of parameters, in terms of number of layers, hidden units, and attention heads.

∗This project was undertaken during an undergraduate internship at UTHealth-SBMI.
The remainder of this paper is organized as follows. Section 2 discusses related work in NLP for cancer and precision medicine. Section 3 describes the methods, including data (§3.1), annotation (§3.2), and automatic concept extraction (§3.3). Section 4 details the results. Section 5 provides a discussion, including an error analysis, implications, and directions for future work. Finally, Section 6 concludes the paper.

2 Related Work

Biomedical Literature NLP for Cancer Cancer is one of the more frequently studied aspects of NLP for biomedical literature articles. Early works such as MedScan [13] employed rule-based systems to extract and interpret information from MEDLINE abstracts. Chun et al. [14] developed a corpus and extracted relations between prostate cancer and genes from abstracts using a maximum entropy classifier. Baker et al. developed a corpus for identifying the hallmarks of cancer from the biomedical literature and proposed a support vector machine (SVM) model [15] and later a convolutional neural network [16] to automatically classify abstracts. A different take on cancer NLP for the biomedical literature is the development of literature-based discovery (LBD) tools such as LION LBD [17] to identify implicit links within the network of literature articles. LION in particular focuses on the molecular biology of cancer. Beyond the biomedical literature, a tremendous amount of NLP research has been conducted for cancer on other data types. Most notable among these are electronic health records, for which several review articles exist that overview cancer NLP for clinical notes. [18,19,20]

Biomedical Literature NLP for Genomics A tremendous amount of NLP work has focused on extracting information related to genomics from the literature. Early work includes EDGAR [21], which identified gene-drug relations from biomedical abstracts. Libbus et al. [22] identified genes from MEDLINE abstracts based on the Gene Ontology [23] for the purpose of linking literature-based data to structured knowledge sources. Work in pharmacogenomics has required extensive use of NLP to build resources such as the use of SemRep [24] or the construction of the pharmacogenomics knowledge base PharmGKB. [25,26,27] In turn, PharmGKB has been utilized as a knowledge base for many further NLP studies. [28,29,30] Similarly, the PGxCorpus [31] is a manually-annotated corpus for pharmacogenomics—similar in many ways to our goal here, but their work is not specific to cancer. Finally, more general biomedical literature NLP has included genomic components, particularly the CRAFT corpus. [32,33]

Biomedical Literature NLP for Precision Oncology There has indeed been some work specific to precision medicine for NLP within the space of the current work. For instance, Deng et al. [34] classifies abstracts with an SVM based on whether they focus on cancer penetrance. Bao et al. [35] extends this with a deep learning model. Instead of extracting the particular concepts, however, these works focus is simply to classify the entire abstract for use in downstream meta-analyses. Next, Hughes et al. [36] reviews how to utilize precision oncology NLP specific for breast cancer. Finally, the TREC Precision Medicine track [7,8,9] is an ongoing information retrieval shared task focusing on identifying articles relevant to precision oncology. This has inspired the creation of many search engines, including our own, [10] for clinical decision support in precision oncology. Of the many search engines to participate in the TREC Precision Medicine track, however, none has successfully integrated biomedical knowledge sources to greatly improve retrieval performance. We believe this is partly due to the fact that it is difficult to properly link the key aspects of precision oncology in an abstract to these powerful knowledge bases. Instead, most use of biomedical knowledge in such search engines is simply to expand synonyms (e.g., through query expansion) which gives at most small boosts to retrieval performance. Our goal in this paper, then, is to lay the groundwork for improvements in precision oncology search and knowledge acquisition by identifying the key elements to precision oncology in biomedical abstracts. This will allow for the downstream linking of these articles with existing biomedical knowledge bases for better semantic comprehension of the precision oncology scientific landscape.

