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Biomedical Text Mining

**SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENT FOR THE
DEGREE OF
BACHELOR OF TECHNOLOGY
(BioInformatics)
(SESSION 2007-2011)**

Submitted by

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Date: th25 May 2011

CERTIFICATE

This is to certify that the thesis entitled Biomedical text mining is submitted by Vishal Mahajan & Arjun Bagai in the partial fulfillment of the award of degree of Bachelor of Technology BioInformatics by **JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT.**

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23/05/11

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Contents

ABSTRACT	7
Chapter 1 - Introduction	
1.1The Problem Statement	8
1.2Objective and Scope of the project	8
1.3Text Mining	9
1.4Approaches to Text Mining	9
1.5Text Mining in Molecular Biology	10
1.6Natural Language Processing Technique	10
1.7Literature Source Diagram	11
1.8Biomedical Text Mining and its Practical Applications	12
Chapter 2 – Text Mining	
2.1What Text Miners are Interested in !	13
2.1.1 Terminologies	13
2.1.2 Relationships	14
2.1.3 Discovery	14
2.1.4 Quality	14
2.1.5Comprehensiveness	15
Chapter 3 – Vector Space Model	
3.1What is a Vector Space Model	16
3.2Stages of Vector Space Model	16
3.2.1 First Stage – Document Indexing	17
3.2.2 Second Stage – Term Weighting	17

3.2.3 Third Stage- Similarity Coefficient	18
3.2.4 User Query Diagram	19
 Chapter 4 – Query Extension Technique and Vector Space Models	
4.1 Knowledge Based Query Extension Technique	20
4.2 Stem Based VSM	20
4.3 Concept Based VSM	21
4.4 Phrase Based VSM	22
 Chapter 5 – The Test Set, OHSUMED	
5.1 Phrase Detection	23
5.2 VSM Models, Accuracy	23
5.2.1 Average Precision Recall Comparison	24
 Chapter 6 – Flow Diagram	
6.1 Integration + Working	28
6.2 Inverted Index	28
6.2.1 Inverted Index for added Documents	30
 Chapter 7 – Appendix	
7.1 For Building Inverted Index in Perl	31
7.1.1 Results In CMD	34

7.1.2 Results Directory	36
7.2Perl Programming in HTML	37
7.2.1 Main HTML Page	37
 Chapter 8 – Results And Conclusions	
8.1 Searching for a disease	51
8.2 Searching for a definition	55
8.3 Searching by line	59
8.4 Searching for symptoms	62
 Chapter 9 – Future Work Of The Project	
9.1 Sublanguage	63
9.2 Lexical And Semantic Sources	63
9.3 Controlled Vocabulary	63
 Chapter 10 – Bibliography	67

Abstract

A Vector Space Model, inverted index i.e an optimized structure, built primarily for retrieval, this basic structure inverts the text so that instead of the view obtained from scanning documents where a document is found and then its terms are seen (a list of documents each pointing to a list of terms it contains). The point of using an index is to increase the speed and efficiency of searches of the document collection. Without some sort of index, a user's query must sequentially scan the document collection, finding those documents containing the search terms. Users are not going to wait so many minutes for a response.

Hence, a sequential scan is simply not feasible. Given this situation a data structure called an inverted index is commonly used by search engines. The index is built which maps terms to documents (pretty much like the index found in the back of this book that maps terms to page numbers), thus resulting in better retrieval of the documents according to the respective user query.

Chapter 1

Introduction

1.1 Problem Statement

The point of using an index is to increase the speed and efficiency of searches of the document collection. Without some sort of index, a user's query must sequentially scan the document collection, finding those documents containing the search terms. Consider the "Find" operation in Windows; a user search is initiated and a search starts through each file on the hard disk. When a directory is encountered, the search continues through each directory.

Users are not going to wait so many minutes for a response. Hence, a sequential scan is simply not feasible. Given this situation a data structure called an *inverted index* is commonly used by search engines

1.2 Objective and scope of the Project

Create a Vector Space Model, and an inverted index for better retrieval of the documents according to the respective user query. A Vector Space Model, inverted index i.e an optimized structure, built primarily for retrieval, this basic structure inverts the text so that instead of the view obtained from scanning documents where a document is found and then its terms are seen (a list of documents each pointing to a list of terms it contains), the index is built which maps terms to documents (pretty much like the index found in the back of this book that maps terms to page numbers).

1.3 Text mining

Text mining is defined as the automatic discovery of new, previously unknown, information from unstructured textual data. It uses NLP technique for discovery process and is often seen as comprising of three major tasks:

- Information retrieval (gathering relevant documents).
- Information extraction (extracting information of interest from these documents).
- Data mining (discovering new associations among the extracted pieces of information).

1.4 Approaches to text mining

- **Three basic types of approaches to text mining are:**
 - **Co-occurrence-based methods** look for concepts that occur in the same unit of text—typically a sentence, but sometimes as large as an abstract—and posit a relationship between them.
 - **Knowledge-based approaches** make use of some sort of knowledge like how language is structured, how biologically relevant facts are stated in the biomedical literature or what are the main fields of bioscientists interests and what kinds of relationships they can have with one another, or what variant forms by which they might be mentioned in the literature, or any subset or combination of these.
 - **Statistical or machine-learning-based approaches** operate by building classifiers that may operate on any level, from labelling part of speech to choosing syntactic parse trees to classifying full sentences or documents.

1.4 Natural Language Processing

NLP – Natural Language Processing is a field of computer science and linguistics concerned with the interactions between computers and human (natural) languages. Natural language generation systems convert information from computer databases into readable human language.

1.5 Text-mining in molecular biology, BioNLP

Text-mining in molecular biology is defined as the automatic extraction of information about genes, proteins and their functional relationships from text documents. Some applications of NLP techniques in biology (which is sometimes called Biomedical Natural Language Processing – BioNLP) can include:

- **bio-entity recognition, protein/gene normalization, interaction extraction and many others.**
- A major problems dealing with NLP tasks is Text segmentation.

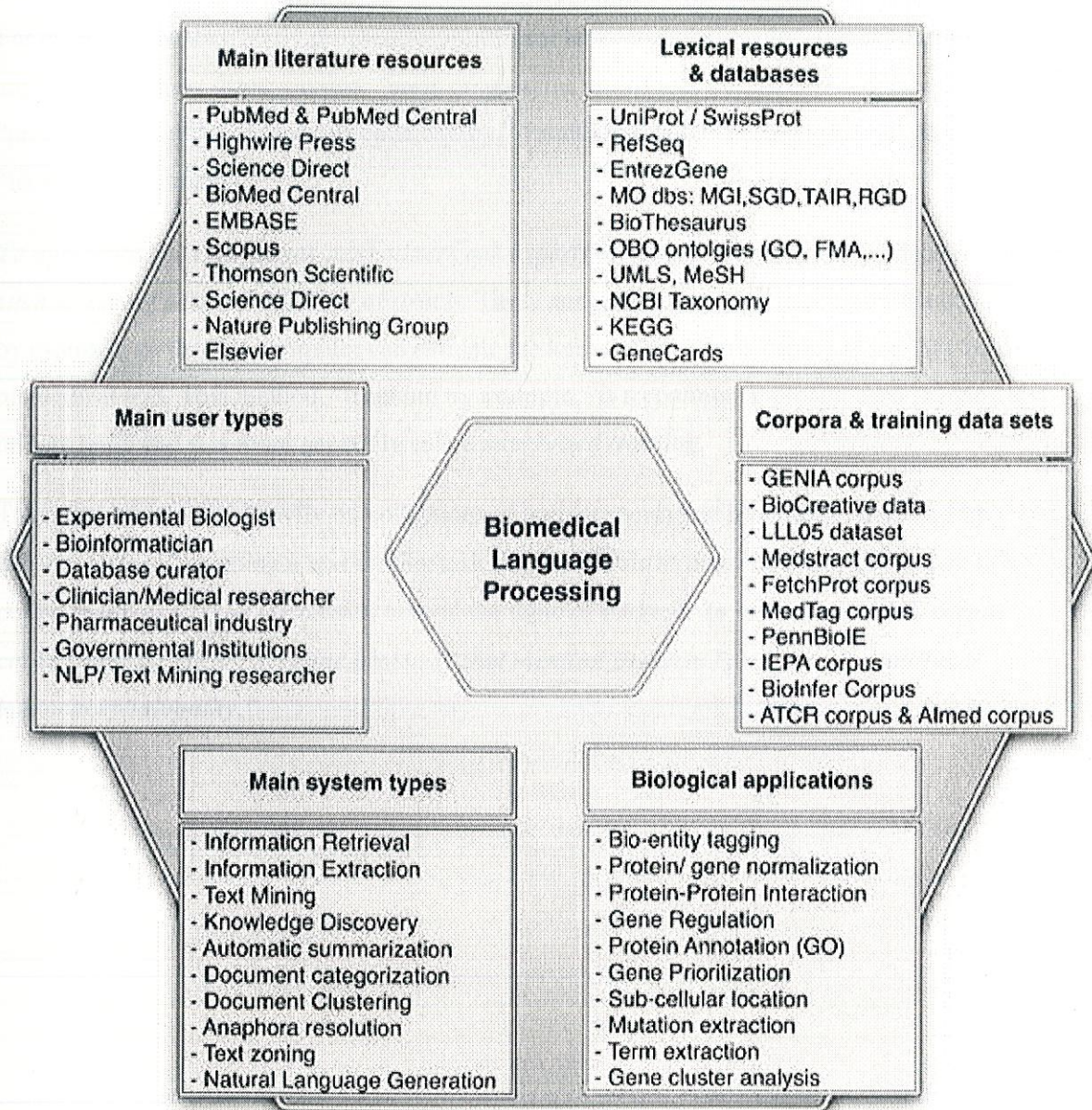
1.6 Natural Language Processing Technique

The fundamental problem is the fact, that a particular meaning may be expressed using different but largely synonymous expressions,

- For example, the information about the interaction between the proteins AKT and GSK-3 can be expressed in many ways, such as: AKT protein phosphorylates GSK-3 enzyme; the phosphorylation of GSK-3 by AKT and GSK-3 is inhibited by AKT.

So, The NLP techniques need to somehow 'decode' the information that is packaged in human language.

1.7 Literature Sources Diagram



1.8 Biomedical Text Mining And Its Practical Applications

For example, the text “early progressive multifocal leukoencephalopathy” could possibly refer to any, or all, of these disease terms: “early progressive multifocal leukoencephalopathy,” “progressive multifocal leukoencephalopathy,” “multifocal leukoencephalopathy,” and “leukoencephalopathy.”

To overcome such dilemmas, text miners ask experts to identify terms within collections of text such as sets of selected Medline abstracts. These annotations are then used to train a computer by example, so that the computer can emulate the knowledge experts deploy when they read biomedical text. This method, “teaching by example,” is a common approach used in many text mining tasks and it is more generally called *supervised training*.

Thus, text miners rely heavily on collections of text (corpora) that have been annotated by experts. Before beginning a text mining task, it is advisable to limit the scope of the task to a corpus made of a set of documents around the topic of interest. *In our case, a PML corpus could comprise all the Medline abstracts that mention the term “progressive multifocal leukoencephalopathy,”*

Chapter 2 –

Text Mining

2.1 What Text Miners are Interested In !

- ☐ Terms
- ☐ Relationships
- ☐ Discovery
- ☐ Quality
- ☐ Comprehensiveness

2.1.1 Terminologies

Text miners are interested in terminologies that are more than just a flat list of terms. Some include term synonyms or relations between terms (taxonomies, ontologies).

For text miners, their usefulness comes from their ability to link to information. Once a text is mapped to one of these terminologies, a bridge is opened between the text and other resources been built manually.

This usefulness justifies efforts such as the National Library of Medicine's manual mapping of Medline abstracts to the Medical Subject Headings (MeSH) terminology. *In our example, MeSH can be used to make the PML corpus more focused by restricting it only to abstracts with the MeSH term "leukoencephalopathy, progressive multifocal."*

2.1.2 Relationships

After recognizing terms, the natural next step is to look for relationships between terms.

