MapReduce Approach for Biomedical Named Entity Using CRF

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ABSTRACT

It has been presented a challenging issue in processing large amount of data, especially in data redundant system. The conditional random field (CRF) model is applied in biomedical named entity recognition. The performance improvement of the CRF model is significant due to the internally sequential feature, which requires a new parallelized solutions. By merging and parallelizing the limited memory Broyolen-Fletcher-Goldfarb-Shanno and Viterbi algorithms. To enhance the capability of estimating parameters, the MRLB algorithm leverages the MapReduce framework. The MRVtb algorithm deduce as if the state sequence by extending the Viterbi algorithm with another MapReduce job.In this MapReduce Approach for Biomedical Named Entity using CRF, we first generate text based biomedical data in which we are loading online health care data and unzip the folder. Secondly we perform NLP operation such as sentence detection, tokenization and Named entity Recognition. The next stage the extraction and taxonomy building task are performed. Pattern matching and searching in the relational database is carried. Finally diagnosis report is generated.

Keyword : - *Biomedical named entity, MapReduce, Conditional Random field*

1. INTRODUCTION

THIS With the rapid development of computational and biological technologies, biomedical literatures are expanding at an exponential rate[1]. Aim is towards identify the words, phrases in biomedical papers is a challenging issue in biomedical named entity recognition. The conditional random field model is applied on biomedical named entity recognition. CRF model provides ability to express long distance dependent and overlapping. This CRF model needs three steps. First, feature selection. Second, parameter estimation. And third model is inference. In this MapReduce framework is enhanced the capacity of estimating parameters by using Viterbi algorithm with a MapReduce job. In this firstly MRCRF i.e. MapReduce CRF is partitioned to large dataset across hadoop environment and minimized replication. Next developed parallel algorithm i.e. MRLB i.e. MapReduce BFGS and MRVtb i.e MapReduce Virterbi. Lastly performance is presented with reported speedupversus sequential CRF under dataset size with hadoop configuration. In first phase each iteration has the following steps. 1) Divide the training set into M subsets of fixed size. 2) Allocate each partition to a single map task. 3)Calculate the gradient vectors using the first map function, where the output of the first map function is a partial weight of gradient vectors. 4) Sum up the partial weight of gradient vectors using the first reduce function to produce the global weight of gradient vectors.5) Output the value of the first reduce function to the HDFS, which is used to update the next estimated parameters in post-processing. The second phase (model inference using the MRVtb algorithm) - The MRVtb algorithm uses the parameters generated by the MRLB algorithm to calculate the most likely state sequence of the training data set. 1) Divide the training set into M subsets of fixed size. 2) Allocate eachpartition to a single map task. 3) Calculate the observation of the subset using the second map function. 4) Output the values of the second map function to the HDFS, which become the final result.

It has been presented a challenging issue in processing large amount of data, especially in data redundant system. The conditional random field (CRF) model is applied in biomedical named entity recognition. The performance improvement of the CRF model is significant due to the internally sequential feature, which requires a new parallelized solutions. By merging and parallelizing the limited memory Broyolen-Fletcher-Goldfarb-Shanno and Viterbi algorithms. To enhance the capability of estimating parameters, the MRLB algorithm leverages the MapReduce framework. The MRVtb algorithm deduce as if the state sequence by extending the Viterbi algorithm with another MapReduce job[1]. In this MapReduce Approach for Biomedical Named Entity using CRF, we first generate text based biomedical data in which we are loading online health care data and unzip the folder. Secondly we perform NLP operation such as sentence detection, tokenization and Named entity Recognition. The next stage the extraction and taxonomy building task are performed. Pattern matching and searching in the relational database is carried. Finally diagnosis report is generated.