3 Methods

The high-level study design for this paper follows the standard supervised NLP pipeline: data identification (Section 3.1), manual data annotation (Section 3.2), and automatic NLP extraction (Section 3.3). Since this is a pilot study, our primary goal has been to identify the key barriers to large-scale system development, which is discussed in more detail in the Discussion (Section 5).
3.1 Data

Since the latest developments of precision oncology research are only publicly available in abstracts, we focus only on abstract-based annotation and extraction. Compared to biomedical research in general, precision oncology is disproportionately less represented in PubMed Central given its funding structure (less open access, more embargoed journal articles) and heavy use of abstract presentations for presenting results—which means many of the latest developments that are so important to capture are not available as full text articles, but only abstracts. We focus on a set of abstracts known to be relevant to precision oncology by annotating only abstracts judged as relevant in the TREC 2017 Precision Medicine track[7]. A random selection of 250 abstracts was chosen from those judged relevant during the assessment process.

3.2 Annotation Process

The 250 abstracts were imported into Brat[32] and double-annotated with the following concept types:

1. **Cancer**. The type of cancer being studied in the article (e.g., “breast cancer”, “non-small cell lung cancer”, “mantle cell lymphoma”, “solid tumor”). If the abstract mentions a type of cancer but it is clearly not the cancer investigated in the study, then it is additionally labeled as a Non-study cancer. If multiple types of cancer are included in the study, all are annotated.

2. **Mutation**. The gene mutation being studied in the article, be it a gene with any mutation (e.g., “KRAS”, “FGFR2”, “PIK3R1”), a specific variant (e.g., “BRAF V600E”, “KRAS G13D”, “NF2 K322”), or some other form of genetic mutation (e.g., “CDK4 Amplification”, “PTEN Inactivating”, “EML4-ALK Fusion transcript”). Similar to cancer type, mutations mentioned in the abstract but not investigated in the study are marked as Non-study mutations.

3. **Population**. The specific population in the study (e.g., “Hunan Province in China”, “never or light smokers”, “adults (> 18 years)”, “European patients”, “no history of chemotherapy for metastatic disease”). As shown by the examples, this can include age, sex, location, ethnicity, cancer status, etc. Populations mentioned in the abstract but not investigated in the study are marked as Non-study populations.

4. **Treatment**. The drug used in the study (e.g., “sorafenib”, “abemaciclib”, “trastuzumab”). If the drug was used as part of a combination, each individual component is annotated separately. If the drug was a comparator but not directly investigated in the study, then it is marked as a Non-study treatment (this is more common than Non-study cancers, mutations, and populations).

5. **Outcome**. The result of the study with regards to the success or failure of the treatment. Non-study outcomes are not annotated. The outcomes are generally a sentence or long phrase describing the overall outcome. E.g.,

- **Main grade 3 or 4 toxicities were rash (11 [13%] of 84 patients given erlotinib vs none of 82 patients in the chemotherapy group), neutropenia (none vs 18 [22%]), anaemia (one [1%] vs three [4%]), and increased amino-transferase concentrations (two [2%] vs 0).**
- **Treatment with crizotinib results in clinical benefit rate of 85%-90% and a median progression-free survival of 9-10 months for this molecular subset of patients.**
- **Although nearly all patients with GIST treated with imatinib experienced adverse events, most events were mild or moderate in nature.**

Additionally, negated concepts were marked as such. While there were negated Cancer annotations (e.g., Two annotators (the first author and a biomedically-trained graduate student) labeled each abstract in batches of 25, reconciling after each batch. Instead of using highly-refined guidelines, the goal of this annotation process was more exploratory in nature. The concepts were defined as above, but no further. The goal was to identify the range of possible ways in which the information can be expressed, without too much regard for maximizing inter-rater agreement.
Table 1: Descriptive statistics of the annotated corpus.

Anecdotally, some concepts had more inconsistent agreement throughout the process (notably POPULATION and OUTCOME), while others had early disagreement that improved over time (such as how to handle acronyms with CANCER and MUTATION). These issues are ultimately reflected in the automatic extraction scores described in Section 3.

