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Syntactic Structures In Medical Discourse And Their Functional Functions

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Abstract: This paper demonstrates a method for determining the syntactic structure of medical terms. We use a model-fitting method based on the Log Likelihood Ratio to classify three-word medical terms as right or left-branching. We validate this method by computing the agreement between the classification produced by the method and manually annotated classifications. The results show an agreement of 75% - 83%. This method may be used effectively to enable a wide range of applications that depend on the semantic interpretation of medical terms including automatic mapping of terms to standardized vocabularies and induction of terminologies from unstructured medical text.

Keywords: Medical term, terminology, experience, method, knowledge, skills, competence.

Introduction: Most medical concepts are expressed via a domain specific terminology that can either be explicitly agreed upon or extracted empirically from domain specific text. Regardless of how it is constructed, a terminology serves as a foundation for information encoding, processing and exchange in a specialized sub-language such as medicine. Concepts in the medical domain are encoded through a variety of linguistic forms, the most typical and widely accepted is the noun phrase (NP). In some even further specialized subdomains within medicine, such as nursing and surgery, an argument can be made that some concepts are represented by an entire predication rather than encapsulated within a single nominalized expression. For example, in order to describe someone's ability to lift objects 5 pounds or heavier above their head, it may be necessary to use a term consisting of a predicate such as [LIFT] and a set of arguments corresponding to various thematic roles such as and (Ruggieri et al., 2004). In this paper, we address typical medical terms encoded as noun phrases (NPs) that are often structurally ambiguous, as in Example 1, and discuss a case for extending the proposed method to non-nominalized terms as well. small1 bowel2 obstruction3 (1) The NP in Example 1 can have at least two interpretations depending on the syntactic analysis: [[small1 bowel2] obstruction3] (2) [small1 [bowel2 obstruction3]] (3) The term in Example 2 denotes an obstruction in the small bowel, which is a diagnosable disorder; whereas, the term in Example 3 refers to a small unspecified obstruction in the bowel. Unlike the truly ambiguous general English cases such as the classical "American History Professor" where the appropriate interpretation depends on the context, medical terms, such as in Example 1, tend to have only one appropriate interpretation. The context, in this case, is the discourse domain of medicine. From the standpoint of the English language, the interpretation that follows from Example 3 is certainly plausible, but unlikely in the context of a medical term. The syntax of a term only shows what interpretations are possible without restricting them to any particular one. From the syntactic analysis, we know that the term in Example 1 has the potential for being ambiguous; however, we also know that it does have an intended interpretation by virtue of being an entry term in a standardized terminology with a unique identifier