1.1 Problem Statement

MapReduce Approach for Biomedical Entity Recognition uses the concept of CRF using Biomedical Named Entity. Unstructured text is used as biomedical terms,Map and Reduce approach is used to improve the performance of system.It deals with big data so used the HADOOP Environment for HDFS framework. Major part of system will include Generate Biomedical data from healthcare dataset, NLP operation, Extraction, Pattern Matching, Generate Diagnosis report. The system is to be developed which will be easily embed into the different application where Biomedical recognition is concern..

1.2 Existing System

Conditional Random Fields (CRFs) are a widely-used approach for supervised sequence labelling, notably due to their ability to handle large description spaces and to integrate structural dependency betweenlabels

To develop tools to analyze biomedical texts as comprehensively and as accurately as possible. To recognize a set of biologically important concepts in unstructured biomedical texts using free and publicly available, open source tools and achieve a level of performance that is competitive with the top performing systems

1.3 Proposed System

- Current methods of improving time efficiency of the CRF model focus on how to reduce the model parameter estimation time. However, the complexity of the model inference step increases quickly with the increase of constraint length of training data set as well. The model inference step can be performed using a modified Viterbi algorithm . In, this dissertation, formulate the Viterbi algorithm within the Map Reduce framework to parallelize the model inference step with a simple strategy.

- An optimization algorithm called Limited memory BFGS (L-BFGS) is a popular method that has been used to do parameter estimation of CRF . However, since it is an iterative algorithm, achieving high parallelism is not easy and demands considerable research attention for developing new parallelized algorithms that will allow them to efficiently handle large-scale data. It is a challenging task to parallelize such a dependent iterative algorithm. The task of making iterations independent of each other and thus leveraging and boosting parallel architectures is nontrivial.

- In Biomedical data structure field ,the often considerable and well-known model is conditional random fields(CRF) has been implemented to incorporate longer distance data information. CRF model plays has been perform a vital role in implementation of Biomedical Named Entity Recognition task in many biomedical text mining and information extraction systems. our main motive is to collect the unstructured data of various decease from various resources and preprocessing it using NLP(Natural language processing) ,these data can store into the Big database called Hadoop, which can be easy and helpful to retrieve the deceases information.

2. LITERATURE SURVEY

Kenli Li, Wei Ai, Zhuo Tang, Fan Zhang, Lingang Jiang, Keqin Li, and Kai Hwang[1] proposed Hadoop Recognition of Biomedical Named Entity Using Conditional RandomFields
Advantage:

- To develop the system with HDFS framework using map reduce, to improve the systemperformance..

Disadvantage:

- Increasing copy threads causes internal communication delay

Chengjie Sun,Yi Guan, Xiaolong Wang, Lei Lin [2]uses the Rich features based Conditional Random Fields for biological named entities recognition..
Advantage:

- Provided an opportunity for natural language processing techniques also provides services to data mining

Disadvantage:

- Information extraction, and word sense disambiguation are particularly challenging in the biological domain with its highly complex

ZHOU Guo Dong SU Jian.[3] proposed the Exploring Deep Knowledge Resources in Biomedical Name Recognition.
Advantage:

- Use of both a closed dictionary from the training set and an open dictionary, as it uses deep knowledge resources such as the name alias phenomenon..

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Thomas Lavergne,Olivier Capp [4]proposed Practical very large scale CRFs
.Advantages:

- Analysis demonstrate that training largescale sparse models can be done efficiently and allows to improve over the performance of smaller models..