Descriptive statistics of the annotated corpus are provided in Table 1. Example annotations from the corpus are shown in Figure 1.

3.3 Automatic Extraction

The abstracts were tokenized and split into sentences using spaCy. A BILOU scheme was used for sequence classification, where B is the first token of a sequence, I an inside token, L the last token, O a token outside any sequence, and U a single-token concept. So “K-ras and PTEN mutations” would be [B-MUTATION, I-MUTATION, L-MUTATION, O, U-MUTATION, O]. Non-study concepts were handled by adding a N- before the concept name (e.g., B-N-TREATMENT).

We follow the standard BERT framework for named entity recognition tasks. Two variants of BioBERT were evaluated: BioBERT BASE v1.1 and BioBERT LARGE v1.1, which are versions of BERT BASE and BERT LARGE respectively pre-trained on both 1 million PubMed abstracts (note that the BioBERT v1.0 models are pre-trained on 200k PubMed abstracts and 200k PubMed Central full-text articles, but BioBERT v1.1 is only pre-trained on abstracts, though a larger number). As such, BioBERT is an ideal starting point for a transformer-based language model to use for our task. BioBERT BASE has 12 layers, 768 hidden units per layer, and 12 attention heads per layer (a total of 110 million parameters); BioBERT LARGE has 24 layers, 1024 hidden units per layer, and 16 attention heads per layer (a total of 340 million parameters). Generally, the larger BERT variant offers some improved performance, but in many cases the performance delta is negligible and not worth the additional computational cost. As such, we experiment with both models to assess whether a larger BERT model would be beneficial in this task.

The data was split 70% for training the BioBERT models, 10% for validation (early stopping), and 20% for testing (results discussed below). The default BioBERT parameters were used other than a learning rate of $2 \times 10^{-5}$, maximum sequence length of 128, training batch size of 32, validation batch size of 8, and test batch size of 8.
### Treatment

- Favorable response to crizotinib in three patients with echinoderm microtubule-associated protein-like 4-anaplastic lymphoma kinase fusion-type oncogene-positive non-small cell lung cancer.

### Background

The echinoderm microtubule-associated protein-like 4 (DML4)-anaplastic lymphoma kinase (ALK) is a recently identified fusion-type oncprotein that exists in approximately 5% of non-small cell lung cancer (NSCLC).

It has been demonstrated that NSCLC driven by EML4-ALK is strongly addicted to this fusion-type oncokine.

A clinical trial of crizotinib (PF-02341066) sponsored by Pfizer has proven this oncogene addiction in humans by demonstrating a high response rate to inhibition of ALK kinase activity.

In the present study, we report on three cases harboring EML4-ALK rearrangement who were enrolled in the trial (A8081001, NCT00585195).

All three patients showed favorable responses to the ALK-specific tyrosine kinase inhibitor.

### Results

Dacomitinib versus erlotinib in patients with EGFR-mutated advanced non-small-cell lung cancer (NSCLC): pooled subset analyses from two randomized trials.

**BACKGROUND:** The irreversible epidermal growth factor receptor (EGFR) inhibitors have demonstrated efficacy in NSCLC patients with activating EGFR mutations, but it is unknown if they are superior to the reversible inhibitors.

Dacomitinib is an oral, small-molecule irreversible inhibitor of all enzymatically active HER family tyrosine kinases.

**METHODS:** The ARCHER 1009 (NCT01360554) and A7471028 (NCT00769647) studies randomized patients with locally advanced/metastatic NSCLC harboring EGFR mutation (exon 19 del or L858R) to either 40 mg dacomitinib or 150 mg erlotinib.

**RESULTS:** Dacomitinib mutation testing was performed centrally on archived tumor samples.

We pooled patients with exon 19 deletion and L858R EGFR mutations from both studies to compare the efficacy of dacomitinib to erlotinib.

