

COMP90055 Computing Project Report

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Information Extraction of biomedical relationships in published colon cancer literature



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To my loving parents...

Declaration

I certify that

- this thesis does not incorporate without acknowledgement any material previously submitted for a degree or diploma in any university; and that to the best of my knowledge and belief it does not contain any material previously published or written by another person where due reference is not made in the text.*
- where necessary I have received clearance for this research from the University's Ethics Committee (Approval Number) and have submitted all required data to the Department*
- the thesis is 8000 words in length (excluding text in images, table, bibliographies and appendices).*

Ruichen Teng
June 2015

Acknowledgements

And I would like to acknowledge ...

Abstract

This is where you write your abstract ...

Table of contents

List of figures	xiii
List of tables	xv
Nomenclature	xvii
1 Introduction	1
1.1 Motivation	1
1.2 Definitions and Assumptions	2
1.3 Research Question	2
1.4 Thesis Structure	2
2 Related Work	5
2.1 Relation Extraction	5
2.2 Named entity recognition	5
2.3 Pattern based Methods	6
2.4 Co-corrence based methods	6
2.5 Rule-Based Methods	6
2.6 Kernel based methods	6
2.7 Feature based methods	6
2.8	6
3 Core	7
3.1 Data Collection	7
3.1.1 Background	7
3.2 Algorithm	8
3.3 System Adaptation	8
3.4 Results	8

4	Conclusion	9
4.1	Conclusion	9
4.2	Definitions and Assumptions	9
4.3	Named entity recognition	9
4.4	Pattern based Methods	9
4.5	Co-corrence based methods	9
4.6	Kernel based methods	9
4.7	Feature based methods	9
4.8	9
5	Getting started	11
5.1	Corpus Construction	11
5.2	System Adaptation	11
5.3	Where does it come from?	11
6	My second chapter	15
6.1	Short title	15
7	My third chapter	21
7.1	First section of the third chapter	21
7.1.1	First subsection in the first section	21
7.1.2	Second subsection in the first section	21
7.1.3	Third subsection in the first section	21
7.2	Second section of the third chapter	22
7.3	The layout of formal tables	22
	References	25
	Appendix A How to install L^AT_EX	27
	Appendix B Installing the CUED class file	31
	Index	33

List of figures

6.1	Minion	16
6.2	Best Animations	19

List of tables

3.1	A nice looking table	8
7.1	A badly formatted table	23
7.2	A nice looking table	23
7.3	Even better looking table using booktabs	23

Nomenclature

Roman Symbols

F complex function

F complex function

Greek Symbols

γ a simply closed curve on a complex plane

γ a simply closed curve on a complex plane

ι unit imaginary number $\sqrt{-1}$

ι unit imaginary number $\sqrt{-1}$

π $\simeq 3.14\dots$

π $\simeq 3.14\dots$

Superscripts

j superscript index

j superscript index

Subscripts

0 subscript index

0 subscript index

Other Symbols

\oint_{γ} integration around a curve γ

\oint_{γ} integration around a curve γ

Acronyms / Abbreviations

CIF Cauchy's Integral Formula

CIF Cauchy's Integral Formula

Introduction

1.1 Motivation

Text mining is the process of searching for patterns in natural language text using methods in computer science, linguistics, and statistics. Despite being unstructured and only human-understandable, text is still our primary media for exchange of information[13]. The prevalence of textual data presents a big challenge to computer-driven natural language understanding. *Information extraction*, in particular, refers to the task of acquiring organized, structured and queryable format of data from the unstructured corpus.

While text mining is widely used in areas like marketing and document verifying, it has received increased attention for its application to biomedical literatures[1, 5, 6]. This trend stems from the direct need of biomedical workers and researchers to cope with information explosion in their field. For instance, MEDLINE(Medical Literature Analysis and Retrieval System Online), the online database of United States National Library of Medicine, has accumulated nearly 0.8 million citations and 2.7 billion searches in 2014 alone[7], with total citations reaching 22 million. Within these publications there are valuable research results that should add to human knowledge. In the meantime, our primary knowledge base in life science - the biomedical databases, are still mostly being populated manually by *biocurators* - the “museum catalogers of the Internet age”[12]. They are professional scientists who read biomedical articles, record relevant data and organize them according to the biomedical database schema. The sheer volume of publications has made this process increasingly unrealistic[4].