The simplest method to identify relationships is using the *co-occurrence* assumption: terms that appear in the same texts tend to be related. For example, if a protein is mentioned often in the same abstracts as a disease, it is reasonable to hypothesize that the protein is involved in some aspect of the disease.

The degree of co-occurrence can be quantified statistically to rank and eliminate statistically weak co-occurrences. *An example using GoGene illustrate the use of simple co-occurrence, the query "leukoencephalopathy, progressive multifocal" in GoGene returns all the genes mentioned in Medline abstracts annotated for PML. The genes that appear most often are likely to be related to PML.*

2.1.3 Discovery

Besides finding relationships, text miners are also interested in *discovering* relationships. **Due to the size of the literature, scientists miss links between their work and other, related work.** Swanson called these links "undiscovered public knowledge."

One method to discover relationships is based on transitive inference. Simply stated, if A is linked to B, and B is linked to C, then there is a chance that A is linked to C.

2.1.4 Quality

The most common measure of output quality in text mining is the F-measure, which is the harmonic mean of two other measures, precision and recall. Both high precision and high recall are desirable, and a high F-measure reflects both because it is the harmonic mean.

Moreover, text mined applications may perform differently in different types of text and this may be reflected in lower F-measures than advertised. When the F-measure attainable is not high enough, one solution is to use text mining as a filter. Filtering with text mining is used as a preliminary step in databases such as MINT , DIP, and BIND.

2.1.5 Comprehensiveness

Doing comprehensive text mining means considering all sources of information—Medline and beyond.

The abstract conveys an article's main findings, but many other pieces of information are elsewhere in the full text, figures, tables, supplementary information, references, databases, Web sites, and multimedia files.

A search for “progressive multifocal leukoencephalopathy” in the Yale Image Finder yields only one figure, while a search for “PML” yields a large number of hits, most of them not relevant because PML is an ambiguous term.

Chapter 3 -

Vector Space Model

3.1 What is a Vector Space Model ?

Vector space model (or term vector model) is an algebraic model for representing text documents (and any objects, in general) as vectors of identifiers, such as, for example, index terms.

It is used in information filtering, information retrieval, indexing and relevancy rankings. Its first use was in the SMART Information Retrieval System.

3.2 Stages Of Vector Space Model

The vector space model procedure can be divided in to three stages -

- The **first stage** is the document indexing where content bearing terms are extracted from the document text.
- The **second stage** is the weighting of the indexed terms to enhance retrieval of document relevant to the user.
- The **last stage** ranks the document with respect to the query according to a similarity measure.

3.2.1 First Stage- Document Indexing

It is obvious that many of the words in a document do not describe the content, words like *the, is*. By using **automatic document indexing** those non significant words (function words) are removed from the document vector, so the document will only be represented by content bearing words .

This indexing can be based on term frequency, where terms that have both high and low frequency within a document are considered to be function words . **Use of a stop list which holds common words to remove high frequency words (stop words).**

In general, 40-50% of the total number of words in a document are removed with the help of a stop list. **Non linguistic methods** for indexing have also been implemented. **Probabilistic indexing** is based on the assumption that there is some statistical difference in the distribution of content bearing words, and function words.

Probabilistic indexing **ranks the terms in the collection w.r.t. the term frequency** in the whole collection. The **function words are modeled by a Poisson distribution** over all documents, as content bearing terms cannot be modeled.

3.2.2 Second Stage- Term Weighting

There are three main factors term weighting:

term frequency factor, collection frequency factor and length normalization factor.

These three factor are multiplied together to make the resulting term weight.

Collection frequency document : These assume that the importance of a term is proportional with the number of document the term appears in ,and leads to a more effective retrieval, i.e., an improvement in precision and recall.

The third possible weighting factor is a **document length normalization factor**. Long documents have usually a much larger term set than short documents, which makes long documents more likely to be retrieved than short documents.

3.2.3 Third Stage- Similarity Coefficients

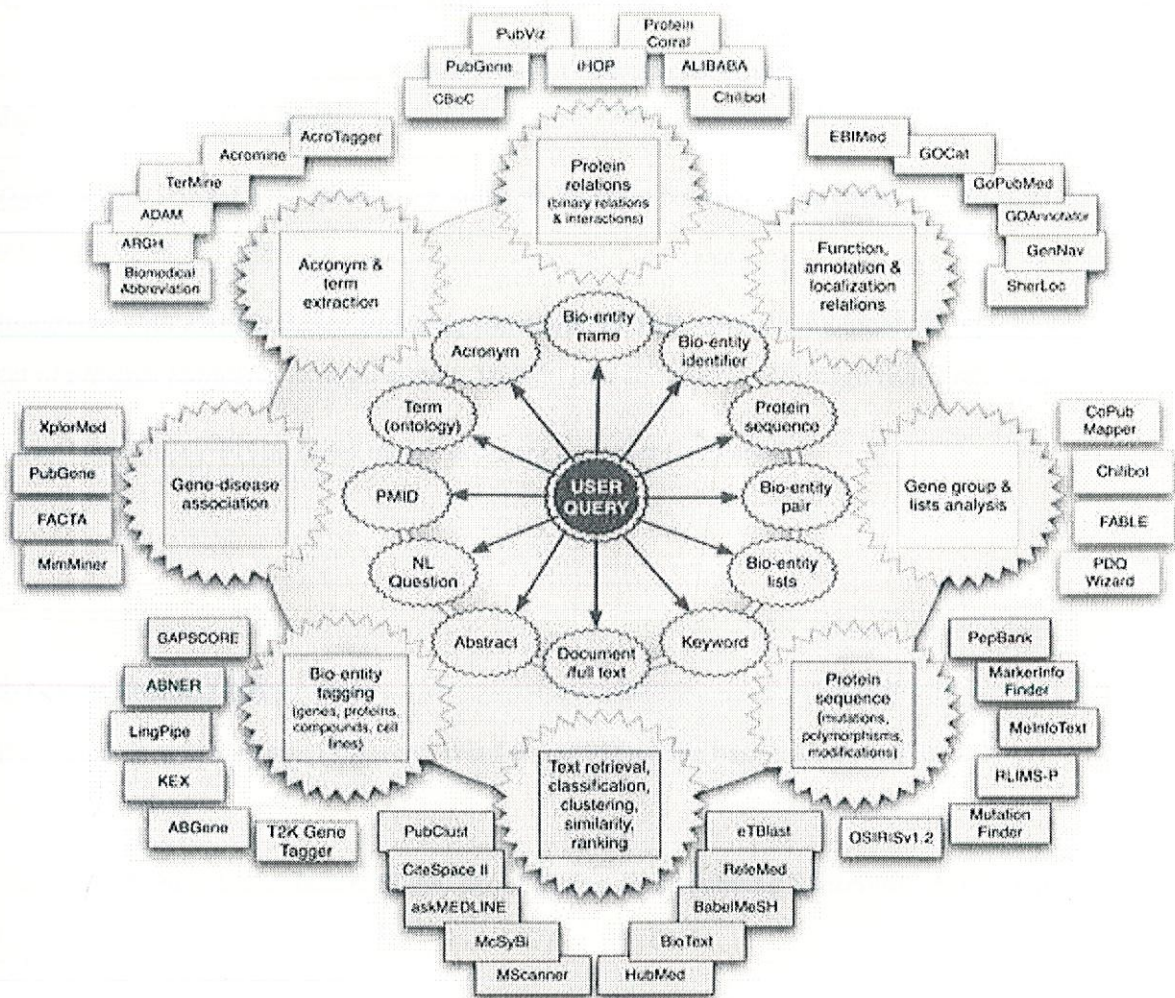
The **similarity in vector space models** is determined by using associative coefficients based on the inner product of the document vector and query vector, where word overlap indicates similarity. The inner product is usually normalized.

The most popular similarity measure is the **cosine coefficient**, which measures the angle between the a document vector and the query vector.

$$\text{cosine} [\{ (|v_1| \cdot |v_2|) / (|v_1| \times |v_2|) \}]$$

Other measures are e.g., Jaccard and Dice coefficients.

3.2.4 User Query Diagram



Chapter 4 –

Query Extension Technique and Vector Space Models

4.1 Query Extension Technique (knowledge based)-

Through Query Extension Technique Document Retrieval easy/improved, because it matches the document Index terms better.

Query with, General concept terms → subst. → Specific concept terms (used in corpus, mined, co-occur, relevant to doc.'s).

Integrated with *Phrase Based indexing technique (VSM)*, where a document is represented as a set of *phrases (concepts + word stems)*, leading to a complete knowledge based retrieval.

Thus, User Query → (via. Indexing) → efficient document retrieval.

4.2 Stem Based VSM-

It is based on **word stems**. Different word stems means the base vectors will be ORTHOGONAL.

The major Limitation of Indexing via. Word Stems is searching Synonyms, hypernyms, hyponyms in documents..

- *Doc (VSM) → vector (of terms)*
- *Wts. Of terms, ← importance of that term, in doc.*
- Stemming: {edema, edemas} → stem word.
- Word Stems in our query-

{hyperthermia},{leukocytosis}, {increased}, {intracranial}, {pressure}.....

The weight of a word stem u in a document a is determined by $W(a,u)$, where a is the document and, u is the word stem, number of times u appears in a is **term frequency**. Similarly, number of documents that contain u is **document frequency**.

- *more often u appears in a , the more important u is in a .*
- *more documents u belongs to, the less important it is.*

4.3 Concept Based VSM

Uses *concepts* instead of single words or word stems, and produces a VSM that better mimics the human thought processes .

Eg. - "increased intracranial pressure"

- stems "increas," "intracran," and "pressur."
- inappropriate fragmentation of concepts.
- concepts represented by, multi-word phrases such as "increased intracranial pressure."

Limitation of Concept Based Vector Space Model is incomplete/quality knowledge resources.

- {Conceptual similarities, derived from knowledge sources}
- *Concepts based, → base v's. of concepts*, Orthogonal

→related, acute angle b/w them.

- Phrases → *synonymous (repr. 1 concept)*

→polysemous (repr. >1 concept)

The **cosine of the angle** between two concept vectors is defined as the **conceptual similarity**, between the corresponding concepts, (0-1). So, 0 → unrelated → Orthogonal.



- $W_t, W(a, X_i) \rightarrow$ *ith concept X_i in a document a .*

Longer Phrase means high weight, so more specific concepts. For Example, “increased intracranial pressure” and “hyperthermia” are identical, but the former concept would obtain a higher weight than the latter.

4.4 Phrase-based VSM

Previous Concept based VSM, treats “cerebral edema” and “cerebral lesion” as unrelated, so, is potentially harmful. Noticing their common component word “cerebral” in the above phrases, **phrase-based VSM** is there to remedy the incompleteness of the knowledge sources.

- In phrase-based VSM, a **document** \rightarrow **represented** \rightarrow **set of phrases.**
- **phrase** \rightarrow **multiple concepts, and several word stems.**

Thus the Advantage of Phrase Based Vector Space Model is that it removes problem of incomplete knowledge.

- So, doc. \rightarrow parse into \rightarrow phrases (based on conceptual Terms)
- *Similarity b/w doc.'s \rightarrow sim. b/w concepts and common word stems.*

Similarity of two documents α and β , is the cosine of the angle between their document vectors. And Conceptual Similarity, i.e b/w i .th concept X_i in α , j .th con. Y_j in β , is the Conceptual contribution to the similarity between two phrases calculation, i.e taking all possible concept pairs into account, where each pair consists of one concept from each phrase.

- $S(X_i, Y_j) \rightarrow$ conc. sim. \rightarrow dist. b/w X & Y concepts.
- $S(X, Y) \rightarrow$ conc. sim. is inversely proportional to the $d(X, Y)$.
- *or, $S(X, Y) \rightarrow 1/\log(\text{no. of descendants of the two}).$*

Example, a general concept like “disease” has much more descendants than a more specific concept like “hyperthermia” has.

Chapter 5 -

The Test Set, OHSUMED

Ohsuned, is the Test Collection comprising of -

- Reference → MEDLINE → title, abstract, author inf.
- Query → patient description.
- Judgement → relevant references.