anchoring its meaning. What we do not know is which syntactic structure generated that interpretation. Being able to determine the structure consistent with the intended interpretation of a clinical term can improve the analysis of unrestricted medical text and subsequently improve the accuracy of Natural Language Processing (NLP) tasks that depend on semantic interpretation. To address this problem, we propose to use a model-fitting method which utilizes an existing statistical measure, the Log Likelihood Ratio. We validate the application of this method on a corpus of manually annotated noun-phrase-based medical terms. First, we present previous work on structural ambiguity resolution. Second, we describe the Log Likelihood Ratio and then its application to determining the structure of medical terms. Third, we describe the training corpus and discuss the compilation of a test set of medical terms and human expert annotation of those terms. Last, we present the results of a preliminary validation of the method and discuss several possible future directions. 2 Previous Work The problem of resolving structural ambiguity has been previously addressed in the computational linguistics literature. There are multiple approaches ranging from purely statistical (Ratnaparkhi, 1998), to hybrid approaches that take into account the lexical semantics of the verb (Hindle and Rooth, 1993), to corpus-based, which is the approach discussed in this paper. (Marcus, 1980) presents an early example of a corpus-based approach to syntactic ambiguity resolution. One type of structural ambiguity that has received much attention has to do with nominal compounds as seen in the work of (Resnik, 1993), (Resnik and Hearst, 1993), (Pustejovsky et al., 1993), and (Lauer, 1995). (Lauer, 1995) points out that the existing approaches to resolving the ambiguity of noun phrases fall roughly into two camps: adjacency and dependency. The proponents of the adjacency model ((Liberman and Sproat, 1992), (Resnik, 1993) and (Pustejovsky et al., 1993)) argue that, given a three word noun phrase XYZ, there are two possible analyzes [[XY]Z] and [X[YZ]]. The correct analysis is chosen based on the “acceptability” of the adjacent bigrams A[XY] and A[YZ]. If A[XY] is more acceptable than A[YZ], then the left-branching analysis [[XY]Z] is preferred. (Lauer and Dras, 1994) and (Lauer, 1995) address the issue of structural ambiguity by developing a dependency model where instead of computing the acceptability of A[YZ] one would compute the acceptability of A[XZ]. (Lauer, 1995) argues that the dependency model is not only more intuitive than the adjacency model, but also yields better results. (Lapata and Keller, 2004) results also support this assertion. The difference between the approaches within the two models is the computation of acceptability. Proposals for computing acceptability (or preference) include raw frequency counts ((Evans and Zhai, 1996) and (Lapata and Keller, 2004)), Latent Semantic Indexing ((Buckeridge and Sutcliffe, 2002)) and statistical measures of association ((Lapata et al., 1999) and (Nakov and Hearst, 2005)). One of the main problems with using frequency counts or statistical methods for structural ambiguity resolution is the sparseness of data; however, (Resnik and Hearst, 1993) used conceptual associations (associations between groups of terms deemed to form conceptual units) in order to alleviate this problem. (Lapata and Keller, 2004) use the document counts returned by WWW search engines. (Nakov and Hearst, 2005) use the χ 2 measure based on statistics obtained from WWW search engines to compute values to determine acceptability of a syntactic analysis for nominal compounds. This method is tested using a set of general English nominal compounds developed by (Lauer, 1995) as well as a set of nominal compounds extracted from MEDLINE abstracts. The novel contribution of our study is in demonstrating and validating a corpus-based method for determining the syntactic structure of medical terms that relies on using the statistical measure of association, the Log Likelihood Ratio, described in the following section. 3 Log Likelihood Ratio The Log Likelihood Ratio (G2) is a “goodness of fit” statistic first proposed by (Wilks, 1938) to test if a given piece of data is a sample from a set of data with a specific distribution described by a hypothesized model. It was later applied by (Dunning, 1993) as a way to determine if a sequence of N words (Ngram) came from an independently distributed sample. (Pedersen et al., 1996) pointed out that there exists theoretical assumptions underlying the G2 measure that were being violated therefore making them unreliable for significance testing. (Moore, 2004) provided additional evidence that although G2 may not be useful for determining the significance of an event, its near equivalence to mutual information makes it an