**RESULTS:** One hundred twenty-nine patients with any EGFR mutation were enrolled; 101 had activating mutations in exon 19 or 21.

**RESULTS:** For patients with exon 19/21 mutations, the median progression-free survival was 14.6 months [95% confidence interval (CI) 9.0-18.2] with dacomitinib and 9.6 months (95% CI 7.4-12.7) with erlotinib [unstratified,

**RESULTS:** The median survival was 26.6 months (95% CI 21.6-41.5) with dacomitinib versus 23.2 months (95% CI 16.0-31.8) with erlotinib (unstratified HR 0.737 [95% CI 0.431-1.259], two-sided log-rank, P = 0.265).

### Distinct clinical outcomes of non-small cell lung cancer patients with epidermal growth factor receptor (EGFR) mutations treated with EGFR tyrosine kinase inhibitors: non-responders versus responders.

**INTRODUCTION:** Treatment with epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKIs) has been associated with favorable progression free survival (PFS) in patients with non-small cell lung cancers (NSCLC) harboring EGFR mutations.

However, a subset of this population doesn’t respond to EGFR-TKI treatment.

Therefore, the present study aimed to elucidate survival outcome in NSCLC EGFR-mutant patients who were treated with EGFR TKIs.

**METHODS:** Among the 580 consecutive NSCLC patients who were treated at our facility between 2008 and 2012, a total of 124 treatment-naive, advanced NSCLC, EGFR-mutant patients treated with EGFR TKIs were identified and grouped into non-responders and responders for analyses.

**RESULTS:** Of 124 patients, 104 (84%) responded to treatment, and 20 (16%) did not; and the overall median PFS was 9.0 months.

Notably, the PFS, overall survival (OS) and survival rates were significantly unfavorable in non-responders (1.8 vs. 10.3 months, hazard ratio (HR) = 29.2, 95% confidence interval (CI), 3.48-63.26, P<0.001.

In multivariate analysis, treatment efficacy strongly affected PFS and OS, independent of covariates (HR=47.22, 95% CI, 17.88-124.73, P<0.001 and HR=2.74, 95% CI, 1.43-5.24, P=0.002, respectively).

However, none of the covariates except of the presence of EGFR exon 19 deletion in the tumors was significantly associated with better treatment efficacy.

**CONCLUSIONS:** A subset of NSCLC EGFR-mutant patients displayed unfavorable survival despite EGFR TKI administration.

This observation reinforces the urgent need for biomarkers effectively predicting the non-responders and for drug development overcoming primary resistance to EGFR TKIs.

In addition, optimal therapeutic strategies to prolong the survival of non-responders need to be investigated.

**Figure 1:** Example annotations
| Annotation  | Precision | Recall | F1   |
|------------|-----------|--------|------|
| Overall    | 60.48     | 70.73  | 65.20|
| CANCER     | 69.31     | 78.65  | 73.68|
| MUTATION   | 59.35     | 69.13  | 63.87|
| POPULATION | 41.82     | 42.59  | 42.20|
| TREATMENT  | 47.79     | 71.05  | 57.14|
| OUTCOME    | 0.0       | 0.0    | 0.0  |

Table 2: Results using BioBERT\textsubscript{BASE} model.

| Annotation  | Precision | Recall | F1   |
|------------|-----------|--------|------|
| Overall    | 63.79     | 71.90  | 67.61|
| CANCER     | 70.54     | 80.06  | 75.00|
| MUTATION   | 61.51     | 68.78  | 64.94|
| POPULATION | 56.25     | 50.00  | 52.94|
| TREATMENT  | 58.59     | 76.32  | 66.29|
| OUTCOME    | 0.0       | 0.0    | 0.0  |

Table 3: Results using BioBERT\textsubscript{LARGE} model.

### 4 Results

The results for the BioBERT\textsubscript{BASE} and BioBERT\textsubscript{LARGE} models are provided in Table 2 and Table 3. Not enough Non-study concepts are present in the test set to merit an evaluation here. We thus focus on boundary extraction and type classification without the Non-study attribute.