3. PROPOSED SYSTEM ARCHITECTURE

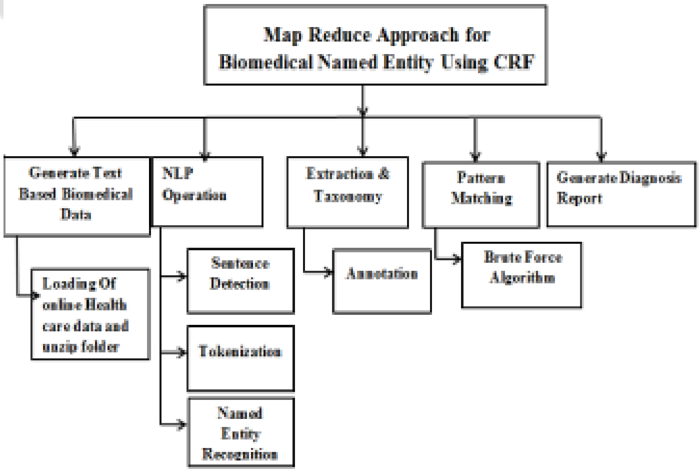
Map Reduce Approach for Biomedical Named Entity Using CRF
Generate Text Based Biomedical Data
NLP Operation
Extraction & Taxonomy
Pattern Matching
Generate Diagnosis Report
Loading Of online Health care data and unzip folder
Sentence Detection
Tokenization
Named Entity Recognition
Annotation
Brute Force Algorithm

Fig -1: System Overview

3.1 Generate text based on biomedical data.

Loading Of online Health care data and unzip folder In this load bio medical data online in Zip folder Format. and another operation is Unzip that folder for further NLP Operation.That Loading and Unzipping can do by Admin.

3.2 NLP operation

- The output of first module is given as input to second module, i.e. the temporary text file. This text file contains content of the medical paper. The data in this file is in unstructured form thus the next task is to perform Natural Language Processing (NLP) operations on this data.
- Input of Module: Temporary text with the medical paper content.
- Output of Module: Text file contains the Adjective Phrases, Adverb Phrases, Conjunction Phrase, Noun phrase, Prepositional phrases, and Verb phrase classified by labels.
- Sentence Detection is first step of NLP operation. Sentence Detector can detect that a punctuation character marks the end of a sentence or not.
- Tokenization is the second step in NLP operation. tokenization Convert a sentence into a sequence of tokens.Divides the text into smallest units (usually words), removing punctuation. Assign a part-of-speech tag to each token in a sentence.
- Named Entity Recognition is the third step of in NLP operation. Named entity recognition classifies tokens in text into predefined categories such as date, location, person, time.

3.3 Extraction and Taxonomy

- In this module the Concept extraction and Taxonomy building task are performed.
- Input Of Module:The input for this module is the table generated by NLP tasks and the master table containing the attributes such as synonyms for disease, specialized lexicon, semantic network.
- Output Of Module: The output of this module is relational database schema containing attributes such as symptom, disease, treatment, side-effect. Identification of sentence task is to identifying sentences published in medical papers as containing information about diseases and treatments and data sets are annotated with the following information: a label indicating that the sentence is informativethat is it containing diseasetreatment information, or a label indicating that the sentence is not informative.
- Annotation is the second task, the sentences have annotation information that states if the relation that exists in a sentence between the disease and treatment is Cure, Prevent, or Side Effect, these are three semantic relation used.

3.4 Pattern Matching

- In this module pattern matching and searching in the relational database are performed. The first task is to accept user query and perform operations on the relational database. For more than one symptom,pattern matching is performed on the database, which matches the symptom with data in the database. In pattern matching, the perceived sequence of tokens is checked for the presence of the constituents of some pattern. The resultant matched pattern is tabulated and cluster of information is formed by the pattern matching algorithm. These patterns are referred while determining the input for the next module i.e. Perceptron optimization.
- Input Of Module: The input for this module will be a sentence containing either disease or symptoms.
- Output Of Module: The result containing symptoms, treatment , side-effects for the disease.

3.5 Generate Diagnosis Report.

- It provides Diagnosis Report of dieses by providing treatment,symtoms,cure etc in GUI.

4. CONCLUSION

The paper proposes a Map reduce approach for Named Entity recognition using CRF .Proposed scheme offers substantial benefits and provides an opportunity to extend Biomedical applications., I have implemented the first module that is Loading of health care data and extraction. In this module firstly load the health dataset into zip format, after unzipping by admin. In Extraction will get symptoms,causes of particular disease.

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