appropriate measure of word association. (McInnes, 2004) applied G2 to the task of extracting three and four word collocations from raw text. G2 , formally defined for trigrams in Equation 4, compares the observed frequency counts with the counts that would be expected if the words in the trigram (3-gram; a sequence of three words) corresponded to the hypothesized model. G 2 = 2 ∗ X x,y,z nxyz ∗ log(nxyz mxyz) (4) The parameter nxyz is the observed frequency of the trigram where x, y, and z respectively represent the occurrence of the first, second and third words in the trigram. The variable mxyz is the expected frequency of the trigram which is calculated based on the hypothesized model. This calculation varies depending on the model used. Often the hypothesized model used is the independence model which assumes that the words in the trigram occur together by chance. The calculation of the expected values based on this model is as follows: mxyz = nx++ ∗ n+y+ ∗ n++z/n+++ (5) The parameter, n+++, is the total number of trigrams that exist in the training data, and nx++, n+y+, and n++z are the individual marginal counts of seeing words x, y, and z in their respective positions in a trigram. A G2 score reflects the degree to which the observed and expected values diverge. A G2 score of zero implies that the observed values are equal to the expected and the trigram is represented perfectly by the hypothesized model. Hence, we would say that the data 'fits' the model. Therefore, the higher the G2 score, the less likely the words in the trigram are represented by the hypothesized model. 4 Methods 4.1 Applying Log Likelihood to Structural Disambiguation The independence model is the only hypothesized model used for bigrams (2-gram; a sequence of two words). As the number of words in an Ngram grows, the number of hypothesized models also grows. The expected values for a trigram can be based on four models. The first model is the independence model discussed above. The second is the model based on the probability that the first word and the second word in the trigram are dependent and independent of the third word. The third model is based on the probability that the second and third words are dependent and independent of the first word. The last model is based on the probability that the first and third words are dependent and independent of the second word. Slightly different formulas are used to calculate the expected values for the different hypothesized models. The hypothesized models result in different expected values which results in a different G2 score. A G2 score of zero implies that the data are perfectly represented by the hypothesized model and the observed values are equal to the expected. Therefore, the model that returns the lowest score for a given trigram is the model that best represents the structure of that trigram, and hence, best 'fits' the trigram. For example, Table 2 shows the scores returned for each of the four hypothesized models for the trigram "small bowel obstruction.

The smallest G2 score is returned by Model 2 which is based on the first and second words being dependent and independent of the third. Based on the data, Model 2 best represents or 'fits' the trigram, "small bowel obstruction". In this particular case that happens to be the correct analysis. The frequency counts and G2 scores for each model were obtained using the N-gram Statistics Package 1 (Banerjee and Pedersen, 2003). 4.2 Data The data for this study was collected from two sources: the Mayo Clinic clinical notes and SNOMED-CT terminology (Stearns et al., 2001). 4.2.1 Clinical Notes The corpus used in this study consists of over 100,000 clinical notes covering a variety of major medical specialties at the Mayo Clinic. These notes document each patient-physician contact and are typically dictated over the telephone. They range in length from a few lines to several pages of text and represent a quasi-spontaneous discourse where the dictations are made partly from notes and partly 1 http://www.d.umn.edu/ tpederse/nsp.html from memory. At the Mayo Clinic, the dictations are transcribed by trained personnel and are stored in the patient's chart electronically. 4.2.2 SNOMED-CT SNOMED-CT (Systematized Nomenclature of Medicine, Clinical Terminology) is an ontological resource produced by the College of American Pathologists and distributed as part of the Unified Medical Language System2 (UMLS) Metathesaurus maintained by the National Library of Medicine. SNOMED-CT is the single largest source of clinical terms in the UMLS and as such lends itself well to the analysis of terms found in clinical reports. SNOMED-CT is used for many applications including indexing electronic medical records, ICU monitoring, clinical decision support, clinical trials, computerized physician order entry, disease

surveillance, image indexing and consumer health information services. The version of SNOMED-CT used in this study consists of more than 361,800 unique concepts with over 975,000 descriptions (entry terms) (SNOMED-CT Fact Sheet, 2004). 4.3 Testset of Three Word Terms We used SNOMED-CT to compile a list of terms in order to develop a test set to validate the G2 method. The test set was created by extracting all trigrams from the corpus of clinical notes and all three word terms found in SNOMED-CT. The intersection of the SNOMED-CT terms and the trigrams found in the clinical notes was further restricted to include only simple noun phrases that consist of a head noun modified with a set of other nominal or adjectival elements including adjectives and present and past participles. Adverbial modification of adjectives was also permitted (e.g. "partially edentulous maxilla"). Noun phrases with nested prepositional phrases such as "fear of flying" as well as three word terms that are not noun phrases such as "does not eat" or "unable to walk" were excluded from the test set. The resulting test set contains 710 items. The intended interpretation of each three word term (trigram) was determined by arriving at a 2Unified Medical Language System is a compendium of over 130 controlled medical vocabularies encompassing over one million concepts. consensus between two medical index experts (kappa=0.704). These experts have over ten years of experience with classifying medical diagnoses and are highly qualified to carry out the task of determining the intended syntactic structure of a clinical term.