The Knowledge Source-

- UMLS → medical lexical knowledge source.
→ lexical and semantic network → VSM

5.1 Phrase Detection-

Given a set of documents (106 queries and 14K), detect any occurrences in a set of phrases. First, detects *all occurrences* of any phrase in a document, and *only keep the longest, most specific phrase*.

Example- although both “edema” and “cerebral edema”, are detected in the sample query, keep only the latter and ignore the former.

5.2 VSM models, accuracy-

- Retrieval accuracy → calc. → Precision-Recall

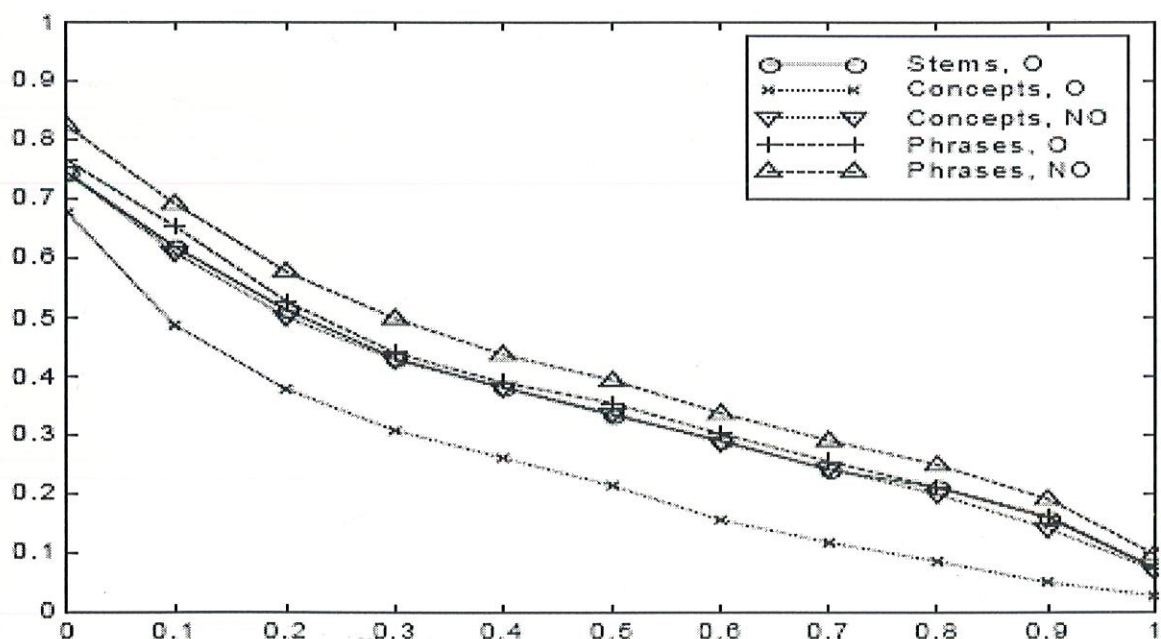
➤ VSM → doc.'s → doc. similarity (14k doc.'s, 105 q.'s)

Rank the documents from the most to the least similar to the query. When a certain number of documents are retrieved, *precision* is the percentage of retrieved documents that are relevant; and *recall* is the percentage of the (relevant/irrelevant) documents that has been retrieved so far.

So, the evaluation of the retrieval accuracy is done by interpolating the precision values at eleven recall points. The overall effectiveness of different VSM can be compared by averaging over the performance of all the 105 queries.

5.2.1 Avg. precision recall comparison-

Effectiveness of VSM Diagram



Comparisons of VSM-

- Stem based VSM-

11 pts. Avg. Precision= 0.363

- **Concept based VSM-**

Precision= 0.260

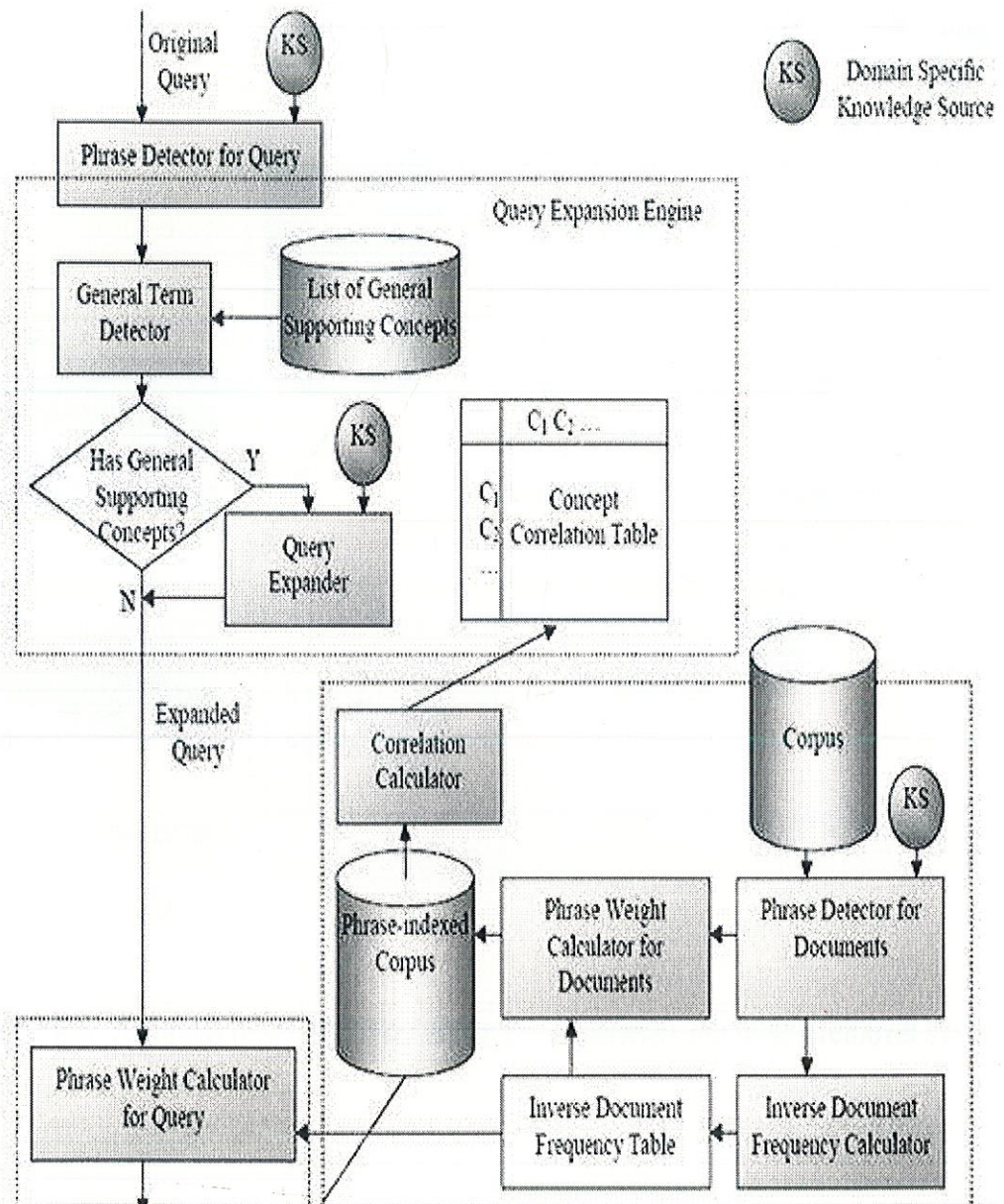
- **Phrase based VSM-** (concepts & word stems)

- Precision=0.420

So, there is 16% improvement in Retrieval Accuracy, the best of the lot.

Chapter 6 –

The Flow Diagram-



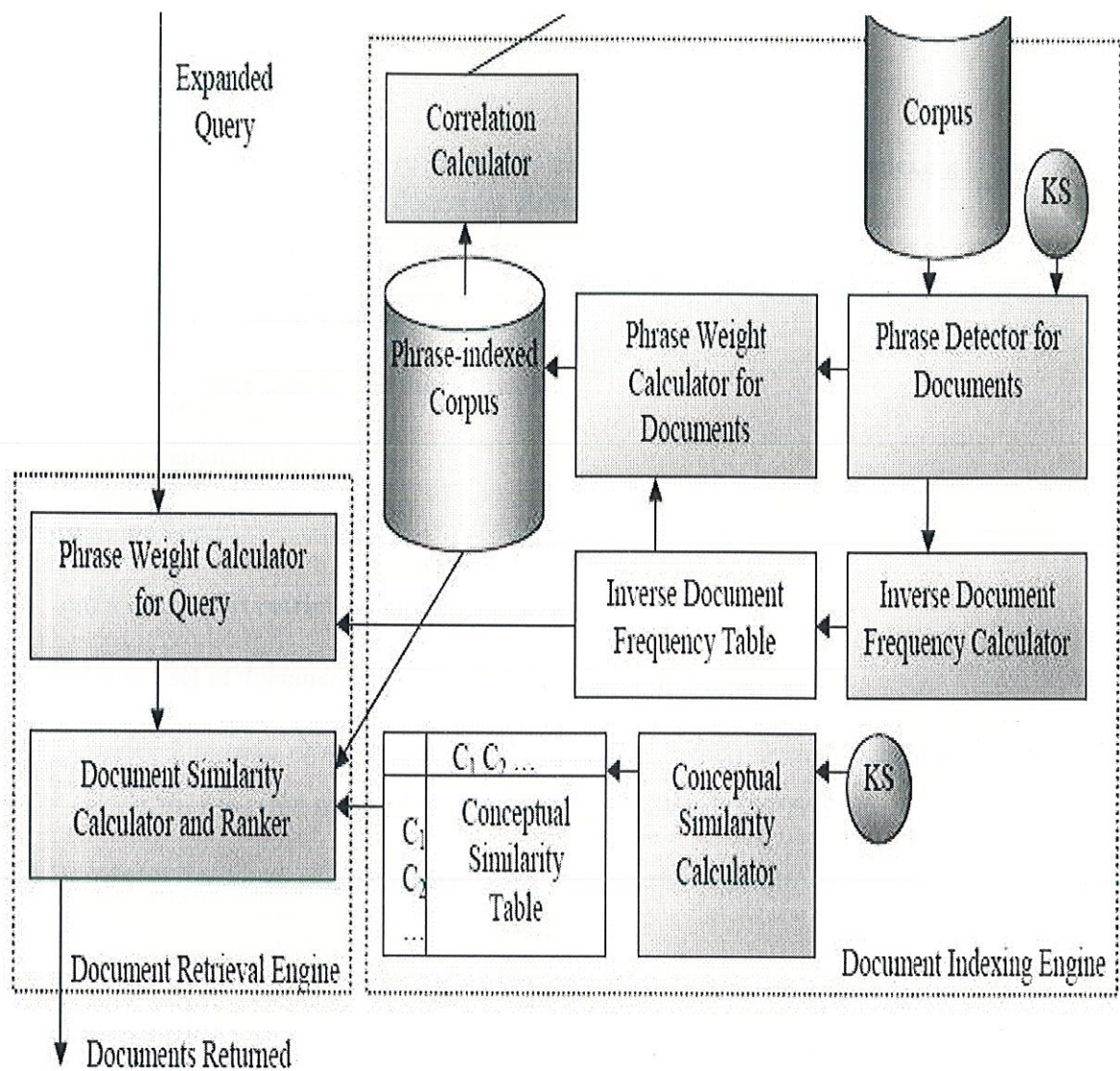


Figure 3. A phrase based indexing and query expansion document retrieval system.

6.1 Integration + Working-

Integration of knowledge based Query Extension technique and Phase based indexing is done because it gives the best accuracy of document Retrieval.

It consists of three subsystems:

- a document indexing engine,

(knowl. based, create data str. for the nxt two)

- a query expansion engine,

(expands the query)

- and a document retrieval engine,

- (returns a set of documents relevant to the user)

Working- query → phrases → (general c. terms → specific c. terms) → small size query, retrieval better → phrase wt. calc. , for query → ranking based on similarity measure

→ Document Retrieval. (Phrase based VSM)

6.2 Inverted Index-

Let's take the Doc.'s for Indexing..