Not only does data overload make knowledge discovery demanding, it also leads to a decline in literature quality. Nowadays biomedical workers and researchers are more prone to drawing wrong conclusions because they simply can not read all the relevant publications, among which oftentimes contradicting results are reported. Needless to say, we are

in desperate need of automatic tools for systematically analyzing documents and extracting information. In fact, it has been argued that text mining is required to improve the coverage of databases[3].

1.2 Definitions and Assumptions

Below are a list of terms which I will use throughout this thesis, detailed examples will be given in the relevant sections, but a general definition is first given here to avoid any confusions that might arise when reading the following paragraphs.

- *Relation Extraction*: In general, relation extraction refers to the process of discovering a relationship between entities in text. In the domain of natural language processing, the relation can be semantic, syntactic, etc, with semantic relations being the most important for knowledge discovery. Relations can be unary, binary and complex with complex relations sometimes intermingled with the concept of events, In this project we are mainly concerned with binary relations as shown. Relation extraction is a form of information extraction where the semantic relations between entities are extracted. Specifically, in this project we focus on the relation extraction among other informations. Biomedical relations covers a wide range of knowledge in this field.
- *Event Extraction*: to be added

1.3 Research Question

This project looks to investigate the application of information extraction system Approximate Subgraph Matching (ASM)[?], on relation extraction tasks, specifically regarding the relation extraction on the variome corpus. In this project we focus on the relation extraction among other informations. Biomedical relations covers a wide range of knowledge in this field. As it turns out, this is not a trivial process, The relation extraction tool has a very promising applications for researchers and medical field workers, pharmaceutical companies, and the general public.

1.4 Thesis Structure

The thesis is organized as follows: chapter 1 will

therefore to allow researchers to identify needed information more efficiently, quote
Based on the information in 1.1 and 1.2, the aim of this project is to develop tools that can
assist the human bio-curation process.

Related Work

This chapter will explore the research related to this thesis.

2.1 Relation Extraction

In general, relation extraction refers to the process of discovering a relationship between entities in text. In the domain of natural language processing, the relation can be semantic, syntactic, etc, with semantic relations being the most important for knowledge discovery. Relations can be unary, binary and complex with complex relations sometimes intermingled with the concept of events. In this project we are mainly concerned with binary relations as shown

2.2 Named entity recognition

Named Entity Recognition, or NER, is the task of identifying elements in text that belong to pre-defined categories like person, organization, etc. Specifically, NER in biomedical text mining aims at identifying things like proteins, diseases, genes, etc. There is extra difficulty for NER in the biomedical domain mainly because of the following reasons.

quote: A survey of current work in biomedical text mining This task has been challenging for several reasons. First, there does not exist a complete dictionary for most types of biological named entities, so simple text-matching algorithms do not suffice. In addition, the same word or phrase can Recognising biological entities in text allows for further extraction of relationships and other information by identifying the key concepts of interest refer to a different thing depending upon context (eg ferritin can be a biological substance or a laboratory test). Conversely, many biological entities have several names (eg PTEN and MMAC1 refer the same gene). Biological entities may also have multi-word names (eg carotid artery), so the problem is additionally complicated by the need to determine name boundaries and resolve overlap of candidate names. Because of the potential utility and

complexity of the problem, NER has attracted the interest of many researchers, and there is a tremendous amount of published research in this topic. With the large amount of genomic information being generated by biomedical researchers, it should not be surprising that in the genomics era, much of the work in biomedical NER has focused on recognising gene and protein names in free text. quote: A survey of current work in biomedical text mining

2.3 Pattern based Methods

Pattern based methods

2.4 Co-corrence based methods

2.5 Rule-Based Methods

2.6 Kernel based methods

2.7 Feature based methods

2.8

Core

3.1 Data Collection

Our dataset is the Variome Corpus[11], which is openly accessible.¹ Verspoor et al. [11] gave a detailed illustration of the document selection and annotation process. I will summarize the main points here.