The first two types are left and right-branching where the left-branching phrases contain a left-adjoining group that modifies the head of the noun phrase. The rightbranching phrases contain a right-adjoining group that forms the kernel or the head of the noun phrase and is modified by the remaining word on the left. The non-branching type is where the phrase contains a head noun that is independently modified by the other two words. For example, in "follicular thyroid carcinoma", the experts felt that "carcinoma" was modified by both "follicular" and "thyroid" independently, where the former denotes the type of cancer and the latter denotes its location. This intuition is reflected in some formal medical classification systems such as the Hospital International Classification of Disease Adaptation (HICDA) where cancers are typically classified with at least two categories - one for location and one for the type of malignancy. This type of pattern is rare. We were able to identify only six examples out of the 710 terms. The monolithic type captures the intuition that the terms function as a collocation and are not decomposable into subunits. For example, "leg length discrepancy" denotes a specific disorder where one leg is of a different length from the other. Various combinations of subunits within this term result in nonsensical expressions. Table 4: Distribution of term types in the test set Type Count %total Left-branching 251 35.5 Right-branching 378 53.4 Non-branching 6 0.8 Monolithic 73 10.3 Total 708 100 Finally, there were two terms for which no consensus could be reached: "heart irregularly irregular" and "subacute combined degeneration". These cases were excluded from the final set. Table 4 shows the distribution of the four types of terms in the test set. 5 Evaluation We hypothesize that general English typically has a specific syntactic structure in the medical domain, which provides a single semantic interpretation. The patterns observed in the set of 710 medical terms described in the previous section suggest that the G2 method offers an intuitive way to determine the structure of a term that underlies its syntactic structure.

Model 1 would represent a term where words are completely independent of each other, which is an unlikely scenario given that we are working with terms whose composition is dependent by definition. This is not to say that in other applications (e.g., syntactic parsing) this model would not be relevant. Model 4 suggests dependence between the outer edges of a term and their independence from the Figure 1: Comparison of the results with two baselines: L-branching and R-branching assumptions middle word, which is not motivated from the standpoint of a traditional context free grammar which prohibits branch crossing. However, this model may be welcome in a dependency grammar paradigm. One of the goals of this study is to test an application of the G2 method trained on a corpus of medical data to distinguish between left and rightbranching patterns. The method ought to suggest the most likely analysis for an NP-based medical term based on the empirical distribution of the term and its components. As part of the

