# Identifying most relevant concepts to describe clinical trial eligibility criteria

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Abstract: Since eligibility criteria of clinical trials are represented as free text, their automatic interpretation and the evaluation of patient eligibility is challenging. Our approach to the criteria processing is based on the identification of contextual patterns and semantic concepts that together define the machine-interpretable meaning. The goal of this research is to find the most relevant concepts occurring in eligibility criteria that need to be mapped to patient record to enable automatic evaluation of patient eligibility. Based on the analysis of annotation of breast cancer trials obtained using different concept recognizers and ontologies from UMLS Thesaurus, we chose to use MetaMap and SNOMED CT to create the mapping set. To prioritize the identified concepts, we used the tf-idf measure and the corpus of over 38, 000 various clinical trials, to detect concepts specific for breast cancer, and cancer in general. The obtained results can guide the mapping order of criteria concepts to patient data. The observed substantial overlap between the terms occurring in criteria from the trials related to breast cancer and other diseases will reduce the cost of extending the trial matching system to other diseases.

## **1 INTRODUCTION**

Clinical trials examine the efficacy of diagnosis and treatment methods through case-control studies, but finding eligible patients is expensive and difficult. A patient is enrolled in a clinical trial only when all the eligibility criteria are fulfilled. They regard i.a. age, gender, the current and prior diagnoses and treatments. The problem is that they are defined in free text e.g. 'No prior cancer except for skin cancer'. In our previous work we built the patterns that capture general meaning of criteria (e.g. 'No prior [] except []') which, when detected, provide crucial context information (Milian et al., 2012). Here, we explore the concepts that occur in eligibility criteria related to a particular disease. Identified concepts will be used to link to corresponding data items in patient record, to enable evaluation of patient eligibility. The links can be defined via the pointers to the type of a source document (e.g. pathology report, discharge summary), and/ or by defining semantic relations (isA, sameAs) to the terminology locally used in a hospital. Such process will require significant manual effort, during the design or evaluation and involvement of medical experts. Since medical ontologies contain hundreds of thousands of concepts, there is a need to extract subsets which are relevant for a particular purpose.

This study presents the experiment conducted to

compare 2 major ontology annotators: Bioportal and MetaMap, and coverage of criteria from ClinicalTrials.gov<sup>1</sup> by the various medical ontologies (section 2). Further, section 3 describes in detail the MetaMap annotation results of eligibility criteria of breast cancer trials, the quantitative characteristics of identified concepts, their distribution over semantic types and analysis of stability of obtained set. Section 4 demonstrates the strategy used to prioritize the detected concepts for creating mappings to patient record, and presents findings about overlap of concepts occurring in various types of trials. Final sections presents related work and conclusions.

## **2 DEFINING A STRATEGY**

#### 2.1 Selecting an ontology annotator

There are two major concepts recognizers available for biomedical text mining: MetaMap (Aronson and Lang, 2010) and NCBO annotator (Musen et al., 2008). This section presents the experiment conducted to compare the results of annotation of both tools on the trials corpus. We used 2135 trials from ClinicalTrials.gov, related only to breast cancer, as it

<sup>&</sup>lt;sup>1</sup>http://clinicaltrials.gov/

is our main domain of interest. Both tools are highly configurable, allow i.a. to select ontologies used for annotations, MetaMap - any from UMLS (which integrates more than 100 vocabularies), Bioportal - 16 out of them. Because SNOMED CT is the largest relevant ontology covered by both tools, we performed the experiment restricting the vocabulary source to this one. MetaMap returns the UMLS identifiers (CUI) of detected concepts, Bioportal - the codes from a local ontology. To compare the results, we used the UMLS API to retrieve the corresponding CUIs of SNOMED ConceptIds, returned by NCBO annotator.

