Unsupervised Learning of Ontology for the Medical Domain

MSc Thesis

Sónia Margarida Ferreira de Bastos
Unsupervised Learning of Ontology for the Medical Domain

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Sónia Margarida Ferreira de Bastos

Department of Computer Science
University of Beira Interior
Covilhã, Portugal
www.di.ubi.pt

HULTIG - Centre of Human Language Technology and Bioinformatics
Department of Computer Science of the University of Beira Interior
Covilhã, Portugal
hultig.di.ubi.pt
Unsupervised Learning of Ontology for the Medical Domain

Author: Sónia Margarida Ferreira de Bastos
Student number: m2149
Email: sonia@hultig.di.ubi.pt
Supervisor: Prof. Dr. Gaël Dias, UBI, Covilhã

Abstract

Tom Gruber (1993) defines Ontology as "an explicit specification of a conceptualization."

Due two the enormous quantity of information available, there is a growing number of applications that perform tasks where lexical-semantic resources are needed, like Information Retrieval, intelligent search or machine translation. This shows that Natural Language Processing is becoming more dependent on semantic information.

One of the main motivations in ontology building is the possibility of knowledge sharing and reuse across different applications. The start point is to fixed a particular domain (like medicine), which is expected to be the base of domain knowledge for a variety of applications. This is a difficult task as the domain knowledge strongly depends on the particular task at hand.

This paper is an approach on ontology learning, for which it was selected the Medical Domain, so that we could have a base to compare and evaluate the resulting ontology.

In our approach, we use different techniques, like Asymmetric Association Measures, clustering algorithm and text rank algorithm, so that we can obtain relations between a set of terms, which are rank by the degree of generality, like the cluster obtained by applying clustering algorithms, with the confidence measure as the values for the similarity matrix, to the set of terms, the generality clusters. Those clusters are then submitted to clustering algorithm, but with Symmetric Conditional Probability values in the similarity matrix, to obtain domain clusters within the generality clusters.

In the future, this ontology may be used in acquisition of Lexical Chains for Text Summarization, as in other Natural Language Processing applications.
There are many people, without whose support and contributions this thesis would not have been possible. I am specially grateful to my supervisor, Gaël Dias for his constant support and help, for professional and personal support, and for getting me interested in the subject of Natural Language Processing and for introducing me to the summarization and ontology building fields. I also want to thank to HULTIG research group, in particular Rumen and João Paulo Cordeiro for sharing their work, which had elements necessary for the progress of my work.

I would like to thank all my friends for all their help and support when sometimes I thought I would not make it.

And finally, I want to thank to my mother, Adélia Simão, my boyfriend, Helder, and his family (especially his mother and grandmother) for all their help, support and incentive.

Thank you for all your support!

Sónia Margarida Ferreira de Bastos
Covilhã, Portugal
August, 2009
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Chapter 1

Introduction

Due to the enormous quantity of information available, there is a growing number of applications that perform tasks where lexical-semantic resources are needed, like Information Retrieval, intelligent search or machine translation. This shows that Natural Language Processing is becoming more dependent on semantic information.

Nowadays, researchers are trying to build ontologies, which are models that aim to represent concepts hierarchically, and the relations between them.

The term ontology comes from the field of philosophy that is concerned with the study of being or existence.

In the computer science field, Tom Gruber [12] defines Ontology as "an explicit specification of a conceptualization."

We can say that an Ontology is a formal representation of a set of concepts within a domain and the relationships between them. Ontologies are used in artificial intelligence, the Semantic Web, software engineering, biomedical informatics, library science, and information architecture as a form of knowledge representation about the world or some part of it.

An example of a published Ontology is WordNet, in which Ontology, in the computer science filed, is defined as "a rigorous and exhaustive organization of some knowledge domain that is usually hierarchical and contains all the relevant entities and their relations".

Most of the Ontologies developed, or currently in development are not publicly available, which implies research and new implementation of ontologies by researchers.

In order to avoid time-consuming human work in its construction and maintenance, we aim to design and, in the future, develop the tools needed to automatically (without supervision) build ontologies without access to existing linguistic resources (thesaurus, lexico-semantic databases, . . . ), maintaining the process as language-independent as possible.

Although we want to maintain it language-independent, we choose the medical domain
Introduction

in English as a place to start. Therefore, our work uses UMLS Metathesaurus, so that we can have a base of comparison for our results. This Metathesaurus contains a collection of medical concepts and terms of the various vocabularies and the relationships between them.

It also uses MEDLINE, a bibliographic database containing over 17 million references to journal articles in life sciences and biomedical information, for gathering a set of documents, so we could count the occurrence and the co-occurrence of the terms, which is necessary to calculate the different measures in our work.

This work is divided in four parts. The first describes the resources we used: (1) UMLS and (2) MEDLINE. The next parts describes all the steps we made in building the Ontology - the association measures, the rank and cluster algorithms, the requirements for their implementation and the problems we found.

Afterwards we make a reference to related work in building ontologies, but for Portuguese language.

For last we present some conclusions and future work.
Chapter 2

Resources

2.1 UMLS - Unified Medical Language System

UMLS is a compendium of vocabularies in several languages in the biomedical sciences and the relations between them (this relations are only available for English). It is produced and distributed by the National Library of Medicine (NLM) - National Institutes of Medicine - USA. All the information about UMLS is available at http://www.nlm.nih.gov/research/umls/.

The use of UMLS Knowledge Sources and the associated software is free of charge for all user.

The Semantic Network and the SPECIALIST Lexicon, and their associated lexical tools, are accessible on the Internet (see [6] and [3]), under open terms. To view the terms and conditions for use of the Semantic Network and of the SPECIALIST Lexicon and Lexical Tools, see [5] and [4].

Since the Metathesaurus includes vocabulary content produced by many different copyright holders as well as the substantial content produced by NLM, it is necessary to establish a license agreement to use the Metathesaurus. This license agreement is set up via the web. After the license agreement is in place, the content of the Metathesaurus may be used under some conditions, available at [2].

2.1.1 UMLS components

The UMLS is made up of three main knowledge components: the Metathesaurus, the Semantic Network and the SPECIALIST Lexicon. It also includes several tools that facilitate their use, including the MetamorphoSys, the install and customization program.

- Metathesaurus is the main part of UMLS, containing a collection of medical concepts and terms of the various vocabularies and the relationships between them. It represents several kinds of relations like hierarchical relations (“a is a part of b” or “c is...
a kind of d”), or associative relations (”e is caused by f” or ”g often occurs close to h”). The use of different names for the same concept or the same name for different concepts, are also faithfully represented in the Metathesaurus [7].

- The Semantic Network, which provides a categorization of all concepts existent in the Metathesaurus and the semantic relationships that can be assigned between these concepts.

- The SPECIALIST Lexicon, which can be applicable in Natural Language Processing, is intended to be a general English lexicon with many biomedical terms. It contains the syntactic, morphological, and orthographic information of each word and term records.

2.1.2 Metathesaurus RRF (Rich Release Format) and ORF (Original Release Format) files

There are two different relational formats: the Riche Release Format (RRF) and the Original Release Format(ORF), available in the MetamorphoSys.

2.1.3 Structure of data

UMLS provides scripts to load the data on the RRF or ORF files into a database. The database server version recommend is MySQL Server 5.0.

For our purpose, we only need 8 tables. Those tables are described in Table 2.1 and their relationship is showed in Figure 2.1. There are also reference to the fields used from each table, which are described in Table 2.2

2.2 MEDLINE - Medical Literature Analysis and Retrieval System Online

MEDLINE is a bibliographic database owned by the National Library of Medicine, U.S.A. It contains over 17 million references to journal articles in life sciences and biomedical information. New citations are added Tuesday through Saturday.

The access to the database is free via the PubMed interface, or by downloading the XML files, after completing and submitting the License Request Form, available at [1].