evaluation, we compute the G2 scores for each of the terms in the test set, and picked the model with the lowest score to represent the structural pattern of the term. We compared these results with manually identified patterns. At this preliminary stage, we cast the problem of identifying the structure of a three word medical term as a binary classification task where a term is considered to be either left or right-branching, effectively forcing all terms to either be represented by either Model 2 or Model 3. 6 Results and Discussion In order to validate the G2 method for determining the structure of medical terms, we calculated the agreement between human experts' interpretation of the syntactic structure of the terms and the interpretation suggested by the G2 method. The agreement was computed as the ratio of matching interpretations to the total number of terms being interpreted. We used two baselines, one established by assuming that each term is left-branching and the other by assuming that each term is rightbranching. As is clear from Table 4, the leftbranching baseline is 35.5% and the right-branching baseline is 53.4% meaning that if we simply assign left-branching pattern to each three word term, we would agree with human experts 35.5% of the time. The G2 method correctly identifies 185 trigrams as being left-branching (Model 2) and 345 trigrams as being right-branching (Model 3). There are 116 right-branching trigrams incorrectly identified as left-branching, and 62 left-branching trigrams incorrectly identified as right- branching. Thus the method and the human experts agreed on 530 (75%) terms out of 708 (kappa=0.473), which is better than both baselines (Figure 1). We did not find any overlap between the terms that human experts annotated as non-branching and the terms whose corpus distribution can be represented by Model 4 ([[XZ]Y]). This is not surprising as this pattern is very rare. Most of the terms are represented by either Model 2 (left-branching) or Model 3 (right-branching). The monolithic terms that the human experts felt were not decomposable constitute 10% of all terms and may be handled through some other mechanism such as collocation extraction or dictionary lookup. Excluding monolithic terms from testing results in 83.5% overall agreement (kappa=0.664). We observed that 53% of the terms in our test set are right-branching while only 35% are leftbranching. (Resnik, 1993) found between 64% and 67% of nominal compounds to be left-branching and used that finding to establish a baseline for his experiments with structural ambiguity resolution. (Nakov and Hearst, 2005) also report a similar percentage (66.8%) of left-branching noun compounds. Our test set is not limited to nominal compounds, which may account for the fact that a slight majority of the terms are found to be right-branching as adjectival modification in English is typically located to the left of the head noun. This may also help explain the fact that the method tends to have higher agreement within the set of right-branching terms (85%) vs. left-branching (62%). We also observed that many of the terms marked as monolithic by the experts are of Latin origin such as the term in Example 9 or describe the functional status of a patient such as the term in Example 10. erythema1 ab2 igne3 (9) difficulty1 swallowing2 solids3 (10) Example 10 merits further discussion as it illustrates another potential application of the method in the domain of functional status terminology. As was mentioned in the introduction, functional status terms may be be represented as a predication with a set of arguments. Such view of functional status terminology lends itself well to a frame-based representation of functional status terms in the context of a database such as FrameNet 3 or PropBank4 . One of the challenging issues in representing functional status terminology in terms of frames is the distinction between the core predicate and the frame elements (Ruggieri et al., 2004). It is not always clear what lexical material should be part of the core predicate and what lexical material should be part of one or more arguments.

The analysis dictates the shape of the frames and how the frames would fit into a network of frames. The G2 method identifies Example 10 as left-branching (Model 2), which suggests that it would be possible to have a parent DIFFICULTY frame and a child CLIMBING DIFFICULTY that would inherit form its parent. An example where this is not possible is the term "difficulty staying asleep" where it would probably be nonsensical or at least impractical to have a predicate such as [STAYING DIFFICULTY]. It would be more intuitive to 3 http://www.icsi.berkeley.edu/framenet/ 4 http://www.cis.upenn.edu/ ace/ assign this term to the DIFFICULTY frame with a frame element whose lexical content is "staying asleep". The method

appropriately identifies the term “difficulty staying asleep” as right-branching (Model 3) where the words “staying asleep” are grouped together. This is an example based on informal observations; however, it does suggest a utility in constructing frame-based representation of at least some clinical terms. 7 Limitations The main limitation of the G2 method is the exponential growth in the number of models to be evaluated with the growth in the length of the term. This limitation can be partly alleviated by either only considering adjacent models and limiting the length to 5-6 words, or using a forward or backward sequential search proposed by (Pedersen et al., 1997) for the problem of selecting models for the Word Sense Disambiguation task. 8 Conclusions and Future Work This paper presented a simple but effective method based on G2 to determine the internal structure of three-word noun phrase medical terms. The ability to determine the syntactic structure that gives rise to a particular semantic interpretation of a medical term may enable accurate mapping of unstructured medical text to standardized terminologies and nomenclatures. Future directions to improve the accuracy of our method include determining how other measures of association, such as dice coefficient and $\chi 2$, perform on this task. We feel that there is a possibility that no single measure performs best over all types of terms. In that case, we plan to investigate incorporating the different measures into an ensemblebased algorithm. We believe the model-fitting method is not limited to structural ambiguity resolution. This method could be applied to automatic term extraction and automatic text indexing of terms from a standardized vocabulary. More broadly, the principles of using distributional characteristics of word sequences derived from large corpora may be applied to unsupervised syntactic parsing. Acknowledgments We thank Barbara Abbott, Debra Albrecht and Pauline Funk for their contribution to annotating the test set and discussing aspects of medical terms. This research was supported in part by the NLM Training Grant in

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