Figure 1 presents the annotation results, the number of concepts recognized by both tools, the overlap between them and the number of concepts found only by one of them. Initially NCBO returned 7081



Figure 1: The number of SNOMED CT concepts detected by Bioportal and MetaMap in the corpus of eligibility criteria from 2135 breast cancer trials.

distinct concepts, which were mapped to 5005 CUIs. The inspection of some of the remaining ones showed that they were flagged in UMLS as duplicate or ambiguous. As can be seen in the figure, MetaMap returned a larger number of concepts (5994 vs 5005). The overlap between both results is 4075, meaning only 59% of entire set (6924), which is rather worrisome. Additionally, both tools detected concepts not found by the other (1919 - MetaMap, 930 - Bioportal). Table 1 provides the details about the top 3 semantic types present in the set of concepts detected exclusively by one of the tool. In the set detected only by MetaMap the majority of concepts have types: Findings, Disease or Syndrome, Laboratory procedure. Third on the list of Bioportal is Therapeutic or Preventive procedure. In most cases, except for Diseases, MetaMap returned more concepts.

The proper evaluation should also consider precision and recall of both tools. However, it would require the involvement of domain experts, which exceeds the scope of this work. In paper (Shah et al., 2009) the authors of Bioportal report that Mgrep (algorithm underlying the service) has higher precision than MetaMap when detecting UMLS concepts having 'Disease or syndrom' semantic type (0.87 vs 0.71), but lower in case of 'Biological processes' (0.6 vs 0.63). Clearly, the performance is dictionary dependent. However, no information on other semantic

Table 1: Number of concepts belonging to particular semantic types, detected only by MetaMap and only by NCBO, percentage of all of a type, detected by corresponding tool.

Sementic Type	Only by	Only by
	MetaMap	NCBO
Finding	185 (43%)	139 (22%)
Disease or Syndrome	151 (26%)	189 (49%)
Laboratory Procedure	100 (59%)	31 (11%)
Therapeutic or Preven-	95 (31%)	55 (21%)
tive Procedure		

types, ontologies, nor recall is provided.

We choose MetaMap for the next experiments, as it detects significantly larger number of concepts.

#### 2.2 Selecting a medical vocabulary

This section presents the MetaMap annotation results of eligibility criteria from 2135 breast cancer clinical trials. The aim is to compare the coverage of criteria by various ontologies to support the choice for further experiments, and learn about the uncovered phrases.

#### Coverage by various ontologies

In total MetaMap detected 768439 UMLS concepts, 10924 distinct. Figure 2 presents the statistics of their source (left bars). Listed are only ontologies which contributed new concepts to the set, ordered by the number of exclusive contributions (right bars).

The majority of concepts are covered by: MTH (UMLS Metathesaurus), CHV (Consumer Health Vocabulary), NCI ( NCI Thesaurus) and SNOMED CT. The figure demonstrates remarkable overlap between the terminologies, emphasized by the small contributions of distinct sources (highest for NCI, SNOMED CT and CHV). The majority of concepts (88%) are defined by multiple ontologies. Based on the number of all detected concepts and unique contributions, NCI seem to be the most appropriate ontology to use for the concept recognition in eligibility criteria of breast cancer trials. However, because SNOMED CT is broadly used in clinical setting, and is still high on the list, we decide to use it for the next experiments.

#### **Uncovered phrases**

Additionally, we analyzed the overall coverage of eligibility criteria by ontologies. Table 2 presents the statistics about phrases distinguished by MetaMap. Both when using entire UMLS and only SNOMED CT, around 32% of phrases remains uncovered. To analyze the quality of obtained mappings, we checked their MetaMap score. When using entire UMLS only



Figure 2: Number of concepts from various UMLS ontologies detected in eligibility criteria of breast cancer trials

34.9% of mappings got the maximal score, SNOMED CT, significantly more, 47.8%. UMLS is a multipurpose source, i.e. includes concepts from vocabularies developed for different purposes, therefore for effective usage needs to be customized.

