

Automatic Detection of Breast Cancer Using Mathematical Morphological Operations and Machine Learning Technique

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ABSTRACT: Breast cancer is the second cause of dead among women. Early detection followed by appropriate cancer treatment can reduce the deadly risk. It is a hereditary disease and does not result from a single cause. The diagnosis of cancer starts with a biopsy. A computer-aided diagnosis (CAD) system based on mammograms enables early breast cancer detection, diagnosis, and treatment. However, the accuracy of existing CAD systems remains unsatisfactory. Various methods are used to detect and recognize cancer cells, from microscopic images and mammography to ultrasonography and magnetic resonance images (MRI). In the present study, Extreme Learning Machine (ELM) classification was performed for 9 features based on image segmentation in the Breast Cancer Wisconsin (Diagnostic) data set in the UC Irvine Machine Learning Repository database. Big Data technology is used to analyze these datasets in a database for accurate exploration and detection over benign and malignant breast masses. Extensive experiments demonstrate the accuracy and efficiency of our proposed mass detection and breast cancer classification method.

Keywords: breast cancer detection, UC Irvine Machine Learning, Extreme Learning Machine, computer-aided diagnosis, magnetic resonance images.

I.INTRODUCTION

GENERAL

Cancer begins when healthy cells in the breast change and grow out of control, forming a mass or sheet of cells called a tumor. A tumor can be cancerous or benign. A cancerous tumor is malignant, meaning it can grow and spread to other parts of the body. A benign tumor means the tumor can grow but will not spread. Breast cancer spreads when the cancer grows into other parts of the body or when breast cancer cells move to other parts of the body through the blood vessels and/or lymph vessels. This is called a metastasis. This guide covers early-stage and locally advanced breast cancer, which includes stages I, II, and III. The stage of breast cancer describes where the cancer is located, how much the cancer has grown, and if or where it has spread. Although breast cancer most commonly spreads to nearby lymph nodes, it can also spread further through the body to areas such as the bones, lungs, liver, and brain. This is called metastatic or stage IV breast cancer. If breast cancer comes back after initial treatment, it can recur locally, meaning in the breast and/or regional lymph nodes. The regional lymph nodes are those nearby the breast, such as the lymph nodes under the arm. It can also recur elsewhere in the body, called a distant recurrence or metastatic recurrence.

Types of breast cancer

Breast cancer can be invasive or noninvasive. Invasive breast cancer is cancer that spreads into surrounding tissues. Noninvasive breast cancer does not go beyond the milk ducts or lobules in the breast. Most breast cancers start in the ducts or lobes and are called ductal carcinoma or lobular carcinoma:

Ductal carcinoma. These cancers start in the cells lining the milk ducts and make up the majority of breast cancers. Ductal carcinoma in situ (DCIS). This is cancer that is located only in the duct. Invasive or infiltrating ductal carcinoma. This is cancer that has spread outside of the duct.

Invasive lobular carcinoma. This is cancer that starts in the lobules. Less common types of breast cancer include:

- Medullary
- Mucinous
- Tubular
- Metaplastic
- Papillary

Inflammatory breast cancer is a faster-growing type of cancer that accounts for about 1% to 5% of all breast cancers. Paget's disease is a type of cancer that begins in the ducts of the nipple. Although it is usually in situ, it can also be an invasive cancer.

Breast cancer subtypes

There are 3 main subtypes of breast cancer that are determined by doing specific tests on a sample of the tumor. These tests will help your doctor learn more about your cancer and recommend the most effective treatment plan. Testing the tumor sample can find out if the cancer is:

Hormone receptor positive. Breast cancers expressing estrogen receptors (ER) and/or progesterone receptors (PR) are called "hormone receptor positive." These receptors are proteins found in cells. Tumors that have estrogen receptors are called "ER positive." Tumors that have progesterone receptors are called "PR positive." Only 1 of these receptors needs to be positive for a cancer to be called hormone receptor positive. This type of cancer may depend on the hormones estrogen and/or progesterone to grow. Hormone receptor-positive cancers can occur at any age, but are more common in women who have gone through menopause. About 60% to 75% of breast cancers have estrogen and/or progesterone receptors. Cancers without these receptors are called "hormone receptor negative."