About 48% of the citations added during 1995-2003 are for cited articles published in the U.S., about 88% are published in English, and about 76% have English abstracts written by authors of the articles. The Appendix A shows a MEDLINE citations. Not all
Table 2.1: Tables used from UMLS

<table>
<thead>
<tr>
<th>Table</th>
<th>Used fields</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRCOC</td>
<td>CUI1, AUI1, CUI2,</td>
<td>Co-occurrence of concepts (concepts that occur together in the same entries)</td>
</tr>
<tr>
<td></td>
<td>AU12, SAB, COT, COF</td>
<td></td>
</tr>
<tr>
<td>MRCONSO</td>
<td>CUI, LUI, SUI, AUI,</td>
<td>Strings or concept names in the Metathesaurus</td>
</tr>
<tr>
<td></td>
<td>STR</td>
<td></td>
</tr>
<tr>
<td>MRDEF</td>
<td>CUI, AUI, DEF</td>
<td>Definitions of atoms (occurrence of each string in a source vocabulary)</td>
</tr>
<tr>
<td>MRHIER</td>
<td>CUI, AUI, PAUI, RELA,</td>
<td>Representation of all hierarchies present in the Metathesaurus</td>
</tr>
<tr>
<td></td>
<td>PTR</td>
<td></td>
</tr>
<tr>
<td>MRREL</td>
<td>CUI1, AUI1, CUI2,</td>
<td>Representation of the relationships between the concepts known to the Metathesaurus</td>
</tr>
<tr>
<td></td>
<td>AU12, REL, RUI</td>
<td></td>
</tr>
<tr>
<td>MRXW_ENG</td>
<td>CUI, LUI, SUI, WD</td>
<td>Words found in each unique Metathesaurus string</td>
</tr>
<tr>
<td>MRXNS_ENG</td>
<td>CUI, LUI, SUI, NWD</td>
<td>Normalized strings(^1) found in each unique Metathesaurus string (only for English)</td>
</tr>
<tr>
<td>MRXNW_ENG</td>
<td>CUI, LUI, SUI, NSTR</td>
<td>Normalized words(^2) found in each unique Metathesaurus string (only for English)</td>
</tr>
</tbody>
</table>

the elements showed (DateCreated, ArticleTitle, etc.) are available for all the citations, like the AbstractText.

Since the objective was to gather a set of documents, a corpus, it was only necessary to keep the abstract text (text delimited by the <AbstractText> tag). It was also kept the title of the article (<ArticleTitle> tag) and the name of the file where it belongs (medline09nXXXX.xml, where XXXX is a number from 0000 to 0593).
Figure 2.1: Entity-Relationship Diagram
<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>AUI</td>
<td>Unique Atom Identifier</td>
</tr>
<tr>
<td>CUI</td>
<td>Unique Concept Identifier</td>
</tr>
<tr>
<td>SUI</td>
<td>Unique String Identifier</td>
</tr>
<tr>
<td>LUI</td>
<td>Unique Term Identifier</td>
</tr>
<tr>
<td>WD</td>
<td>Word</td>
</tr>
<tr>
<td>NWD</td>
<td>Normalized Word</td>
</tr>
<tr>
<td>STR</td>
<td>String</td>
</tr>
<tr>
<td>NSTR</td>
<td>Normalized String</td>
</tr>
<tr>
<td>DEF</td>
<td>Definition of atom</td>
</tr>
<tr>
<td>PAUI</td>
<td>Unique identifier of atom's immediate parent</td>
</tr>
<tr>
<td>RELA</td>
<td>Relationship of atom to its immediate parent</td>
</tr>
<tr>
<td>RUI</td>
<td>Unique Relationship Identifier</td>
</tr>
<tr>
<td>REL</td>
<td>Relationship of second concept or atom to first concept or atom</td>
</tr>
<tr>
<td>PTR</td>
<td>Path to the top of the hierarchical context from this atom, represented as a list of AUIs, separated by periods (.) The first one in the list is top of the hierarchy; the last one in the list is the immediate parent of the atom, which also appears as the value of PAUI.</td>
</tr>
<tr>
<td>SAB</td>
<td>Abbreviated source name</td>
</tr>
<tr>
<td>COT</td>
<td>Type of co-occurrence</td>
</tr>
<tr>
<td>COF</td>
<td>Frequency of co-occurrence</td>
</tr>
</tbody>
</table>

Table 2.2: UMLS database used fields
Chapter 3

Ontology Learning

3.1 Ontology

In [12], Tom Gruber defines Ontology as "an explicit specification of a conceptualization."

For knowledge-based systems, it can only be represented what "exists", creating a set of objects. This set of objects, and the relationships between them, are shown in the representational vocabulary with which a knowledge-based program represents knowledge. Therefore, an ontology can be described by defining a set of representational terms. In this ontology, definitions associate the entities (classes, terms, relations, ...) with text describing the meaning of each entity.

In the Artificial Intelligence field, Ontology was initially defined by Neches et al. ([19]): "An ontology defines the basic terms and relations comprising the vocabulary of a topic area as well as the rules for combining terms and relations to define extensions to the vocabulary."

In [11], Pérez and Corcho identify the main components used in Ontologies:

1. Concepts are used in a broad sense and can be abstract or concrete, elementary or composite, real or fictitious. A concept can be anything that was said about something and the description of a task, function, action, etc.

2. Taxonomies are used to organize ontological knowledge in the domain using generalization/specialization relationships.

3. Relations represent the connection between concepts of the domain and are formally defined as any subset of a product of n sets, this is, \( R = C_1 \times C_2 \times C_3 \times \ldots \times C_n \) where \( C_1, C_2, C_3, \ldots, C_n \) represent concepts.

4. Functions are considered as a special kind of relations where the value of the last argument is unique for a list of values of the n-1 preceding arguments.
3.1 Ontology

5. **Axioms** are included in an ontology to constrain its information (Example: a square is a rectangle which has four equal sides), verifying its correctness or deducting new information.

6. **Instances/Individuals/Facts/Claims** are used to represent elements in the domain. Instances represent elements of a given concept. Facts represent a relation which holds between elements. Individuals refer to any element in the domain which is not a class. Claims represent assertions of a fact by an instance.

There are many types of relationships that can be established between terms. In [18], Miller lists the relations present in WordNet, which can be present in any Ontology:

- **Synonym** - terms having the same or nearly the same meaning. Example: *Ache* and *Pain.*
- **Antonym** - terms having an opposite meaning. Example: *Healthy* and *Unwell.*
- **Hyponym** - a term that is less general than another. Example: *Aorta* and *Arteries.*
- **Hypernym** - a term that is more general than another. Example: *Blood Vessels* and *Arteries.*
- **Meronym** - a term that is a part of another term. Example: *Eyes* and *Head* - Eyes is a part of head.
- **Holonym** - a term which names the whole of another term. Example: *Head* and *Nose* - Head has a nose.
- **Troponym** - same as hyponym, but it’s applied to verbs, this is a verb that indicates a manner of doing something by replacing a verb of a more generalized meaning. Example *to march* and *to walk.*
- **Entailment** - encodes the relations between verbs.

In [21], van Heijst et al. classify ontologies according to two dimensions: (1) the amount and type of structure of the conceptualization, and (2) the subject of the conceptualization.

In (1), they distinguish three categories:

1. **Terminological ontologies** which specify the terms that are used to represent knowledge in the domain of discourse. Example: UMLS.
2. **Information ontologies** which specify the record structure of databases.
3. **Knowledge modelling ontologies** specify conceptualizations of the knowledge. This ontologies usually have a richer internal structure than information ontologies. Also, they are often tuned to a particular use of the knowledge that they describe.

In (2), there are four categories:

1. **Application ontologies** which contains all the definitions that are needed to model the knowledge required for a particular application. They are a mix of concepts taken from domain ontologies and generic ontologies.

2. **Domain ontologies** express conceptualizations that are specific for particular domains.

3. **Generic ontologies** are similar to domain ontologies, but the concepts that they define are considered to be generic.

4. **Representation ontologies** provide a representational framework without making claims about the world. They provide primitives used to describe domain ontologies and generic ontologies.

Not agreeing with van Heijst, Guarino ([13]) suggest that a distinction can be made based on (1) the degree of detail used to characterize a conceptualization and (2) the subject of the conceptualization.