- D1: The GDP increased 2 percent this quarter.
- D2: The spring economic slowdown continued to spring downwards this quarter.

- 2 ->[D1]
- continued ->[D2]
- downwards -> [D2]
- economic -> [D2]
- GDP -> [D1]
- increased -> [D1]
- percent -> [D1]
- quarter ->[D1] à [D2]
- slowdown -> [D2]
- spring -> [D2]
- the -> [D1] -> [D2]
- this ->[D1] -> [D2]
- to -> [D2]

D1	
documentID	1
distinctTerms	
term	tf
increased	1
quarter	1
2	1
gdp	1
percent	1

D2	
documentID	2
distinctTerms	
term	tf
spring	2
quarter	1
economic	1
slowdown	1
continued	1

Inverted Index, Document 1 –

Index			
increased	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1
1	1		
quarter	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1
1	1		
two	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1
1	1		
GDP	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1
1	1		
percent	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1
1	1		

6.2.1 Inverted Index for added documents

Index					
increased	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1		
1	1				
quarter	→ <table><tr><td>1</td><td>1</td></tr></table> → <table><tr><td>2</td><td>1</td></tr></table>	1	1	2	1
1	1				
2	1				
two	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1		
1	1				
GDP	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1		
1	1				
percent	→ <table><tr><td>1</td><td>1</td></tr></table>	1	1		
1	1				
spring	→ <table><tr><td>2</td><td>2</td></tr></table>	2	2		
2	2				
economic	→ <table><tr><td>2</td><td>1</td></tr></table>	2	1		
2	1				
slowdown	→ <table><tr><td>2</td><td>1</td></tr></table>	2	1		
2	1				
continued	→ <table><tr><td>2</td><td>1</td></tr></table>	2	1		
2	1				

Chapter 7 –

Appendix

7.1 For building inverted index in Perl –

```
print "Search\t";

$search=<stdin>;

chomp($search);

#$search=uc($search);

@stoplist=qw(is an the with or between are not has had but can many what when who in it where
when why on);

@search=split("\s+",$search);

for($i=0;$i<scalar(@stoplist);$i++)
{
    for($j=0;$j<scalar(@search);$j++)
    {
        if ($stoplist[$i] eq $search[$j])
        {
            splice(@search,$j,1);
        }
    }
}

$dirtoget="prj4";

opendir(prj4, $dirtoget) || die("Cannot open directory");
```

```

@thefiles= readdir(prj4);

closedir(prj4);

%it=();

foreach $f (@thefiles)
{
    unless ( ($f eq ".") || ($f eq "..") )
    {
        %l=NULL;

        open(F1,"./prj4/"$.f);

        $data=<F1>;

        close (F1);

        open(F2,">./results/"$.f);

        for($i=0;$i<scalar(@search);$i++)
        {
            $l{$search[$i]}=0;

            $l{$search[$i]}=($data=~tr/$search[$i]/);

            if($l{$search[$i]} eq "")
            {
                $l{$search[$i]}=0;
            }

            print "\t$search[$i]=>$l{$search[$i]}\t\t";
        }
    }
}

```



```

        print F2      "\t$search[$i]=>$l{$search[$i]}\t\n";
    }

    $total=0;

    close(F2);

    foreach $key(keys%l)
    {

        $total=$total+$l{$key};

    }

    $it{$f}=$total;

    }

    print "\n\n\n"

}

print "the identification table list";

foreach my $key(sort {$it{$b} <=> $it{$a}} keys %it)
{

    print "\n".$key . "=> " . $it{$key};

}

◇;

```

7.1.1 Results in cmd -

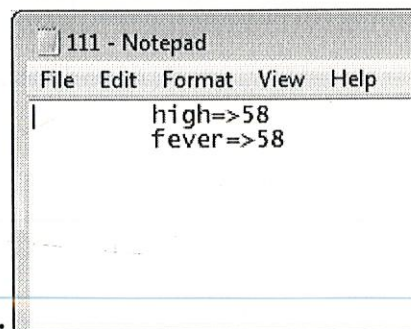
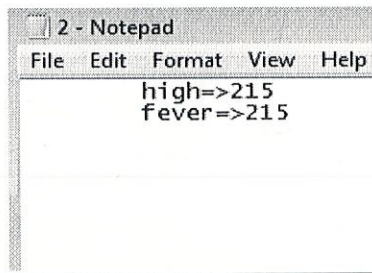
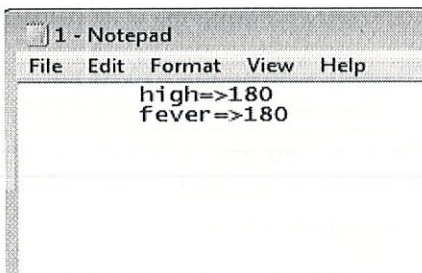
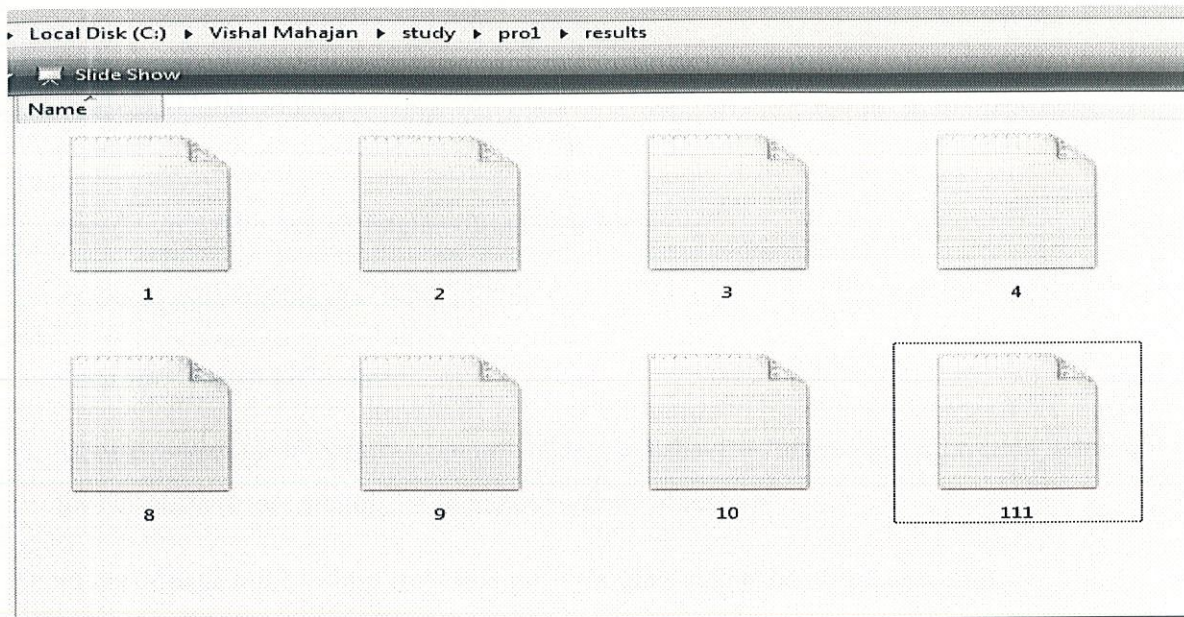
```
C:\Windows\system32\cmd.exe - pro3.pl
Microsoft Windows [Version 6.0.6000]
Copyright (c) 2006 Microsoft Corporation. All rights reserved.

C:\Users\wisha>cd Desktop
C:\Users\wisha\Desktop>cd pro1
C:\Users\wisha\Desktop\pro1>pro3.pl
Search the high fever

high=>180 fever=>180
high=>104 fever=>104
high=>58 fever=>58
high=>215 fever=>215
high=>3 fever=>3
high=>129 fever=>129
high=>0 fever=>0
high=>129 fever=>129
high=>62 fever=>62
high=>145 fever=>145
high=>126 fever=>126

the identification table list
2.txt=> 430
1.txt=> 360
8.txt=> 290
6.txt=> 258
4.txt=> 258
9.txt=> 252
10.txt=> 208
7.txt=> 124
11.txt=> 116
3.txt=> 6
5.txt=> 0
```


7.1.2 Results Directory –



7.2 Perl Programming with HTML –

7.2.1 Main HTML page –

[illegible]

SEARCH PAGE –

```
<html>

<head><title>Bio Search Engine</head></title>

<body bgcolor=CC9900>

<marquee behavior="alternate"></marquee><br>

<br>

<font size=6 color=990000> <center> <marquee behavior="alternate">A inverted index tool for
bio-medical text mining...</marquee></font> </center>

<a href="page1.html"></a>&nbsp;

<a href="define.html"></a>&nbsp;

<a href="line.html"></a>&nbsp;

<a href="sym.html"></a>&nbsp;

<a href="contact.html"></a><br><br>

<form action="http://localhost/cgi-bin/vishal/pro_v.cgi" method="get">

<input type="text" name="text" size="90"/></p>

<input type="submit" value="search"/>

</form>

</body>

</html>
```


DEFINITION SEARCH –

```
<html>

<head><title>Bio Search Engine</head></title>

<body bgcolor=CC9900>

<marquee behavior="alternate"></marquee><br>

<br>

<font size=6 color=990000> <center> <marquee behavior="alternate">A inverted index tool for
bio-medical text mining...</marquee></font> </center>

<a href="page1.html"></a>&nbsp;

<a href="define.html"></a>&nbsp;

<a href="line.html"></a>&nbsp;

<a href="sym.html"></a>&nbsp;

<a href="contact.html"></a><br><br>

<form action="http://localhost/cgi-bin/vishal/vis_define.cgi" method="get">

<p><font size=4 color=990000><b>D</b>efine</font><input type="text" name="text"
size="90"/></p>

<input type="submit" value="search"/>

</form>

</body>

</html>
```

SEARCH BY LINE –

```
<html>

<head><title>Bio Search Engine</head></title>

<body bgcolor=CC9900>

<marquee behavior="alternate"></marquee><br>

<br>

<font size=6 color=990000> <center> <marquee behavior="alternate">A inverted index tool for
bio-medical text mining...</marquee></font> </center>

<a href="page1.html"></a>&nbsp;

<a href="define.html"></a>&nbsp;

<a href="line.html"></a>&nbsp;

<a href="sym.html"></a>&nbsp;

<a href="contact.html"></a><br><br>

<form action="http://localhost/cgi-bin/vishal/vis_line.cgi" method="get">

<p><font size=4 color=990000><b>S</b>earch By Line</font><input type="text" name="text"
size="90"/ ></p>

<input type="submit" value="search"/>

</form>

</body>

</html>
```


SEARCH BY SYMPTOMS-

```
<html>

<head><title>Bio Search Engine</head></title>

<body bgcolor=CC9900>

<marquee behavior="alternate"></marquee><br>

<br>

<font size=6 color=990000> <center> <marquee behavior="alternate">A inverted index tool for
bio-medical text mining...</marquee></font> </center>

<a href="page1.html"></a>&nbsp;

<a href="define.html"></a>&nbsp;

<a href="line.html"></a>&nbsp;

<a href="sym.html"></a>&nbsp;

<a href="contact.html"></a><br><br>

<form action="http://localhost/cgi-bin/vishal/vis_sym.cgi" method="get">

<p><font size=4 color=990000><b>S</b>ympoms</font><input type="text" name="text"
size="90"/></p>

<input type="submit" value="search"/>

</form>

</body>

</html>
```

[illegible]