Table 2: Statistics about phrases from breast cancer trials

Phrases	UMLS	SNOMED CT
Uncovered	31.6 %	32 %
Max mapping sore	34.9%	47.8%

Finally, we examined the unmatched phrases (see Figure 3), observing mainly lay terms, which is a promising finding about UMLS coverage. However, these provide the context, therefore their recognition is also crucial for automated interpretation of criteria.

or	:	-	)	and	be	must	(	have	>
is	are	that	,	;	<	who	of	since	and/or
as	would	if	for	).	will	may	e.g.	has	with
OR	been	but	had	either	unless	should	Must	in	of the
any	than	by	which	If	Have	they	to	can	Has

Figure 3: The most frequent words in eligibility criteria, uncovered by ontologies.

## **3 ESTIMATING EFFORT**

Using selected annotator and ontology (MetaMap and SNOMED CT), in this section, we investigate which parts of SNOMED CT are actually relevant for describing eligibility criteria of medical trials and estimate the effort indicators for mapping terms in eligibility criteria to patient data.

## 3.1 Distribution of SNOMED CT concepts over semantic types

Annotation of criteria with SNOMED CT resulted in detection of 393,511 occurrences of 5994 distinct concepts. Figure 4 presents the distribution of all detected concepts over the top 25 semantic types. Figure 5 presents the cardinality of top 25 mostly represented semantic types. The most frequent concepts have types: Qualitative Concept (13%), Temporal Concept (10%), Therapeutic or Preventive Procedure (8%). The majority of distinct concepts belong to: Disease or Syndrome (10%), Finding (7%), Organic Chemical, Pharmacologic Substance (6%).

For mappings, the "cardinality of the type" is an indicator of the effort needed to map this type to patient data, while the "frequency of the type" is an indicator of how many trials will be covered by such a mapping. In loose terms, the size of a semantic type is the "cost" of mapping, while the frequency is its "benefit". So ideally, we would like to find semantic types with high benefit and low cost. Figure 6 shows this benefit/cost ratio (frequency/ cardinality) corresponding to the highest ranking 25 semantic types. The situation is most "profitable" for the type "Research activity" which occurs over 5k times and contains only 4 concepts. Next are "Patient or Disabled Group", "Hormone", "Amino Acid, Peptide". Only few types contain concept that frequently occur and are limited in number. The majority occurs sporadically with relatively large number of concepts, as the ratio decreases very slowly. Concluding, the long tails on the above graphs show that the mapping effort will spread over many semantic types, and we cannot focus only on most frequent or largest types. However, presented ordering should help to optimize the effort.

#### 3.2 Verifying stability of annotation set

By annotating the large corpus of trials we wanted to obtain the set of concepts that is sufficiently broad to cover the majority of trials, including those not presented in the initial corpus. To verify this idea, we analyzed how the number of distinct concepts occurring in eligibility criteria is growing with the number of trials fed to the annotator. The results are plotted for the major semantic types in Figure 7. Initially, the number of concepts grows rapidly, independently of the type, then, the curves gradually slow down because of the trials similarities. As expected, the number of concepts belonging to some types keeps growing considerably, e.g. Disease or Syndrome, while in other cases it stabilizes sooner, e.g. Laboratory or Test Result. Figure 7 shows only the behavior of semantic types with highest cardinality. The semantic types in the tail of Figure 5 show a more promising behaviour: their

Population Group idea of concept Patrone Function OF8715 MARTINGTON Jusenesdie Occupation of Nautacured object entrealth Cae Activity Research Activity Laboraton Procedure Patent of Disbed Grid Diagnostic Procedu Oreanism Attribu Quantitative Conc Body Part, Organ Pramaologi Substa Temporal Cont runctional conc Neoplastic Prot Intellectual Prot spatialcon Jutic or Preve Therape





Figure 5: Distribution of cardinality of semantic types



Figure 6: The ratio: semantic type frequency / cardinality

growth is small after an initial growth period, hence for these semantic types there seem to exist a "core set of concepts" used in eligibility criteria. However, we cannot expect to obtain a complete and stable set of all concepts. Extending the trial matching system, will require some effort of defining new mappings.