HER2 positive. About 10% to 20% of breast cancers depend on the gene called human epidermal growth factor receptor 2 (HER2) to grow. These cancers are called "HER2 positive" and have many copies of the HER2 gene or high levels of the HER2 protein. These proteins are also called "receptors." The HER2 gene makes the HER2 protein, which is found on the cancer cells and is important for tumor cell growth. HER2-positive breast cancers grow more quickly. They can also be either hormone receptor positive or hormone receptor negative. Cancers that have no or low levels of the HER2 protein and/or few copies of the HER2 gene are called "HER2 negative."

Triple negative. If a tumor does not express ER, PR, or HER2, the tumor is called "triple negative." Triple-negative breast cancer makes up about 15% to 20% of invasive breast cancers. Triple-negative breast cancer seems to be more common among younger women, particularly younger black and Hispanic women. Triple-negative cancer is also more common in women with a mutation in the BRCA1 or BRCA2 genes. Experts recommend that all people with triple-negative breast cancer younger than 60 be tested for BRCA gene mutations.

II. LITERATURE SURVEY

Title : Investigating the role of model-based and model-free imaging biomarkers as early predictors of neoadjuvant breast cancer therapy outcome

Author : Eleftherios Kontopodis, Maria Venianaki, Georgios C. Manikis, Katerina Nikiforaki, Ovidio Salvetti, Efrosini Papadaki, Georgios Z. Papadakis, Apostolos H. Karantanas, Kostas Marias

Description : Imaging biomarkers (IBs) play a critical role in the clinical management of breast cancer (BRCA) patients throughout the cancer continuum for screening, diagnosis and therapy assessment especially in

the neoadjuvant setting. However, certain model-based IBs suffer from significant variability due to the complex workflows involved in their computation, whereas model-free IBs have not been properly studied regarding clinical outcome. In the present study, IBs from 35 BRCA patients who received neoadjuvant chemotherapy (NAC) were extracted from dynamic contrast enhanced MR imaging (DCE-MRI) data with two different approaches, a model-free approach based on pattern recognition (PR), and a model-based one using pharmacokinetic compartmental modeling. Our analysis found that both model-free and model-based biomarkers can predict pathological complete response (pCR) after the first cycle of NAC.

Title : Focused Microwave Breast Hyperthermia Monitored by Thermoacoustic Imaging: A Computational Feasibility Study Applying Realistic Breast Phantoms

Author : Lifan Xu, and Xiong Wang

Description : Focused microwave breast hyperthermia (FMBH) represents a newly emerging technique endowed with advantages of high accuracy and low side effect for treating breast tumors. Practical application of the FMBH approach requires monitoring of microwave power deposition in the breast. Microwave-induced thermoacoustic imaging (MITAI) is naturally feasible for such power deposition monitoring task. This work conducts a computational study to evaluate feasibility of the novel FMBH-MITAI modality using realistic breast phantoms. Basic configuration and rationale of both FMBH and MITAI are introduced. Compressive sensing (CS) technique has to be applied in MITAI for sparse acoustic measurement in the FMBH-MITAI modality. Procedure of the computational study consists of microwave simulation, thermoacoustic numerical simulation, CS imaging, and performing the iterative optimization. Simulated results show that CS based MITAI is able to serve as a reliable monitoring mechanism to efficiently guide the iterative optimization toward the best obtainable focusing condition in most of the simulated scenarios

Title : Construction and Characterization of a Novel Single Pixel Beta Detector for Intra-operative Guidance in Breast conserving Surgery

Author : Amritpal Singh, Ryerson University, Toronto, John Dillon Odette Cancer Centre, Toronto, Ananth Ravi, Odette Cancer Centre, Toronto

Description : Breast-conserving surgery is imprecise requiring re-excision in up to 40% of cases. One potential method of improving breast-conserving surgery accuracy is to use a beta particle detector to evaluate the surface of the excised tissue for any cancerous deposits, intra-operatively. Patients could be injected with a radiopharmaceutical that emits beta particles and preferentially accumulates within cancer cells. Cancer cells found on the surface of the excised tissue indicate that the surgery is incomplete. The purpose of this study is to develop and analyze a novel single pixel beta sensitive detector.