In (1), Guarino distinguish two kinds of ontologies:

1. **Documenting ontologies**, or off-line ontologies, are very rich in details and gets closer to specifying the intended conceptualization.

2. **Shareable ontologies**, or on-line ontologies, are very simple ontologies, which are developed with particular inferences, previously agreed by the user on the underlying conceptualization.

In (2), ontologies are distinguish in:

1. **Domain ontologies** express conceptualizations that are specific for particular domains.

2. **Method ontologies** express conceptualizations of a specific task or method, including all the concepts necessary to describe the inferential process, from the very abstract concepts to the more specialized concepts.

3. **Application ontology** which contains the definitions specific to a particular application.
3.2 Building an Ontology

Making an Ontology is a complex and slow process. Preparing a computer to do so without supervision is an even more complex and slow process.

First of all, it is necessary to prepare a base, so that we could compare and, in the future, evaluate the results of our work. To do so, we started by searching for a base of knowledge in the medical domain, the UMLS (see section 2.1). The next step was to select the words we would use. This selection was made for four domains in Medicine: (1) Cardiovascular System; (2) Digestive System; (3) Respiratory System and (4) Nervous System. For each of these domains/terms, it was chosen five hyponyms (if they exist), this is, five words that are directly below in the hierarchy present in UMLS. The process was repeated until we had six levels of generality, as showed in Appendix B.

Then, we processed the XML files from MEDLINE, saving the title, abstract text and the name of the file were the article was, as described in section 2.2.

3.3 Similarity Matrix

The next step is to calculate the Similarity Matrix. For this, we need to calculate the asymmetry between the terms, using Asymmetric Association Measures. From all the existing, we enumerate only seven, from which we used the Confidence measure during our work.

3.3.1 Asymmetric Association Measures

As stated by [16], asymmetry is important in Natural Language Processing, therefore in all of its strands, like ontology building. The asymmetry allows us to induce oriented associations between terms, like dentition and mouth. When someone hears dentition, they may think about mouth, but when hearing mouth more common elements will come to mind, like tongue or teeth. In this case, there is an oriented associations between dentition and mouth (dentition → mouth) which indicates that dentition attracts more mouth, than mouth attracts dentition, this is, mouth is more likely to be a more general term than dentition.

Therefore, we can use asymmetric association measures, presented below, to measure the degree of attractiveness between to terms, $x$ and $y$, where $f(x, y)$, $P(x)$, $P(x, y)$ and $N$ are respectively the frequency function, the marginal probability function, the joint probability function, the number of documents in the corpus.

$$
Braun-Blanquet = \frac{f(x, y)}{\max(f(x, y) + f(x, \overline{y}), f(x, y) + f(\overline{x}, y))}
$$

(3.1)
3.3 Similarity Matrix

J measure = \[
\max \left[ \begin{array}{c}
P(x, y) \log \frac{P(y|x)}{P(y)} + P(x, \neg y) \log \frac{P(\neg y|x)}{P(\neg y)} \\ P(x, y) \log \frac{P(x|y)}{P(x)} + P(\neg x, y) \log \frac{P(\neg x|y)}{P(\neg x)}
\end{array} \right]
\] (3.2)

Confidence = \max [P(x|y), P(y|x)] (3.3)

Laplace = \max \left[ \frac{N.P(x, y) + 1}{N.P(x) + 2}, \frac{N.P(x, y) + 1}{N.P(y) + 2} \right] (3.4)

Conviction = \max \left[ \frac{P(x)P(\neg y)}{P(x, \neg y)}, \frac{P(\neg x)P(y)}{P(\neg x, y)} \right] (3.5)

Certainty Factor = \max \left[ \frac{P(y|x) - P(y)}{1 - P(y)}, \frac{P(x|y) - P(x)}{1 - P(x)} \right] (3.6)

Added Value = \max [ P(y|x) - P(y), P(x|y) - P(x) ] (3.7)

All these measures evaluate the maximum value between the attraction of \( x \) upon \( y \) and the attraction of \( y \) upon \( x \) to show the asymmetry between \( x \) and \( y \). The maximum value decides the direction of the general-specific association, this is, \((x \rightarrow y)\) or \((y \rightarrow x)\).

Although all the measures were calculated and saved, we used only the Confidence measure to describe our work. In the future, it will be tested with the other measures, so that we can compare the results and choose the one with better results.

3.3.2 Calculating the Similarity Matrix

The final values of the Asymmetric Association Measures were calculated by steps, this is, it was first calculated the values of each part \((f(x, y) e f(y, x))\), which was saved in a matrix (see table 3.1). Then, we calculated the maximum value \((\max [f(x, y), f(y, x)])\), saving it in the matrix by putting 0 (zero) in the minimum value, originating the Similarity Matrix (see table 3.2).
3.4 TextRank Algorithm

The use of a TextRank algorithm based on a graph is a way to decide the importance of a vertex (in our case, a term) within a graph, based on the information recursively drawn from the graph. With the use of a graph-based ranking algorithm, we intend to show that more general terms will be more likely to have incoming associations as they will be associated to many specific terms. In the other and, more specific terms will have more outgoing associations than incoming associations as they attract general terms (See Figure 3.1). Therefore, a graph-based ranking algorithms should give more strength to general terms than specific ones, ranking the term from general to specific.

Before using a graph-based ranking algorithms, we need to build a direct graph. As stated above (See section 3.3.1), if a term $x$ attracts more another term $y$, than $y$ attracts $x$, it will be created an edge between $x$ and $y$ as follows ($x \rightarrow y$), so that we can give more credit to general words.

Formally, a directed graph $G = (V, E)$ can be defined with the set of vertices $V$ (in our case, a set of terms) and a set of edges $E$, where $E$ is a subset of $V \times V$ (in our case,
Figure 3.1: Directed Graph based on the Confidence measure.

a similarity matrix calculated by the asymmetric association measure value between two terms - See table 3.2).

In Figure 3.1, we show the directed graph obtained by using the first terms selected from UMLS, this is, the set $V=\{"Cardiovascular System", "Digestive System", "Respiratory System", "Nervous System", "Blood Vessels"\}$. The weight of the edges have been calculated by the Confidence Association Measure (Equation 3.3) based on the corpus\(^1\) counts. The Joint Probability between two terms, $P(x, y)$, is calculated by the number of documents where the terms $x$ and $y$ appear together divided by the total number of documents in the corpus. The Marginal Probabilities $P(x)$ and $P(y)$ are calculated by the same process.

By using a graph-based algorithm, we aim to produce an ordered list of terms from the most general (with the highest value) to the most specific (with the lowest value).

The algorithm used is the one proposed by [17], which can be used by Weighted and Unweighted Direct Graphs.

For a given vertex $V_i$, let $In(V_i)$ be a set of vertices that point to it, and $Out(V_i)$ a set of vertices that vertex $V_i$ points to. The score of a vertex $V_i$ is defined by:

$$S(V_i) = (1 - d) + d \times \sum_{V_j \in In(V_i)} \frac{1}{|Out(V_j)|} \times S(V_j) \quad (3.8)$$

where $d$ is a damping factor that can be set between 0 and 1 (usually set to 0.85), which has the role of integrating into the model the probability of jumping from a given vertex to another random vertex in the graph.

To take into account the weight of the edges, it is introduced a new formula:

\(^1\)set of texts extracted from the MEDLINE XML files
3.5 Determination of clusters of words

Cluster analysis or clustering is a filed of research that belongs to data analysis and machine learning major domains.

Clustering divides a set of data into groups whose members are similar to each other. Each object (called "term" in the following), is assigned to the group it is more similar to. For instance, "Hospital" and "Doctor’s office" are similar for both represent a place were medicine is practiced, therefore, they can be placed in the same group.

The main objective in clustering is placing similar terms in the same group and dissimilar words in different groups, which are called clusters.