PAGE –

```
<html>

<head><title>Bio Search Engine</head></title>

<body bgcolor=CC9900>

<marquee behavior="alternate"></marquee><br>

<br>

<font size=6 color=990000> <center> <marquee behavior="alternate">A inverted index tool for
bio-medical text mining...</marquee></font> </center>

<a href="page1.html"></a>&nbsp;

<a href="define.html"></a>&nbsp;

<a href="line.html"></a>&nbsp;

<a href="sym.html"></a>&nbsp;

<a href="contact.html"></a><br><br>

<form action="http://localhost/cgi-bin/vishal/pro_v.cgi" method="get">

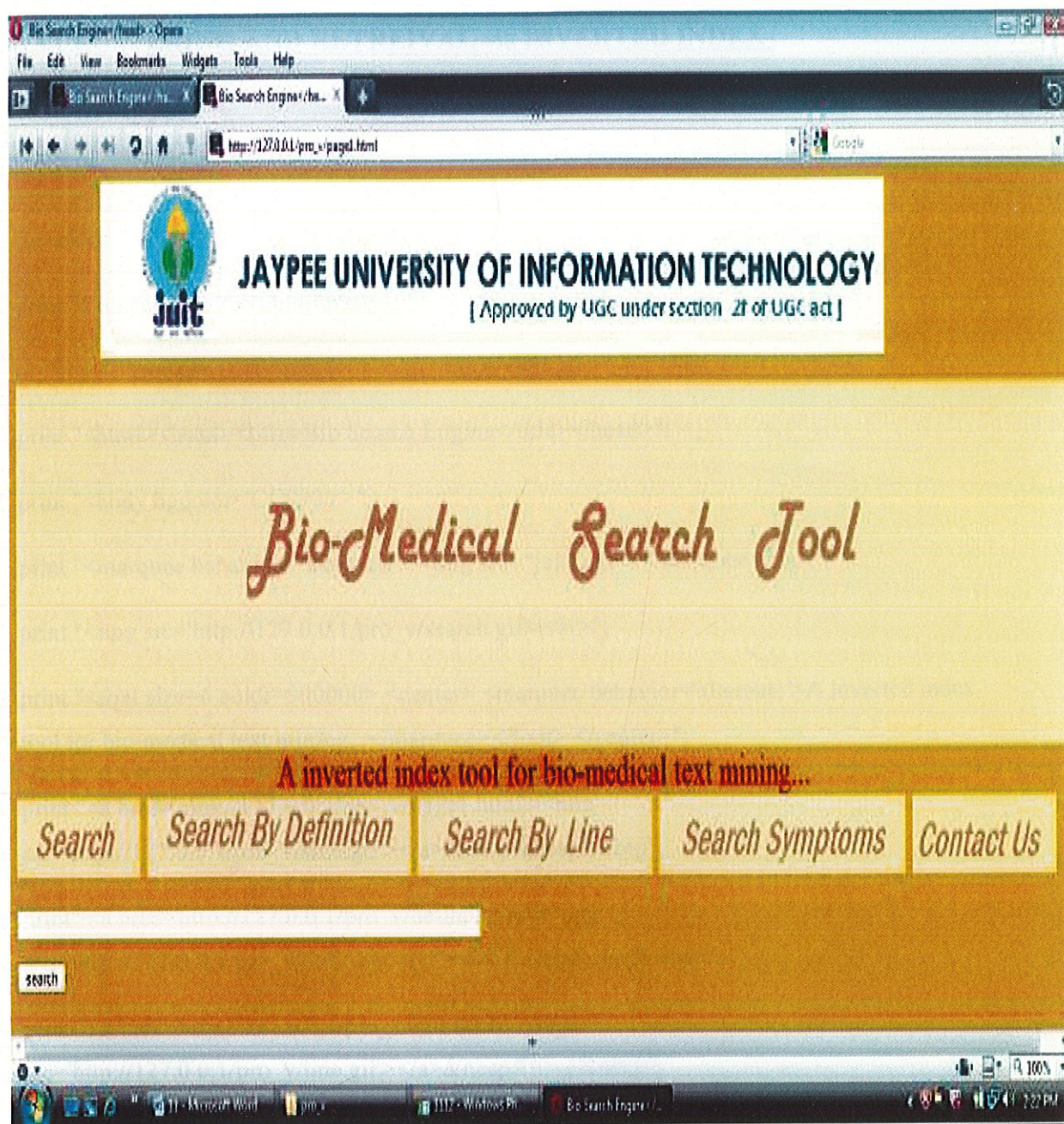
<input type="text" name="text" size="90"/></p>

<input type="submit" value="search"/>

</form>

</body>

</html>
```

7.3 CLUSTERING AND RETREIVAL via INVERTED INDEX-

```
#!/c:/Perl/bin/perl

use CGI;

use strict;

print "Content-type: text/html\n\n";

my $cgi=new CGI;

print "<html><head><title>Bio Search Engine</title></head>";

print "<body bgcolor='CC9900'>";

print "<marquee behavior='alternate'><img src='juil.gif'></marquee><br>";

print "<img src='http://127.0.0.1/pro_v/search.gif'><br>";

print "<font size=6 color=990000> <center> <marquee behavior='alternate'>A inverted index  
tool for bio-medical text mining...</marquee></font> </center>";

print "<a href='http://127.0.0.1/pro_v/page1.html'><img  
src='http://127.0.0.1/pro_v/srch.gif'></a>&nbsp;&nbsp;&nbsp;";

print "<a href='http://127.0.0.1/pro_v/define.html'><img  
src='http://127.0.0.1/pro_v/definition.gif'></a>&nbsp;&nbsp;&nbsp;";

print "<a href='http://127.0.0.1/pro_v/line.html'><img  
src='http://127.0.0.1/pro_v/line.gif'></a>&nbsp;&nbsp;&nbsp;";

print "<a href='http://127.0.0.1/pro_v/sym.html'><img  
src='http://127.0.0.1/pro_v/sym.gif'></a>&nbsp;&nbsp;&nbsp;";

print "<a href='http://127.0.0.1/pro_v/contact.html'><img  
src='http://127.0.0.1/pro_v/contact.gif'></a><br><br><br>";
```

```

my $search=$cgi->param("text");

$search=lc($search);

#print "<p>here1 $search</p>";

my @stoplist=qw(is an the with or between are not has had but can many what when who in it
where when why on );

my @search=split("\s+",$search);

for(my $i=0;$i<scalar(@stoplist);$i++)
{
    for(my $j=0;$j<scalar(@search);$j++)
    {
        if ($stoplist[$i] eq $search[$j])
        {
            splice(@search,$j,1);
        }
    }
}

foreach my $x(@search)
#{
    #print "<p>here2 $x</p>";
#}

my $dirtoget="C:/Users/vishal/Desktop/pro1/prj4";

opendir(prj4, $dirtoget) || die("Cannot open directory");

my @thefiles= readdir(prj4);

```



```

#foreach my $y(@thefiles)

#{

#print "<p>here3 $y</p>";

#}

closedir(prj4);

my %it=();

foreach my $f (@thefiles)

{

    unless ( ($f eq ".") || ($f eq "..") )

    {

        my %l=();

        open(F1,"C:/Users/vishal/Desktop/pro1/prj4/$f");

        my @data=<F1>;

        close (F;

        for(my $i=0;$i<scalar(@search);$i++)

        {

            $l{$search[$i]}=0;

            my $ref=0;

            foreach my $data1(@data)

            {

                my @data1=split('\s+', $data1);

```



```

        {

            $total=$total+$l{$key};

        }

        $it{$f}=$total;

    }

    print "<p></p><p></p><p></p><p></p>"

}

print "<table border=1 cellspacing=50 cellpadding=10>";

print "<tr align='center' valign='top'>";

print "<th><font color=990000><h2>Rank</font></h2></th>";

print "<th><font color=990000><h2>File Name</font></h2></th>";

print "<th><font color=990000><h2>weights</font></h2></th>";

print "</tr>";

my $rank=1;

foreach my $key(sort {$it{$b} <=> $it{$a}} keys %it)

{

    if($it{$key}!=0)

    {

        print "<tr align='center' valign='center'>";

        print "<td><font color=white>$rank</font></td>";

        print "<td><a href='http://127.0.0.1/pro_v/prj4/$key'>$key </a></td>";
    }
}

```

```
print "<td><font color=white>${$key}</font></td>";
```

```
$rank++;
```

```
}}
```