Title : Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images

Author : Yangqin Feng, Lei Zhang, Senior Member, IEEE, Juan Mo

Description : Classifying breast cancer histopathological images automatically is an important task in computer assisted pathology analysis. However, extracting informative and non-redundant features for histopathological image classification is challenging due to the appearance variability caused by the heterogeneity of the disease, the tissue preparation, and staining processes. In this paper, we propose a new feature extractor, called deep manifold preserving auto encoder, to learn discriminative features from unlabeled data. Then, we integrate the proposed feature extractor with a softmax classifier to classify breast cancer histopathology images. Specifically, it learns hierarchical features from unlabeled image patches by minimizing the distance between its input and output, and simultaneously preserving the geometric structure of the whole input data set. After the unsupervised training, we connect the encoder layers of the trained deep manifold preserving autoencoder with a softmax classifier to construct a cascade model and fine-tune this deep neural network with labeled training data

Title : On Combining Biclustering Mining and AdaBoost for Breast Tumor Classification

Author : Qinghua Huang, Yongdong Chen, Longzhong Liu, Dacheng Tao Fellow, IEEE, and Xuelong Li

Description : Breast cancer is now considered as one of the leading causes of deaths among women all over the world. Aiming to assist clinicians in improving the accuracy of diagnostic decisions, computer-aided diagnosis (CAD) system is of increasing interest in breast cancer detection and analysis nowadays. In this paper, a novel computer-aided diagnosis scheme with human-in-the-loop is proposed to help clinicians identify the benign and malignant breast tumors in ultrasound. In this framework, feature acquisition is performed by a user-participated feature scoring scheme that is based on Breast Imaging Reporting and Data System (BI-RADS) lexicon and experience of doctors. Biclustering mining is then used as a useful tool to discover the column consistency patterns on the training data. The patterns frequently appearing in the tumors with the same label can be regarded as a potential diagnostic rule. Subsequently, the diagnostic rules are utilized to construct component classifiers of the Adaboost algorithm via a novel rules combination strategy which resolves the problem of

classification in different feature spaces (PC-DFS). Finally, the AdaBoost learning is performed to discover effective combinations and integrate them into a strong classifier

III. OBJECTIVE

In this paper we are isolating cancer data by utilizing Hadoop instrument adjacent some Hadoop common systems like hdfs, map reduce, sqoop, and hive. By utilizing these devices preparing of information with no confinement is conceivable, no information lost issue, we can get high throughput, upkeep cost comparatively incredibly less and it is an open source programming, it is extraordinary on the majority of the stages since it is Java based. In Cancer data, we have every patients data, with their progress and their treatment reports.

IV. EXISTING SYSTEM

Existing concept deals with providing backend by using MySQL which contains lot of drawbacks i.e. data limitation is that processing time is high when the data is huge and once data is lost we cannot recover so thus we proposing concept by using Hadoop framework.

DRAWBACKS IN EXISTING SYSTEM:

- ✓ We can process limitation of data.
- ✓ We get results with take more time and maintenance cost is very high.

V. PROPOSED SYSTEM

Proposed concept deals with providing database by using Hadoop tool we can analyze no limitation of data and simple add number of machines to the cluster and we get results with less time, high throughput and maintenance cost is very less and we are using partitions and bucketing techniques in Hadoop.

ADVANTAGES IN PROPOSED SYSTEM:

- ✓ No data loss problem
- ✓ Efficient data processing.

VI. METHODOLOGIES OF ANALYZING CANCER

GENERAL

In this paper we are isolating Cancer information by utilizing Hadoop structure close-by some Hadoop regular systems like hdfs, MapReduce, sqoop and hive. By utilizing these contraptions we can process no confinement of information, no information lost issue, we can get high throughput, keep up expense in like way less and it is an open wellsprings of programming, it is extraordinary on the majority of the stages since it is Java based

METHODOLOGIES

Following modules involves

MODULES

- Existing Application (MySQL)
- Connector (Sqoop)
- Analysis Query Language (Hive)
- Analysis Latin Script (Pig)
- Processing (MapReduce)

VII. MODULE DIAGRAMS & MODULE DESCRIPTION

Existing Application (MySQL)

In MySQL is a relational database management system. RDBMS uses relations or tables to store Breast Cancer data as a matrix of rows by columns with primary key. With MySQL language, Breast Cancer data in tables can be collected, stored, processed, retrieved, extracted and manipulated mostly for business purpose. Existing concept deals with providing backend by using MySQL which contains lot of drawbacks i.e. data