Several ways of clustering have been explored, originating some types of algorithm. There are the hard-clustering techniques, which assigns each term to a single cluster. Inversely, in fuzzy-clustering methods, terms can belong to more than one cluster, and associ-

\[ WS(V_i) = (1 - d) + d \times \sum_{V_j \in In(V_i)} \frac{w_{ji}}{\sum_{V_k \in Out(V_j)} w_{jk}} \times WS(V_j) \quad (3.9) \]

In our work, we use the Weight Direct Graph to calculate the terms rank. After running the algorithm, a score is associated to each vertex, representing the importance of the vertex within the graph. In Table 3.3, we show the result for the terms included in the set \( V \) described above. The results for all the terms selected from UMLS is shown in Appendix C.

<table>
<thead>
<tr>
<th>Pos.</th>
<th>AUI</th>
<th>Term</th>
<th>Rank Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>A0091423</td>
<td>Nervous System</td>
<td>3.4234311255891776</td>
</tr>
<tr>
<td>8</td>
<td>A0031694</td>
<td>Blood Vessels</td>
<td>0.9797096311214579</td>
</tr>
<tr>
<td>51</td>
<td>A0035256</td>
<td>Cardiovascular System</td>
<td>0.19773753019147863</td>
</tr>
<tr>
<td>62</td>
<td>A0111426</td>
<td>Respiratory System</td>
<td>0.17384242429857602</td>
</tr>
<tr>
<td>74</td>
<td>A0048766</td>
<td>Digestive System</td>
<td>0.15000000000000002</td>
</tr>
</tbody>
</table>

Table 3.3: Partial results of WordRank

Although the results do not correspond to the reality - Cardiovascular System, Respiratory System, Digestive System should be higher in the rank, for they are more general, we can consider them satisfactory. The position of these terms can be related to the fact that, usually, when talking about them, the term is not used, this is, we can talk about "Blood Vessels" without talking about "Cardiovascular System". Therefore, more general words can be considered more specific.

3.5 Determination of clusters of words
Ontology Learning 3.5 Determination of clusters of words

ated with each term is a set of values which indicate the strength of the association between that term and a particular cluster.

In our work, we tried to group the terms by degree of generality. For that, we used the K-Means algorithm (See subsection 3.5.1), which allows us to define the number of cluster (\( k \)), and the PoBOC algorithm (See subsection 3.5.2), that defines the better clusters for the data set, without defining the number of clusters \( a \ priori \).

Then, we calculate the degree of generality by using the values returned by the TextRank algorithm, so that we could have the clusters ranked by degree of generality.

3.5.1 K-Means

K-Means algorithm was introduced by MacQueen in 1967, and is one of the most common clustering algorithm that groups data with similar characteristics together. The data in the same cluster will have similar characteristics, which are dissimilar from the data in other cluster.

The steps of the algorithm are:

1. Introducing the number of clusters (\( k^2 \)) and the data set to be clustered.

2. Choose the \( k \) initial clusters, by randomly choosing \( k \) rows of data from the data set.

3. Each row of data (each term) will be assigned to one of the initial clusters. After evaluating the similarity between the row of data and the initial clusters, the row of data is assigned to the cluster it is most similar to (the nearest cluster). Measures like Distance Measure and Asymmetric Association Measures can be use to calculate the similarity. In our case, we used the Confidence Measure.

4. The Arithmetic Mean, or center, of each cluster is re-calculated (the initial Arithmetic Mean is the set of values of the data row chosen for the initial cluster). The Arithmetic Mean of a cluster is the mean of all the individual data rows (terms) in the cluster. For example, with the set of values for the Confidence and Laplace measures (\{Confidence, Laplace\}), if a cluster contains two data rows with the measurements for \textit{mouth} = \{0.0547, 1.2541\} and \textit{dentition} = \{0.258741, 0.0125454\}, then the arithmetic means is represented by \( Cl_{\text{mean}} = \{\text{Confidence}_{\text{mean}}, \text{Laplace}_{\text{mean}}\} \), where \( \text{Confidence}_{\text{mean}} = (0.0547 + 0.258741)/2 \) and \( \text{Laplace}_{\text{mean}} = (1.2541 + 0.0125454)/2 \). The arithmetic means of this cluster is \{0.1567205, 0.6333227\}.

\(^2\)In our case, we used \( k = 6 \), so that we could compare with the UMLS structure.
5. Each row of data (each term) will be re-assigned to one of the new clusters initiated by the Arithmetic Mean.

6. The steps 4 and 5 are repeated until stable clusters are formed, this is, until the repetition of the k-means algorithm does not create different or new clusters as the cluster center or Arithmetic Mean of the formed cluster is the same as the old cluster center.

Although the procedure will terminate, it does not necessarily find the most optimal clusters and, as the algorithm is sensitive to the initial randomly selected cluster center, the result can be different every time we run the algorithm.

The implementation of the k-means algorithm is the one developed by Cleuziou ([10]), the OKM algorithm (Overlapping k-Means).

In his approach, Cleuziou defines an objective criterion: given a set of data vectors \( \chi = \{x_i\}_{i=1}^{n} \) with \( x_i \in \mathbb{R}^p \), the goal of the OKM algorithm (Overlapping k-means) is to find a k-way coverage \( \{\pi_c\}_{c=1}^{k} \) of the date (where \( \pi_c \) represents the \( c^{th} \) cluster) such that the following objective is minimized:

\[
J(\{\pi_c\}_{c=1}^{k}) = \sum_{x_i \in \chi} \| x_i - \phi(x_i) \|^2
\]  

Each \( x_i \) belongs at least to one cluster, since \( \{\pi_c\}_{c=1}^{k} \) is a coverage, which is such that \( \cup_{c=1}^{k} \pi_c = \chi \). This way, \( \phi(x_i) \) indicates the "image" of \( x_i \) defined by combination of the prototypes \( (m_c) \) for the clusters \( x_i \) belong to:

\[
\phi(x_i) = \sum_{A_i \mid x_i \in \pi_i} \frac{m_c}{|A_i|} 
\]

where \( A_i \) denotes the set of assignment for \( x_i : \{m_c \mid x_i \in \pi_i\} \).

The Figure 3.2 gives an overview of the OKM algorithm.

The OKM implementation allows a term to belong to more than one clusters, but, in our work, we are only interested (for now) to have a term belonging to only one cluster. Therefore, when executing OKM we use the option \(-o=0\) which indicates that the algorithm should use hard clustering. With \(-o=1\), the algorithms use overlapping clusters, this is, a term can be assigned to more than one cluster.

The Appendix D lists the clusters resulting from the K-Means algorithm, after they were rank by the degree of generality (See section 3.6).
3.5.2 PoBOC

The algorithm PoBOC (Pole-Based Overlapping Clustering) is a method which can be viewed as a compromise between hard and fuzzy-clustering approaches [9].

One of the advantages of PoBOC, with regard to methods based on centroids is that each group is represented by a pole, this is, a set of objects, instead of only one object, which is a less specific representation of a group.

The algorithm PoBOC takes the previous calculated similarity matrix (See subsection 3.3.2) as input and builds in a hierarchy of concepts in which an object may belong to several concepts, this is, produces a set of overlapping clusters hierarchically organized.

From the similarity matrix $SM$ defined on $X \times X$ over set of terms $X = x_1, x_2, \ldots, x_n$, the algorithm executes the following steps:

1. construction of the similarity graph $G_S(X, V)$, where $V$ is the set of edges between

\[
\text{OKM}(X, t_{\text{max}}, \epsilon)
\]

**Input:** $X$: a set of data vectors in $\mathbb{R}^p$; $t_{\text{max}}$: optional maximum number of iterations; $\epsilon$: optional threshold on the objective

**Output:** $\{\pi_k^{(i)}\}_{k=1}^k$: final coverage of the points

1. Draw randomly $k$ initial cluster prototypes $\{m_e^{(0)}\}_{e=1}^k$ in $\mathbb{R}^p$ or $X$.

2. For each $x_i \in X$ compute the assignments $A_i^{(0)} = \text{ASSIGN}(x_i, \{m_e^{(0)}\}_{e=1}^k)$ and derive the initial coverage $\{\pi_e^{(0)}\}_{e=1}^k$ such that

\[
\pi_e^{(0)} = \{x_i | m_e^{(0)} \in A_i^{(0)}\}
\]

3. Set $t = 0$.

4. For each cluster $\pi_e^{(t)}$ successively, compute the new prototype

\[
m_e^{(t+1)} = \text{PROTOTYPE}(\pi_e^{(t)})
\]

5. For each $x_i \in X$ compute the assignments $A_i^{(t+1)} = \text{ASSIGN}(x_i, \{m_e^{(t+1)}\}_{e=1}^k, A_i^{(0)})$, and derive the new coverage $\{\pi_e^{(t+1)}\}_{e=1}^k$.