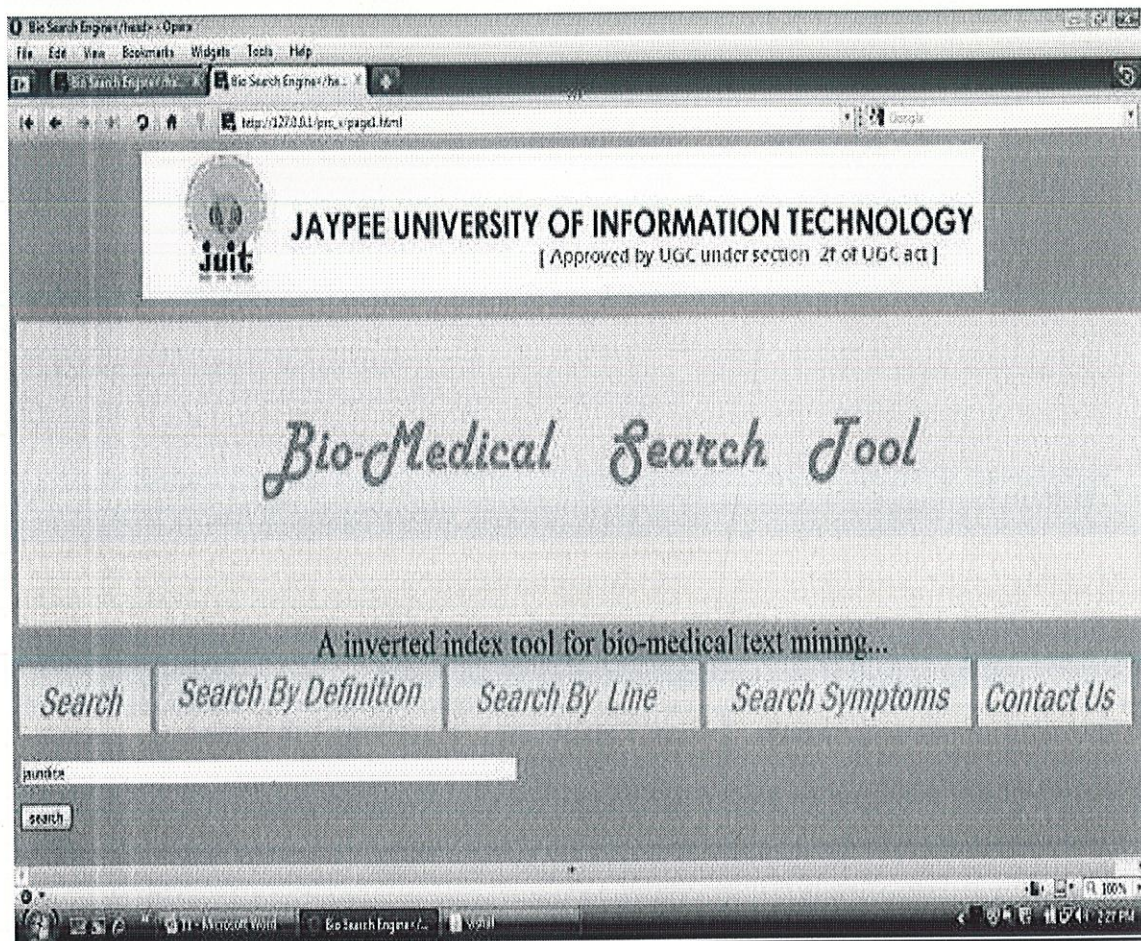
```
print"</table>";
```

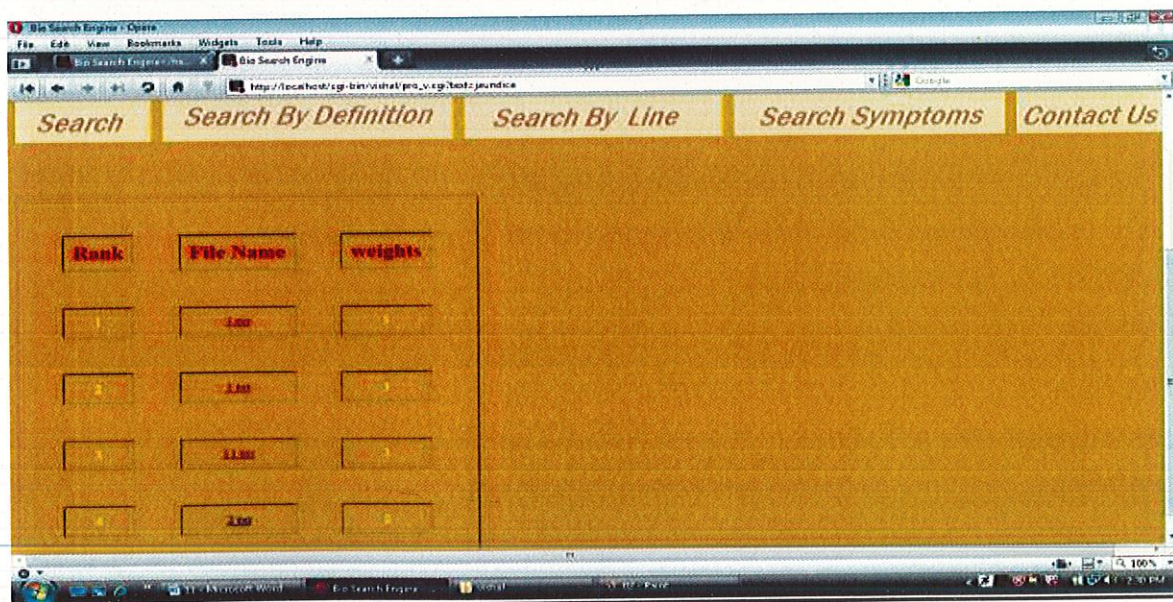
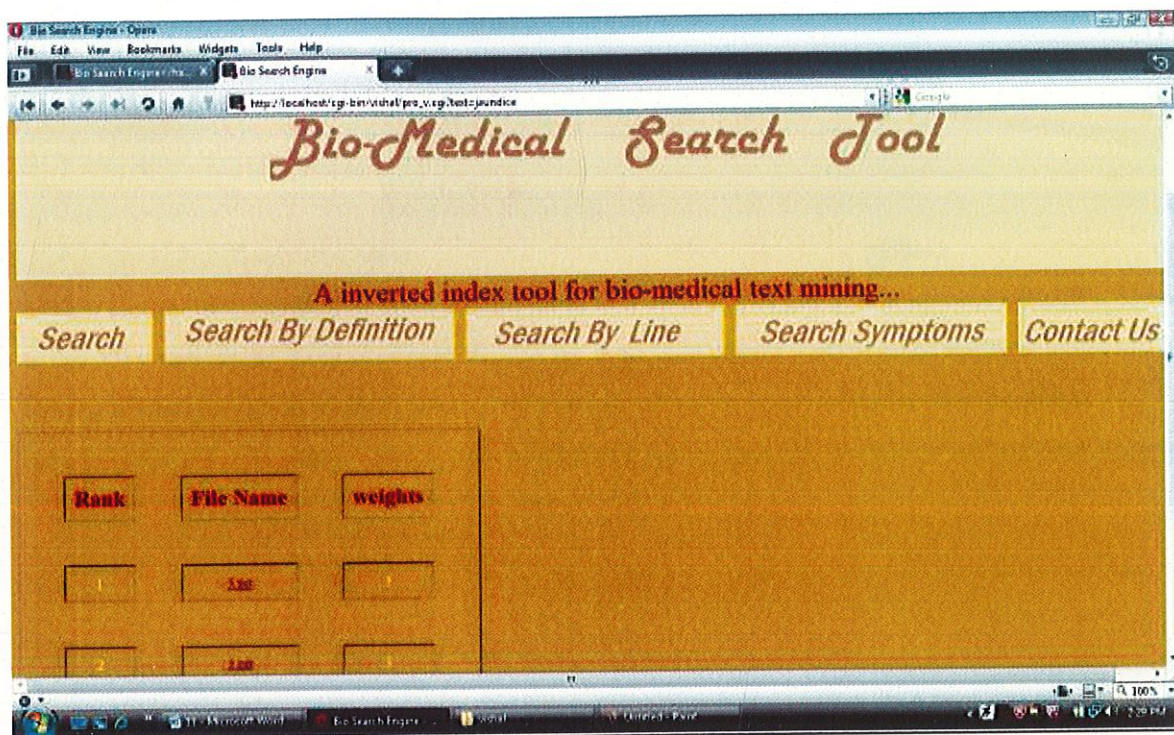
```
print "</body></html>";
```


Chapter 8 –

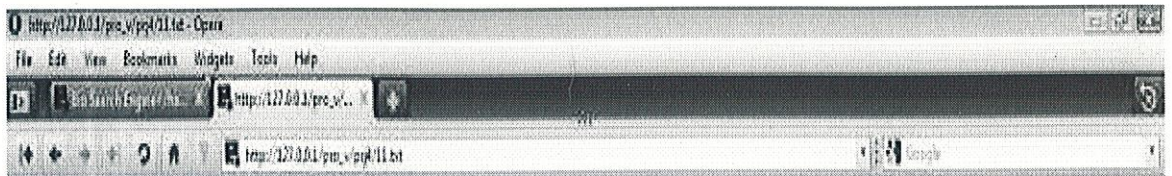
RESULTS AND CONCLUSIONS

8.1 Searching for a disease



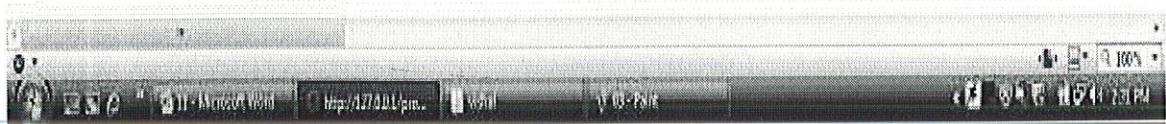


So the best retrieved document is read, henceforth-



Jaundice is a condition easily recognized by its symptoms of yellowed skin and sclera (the whites of the eyes), due to an accumulation of bilirubin in the body. Red blood cells live about 120 days then die and are flushed through the body. In this process, bilirubin is produced when the hemoglobin of red blood cells is broken down. Jaundice is not dangerous in itself but can indicate potentially serious underlying conditions that should be diagnosed and treated by a physician. Knowing how bilirubin is processed, causes for accumulation can be narrowed to one of three key possibilities, which create the three basic classes of jaundice:

- Pre-hepatic or hemolytic: Too many red blood cells are broken down.
- Hepatic: Liver does not process the bilirubin correctly.
- Post-hepatic or extrahepatic: Bile is unable to pass properly.



```
#!c:/Perl/bin/perl
```

use CGI;

```
use strict;
```

```
print "Content-type: text/html\n\n";
```

```
my $cgi=new CGI;
```

```
print "<html><head><title>Bio Search Engine</title></head>";
```

```
print "<body bgcolor='CC9900'>";
```

```
print "<marquee behavior='alternate'><img src='juit1.gif'></marquee><br>";
```

```
print "<img src='http://127.0.0.1/pro_v/search.gif'><br>";
```

```
print "<font size=6 color=990000> <center> <marquee behavior='alternate'>A inverted index  
tool for bio-medical text mining...</marquee></font> </center>";
```

```
print "<a href='http://127.0.0.1/pro_v/page1.html'><img  
src='http://127.0.0.1/pro_v/srcch.gif'></a>&nbsp&nbsp&nbsp&nbsp";
```

```
print "<a href='http://127.0.0.1/pro_v/define.html'><img  
src='http://127.0.0.1/pro_v/definition.gif'></a>&nbsp&nbsp&nbsp";
```

```
print "<a href=http://127.0.0.1/pro_v/line.html"><img  
src='http://127.0.0.1/pro_v/line.gif'></a>&nbsp&nbsp&nbsp";
```

```
print "<a href=http://127.0.0.1/pro_v/sym.html"><img  
src='http://127.0.0.1/pro_v/sym.gif'></a>&nbsp&nbsp&nbsp&nbsp";
```

```
print "<a href='http://127.0.0.1/pro_v/contact.html'><img  
src='http://127.0.0.1/pro_v/contact.gif'></a><br><br><br><br>";
```



```

my $search=$cgi->param("text");

$search=lc($search);

$search=$search.".txt";

open(F1,"C:/Users/vishal/Desktop/pro1/definitions/$search");

my @data=<F1>;

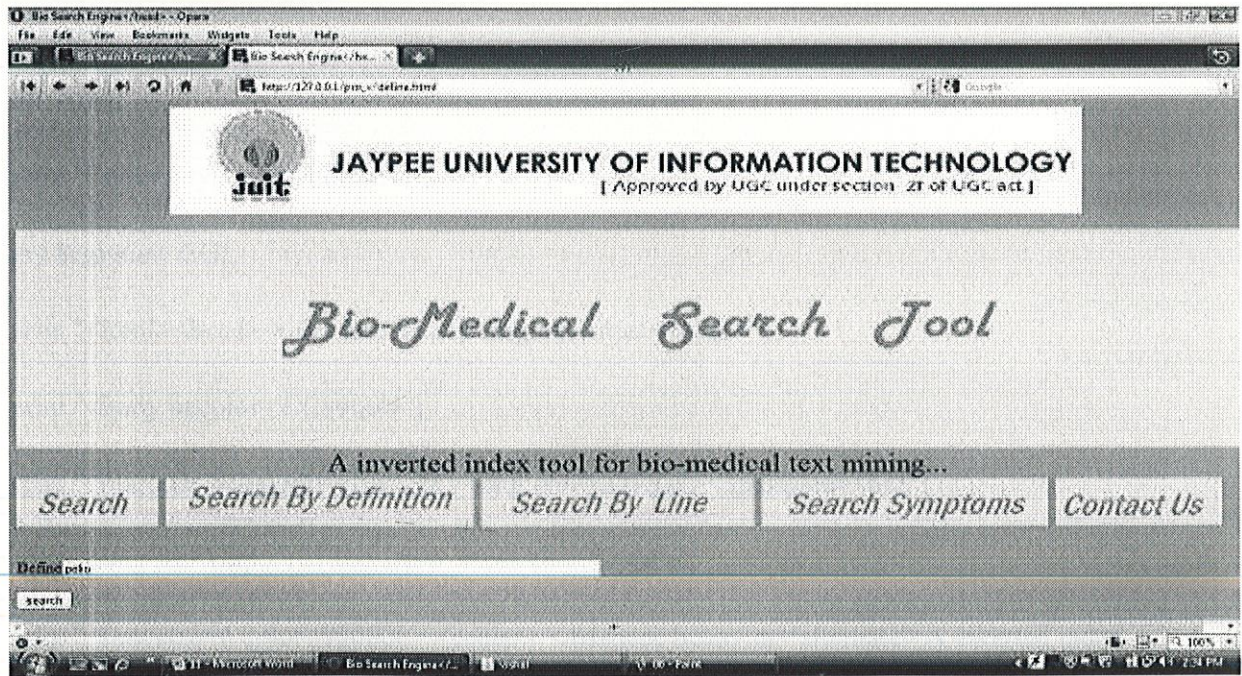
foreach my $d(@data)

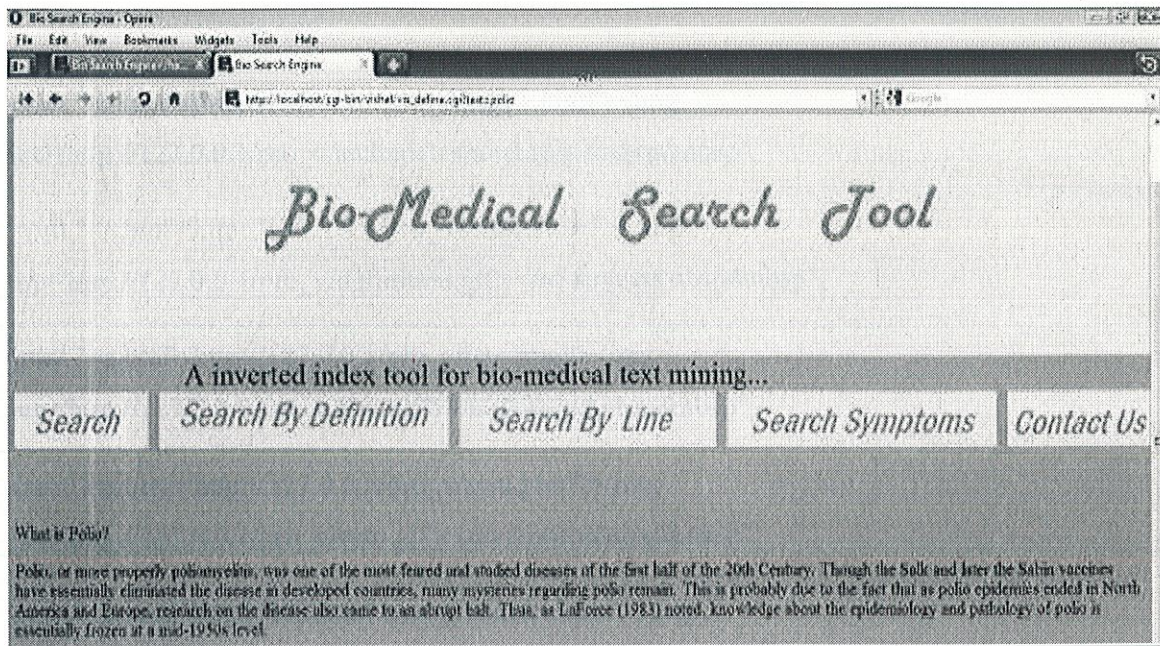
{
    print "<p><font size=4 color=990000>$d</p>";
}

print "</body></html>";