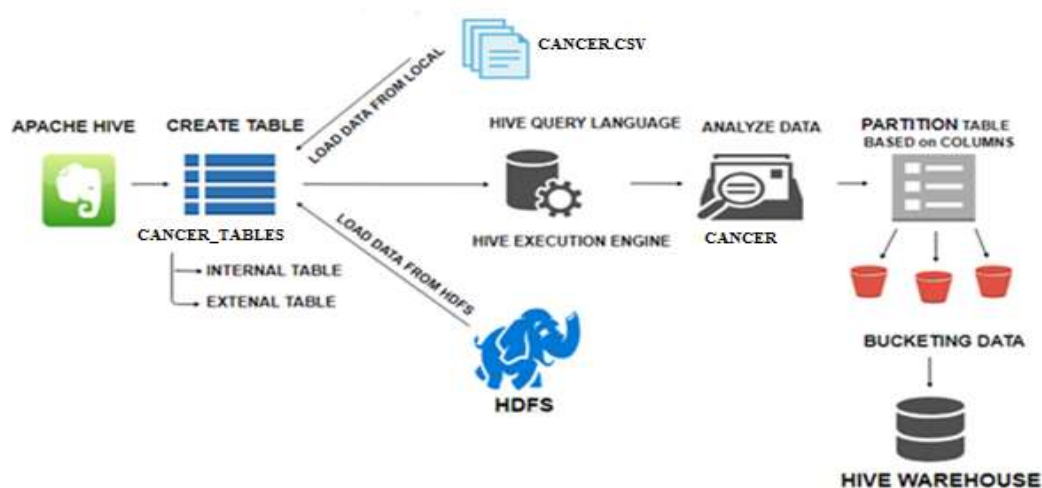
limitation is that processing time is high when the data is huge and once data is lost we cannot recover so thus we proposing concept by using Hadoop tool.

Connector (Sqoop)

Sqoop is a command-line interface application for transferring Breast Cancer data between relational databases (MySQL) and Hadoop. Here in MySQL database having Breast Cancer data have to import it to HDFS using Sqoop. Breast Cancer data can be moved into HDFS/Hive from MySQL and then it will generate the java classes. In previous cases, flow of data was from RDBMs to HDFS. Using "export" tool, we can import data from HDFS to RDBMs. Before performing export, Sqoop fetches table metadata from MySQL database. Thus we first need to create a table with required metadata.

Analysis Query Language (Hive)

Hive is a data ware house system for Hadoop that runs SQL like queries called HQL (Hive query language) which gets internally converted to map reduce jobs. In Hive, Breast Cancer data tables and databases are created first and then data is loaded into these tables. Hive as Breast Cancer data warehouse designed for managing and querying only structured data that is stored in tables. Hive organizes Breast Cancer data tables into partitions. It is a way of dividing a table into related parts based on the values of partitioned columns. Using partition, it is easy to query a portion of the given dataset. Tables or partitions are sub-divided into buckets, to provide extra structure to the Breast Cancer data that may be used for more efficient querying. Bucketing works based on the value of hash function of some column of a table.



Analysis Latin Script (Pig)

To analyze Breast Cancer data using Pig, programmers need to write scripts using Pig Latin language and execute them in interactive mode using the Grunt shell. All these scripts are internally converted to Map and Reduce tasks. After invoking the Grunt shell, you can run your Pig scripts in the shell. Except LOAD and STORE, while performing all other operations, Pig Latin statements take a relation as input and produce another relation as output. As soon as you enter a Load statement in the Grunt shell, its semantic checking will be carried out. To see the contents of the schema, you need to use the Dump operator. Only after performing the dump operation, the MapReduce job for loading the data into the file system will be carried out. Pig provides many built-in operators to support data operations like grouping, filters, ordering, etc.

Processing (MapReduce)

MapReduce is a framework using which we can write applications to process huge amounts of Breast Cancer data, in parallel, on large clusters of commodity hardware in a reliable manner. MapReduce is a processing technique and a program model for distributed computing based on java. The MapReduce algorithm contains two important tasks, namely Map and Reduce. MapReduce program executes in three stages, namely map stage, shuffle stage, and reduce stage. The map or mapper's job is to process the input data. Generally the input data is in the form of file or directory and is stored in the Hadoop file system (HDFS). The input file is passed to the mapper function line by line. The mapper processes the data and creates several small chunks of data. This stage

is the combination of the Shuffle stage and the Reduce stage. The Reducer's job is to process the data that comes from the mapper. After processing, it produces a new set of output, which will be stored in the HDFS.

VIII. SYSTEM TECHNIQUES

MapReduce is a processing technique and a program model for distributed computing based on java. The MapReduce algorithm contains two important tasks, namely Map and Reduce. Map takes a set of data and converts it into another set of data, where individual elements are broken down into tuples (key/value pairs). Secondly, reduce task, which takes the output from a map as an input and combines those data tuples into a smaller set of tuples. As the sequence of the name MapReduce implies, the reduce task is always performed after the map job.