6. If not converged or $t_{\text{max}} > t$ or $J(\{\pi_e^{(t)}\}) - J(\{\pi_e^{(t+1)}\}) > \epsilon$, set $t = t + 1$ and go to Step 4; Otherwise, stop and output final clusters $\{\pi_e^{(t+1)}\}_{e=1}^k$.

Figure 3.2: OKM overview.
the terms;

2. extraction of complete sub-graphs from $G_S(X, V)$, the "poles";

3. multi-assignment of the terms to the poles;

4. hierarchical organization of the obtained groups.

In the first step, $X$ is already defined as the set of terms obtained from UMLS, and is the base of the similarity graph denoted by $G_S(X, V)$. $V$ is the set of edges between the terms. We can say there is an edge between two terms $x_i$ and $x_j$ if $x_i$ belongs to the neighborhood of $x_j$ and vice-versa, which can be defined by:

$$s(x_i, x_j) \geq \max\left\{ \frac{1}{n} \sum_{x_k \in X} s(x_i, x_k), \frac{1}{n} \sum_{x_k \in X} s(x_j, x_k) \right\}$$  \hspace{1cm} (3.12)

With this definition, exists an edge between $x_i$ and $x_j$ if their similarity is greater than both the average similarity between $x_i$ and the whole set of objects and the average similarity between $x_j$ and the whole set of objects. This allows to take into consideration the density around each object.

The second step uses two heuristics to extract the poles from the similarity graph. A pole $P_k$ is a subset of $X$ such that the sub-graph $G_S(P_k, V(P_k))$ is a clique-graph, this is, $\forall x_i \in P_k, \forall x_j \in P_k, (x_i, x_j) \in V(P_k))$ with $V(P_k)$ the subset of edges associated with $P_k$.

The Poles are derived from the similarity graph $G_S(X, V)$ by selecting a particular point and adding connected vertices to the pole in construction. The first vertex select ($x^1$) is the one with the lower average similarity with the objects, among the set of vertices having at least one connected vertex. The set of vertices having at least one connect vertex, $E$, is include in $X$ ($E \subset X$). $x^1$ is defined by:

$$x^1 = \arg \min_{x_i \in E} \frac{1}{|X|} \sum_{x_j \in X} s(x_i, x_j)$$  \hspace{1cm} (3.13)

The next vertices $\{x^2, x^3, \ldots, x^m\}$ are chosen in order to reduce the similarity with the poles previously built:

$$x^k = \arg \min_{x_i \in E} \frac{1}{k-1} \sum_{m=1, \ldots, k-1} \frac{1}{|P_m|} \sum_{x_j \in P_m} s(x_i, x_j)$$  \hspace{1cm} (3.14)

The process stops when the sum in the previous equation is greater than the average similarity of the whole set of objects. The number of poles is determined by 3.14, and correspond to the number of clusters.
The next step is the multi-assignment of the terms to one or several poles, among the set of poles \( P = \{P_1, \ldots, P_l\} \). This step plays an important role in the construction of overlapping clusters in PoBOC. The advantage of assigning an object to several clusters is that way we can have a word with several senses in different clusters. Each cluster should represent optimally a sense of the word. In other soft-clustering algorithms, the assignment method is often based on a global threshold applied on a membership matrix obtained with a fuzzy-clustering method.

Cleziou et al. ([9]) proposes a new approach for the multi-assignment of objects to the poles based on the relative similarity between objects and poles. Let \( X = x_1, \ldots, x_n \) be the set of objects, let \( P = P_1, \ldots, P_n \) be the set of poles and \( U \) be the membership matrix on \( P \times X \) defined by:

\[
u(P_i, x_j) = \frac{1}{|P_i|} \sum_{x_k \in P_i} s(x_j, x_k)
\]

Given an object \( x_j \), \( P_{j,1} \) is the most similar pole for \( x_j \) (\( P_{j,1} = \arg \max_{P_i \in P} u(P_i, x_j) \)), \( P_{j,2} \) the second most similar pole for \( x_j \), and so on. \( P_{j,l} \) is the least similar pole for \( x_j \). The following condition \( \text{Assign}(x_j, P_{j,k}) \) is used to test whether the object \( x_j \) is assigned to the pole \( P_{j,k} \):

\[
\text{Assign}(x_j, P_{j,k}) \text{ iff one of the following properties is satisfied:}
\]

i) \( k = 1 \),

ii) \( 1 < k < l, u(P_{j,k}, x_j) \geq \frac{u(P_{j,k-1}, x_j) + u(P_{j,k+1}, x_j)}{2} \) and \( \forall k', \text{Assign}(x_j, P_{j,k'}) \)

where \( l \) is the number of resulting overlapping clusters.

For each object, the set of poles is ordered by his average similarity with the object. The property i) allows to assign each object to at least one pole (the most similar) and ii) allows to assign an object \( x_j \) to a pole \( P_{j,k} \) by considering the similarity with the previous pole \( P_{j,k-1} \) and the next pole \( P_{j,k+1} \) w.r.t. the order associated to \( x_j \). The assignment is based on the relative position (similarity) of the object with regards to the poles previously obtained.

The last step is the hierarchical organization of groups, which allows to control the number of final clusters obtained from the set of groups. This will be used so that it could be found a better characterization of the groups, and then to get a better set of clusters.

To get a hierarchical organization, Cleziou et al. propose to apply the hierarchical agglomerative clustering method "single-link", described by Kain, Murty and Flynn ([8]). Starting with the groups previously built \( C = C_1, \ldots, C_I \) where \( C_i = x_j \text{ assigned to } P_i \). Since the similarity matrix is normalized, we have \( \forall x_i \in X, s(x_i, x_i) = 1 \) and the similarity between two groups is defined by:
3.6 Cluster Ranking

The organization of clusters is built as follows: the two most similar groups are agglomerated and this process is repeated until we get only one group. This organization is represented by a binary tree where the leaves correspond to the initial set of groups.

After the execution of PoB0C in our set of terms, the algorithm returns a set of clusters, from which we only use the ones with more than one term.

The Appendix E lists the clusters resulting from the PoB0C algorithm, after they were rank by the degree of generality (See section 3.6).

3.6 Cluster Ranking

As the base of comparison of our work is ranked by degree of generality and this does not happens with the cluster returned by the algorithm, it is necessary to rank the clusters. This is done using the value obtained with the TextRank algorithm (See section 3.4 and Appendix C).

For each cluster we calculate the average of the TextRank value of the terms assign to it.

For example, using the following clusters, obtained by the PoB0C algorithm:

<table>
<thead>
<tr>
<th>GenCluster 2</th>
<th>GenCluster 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>(0.1) ——&gt; Cardiovascular System</td>
<td>(0.5) ——&gt; Blood Vessels</td>
</tr>
<tr>
<td>(1.2) ——&gt; Digestive System</td>
<td>(1.46) ——&gt; Oropharynx</td>
</tr>
<tr>
<td>(2.3) ——&gt; Respiratory System</td>
<td>(2.93) ——&gt; Geniculate Ganglion</td>
</tr>
<tr>
<td>(3.4) ——&gt; Nervous System</td>
<td></td>
</tr>
</tbody>
</table>

and the TextRank values, with the values rounded to five decimal places:

<table>
<thead>
<tr>
<th>AUI</th>
<th>Term</th>
<th>Rank Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>A0091423</td>
<td>Nervous System</td>
<td>3.30660</td>
</tr>
<tr>
<td>A0031694</td>
<td>Blood Vessels</td>
<td>0.92931</td>
</tr>
<tr>
<td>A0095412</td>
<td>Oropharynx</td>
<td>0.27398</td>
</tr>
<tr>
<td>A0035256</td>
<td>Cardiovascular System</td>
<td>0.19745</td>
</tr>
<tr>
<td>A0111426</td>
<td>Respiratory System</td>
<td>0.17371</td>
</tr>
<tr>
<td>A0048766</td>
<td>Digestive System</td>
<td>0.15000</td>
</tr>
<tr>
<td>A0062894</td>
<td>Geniculate Ganglion</td>
<td>0.15000</td>
</tr>
</tbody>
</table>

we obtain the following values:

\[
RankValue(\text{GenCluster2}) = \frac{3.30660 + 0.19745 + 0.17371 + 0.15000}{4} = 0.95694
\]

and
3.7 Domain Clustering

The next step is to determine domain clusters within the generality clusters obtained.