```

8.2 Searching for the definition





SEARCH BY LINE –

```
#!/c:/Perl/bin/perl
```

```
use CGI;
```

```
use strict;
```

```
print "Content-type: text/html\n\n";
```

```
my $cgi=new CGI;
```

```
print "<html><head><title>Bio Search Engine</title></head>";
```

```
print "<body bgcolor='CC9900'>";
```

```
print "<marquee behavior='alternate'><img src='juit1.gif'></marquee><br>";
```

```
print "<img src='http://127.0.0.1/pro_v/search.gif'><br>";
```

```
print "<font size=6 color=990000> <center> <marquee behavior='alternate'>A inverted index  
tool for bio-medical text mining...</marquee></font> </center>";
```



```

print "<a href='http://127.0.0.1/pro_v/page1.html'><img
src='http://127.0.0.1/pro_v/srch.gif'></a>&nbsp;&nbsp;&nbsp;";

print "<a href='http://127.0.0.1/pro_v/define.html'><img
src='http://127.0.0.1/pro_v/definition.gif'></a>&nbsp;&nbsp;&nbsp;";

print "<a href='http://127.0.0.1/pro_v/line.html'><img
src='http://127.0.0.1/pro_v/line.gif'></a>&nbsp;&nbsp;&nbsp;";

print "<a href='http://127.0.0.1/pro_v/sym.html'><img
src='http://127.0.0.1/pro_v/sym.gif'></a>&nbsp;&nbsp;&nbsp;";

print "<a href='http://127.0.0.1/pro_v/contact.html'><img
src='http://127.0.0.1/pro_v/contact.gif'></a><br><br><br><br>";

my $search=$cgi->param("text");

my $dirtoget="C:/Users/vishal/Desktop/pro1/prj4";

opendir(prj4, $dirtoget) || die("Cannot open directory");

my @thefiles= readdir(prj4);

closedir(prj4);

my %it=();

foreach my $f (@thefiles)

{

    unless ( ($f eq ".") || ($f eq "..") )

    {

        open(F1,"C:/Users/vishal/Desktop/pro1/prj4/$f");
    }
}

```

```

my @data=<F1>;

close (F1);

my $ref=0;

foreach my $data1(@data)
{
    if($data1=~/$search/g)
    {
        $ref++;
    }
}

$it{$f}=$ref;
}

}

print "<table border=1 cellpadding=10>";

print "<tr align='center' valing='top'>";

print "<th><font color=990000><h2>Rank</font></h2></th>";

print "<th><font color=990000><h2>File Name</font></h2></th>";

print "<th><font color=990000><h2>Weights</font></h2></th>";

print "</tr>";

my $rank=1;

foreach my $key(sort {$it{$b} <=> $it{$a}} keys %it)
{

```



```

if($it{$key}!=0)

{

print "<tr align='center' valign='center'>";

print "<td><font color=white>$rank</font></td>";

print "<td><a href='http://127.0.0.1/pro_v/prj4/$key'>$key </a></td>";

print "<td><font color=white>$it{$key}</font></td>";


$rank++;

}

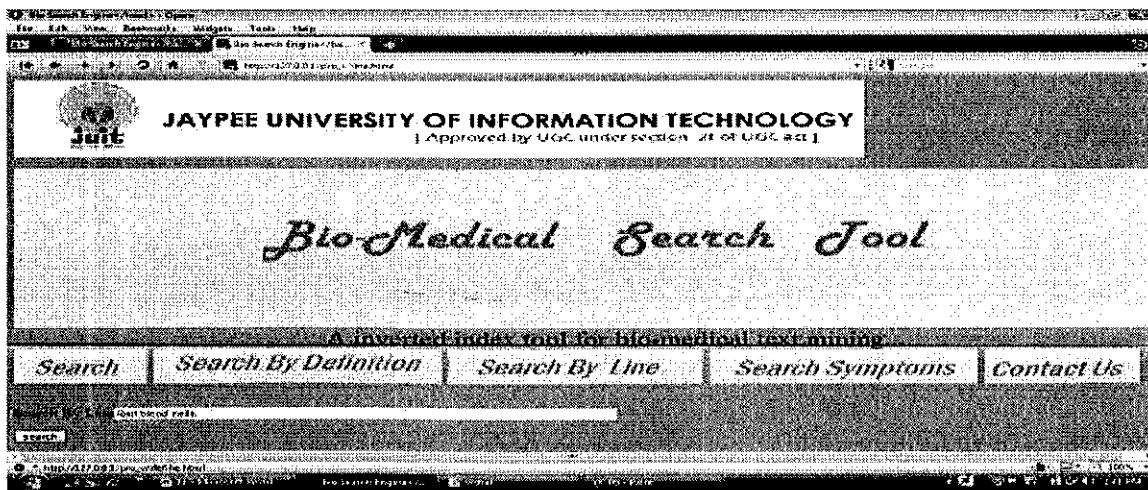
}

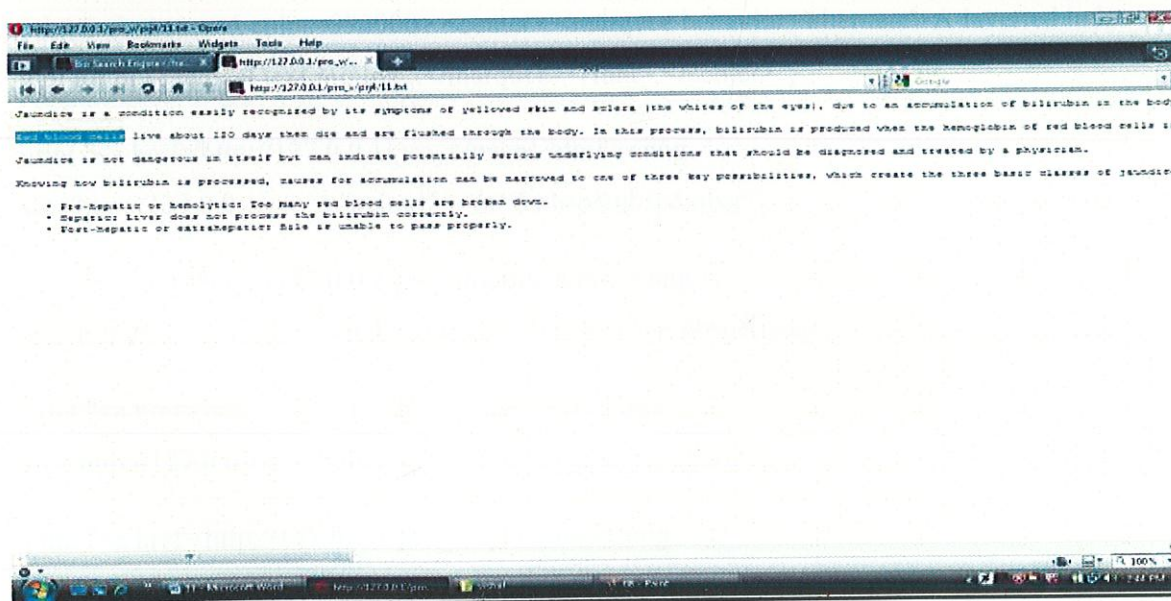
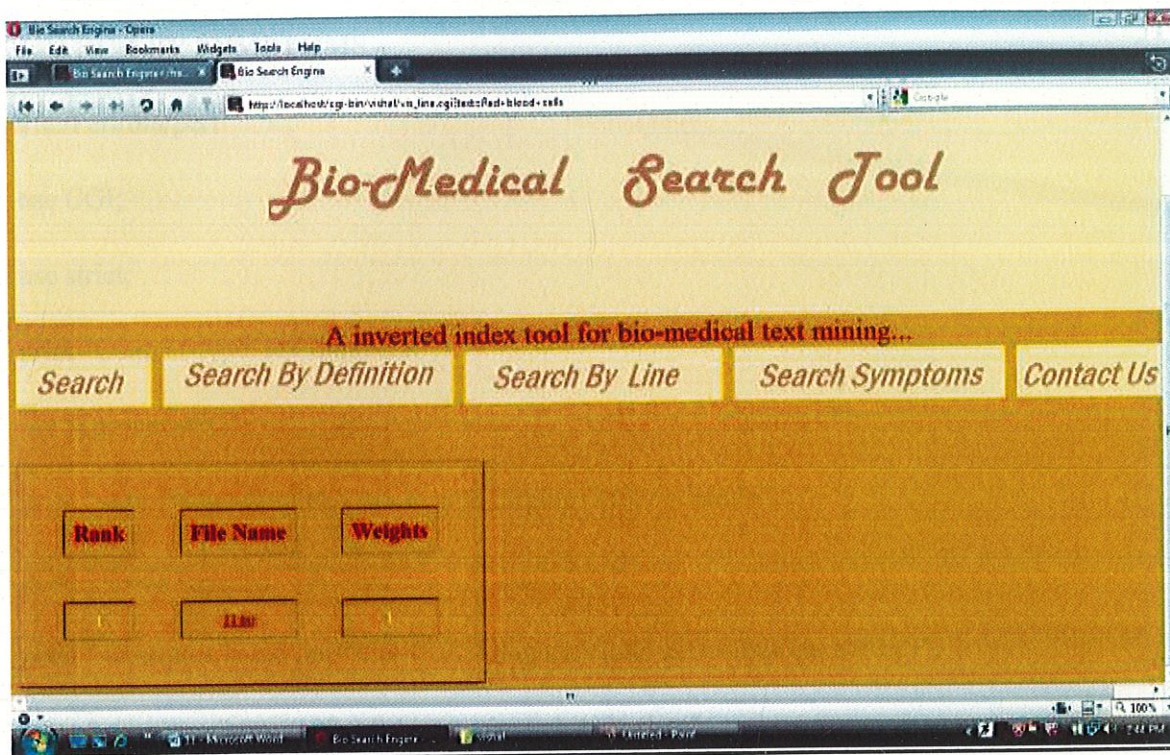
print"</table>";

print "</body></html>";