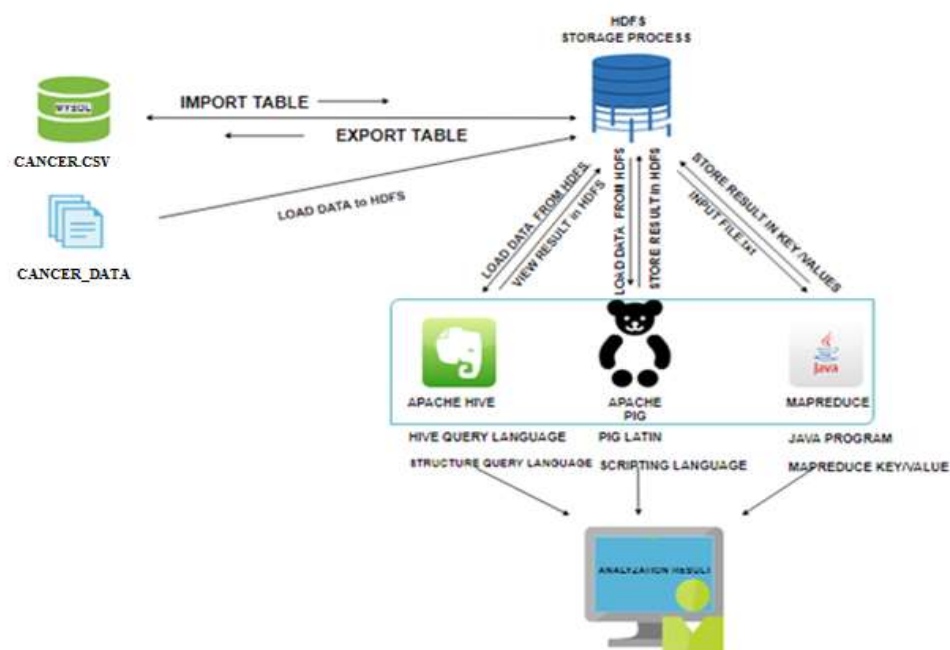
The major advantage of MapReduce is that it is easy to scale data processing over multiple computing nodes. Under the MapReduce model, the data processing primitives are called mappers and reducers. Decomposing a data processing application into mappers and reducers is sometimes nontrivial. But, once we write an application in the MapReduce form, scaling the application to run over hundreds, thousands, or even tens of thousands of machines in a cluster is merely a configuration change. This simple scalability is what has attracted many programmers to use the MapReduce model.

Algorithm

- Generally MapReduce paradigm is based on sending the computer to where the data resides!
- MapReduce program executes in three stages, namely map stage, shuffle stage, and reduce stage.
 - **Map stage:** The map or mapper's job is to process the input data. Generally the input data is in the form of file or directory and is stored in the Hadoop file system (HDFS). The input file is passed to the mapper function line by line. The mapper processes the data and creates several small chunks of data.
 - **Reduce stage:** This stage is the combination of the **Shuffle** stage and the **Reduce** stage. The Reducer's job is to process the data that comes from the mapper. After processing, it produces a new set of output, which will be stored in the HDFS.

IX. DESIGN ENGINEERING

SYSTEM ARCHITECTURE



EXPLANATION

This architecture explains the process or flow of the project. First we should import csv file into hdfs to processing that huge data in Hadoop open source framework. And we can process that data with the help of three tools namely pig, hive, MapReduce and finally we get output what we want result from the dataset, what we have in this project.

X. DEVELOPMENT TOOLS

GENERAL

This chapter is about the software language and the tools used in the development of the project. The platform used here is JAVA and Big Data.

FEATURES OF JAVA &BIG DATA

JAVA &HADOOP Framework

Java is a programming language originally developed by James Gosling at Microsystems and released in 1995 as a core component of Sun Microsystems' Java platform. The language derives much of its syntax from C and C++ but has a simpler object model and fewer low-level facilities. Java applications are typically compiled to byte code that can run on any Java Virtual Machine (JVM) regardless of computer architecture. Java is general-purpose, concurrent, class-based, and object-oriented, and is specifically designed to have as few implementation dependencies as possible. It is intended to let application developers "write once, run anywhere".

Java is considered by many as one of the most influential programming languages of the 20th century, and is widely used from application software to web applications. The Java framework is a new platform independent that simplifies application development internet. Java technology's versatility, efficiency, platform portability, and security make it the ideal technology for network computing. From laptops to datacenters, game consoles to scientific supercomputers, cell phones to the Internet, Java is everywhere!