#### 4 PRIORITIZING CONCEPTS

Performed annotation led to the recognition of several thousands of concepts in eligibility criteria from breast cancer trials. In this section, we prioritize them,





to suggest the order used to map the terms to patient record. Previous section provides insights aggregated for semantic types. Here, we focus on concrete terms. To prioritize the breast cancer concepts, apart from concept frequency we take into account concepts specificity for breast cancer, by comparing their usage in other trials. Next, we rank higher concepts that are specific to cancer trials in general, again as compared to their use in any trial. Furthermore, we verify the coverage of eligibility criteria from various trials, by the top ranking concepts in breast cancer.

#### 4.1 Description of a method

The concepts specificity for breast cancer was measured using the tf-idf weight (Jones, 1972), commonly applied in information retrieval field to detect relevant terms (t) in a document (d) (see Formula 1).

$$tf * idf(t, d, D) = tf(t, d) * log(\frac{|D|}{|\{d \in D\}|})$$
 (1)

It grows proportionally to the term frequency (tf), and inversely proportionally to the number of containing it documents in a corpus D ( idf).

First, to rank higher concepts specific to breast cancer, we concatenated all corresponding eligibility criteria in one document, and as a corpus we used eligibility criteria from all trials related to cancer. Analogously, to give the priority to the concepts specific to cancer in general, we used as corpus trials studying other diseases. We categorized the trials using their meta data - each defines a list of studied conditions. The numbers of applied trials are listed in table 3.

Table 3: Size of corpora used in the experiment

Condition	Trials	Concepts
Breast cancer	2135	5994
Cancer	12022	13547
Non-cancer	23963	19428

#### 4.2 Top ranking concepts

Using the described strategy, we obtained the ordering of concepts. 10 most typical for breast cancer trials, and cancer in general, are listed in table 4. The first on breast cancer list is "Carcinoma of breast", cancer - "Metastatic to". The outcome follows the intuition, demonstrating the effectiveness of tf-idf. The obtained ranking should help to optimize the mapping effort needed to build a recruitment support tool.

Table 4: The most relevant concepts for BC and cancer trials

Most relevant for BC	Most relevant for cancer
Carcinoma of breast	Metastatic to
Breast cancer	Before
Invasive	Chemotherapy regimen
HER-2/neu	Concurrent
Concurrent	Radiotherapy
Before	Chemotherapy
Specific	Therapeutic procedure
Breast	Malignant neoplasm
Entire breast	Neoplasms - malignant
Immunologic adjuvant	Radiotherapy

#### 4.3 Coverage in other types of trials

Here, we present the result of the experiment aimed to analyze the extensibility of our approach to other diseases. We want to verify how many concepts relevant for breast cancer, are also used in eligibility criteria of trials studying other diseases. The trials were clustered based on the top frequently occurring conditions in the corpus of cancer and non cancer trials. We performed the experiment with the top 2000 concepts according to the tf-idf weight. The ordering reflects the concepts weights of on the merged list of breast cancer and cancer specific items. Table 5 presents the statistics about the trials groups, overlaps of the top breast cancer concept and the percentage of all detected concepts in a group.

Table 5: Coverage of criteria related to various diseases, by the most relevant 2000 breast cancer concpets.

Condition	Trials	Overlaping concepts
Prostate cancer	1214	1657 (24%)
Lung cancer	854	1662 (38%)
Lymphoma	616	1476 (42%)
Leukemia	615	1378 (42%)
Healthy	2760	1480 (21%)
HIV	1881	1430 (25%)
Obesity	844	1217 (31%)
Hypertension	804	1185 (34%)

The highest overlap occurs between breast and lung cancer trials. As expected, there is a bigger overlap between trials about breast cancer and other cancers, than those about non cancer conditions (considering also the number of compared trials). In all cases more than half of top ranking concepts for breast cancer, are also detected in eligibility criteria related to other diseases. This finding indicates that the substantial part of mappings can be reused if the trial matching algorithm should be extended to others diseases.