For this, we use the Symmetric Conditional Probability (SCP) measure, which calculates numerically the similarity between terms, based on the co-occurrence frequency acquired from the corpus.

The SCP measure is defined by:

$$SCP(w_1, w_2) = \frac{p(w_1 | w_2) \times p(w_2 | w_1)}{p(w_1) \times p(w_2)}$$  \hspace{1cm} (3.17)

This process is done by:

1. Calculate the SCP measure between the terms within each Cluster.
2. Build similarity matrix for each cluster, using the SCP values.
3. Re-use the clustering algorithm in the clusters returned from the first use (See section 3.5.2).
4. Rank the clusters (See section 3.6).

The domain cluster obtained for the first generality cluster (GenCluster 1), with PoBOC algorithm, is:

**DomCluster 1**

(0, 6) ----> Nose
(1, 13) ----> Salivary Glands
(2, 15) ----> Maxillary Sinus
(3, 17) ----> Submandibular Gland

**DomCluster 2**

(0, 3) ----> Pancreas
(1, 7) ----> Pleura

$$RankValue(\text{GenCluster} 4) = \frac{0.92931 + 0.27398 + 0.15000}{3} = 0.45110$$

Comparing the two values, the higher value is $RankValue(\text{GenCluster} 4)$, therefore, "GenCluster 2" is more general than "GenCluster 4", appearing before in the cluster ranked list, as we can see in Appendix E.
3.8 Problems found

Building a language-independent Ontology without supervision is a difficult process, during which several problems can be found. During the elaboration of this work we encountered the following problems:

1. The small size of the documents in the corpus. As MEDLINE only keeps references to journal articles, only the abstracts of some articles are in those references.

2. As we intend to keep the system language-independent, the variations of the terms are treated distinctly. For example, *lung* and is plural, *lungs*, can be treated as the same term in a language-dependent system, but, on a language-independent system, they are completely different terms, as the rules to inflict terms variations are language-dependent.

3. The more general terms, like *Cardiovascular System*, are rarely used, therefore, they can be wrongly classified. So, more general words can be considered more specific, and vice-versa.

4. The size of the compound terms, this is, the number of words that defines the compound term, complicates the process, as the bigger the term is, more difficult it is to find it in the corpus.
Oliveira ([20]) also aims to the automatic creation of a lexical Ontology, but for the Portuguese language.

The resulting Ontology of Oliveira’s work is intended to be in the public domain and freely available for download, so it could be used by the Portuguese NLP community and other researchers that need Portuguese lexical knowledge in their work.

Lexical capabilities of NLP systems are weak, as there is intensive work involved in manually encoding lexical entries, which is impractical and undesirable. NLP tools should be used in order to automate part of the process, decreasing the manual input.

Oliveira talks about lexical database, where concepts are organized in a network and relate with other concepts by means of semantic relations, which are present in text.

As Oliveira’s work is language-dependent, he can take advantage of the language characteristics, like textual patterns which can be used to identify semantic relations. He also intends to use machine readable dictionaries (MRDs) to acquire general knowledge and then corpora to complete specific lexical gaps.

Oliveira’s choice on using MRDs is related to the fact that "MRDs are highly structured, they are a substantial source of general lexical knowledge, and the "authorities" of word sense". They are also used for word sense disambiguation (WSD). He intends to use PAPEL ¹ as a base his our ontology, by analysing its structure and relations in order to improve the grammars, the extraction tools and, therefore, the quality of the relations. Besides PAPEL, he is also planning on using other MRDs, like the portuguese version of Wiktionary (http://pt.wiktionary.org), with the objective of improving is work.

Resembling our work, Oliveira will also extract relations from textual resources, like textual corpora, which should be viewed as the main source of domain-specific information

¹A lexicial resource for Portuguese, consisting of relations between terms, extracted after processing the definitions of a major general dictionary
Related Work

([14]). Therefore, Oliveira will try to develop tools to extract relations from corpora, which will be used to enrich the main Ontology, or to build new ones based on the texts.

For extracting relations from corpora, Oliveira refers Hearst’s work ([15]), which propose an automatic method to discover lexico-syntactic patterns, used for the acquisition of hyponyms. Other researchers used Hearst proposal, not only for the hyponyms, but also for other relations like meronymy or causality.

He will also try to adapt the tools used to extract relations from MRDs to textual resources, knowing that extraction from unrestricted text is a more difficult task, as this text is not structured, its vocabulary not controlled and may contain several features like metaphors and anaphora.

The main relation with our work is the extraction of relations from corpora, although Oliveira uses different methods, as we will be working for a specific language, Portuguese, taking advantage of its characteristics, as the rules of words derivations.
Chapter 5

Conclusions and Future Work

We can say that ontologies will play a crucial role in future knowledge-based systems if they will be designed in such a way as to minimize the effects of the interaction problem. Ontologies are described in the knowledge level, its objective is to characterize a conceptualization, trying to describe the interpretations of each object, in our case, of each term.

As described in section 3.1, an Ontology is defined as an explicit specification of a conceptualization, by Tom Gruber (1993).

Many types of relations, described by Pérez and Corcho (2000), can be extracted from corpora, but some of them are language-dependent, therefore, were not taken into count in our research, as we want to build a language-independent ontology.

Many work was done, and there much more to be done (See section 5.1), as building a language-independent ontology is a very complex and prolonged process.

Using features like asymmetric association measures and Symmetric Conditional Probability allowed us to define relations between terms, without being necessary the access to lexical resources already built. Although, some of these relations were not what we expected, mainly due to the problems described in section 3.8.

Those wrongly defined relations committed the result obtained in the rest of our approach. Still, the result can be considered satisfactory as we obtained the following domain clusters: $C_1 = \{'GastrointestinalTract', 'Liver', 'LowerGastrointestinalTract'\}$ and $C_2 = \{'Larunx', 'Lung', 'Hypopharynx', 'Nasopharynx'\}$ which belong to 'Digestive System' and 'Respiratory System', respectively.

Therefore, we can say that, besides not concluding our work, we obtain satisfactory results, thus making our approach a point of start for developing language-independent ontologies.

The next section describes the future work, need to complete our approach, and some items that can improve our work.
5.1 Future work

As this thesis is incomplete, this is, the main objective was not achieved, there is some work to be done:

i) Find synonymy clusters for each domain clusters obtain in 3.7.

ii) Calculate the similarity between terms within the domain clusters, using word-context vectors, building a similarity matrix.

iii) Interconnect the clusters. This can be done by:
   a) Interconnect domain clusters;
   b) Interconnect synonym clusters.

iv) Test and evaluate our ontology.

   After this, we can improve our ontology by:

   i) Use word-context vectors in relations extraction.

   ii) Use bigger documents, so we can improve the terms classification.

   iii) Find a way of derive the score for compound terms, as it is difficult to calculate by the method used.
Bibliography


Appendix A

Example of a MEDLINE entry

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        <PubDate>
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  <Abstract>
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  </Abstract>
</MedlineCitation>
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lesions in the posterior segment of the eye were associated with the deposit of cells on the margin of the pupil and the posterior surface of the cornea.