3.1.1 Background

A major part of the current biomedical research lies in understanding the relations between human genetic variation and disease phenotypes. The *Human Variome Project*, or *HVP*, is a global initiative to collect all genetic variation information affecting human health[9]. In particular, it acts as a liaison between individuals and organizations to integrate the genetic variants into databases that are open to the general public[11]. The *International Society for Gastrointestinal Hereditary Tumours (InSiGHT)*, is an international organization which aims to benefit patients with hereditary gastrointestinal(GI) tumours by research, education and personal assistance. In 2008, InSiGHT and HVP began a collaboration which propels InSiGHT to refine its process in the integration and interpretation of genetic variants. Consequently, a substantial effort was made to understand the mutation of mismatch repair(MMR) genes, the cause of Lynch Syndrome - one of the main syndromes of GI cancer[10]. A total of 10 full-text articles were selected from PubMed Central® by searching the common Lynch syndrome genes. These documents are mostly about inherited colon cancer. The annotation schema, also known as the Variome Annotation Schema[11], include 11 entity types and 13 relation types. as can be seen in the table here

In short, the corpus is Inspired by needs of inSiGHT database, but intended for broader applications. Documents relevant to the genetics of Lynch syndrome, which covers inherited colon cancer as well as certain other cancers. Selected with PubMed Central To train tools

¹<http://www.opennicta.com.au/home/health/variome>

Table 3.1 A nice looking table

Dental measurement	Species I		Species II	
	mean	SD	mean	SD
I1MD	6.23	0.91	5.2	0.7
I1LL	7.48	0.56	8.7	0.71
I2MD	3.99	0.63	4.22	0.54
I2LL	6.81	0.02	6.66	0.01
CMD	13.47	0.09	10.55	0.05
CBL	11.88	0.05	13.11	0.04

for mining genetic variation and its relationship to disease Here in this information extraction task, we treat the manually annotated data as the *gold data*,

3.2 Algorithm

To separate Named Entity Recognition from Relation Extraction problem, the named entity annotations are provided in training, development and test sets. Effectively, this is just asking computer to extract possible relations between these entities without worrying how to recognize them accurately. Of course, named entity recognition is an important step in a real relation extraction task as cite cite, because biological named entity recognition is such a complex problem and sometimes the relation extraction success would depend on the accuracy of NER. Named entity recognition is the process of Iis project cite the performance of the subgraph matching method, as an instance-based learning strategy (Alpaydin, 2004), is dependent on having good training examples that express the events in a range of syntactic structures, cite

3.3 System Adaptation

3.4 Results

Conclusion

4.1 Conclusion

cite The focus must be more on helping biomedical researchers to solve real-world problems that are inhibiting the pace of research and less on evaluations based on system output independent of meeting user needs. cite

4.2 Definitions and Assumptions

4.3 Named entity recognition

Named entity recognition is the process of Iis project

4.4 Pattern based Methods

4.5 Co-corrence based methods

Syntactic parsing is particularly useful for relations that are distant in their expression. cite
Distant supervision for relation extraction without labeled data cite

4.6 Kernel based methods

4.7 Feature based methods

4.8

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How to install L^AT_EX

Windows OS

TeXLive package - full version

1. Download the TeXLive ISO (2.2GB) from
<https://www.tug.org/texlive/>
2. Download WinCDEmu (if you don't have a virtual drive) from
<http://wincdemu.sysprogs.org/download/>
3. To install Windows CD Emulator follow the instructions at
<http://wincdemu.sysprogs.org/tutorials/install/>
4. Right click the iso and mount it using the WinCDEmu as shown in
<http://wincdemu.sysprogs.org/tutorials/mount/>
5. Open your virtual drive and run setup.pl

or

Basic MikTeX - T_EX distribution

1. Download Basic-MiK_TE_X(32bit or 64bit) from
<http://miktex.org/download>
2. Run the installer
3. To add a new package go to Start » All Programs » MikTeX » Maintenance (Admin)
and choose Package Manager
4. Select or search for packages to install

TexStudio - T_EX editor

1. Download TexStudio from
<http://texstudio.sourceforge.net/#downloads>
2. Run the installer

Mac OS X

MacTeX - T_EX distribution

1. Download the file from
<https://www.tug.org/mactex/>
2. Extract and double click to run the installer. It does the entire configuration, sit back and relax.