### **5 RELATED WORK**

The problem of identification of subsets of ontologies can be compared to the problem of formal ontology modularization. In (Clark and Parsia, 2008) the authors provide an overview of existing methods, evaluate them from the perspective of correctness, completeness, minimality and importsafety. According to their findings locality-based modules are proven to be correct and complete and are empirically-shown to approximate minimality better than ad-hoc and other formal algorithms. These methods are applicable when the extracted module should be sufficient for reasoning, which is not our concern.

In (Milian et al., 2009) we aimed to detect the subset of UMLS related to breast cancer treatment, by expanding the initial set of concepts (those considered at the decision points in treatment guidelines) via the ontology hierarchy and the UMLS semantic network.

With respect to the analysis of eligibility criteria, (Ross et al., 2010) provide an informative overview of types of criteria, based on randomly-chosen 1000 eligibility criteria from ClinicalTrials.gov. They categorized them along several axes: complexity, semantic patterns, clinical content and data sources. They demonstrated a large semantic and clinical variability of criteria across the trials. They argue that the majority of criteria present the challenges for automatic evaluation because of semantic connectors hard to express with current representation languages, temporal constraints, need for clinical judgment or lack of expected data in patient record.

## 6 CONCLUSIONS

The work described in this paper is part of our research aimed at supporting patient recruitment and trial study feasibility. It focuses on the analysis of semantics of eligibility criteria, detecting parts of medical ontologies relevant for a particular disease.

First, we investigated which annotation tool, MetaMap or NCBO annotator, is more appropriate for our task. We compared the overlap of concepts detected by both in eligibility criteria of 2135 breast cancer trials. The results show that the intersection accounts for only 59% of entire set. Because of the advantage of MetaMap in the number of detected concepts we decided to use it for further experiments. In future work it could be interesting to define a voting algorithm which takes into account precision and recall of both tools corresponding to particular types of criteria or semantic types. Second, we analyzed the source and semantic types of detected concepts. The findings indicate the high majority of concepts (88%) is defined by more than one ontology covered by UMLS, majority by MTH, CHV, NCI and SNOMED CT. The highest number of unique contributions is provided by NCI, SNOMED CT and CHV. We chose SNOMED CT for the next experiments, because of its wide usage in clinical setting and good scores in the comparison. It should be noted that in 32% of criteria phrases MetaMap did not detect any concept, which indicates that additional processing is needed to recognize the context in which recognized terms occur. Only approximately 35% of phrases annotated with UMLS obtained the maximal mapping score, and 48% in case of using only SNOMED CT.

The analysis of the distribution of the detected concepts over various semantic types and their frequency revealed that the mapping effort will need to be spread over many types. Furthermore, we analyzed the stability of obtained concept set by studying its growth while adding new trials. While some stability of the growth curve can be observed, specially for some semantic types, we cannot expect that obtained annotation set is complete. Extending the solution to other trials will involve creating more mappings.

Finally, we put the semantic of breast cancer trials into broader perspective of over 38, 000 clinical trials studying other diseases. We used tf-idf measure to find concepts that are specific for breast cancer, and cancer in general, and used the results to prioritize them. We also verified the overlap between the top 2000 ranking concepts for breast cancer and concepts occurring in other types of eligibility criteria and find out that the substantial part is repeated: in all cases above 1100, in other cancer types above 1300.

We believe that this analysis provides insights about semantics of eligibility criteria that can be used to prioritize the mapping process of eligibility criteria to patient record, and enhance building the recruitment support tool. The approach was demonstrated on the breast cancer domain, but it can be easily reused for other diseases.

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