In almost every case, the BioBERT\textsubscript{LARGE} results outperform the BioBERT\textsubscript{BASE} results (the lone exception being MUTATION recall, while neither model successfully extracts any OUTCOME). The differences between BioBERT\textsubscript{BASE} and BioBERT\textsubscript{LARGE} are often several points, including substantial boosts for both POPULATION (+10.74 F1) and TREATMENT (+9.15 F1). Notably, the improvements from BioBERT\textsubscript{BASE} to BioBERT\textsubscript{LARGE} are roughly proportional to the number of available annotations for training, with the most common concept type (MUTATION) receiving the smallest boost.

For both models, their performance across the different concept types was roughly proportional to the number of annotations for training. While there were more MUTATION annotations than CANCER annotations, there was a far greater variety of MUTATION mentions than CANCER mentions, which likely explains why CANCER outperforms MUTATION in both models by roughly 10 points of F1. TREATMENT is the next most common concept type, and while for BioBERT\textsubscript{BASE} this performs 6.73 points of F1 worse than MUTATION, for BioBERT\textsubscript{LARGE} TREATMENT actually outperforms MUTATION by 1.35 points of F1. Meanwhile, for both models POPULATION is the second-worst-performing concept type, while as mentioned neither model correctly identifies a single OUTCOME. The latter is almost certainly due to the combination of few annotations (130 in the entire corpus) and long, complex nature of each concept span (28.5 tokens). Clearly, OUTCOME extraction is not an ideal named entity recognition task and should be handled by a different type of extraction (e.g., sentence classification).

Finally, it is interesting that with the exception of POPULATION for BioBERT\textsubscript{LARGE}, all concepts have higher recall than precision. This requires further investigation, but one possibility is that the BERT models are good at identifying instances very similar to those in the training data, but additionally predict spans with high biomedical similarity that are nonetheless not one of the annotated concepts.
5 Discussion

This work is an initial feasibility study on the extraction of key variables for precision oncology from biomedical literature abstracts. We focus on identifying the type of cancer, mutation, population information, treatment, and outcomes. A small corpus of 250 abstracts was manually annotated, then two BioBERT models were evaluated. While none of the five concept types performed up to the level one would hope, CANCER performed reasonably well (F1 of 75.00), while MUTATION and TREATMENT showed promise (F1 of 64.94 and 66.29, respectively). POPULATION performed below a level that is likely usable (F1 of 52.94), while OUTCOME was not successfully extracted at all. Here, we discuss the successes and shortcomings of this feasibility pilot and what should come next to address the key problems.

The most obvious need for improvement is the small size of the dataset. Our point of reference for appropriate dataset sizes is the NCBI Disease Corpus[39,40] which has 793 abstracts, or roughly three times the size of what is presented here. BioBERT’s performance on that corpus is an F1 of 89.71, which we can assume is a rough upper bound for automatic extraction if the corpus was scaled up. We will note, however, that even the CANCER, MUTATION, and TREATMENT concepts themselves are more diverse than what is in the NCBI Disease Corpus, and the lexical variation seen with even these concepts is likely greater (especially TREATMENT, see Figure 1), so this would be an ambitious upper bound. Ultimately, it seems clear that increasing the corpus size would be beneficial.

Regarding the lower-performance concepts, it is likely that POPULATION needs to be refined as a concept, which would allow it to incorporate pre-defined lexicons. In this study we intentionally did not define this concept narrowly in order to assess the range of populations mentioned in abstracts. Going forward, however, we can focus on the set of populations that are critically important to precision oncology. These usually differ from the normal medical notion of a population. Instead of demographics, in precision oncology the cancer and treatment history are primary populations of interest (e.g., “treatment-naive” in Figure 1 refers to patients who have not yet undergone chemotherapy). Regarding OUTCOME, this is clearly an item that is more appropriately tackled as a sentence classifier than via entity extraction. As can be seen in Figure 1, the OUTCOME sentences have fairly clear features not seen in the other sentences, so it is likely that a sentence classifier could identify these with relatively high efficacy.