TexStudio - T_EX editor

1. Download TexStudio from
<http://texstudio.sourceforge.net/#downloads>
2. Extract and Start

Unix/Linux

TeXLive - T_EX distribution

Getting the distribution:

1. TeXLive can be downloaded from
<http://www.tug.org/texlive/acquire-netinstall.html>.
2. TeXLive is provided by most operating system you can use (rpm,apt-get or yum) to get TeXLive distributions

Installation

1. Mount the ISO file in the mnt directory

```
mount -t iso9660 -o ro,loop,noauto /your/texlive####.iso /mnt
```

2. Install wget on your OS (use rpm, apt-get or yum install)
3. Run the installer script install-tl.

```
cd /your/download/directory
./install-tl
```

4. Enter command 'i' for installation
5. Post-Installation configuration:
<http://www.tug.org/texlive/doc/texlive-en/texlive-en.html#x1-320003.4.1>
6. Set the path for the directory of TexLive binaries in your .bashrc file

For 32bit OS

For Bourne-compatible shells such as bash, and using Intel x86 GNU/Linux and a default directory setup as an example, the file to edit might be

```
edit ~/.bashrc file and add following lines
PATH=/usr/local/texlive/2011/bin/i386-linux:$PATH;
export PATH
MANPATH=/usr/local/texlive/2011/texmf/doc/man:$MANPATH;
export MANPATH
INFOPATH=/usr/local/texlive/2011/texmf/doc/info:$INFOPATH;
export INFOPATH
```

For 64bit OS

```
edit ~/.bashrc file and add following lines
PATH=/usr/local/texlive/2011/bin/x86_64-linux:$PATH;
export PATH
MANPATH=/usr/local/texlive/2011/texmf/doc/man:$MANPATH;
export MANPATH
```

```
INFOPATH=/usr/local/texlive/2011/texmf/doc/info:$INFOPATH;  
export INFOPATH
```

Fedora/RedHat/CentOS:

```
sudo yum install texlive  
sudo yum install psutils
```

SUSE:

```
sudo zypper install texlive
```

Debian/Ubuntu:

```
sudo apt-get install texlive texlive-latex-extra  
sudo apt-get install psutils
```

Installing the CUED class file

\LaTeX .cls files can be accessed system-wide when they are placed in the $\langle\text{texmf}\rangle/\text{tex}/\text{latex}$ directory, where $\langle\text{texmf}\rangle$ is the root directory of the user's \TeX installation. On systems that have a local texmf tree ($\langle\text{texmflocal}\rangle$), which may be named “ texmf-local ” or “ localtexmf ”, it may be advisable to install packages in $\langle\text{texmflocal}\rangle$, rather than $\langle\text{texmf}\rangle$ as the contents of the former, unlike that of the latter, are preserved after the \LaTeX system is reinstalled and/or upgraded.

It is recommended that the user create a subdirectory $\langle\text{texmf}\rangle/\text{tex}/\text{latex}/\text{CUED}$ for all CUED related \LaTeX class and package files. On some \LaTeX systems, the directory look-up tables will need to be refreshed after making additions or deletions to the system files. For \TeX Live systems this is accomplished via executing “ texhash ” as root. $\text{MIK}\text{\TeX}$ users can run “ initexmf -u ” to accomplish the same thing.

Users not willing or able to install the files system-wide can install them in their personal directories, but will then have to provide the path (full or relative) in addition to the filename when referring to them in \LaTeX .

Index

LaTeX class file, 1, 5