```

8.3 Searching by Line






```
#!c:/Perl/bin/perl
```

```
use strict;
```

```
my $cgi=new CGI;
```

```
print "<body bgcolor='CC9900'>";
```

```
print "<marquee behavior='alternate'><img src='juit1.gif'></marquee><br>";
```

```
print "<img src='http://127.0.0.1/pro_v/search.gif'><br>";
```

```
print "<font size=6 color=990000> <center> <marquee behavior='alternate'>A inverted index  
tool for bio-medical text mining...</marquee></font> </center>";
```

```
print "<a href='http://127.0.0.1/pro_v/page1.html'><img  
src='http://127.0.0.1/pro_v/src/gif'></a>&nbsp&nbsp&nbsp";
```

```
print "<a href='http://127.0.0.1/pro_v/define.html'><img  
src='http://127.0.0.1/pro_v/definition.gif'></a>&nbsp&nbsp&nbsp";
```

```
print "<a href='http://127.0.0.1/pro_v/line.html'><img  
src='http://127.0.0.1/pro_v/line.gif'></a>&nbsp&nbsp&nbsp";
```

```
print "<a href='http://127.0.0.1/pro_v/sym.html'><img  
src='http://127.0.0.1/pro_v/sym.gif'></a>&nbsp&nbsp&nbsp";
```

```
print "<a href='http://127.0.0.1/pro_v/contact.html'><img  
src='http://127.0.0.1/pro_v/contact.gif'></a><br><br><br><br>";
```

```
my $search=$cgi->param("text");
```



```

$search=lc($search);

$search=$search.".txt";

open(F1,"C:/Users/vishal/Desktop/pro1/symptoms/$search");

my @data=<F1>;

foreach my $d(@data)
{

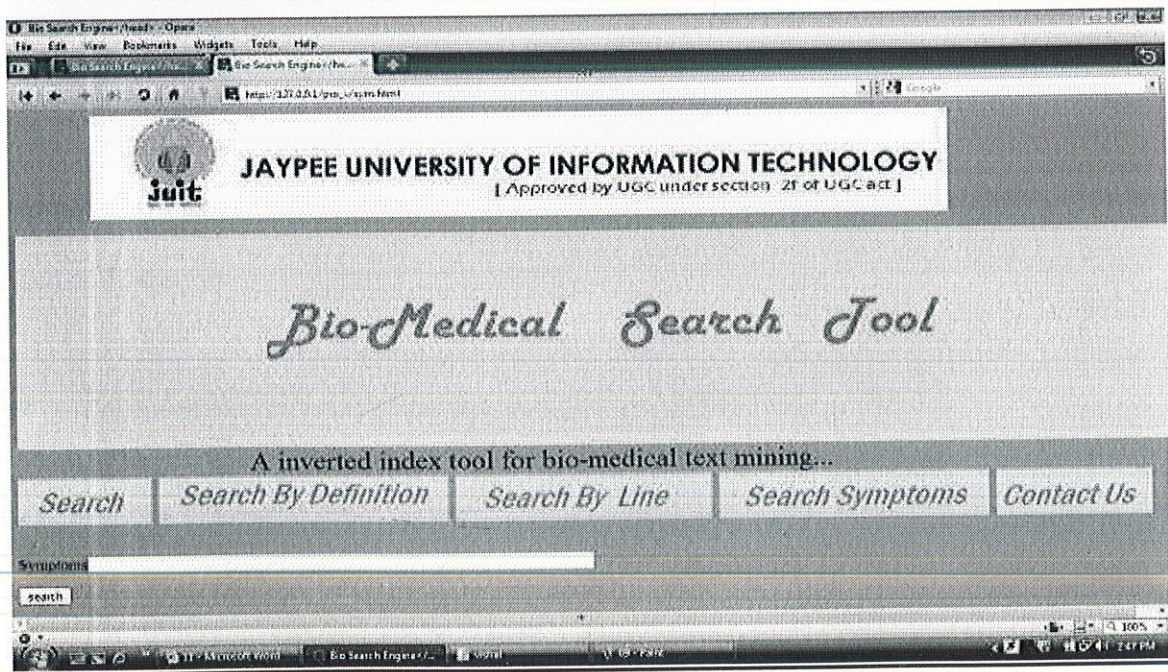
    print "<p><font size=4 color=990000>$d</p>";

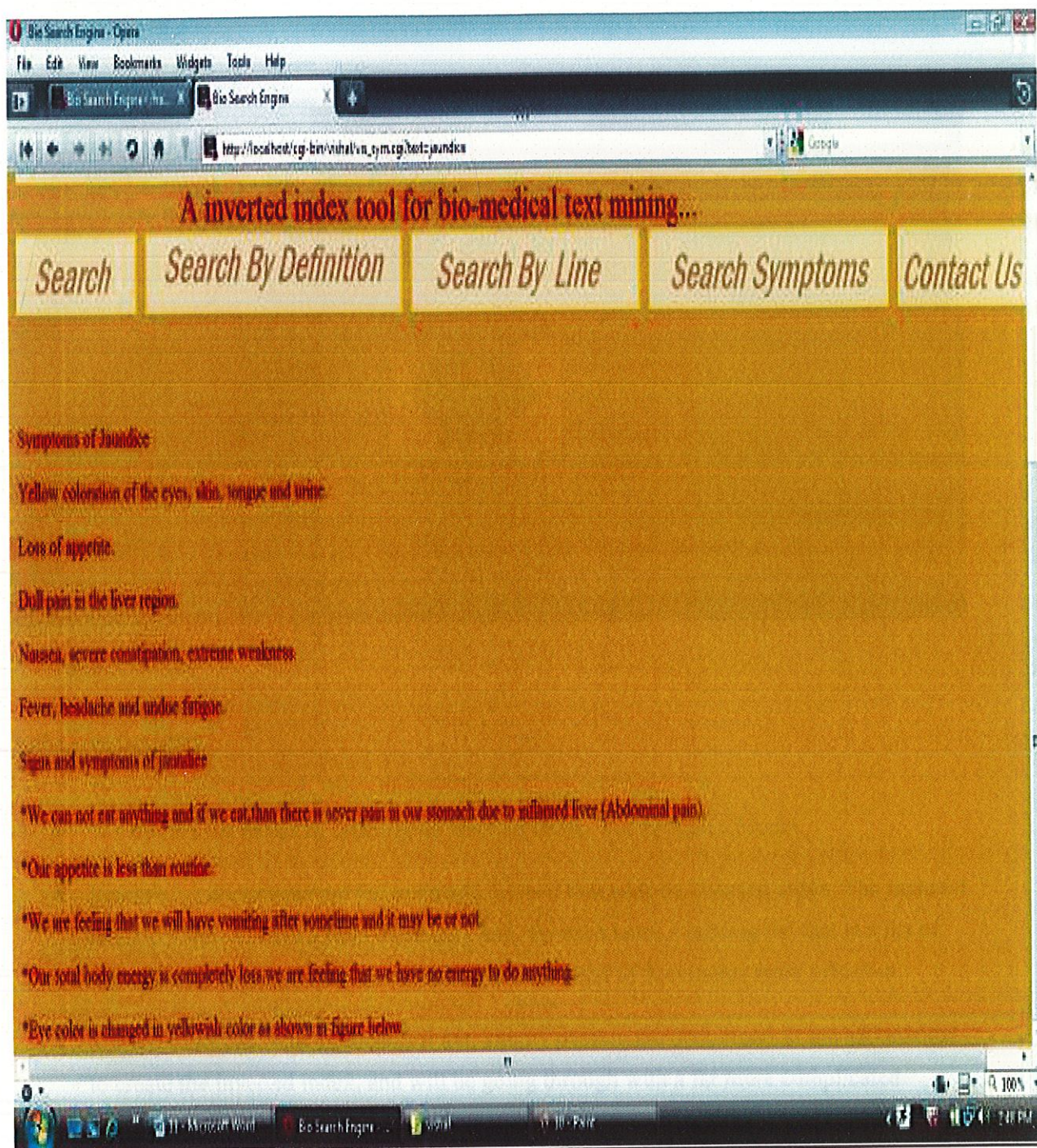
}

print "</body></html>";

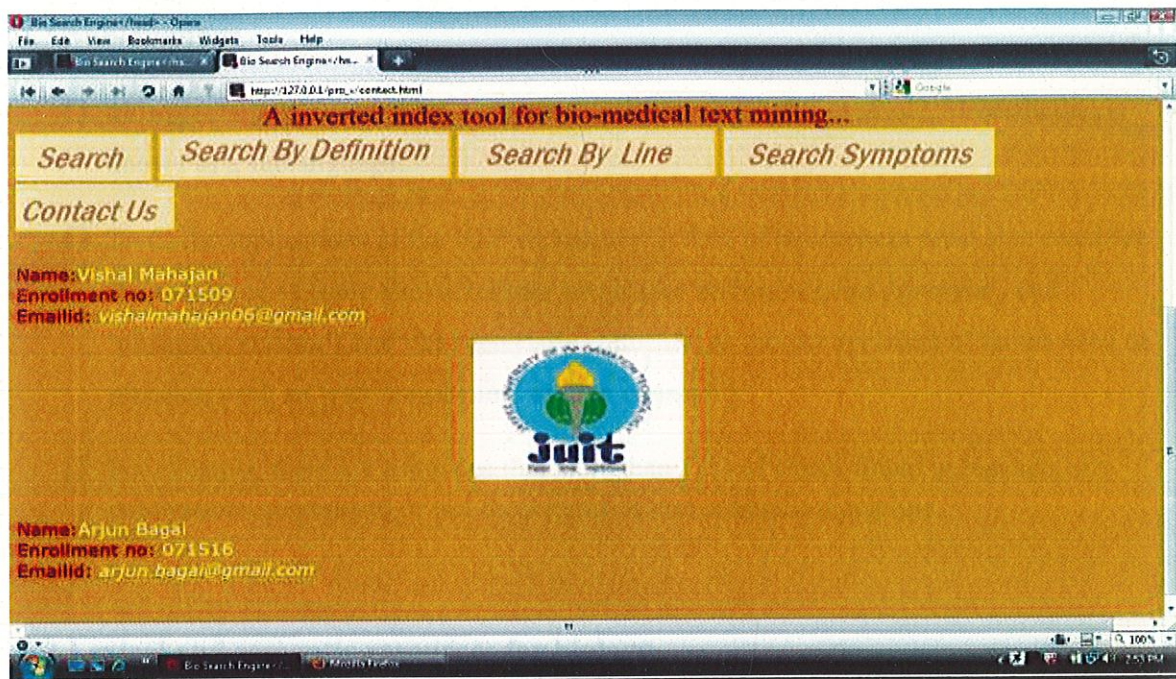
```

8.4 Searching for Symptoms





CONTACT US –



8.5 Conclusions

- We studied the basics of creating an inverted index, Vector Space Model.
- Essentially, documents are fed to an add method that adds an inverted index. The inverted index consists of both a term dictionary and, for each term, a posting list that is a list of documents that contain the term, making the retrieval of documents more effective.
- We went through with an IndexBuilder, simply passing the documents to the add method to create the inverted index, and will be going through with a far more complicated IndexBuilder in the time to come.

Chapter 9 – Future Work of the Project

9.1 Sublanguage

- ☐ This specialized usage of language in a specific domain (for example, biomedicine) is known as a sublanguage.
- ☐ Thus, the applications of the NLP techniques in field of biosciences must also **consider the existence of some characteristic terms (for instance, 'gene', 'protein', and 'phosphorylation') and characteristic collocations (co-occurrences of terms used as phrases, such as 'cell membrane' or 'ion channel')**.
- ☐ For example, there are estimates that more than 12% of words found in biochemistry publications correspond to technical terms of that scientific discipline.

9.2 Lexical and semantic resources for biology

- ☐ Functional descriptions of bio-entities, **relevant biological processes, or experimental techniques** are often **expressed in scientific papers using domain-specific technical terms**.
- ☐ *Terminological repositories and dictionaries are important resources to assist in the interpretation of scientific articles, assisting authors in consistent use of domain specific terminology.*

9.3 Controlled vocabulary

- ☐ So-called controlled vocabulary is a set of predefined, authorized terms that have been preselected by the designer of the vocabulary. **One of the example is MeSH database, however one of the most popular and widely used controlled vocabulary is Gene Ontology database**, that describes gene products in terms of their associated biological processes, cellular components and molecular functions in a species-independent manner.

Chapter 10

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