The comparison of BioBERT_BASE and BioBERT_LARGE is instructive. At the current size of the corpus, the larger model provides more than sufficient benefit to justify its additional complexity. Perhaps in a larger corpus, the base model will close the gap. In other works (e.g., Ji et al.[41]), the larger model performed no better than the base model. These experiments, then, should be revisited with a larger corpus.

Another logical place for improvement is the use of knowledge resources. In this study, we hoped to assess the performance of BioBERT alone, but future work should incorporate existing knowledge resources such as the NCI Thesaurus[42] for cancer names and COSMIC[43] for gene mutations. Above, we stated the NCBI Disease Corpus performance is a good estimate of an upper bound, but the one advantage of focusing exclusively on precision oncology is that more detailed knowledge resources can be brought to bear: a more specific domain allows us to make domain-specific assumptions. This could be critical for improving performance, but there is one important note of caution which also justifies our initial reasoning to evaluate a resource-free approach. Since precision oncology moves quickly as a field, the lexicon of terms used in papers is oftentimes well ahead of knowledge resources. A new oncogene may be identified months or years before it is incorporated into the appropriate knowledge base. Over-reliance on these knowledge sources may increase the NLP performance on the annotated corpus while simultaneously reducing the model’s ability to recognize the very emerging concepts we are most focused on identifying. Thus, these knowledge resources cannot be integrated naively, and care should be taken in this process.

A final avenue for improvement focuses on the machine learning aspects. This includes adjusting the tagging scheme—we used BILOU in this study, but given the variance in concept length (see Table 1) other tagging schemes may be more appropriate. Not every concept type need use the same tagging scheme, either. E.g., the shorter MUTATION concepts may utilize a more simple BIO scheme. Additionally, the only form of transfer learning we experimented with in this paper is the use of the BioBERT model itself, which effectively transfers a language model pre-trained on large amounts of biomedical text. After the language modeling, but prior to fine-tuning the model on this precision oncology corpus, other existing datasets may be utilized for transfer learning, such as the NCBI Disease Corpus[39,40].
and PGxCorpus\textsuperscript{[31]}. This would effectively reduce the need to scale up the size of our own manual corpus, though we do not believe that even with transfer learning the current corpus size is sufficient.

**Limitations** The data evaluated in this study was taken from the TREC Precision Medicine track,\textsuperscript{[7]} and specifically the subset of abstracts marked as relevant for one of the topics. As such, it is certainly not representative of the full array of biomedical literature. This decision was made for annotation convenience—these abstracts were known to be highly relevant to precision oncology. However, the real bias introduced here is the manual nature in which they were chosen. Identifying potentially relevant abstracts to annotate via keywords or machine learning would result in a corpus that is more appropriate, as these methods could be re-applied when using the precision oncology NLP model on new abstracts. A second limitation is the training of the annotators was intentionally kept minimal so as to encourage exploration of potential concepts. Also, only one of the two annotators was biomedically trained. We have discussed the need for additional manual annotation, but this will also need to come with additional training and more refined guidelines to ensure annotation quality.

6 **Conclusion**

This work presents a pilot study for NLP information extraction of terms related to precision oncology from biomedical literature abstracts. Five concept types were targeted: CANCER, MUTATION, POPULATION, TREATMENT, and OUTCOME. A small corpus of 250 abstracts was manually annotated and reconciled. Two BioBERT models were evaluated for automatic extraction, with the best results ranging in F1 of 75.0 (for CANCER) to a complete inability to extract OUTCOME information. We finally discussed a set of opportunities for future work to improve these results, including a larger corpus, use of existing biomedical knowledge resources, and additional transfer learning.

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