Objectives of JAVA & BIGDATA

To see places of Java in Action in our daily life, explore java.com.

Why Software Developers Choose Java

Java has been tested, refined, extended, and proven by a dedicated community. And numbering more than 6.5 million developers, it's the largest and most active on the planet. With its versatility, efficiency, and portability, Java has become invaluable to developers by enabling them to:

- Write software on one platform and run it on virtually any other platform
- Create programs to run within a Web browser and Web services
- Develop server-side applications for online forums, stores, polls, HTML forms processing, and more
- Combine applications or services using the Java language to create highly customized applications or services
- Write powerful and efficient applications for mobile phones, remote processors, low-cost consumer products, and practically any other device with a digital heartbeat

Some Ways Software Developers Learn Java

- Today, many colleges and universities offer courses in programming for the Java platform. In addition, developers can also enhance their Java programming skills by reading Sun's java.sun.com Web site, subscribing to Java technology-focused newsletters, using the Java Tutorial and the New to Java Programming Center, and signing up for Web, virtual, or instructor-led courses.

WORKING WITH SQOOP

Sqoop

The traditional application management system, that is, the interaction of applications with relational database using RDBMS, is one of the sources that generate Big Data. Such Big Data, generated by RDBMS, is stored in **Relational Database Servers** in the relational database structure.

When Big Data storages and analyzers such as MapReduce, Hive, HBase, Cassandra, Pig, etc. of the Hadoop ecosystem came into picture, they required a tool to interact with the relational database servers for importing and exporting the Big Data residing in them. Here, Sqoop occupies a place in the Hadoop ecosystem to provide feasible interaction between relational database server and Hadoop's HDFS.

Sqoop: "SQL to Hadoop and Hadoop to SQL"

Sqoop is a tool designed to transfer data between Hadoop and relational database servers. It is used to import data from relational databases such as MySQL, Oracle to Hadoop HDFS, and export from Hadoop file system to relational databases. It is provided by the Apache Software Foundation.

How Sqoop Works?

The following image describes the workflow of Sqoop.

Sqoop Import

The import tool imports individual tables from RDBMS to HDFS. Each row in a table is treated as a record in HDFS. All records are stored as text data in text files or as binary data in Avro and Sequence files.

Sqoop Export

The export tool exports a set of files from HDFS back to an RDBMS. The files given as input to Sqoop contain records, which are called as rows in table. Those are read and parsed into a set of records and delimited with user-specified delimiter.

WORKING WITH HIVE

Hive

Introduction:

The term 'Big Data' is used for collections of large datasets that include huge volume, high velocity, and a variety of data that is increasing day by day. Using traditional data management systems, it is difficult to process Big Data. Therefore, the Apache Software Foundation introduced a framework called Hadoop to solve Big Data management and processing challenges.

The Hadoop ecosystem contains different sub-projects (tools) such as Sqoop, Pig, and Hive that are used to help Hadoop modules.

- **Sqoop:** It is used to import and export data to and fro between HDFS and RDBMS.
- **Hive:** It is a platform used to develop SQL type scripts to do Map Reduce operations.

WORKING WITH PIG

What is pig?

Apache Pig is a high level data flow platform for execution Map Reduce programs of Hadoop. The language for Pig is pig Latin.

The Pig scripts get internally converted to Map Reduce jobs and get executed on data stored in HDFS. Every task which can be achieved using PIG can also be achieved using java used in Map reduce.

Why do we need apache pig

Programmers who are not so good at Java normally used to struggle working with Hadoop, especially while performing any MapReduce tasks. Apache Pig is a boon for all such programmers.

FUTURE ENHANCEMENTS

Apache Spark is an open source processing engine built around speed, ease of use, and analytics. If you have large amounts of data that requires low latency processing that a typical Map Reduce program cannot provide, Spark is the alternative. Spark provides in-memory cluster computing for lightning fast speed and supports Java, Scala, and Python APIs for ease of development.

XI. CONCLUSION

In this paper, we presented a study on Breast Cancer data and prediction regarding research paper using Extreme learning method. To analyze the Breast Cancer data in Hadoop ecosystem and to improve the accurate analysis of breast cancer. Hadoop ecosystem is using hive, pig, map reduce tools for processing so that output will take less time to process and result will be very fast. Hence in this project, Breast Cancer data which is traditionally going to store in RDBMS going to less performance hence by using Hadoop tool it will be faster and efficiently processing the data.

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