2. The path of wandering cells in relation to localized inflammatory lesions in the eye is discussed.

3. The pathologic findings of a case of chorioretinitis at the optic disc are described.

4. An explanation is offered for the sector-formed defect in the visual field of such cases.

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</MedlineCitation>
Appendix B

Structure of terms selected from UMLS

Cardiovascular System
  – Blood Vessels
    Arteries
      – Aorta
        Aorta, Abdominal
        Sinus of Valsalva
        Aorta, Thoracic
      – Arterioles
      – Axillary Artery
      – Basilar Artery
      – Brachial Artery
    Endothelium, Vascular
      – Tunica Intima
      – Pericytes
    Microcirculation
      – Arterioles
      – Capillaries
      – Venules
      – Arteriovenous Anastomosis
    Muscle, Smooth, Vascular
      – Tunica Media
    Retinal Vessels
      – Retinal Artery
      – Retinal Vein
    – Blood–Air Barrier
    – Blood–Brain Barrier
    – Blood–Retinal Barrier
    – Blood–Testis Barrier

Digestive System
  – Biliary Tract
    Bile Ducts
      – Bile Ducts, Intrahepatic
        Bile Canaliculi
Structure of terms selected from UMLS

- **Bile Ducts, Extrahepatic**
  - Common Bile Duct
    - Ampulla Of Vater
    - Sphincter Of Oddi
  - Cystic Duct
  - Hepatic Duct, Common

- **Gallbladder**

- **Gastrointestinal Tract**

  - **Intestines**
    - **Intestinal Mucosa**
      - Paneth Cells
      - Goblet Cells
      - Enterocytes
    - **Intestine, Large**
      - Cecum
      - Appendix
    - **Colon**
      - Colon, Ascending
      - Colon, Transverse
      - Colon, Descending
      - Colon, Sigmoid
    - **Rectum**
    - **Anal Canal**
    - **Intestine, Small**
      - Duodenum
        - Brunner Glands
        - Ampulla Of Vater
          - Sphincter Of Oddi
      - Ileum
        - Ileocecal Valve
        - Meckel Diverticulum
      - Jejunum

- **Pharynx**

- **Upper Gastrointestinal Tract**

  - **Duodenum**
    - Brunner Glands
    - Ampulla Of Vater
      - Sphincter Of Oddi
  - **Esophagus**
    - Esophagogastric Junction
      - Esophageal Sphincter, Lower
    - Esophageal Sphincter, Upper
  - **Stomach**
    - Cardia
    - Esophagogastric Junction
      - Esophageal Sphincter, Lower
    - **Gastric Fundus**
    - **Gastric Mucosa**
      - Enterochromaffin Cells
      - Parietal Cells, Gastric
      - Gastrin-Secreting Cells
      - Somatostatin-Secreting Cells
      - Chief Cells, Gastric
    - **Pyloric Antrum**
Structure of terms selected from UMLS

Lower Gastrointestinal Tract
- Ileum
  - Ileocecal Valve
  - Meckel Diverticulum
- Intestine, Large
  - Cecum
    - Appendix
  - Colon
    - Colon, Ascending
    - Colon, Transverse
    - Colon, Descending
    - Colon, Sigmoid
  - Rectum
  - Anal Canal
- Jejunum

Mouth
- Dentition
- Salivary Glands
  - Parotid Gland
  - Salivary Glands, Minor
  - Sublingual Gland
  - Submandibular Gland
  - Salivary Ducts
- Tongue
  - Lingual Frenum
  - Taste Buds
- Liver
  - Bile Ducts, Intrahepatic
    - Bile Canaliculi
- Pancreas
  - Islets of Langerhans
    - Glucagon–Secreting Cells
    - Insulin–Secreting Cells
    - Somatostatin–Secreting Cells
    - Pancreatic Polypeptide–Secreting Cells
  - Pancreatic Ducts
  - Pancreas, Exocrine

Respiratory System
- Larynx
  - Glottis
    - Vocal Cords
  - Laryngeal Cartilages
    - Arytenoid Cartilage
    - Cricoid Cartilage
    - Epiglottis
    - Thyroid Cartilage
  - Laryngeal Mucosa
    - Goblet Cells
  - Laryngeal Muscles
- Lung
  - Bronchi
  - Extravascular Lung Water
  - Pulmonary Alveoli
Structure of terms selected from UMLS

- Blood–Air Barrier

- Nose
  - Nasal Bone
  - Nasal Cavity
  - Nasal Mucosa
    - Olfactory Mucosa
      - Olfactory Receptor Neurons
      - Goblet Cells
  - Nasal Septum
  - Vomeronasal Organ

- Paranasal Sinuses
  - Ethmoid Sinus
  - Frontal Sinus
  - Maxillary Sinus
  - Sphenoid Sinus

- Pharynx
  - Hypopharynx
  - Nasopharynx
  - Pharyngeal Muscles
    - Esophageal Sphincter, Upper
  - Oropharynx
  - Tonsil

- Pleura

Nervous System

- Ganglia
  - Ganglia, Autonomic
    - Ganglia, Parasympathetic
    - Ganglia, Sympathetic
    - Stellate Ganglion
    - Superior Cervical Ganglion
  - Satellite Cells, Perineuronal
    - Ganglia, Sensory
      - Ganglia, Spinal
      - Geniculate Ganglion
    - Nodose Ganglion
    - Spiral Ganglion
    - Trigeminal Ganglion
    - Ganglia, Invertebrate

- Nerve Net
  - Ependyma
  - Neurilemma

- Nerve Tissue

- Neural Pathways
  - Afferent Pathways
    - Auditory Pathways
    - Olfactory Pathways
    - Spinothalamic Tracts
    - Visual Pathways
    - Visceral Afferents
  - Efferent Pathways
    - Extrapyramidal Tracts
    - Pyramidal Tracts

Medial Forebrain Bundle
Structure of terms selected from UMLS

Internal Capsule
Perforant Pathway
  − Neuroglia
    Astrocytes
    Oligodendroglia
      − Myelin Sheath
    Schwann Cells
      − Myelin Sheath
    Neurilemma
    Ranvier's Nodes
Satellite Cells, Perineuronal
Microglia
## Appendix C

### Results of TextRank - Confidence measure

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Results of TextRank - Confidence measure

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Appendix D

Results of K-Means - Ranked

GenCluster 1

( 0, 7) --> Blood–Testis Barrier
( 1, 9) --> Gastrointestinal Tract
( 2, 10) --> Liver
( 3, 24) --> Retinal Vessels
( 4, 25) --> Bile Ducts
( 5, 31) --> Islets of Langerhans
( 6, 76) --> Tongue
( 7, 77) --> Bile Canaliculi
( 8, 102) --> Sinus of Valsalva
( 9, 103) --> Common Bile Duct
(10, 125) --> Appendix

GenCluster 2

( 0, 0) --> Cardiovascular System
( 1, 1) --> Digestive System
( 2, 8) --> Biliary Tract
( 3, 12) --> Larynx
( 4, 13) --> Lung
( 5, 14) --> Nose
( 6, 15) --> Pharynx
( 7, 17) --> Ganglia
( 8, 22) --> Arteries
( 9, 26) --> Gallbladder
(10, 28) --> Upper Gastrointestinal Tract
(11, 29) --> Lower Gastrointestinal Tract
(12, 33) --> Glottis
(13, 34) --> Laryngeal Mucosa
(14, 35) --> Laryngeal Muscles
(15, 38) --> Pulmonary Alveoli
(16, 39) --> Nasal Cavity
(17, 40) --> Nasal Mucosa
(18, 41) --> Nasal Septum
(19, 43) --> Hypopharynx
(20, 44) --> Nasopharynx
(21, 47) --> Afferent Pathways
Results of K-Means - Ranked

(22, 50) —> Internal Capsule
(23, 57) —> Arterioles
(24, 60) —> Brachial Artery
(25, 64) —> Venules
(26, 66) —> Retinal Artery
(27, 69) —> Duodenum
(28, 70) —> Esophagus
(29, 73) —> Jejunum
(30, 74) —> Dentition
(31, 84) —> Goblet Cells
(32, 85) —> Olfactory Mucosa
(33, 86) —> Vomeronasal Organ
(34, 87) —> Ethmoid Sinus
(35, 88) —> Frontal Sinus
(36, 90) —> Sphenoid Sinus
(37, 91) —> Tonsil
(38, 95) —> Trigeminal Ganglion
(39, 96) —> Auditory Pathways
(40, 98) —> Visual Pathways
(41, 99) —> Visceral Afferents
(42, 109) —> Rectum
(43, 110) —> Anal Canal
(44, 112) —> Esophagogastric Junction
(45, 113) —> Cardia
(46, 114) —> Gastric Fundus
(47, 115) —> Gastric Mucosa
(48, 117) —> Ileocecal Valve
(49, 118) —> Parotid Gland
(50, 121) —> Taste Buds
(51, 126) —> Sphincter of Oddi
(52, 127) —> Enterochromaffin Cells

GenCluster 3

(0, 2) —> Respiratory System
(1, 3) —> Nervous System
(2, 4) —> Blood Vessels
(3, 5) —> Blood-Brain Barrier
(4, 18) —> Nerve Net
(5, 19) —> Nerve Tissue
(6, 20) —> Neural Pathways
(7, 21) —> Neuroglia
(8, 23) —> Microcirculation
(9, 30) —> Mouth
(10, 36) —> Bronchi
(11, 37) —> Extravascular Lung Water
(12, 45) —> Oropharynx
(13, 46) —> Ependyma
(14, 48) —> Efferent Pathways
(15, 51) —> Perforant Pathway
(16, 52) —> Astrocytes
(17, 53) —> Oligodendroglia
(18, 54) —> Schwann Cells
(19, 55) —> Microglia

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Results of K-Means - Ranked

( 20, 56) → Aorta
( 21, 59) → Basilar Artery
( 22, 61) → Tunica Intima
( 23, 62) → Pericytes
( 24, 63) → Capillaries
( 25, 65) → Tunica Media
( 26, 89) → Maxillary Sinus
( 27, 92) → Geniculate Ganglion
( 28, 93) → Nodose Ganglion
( 29, 97) → Olfactory Pathways
( 30, 100) → Pyramidal Tracts
( 31, 101) → Myelin Sheath

GenCluster 4

( 0,  6) → Blood–Retinal Barrier
( 1, 27) → Intestines
( 2, 58) → Axillary Artery
( 3, 67) → Retinal Vein
( 4, 68) → Intestinal Mucosa
( 5, 71) → Stomach
( 6, 72) → Ileum
( 7, 83) → Thyroid Cartilage
( 8, 104) → Cystic Duct
( 9, 105) → Paneth Cells
(10, 106) → Enterocytes
(11, 107) → Cecum
(12, 108) → Colon
(13, 111) → Ampulla of Vater
(14, 116) → Pyloric Antrum
(15, 119) → Sublingual Gland
(16, 124) → Superior Cervical Ganglion

GenCluster 5

( 0, 11) → Pancreas
( 1, 32) → Pancreatic Ducts
( 2, 42) → Paranasal Sinuses
( 3, 75) → Salivary Glands
( 4, 78) → Insulin–Secreting Cells
( 5, 79) → Vocal Cords
( 6, 80) → Arytenoid Cartilage
( 7, 81) → Cricoid Cartilage
( 8, 82) → Epiglottis
( 9, 120) → Submandibular Gland

GenCluster 6

( 0, 16) → Pleura
( 1, 49) → Medial Forebrain Bundle
( 2, 94) → Spiral Ganglion
( 3, 122) → Olfactory Receptor Neurons
( 4, 123) → Stellar Ganglion
Appendix E

Results of PoBOC - Ranked

GenCluster 1

( 0, 9) ➔ Biliary Tract
( 1, 10) ➔ Gastrointestinal Tract
( 2, 11) ➔ Liver
( 3, 12) ➔ Pancreas
( 4, 13) ➔ Larynx
( 5, 14) ➔ Lung
( 6, 15) ➔ Nose
( 7, 17) ➔ Pleura
( 8, 30) ➔ Lower Gastrointestinal Tract
( 9, 39) ➔ Pulmonary Alveoli
(10, 41) ➔ Nasal Mucosa
(11, 44) ➔ Hypopharynx
(12, 45) ➔ Nasopharynx
(13, 76) ➔ Salivary Glands
(14, 85) ➔ Goblet Cells
(15, 90) ➔ Maxillary Sinus
(16, 109) ➔ Colon
(17, 121) ➔ Submandibular Gland

GenCluster 2

( 0, 1) ➔ Cardiovascular System
( 1, 2) ➔ Digestive System
( 2, 3) ➔ Respiratory System
( 3, 4) ➔ Nervous System

GenCluster 3

( 0, 23) ➔ Arteries
( 1, 37) ➔ Bronchi
( 2, 52) ➔ Perforant Pathway
( 3, 54) ➔ Oligodendroglia
( 4, 57) ➔ Aorta
( 5, 63) ➔ Pericytes
( 6, 64) ➔ Capillaries
( 7, 69) ➔ Intestinal Mucosa

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Results of PoBOC - Ranked

GenCluster 4

(8, 70) —> Duodenum
(9, 71) —> Esophagus
(10, 72) —> Stomach

GenCluster 5

(0, 5) —> Blood Vessels
(1, 46) —> Oropharynx
(2, 93) —> Geniculate Ganglion

GenCluster 6

(0, 53) —> Astrocytes
(1, 55) —> Schwann Cells
(2, 56) —> Microglia

GenCluster 7

(0, 12) —> Pancreas
(1, 39) —> Pulmonary Alveoli
(2, 75) —> Dentition
(3, 118) —> Ileocecal Valve
(4, 120) —> Sublingual Gland
(5, 121) —> Submandibular Gland

GenCluster 8

(0, 8) —> Blood–Testis Barrier
(1, 25) —> Retinal Vessels
(2, 26) —> Bile Ducts
(3, 32) —> Islets of Langerhans
(4, 73) —> Ileum
(5, 77) —> Tongue
(6, 103) —> Sinus of Valsalva
(7, 104) —> Common Bile Duct
(8, 126) —> Appendix

GenCluster 9

(0, 24) —> Microcirculation
(1, 66) —> Tunica Media
(2, 67) —> Retinal Artery

GenCluster 10

(0, 59) —> Axillary Artery
(1, 90) —> Maxillary Sinus
Results of PoBOC - Ranked

GenCluster 11

( 0, 42) → Nasal Septum
( 1, 88) → Ethmoid Sinus
( 2, 90) → Maxillary Sinus

GenCluster 12

( 0, 27) → Gallbladder
( 1, 105) → Cystic Duct
( 2, 106) → Paneth Cells
( 3, 113) → Esophagogastric Junction

GenCluster 13

( 0, 74) → Jejunum
( 1, 89) → Frontal Sinus

GenCluster 14

( 0, 43) → Paranasal Sinuses
( 1, 80) → Vocal Cords
( 2, 81) → Arytenoid Cartilage
( 3, 82) → Cricoid Cartilage
( 4, 83) → Epiglottis

GenCluster 15

( 0, 68) → Retinal Vein
( 1, 84) → Thyroid Cartilage
( 2, 115) → Gastric Fundus

GenCluster 16

( 0, 6) → Blood–Brain Barrier
( 1, 62) → Tunica Intima

GenCluster 17

( 0, 21) → Neural Pathways
( 1, 22) → Neuroglia
( 2, 101) → Pyramidal Tracts

GenCluster 18

( 0, 33) → Pancreatic Ducts
( 1, 79) → Insulin–Secreting Cells
( 2, 80) → Vocal Cords

GenCluster 19

( 0, 105) → Cystic Duct
( 1, 107) → Enterocytes
( 2, 108) → Cecum
Results of PoBOC - Ranked

GenCluster 20

( 3, 125) ——> Superior Cervical Ganglion

( 0, 28) ——> Intestines
( 1, 111) ——> Anal Canal
( 2, 113) ——> Esophagogastric Junction
( 3, 114) ——> Cardia

GenCluster 21

( 0, 20) ——> Nerve Tissue
( 1, 49) ——> Efferent Pathways

GenCluster 22

( 0, 95) ——> Spiral Ganglion
( 1, 124) ——> Stellate Ganglion