



International Journal of Innovative Research in Computer and Communication Engineering

(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

Big Data Solution for Predicting the Risk of Readmission for the Patients

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ABSTRACT: Nowadays a lot of such new technologies are coming. So, we are using those technologies to predict and analyse for the disease.. It involves integration of clinical factors with health conditions, disease parameters, hospital care, quality parameters and variety of variables specified to each health care provider making the task increasingly complex. Using the bigdata concept we can predict the disease and can also analyse it. The required tools are HDFS and HIVE in hadoop concept.

1. INTRODUCTION

Medical data mining has great potential for exploring the hidden patterns in the data sets of the medical domain. These patterns can be utilized for clinical diagnosis. However, the available raw medical data are widely distributed, heterogeneous in nature, and voluminous. These data need to be collected in an organized form. This collected data can be then integrated to form a hospital information system. Data mining technology provides user oriented approach to novel and hidden patterns in the data.

It was prohibitively difficult to store, manage and mine large volumes of structured and semi-structured health record datasets prior to the recent advances in big data infrastructure . One of the emergent abilities of new shared nothing, distributed, and parallel computing infrastructure is the ability to perform similar operations on large amount (petabytes) of data. These infrastructures are evolving to be able to process such large volumes, high velocity, and diverse types of data (variety of data due to the inherent nature of bringing computation closer to where the data is which is unlike the prior paradigm of having to move data around for large computations to happen. Within the healthcare informatics setting, this ability to process large amount of diverse unstructured semi-structured, and structured data enables clinical informatics to develop new insights and discovery new knowledge by combining data from various sources.

1.1.CONTRIBUTION

This research seeks to aid the development of a predictive system by examining the use of medical history to examine information about disease correlations and inexpensively assess risk. Due to common genetic, molecular, environmental, and lifestyle-based individual risk factors, most diseases do not occur in isolation .Share risk and environmental factors have similar consequences prompting the co-occurrence of related diseases in the same patient. Therefore, a patient diagnosed for a combination of diseases and exposed to specific

environmental, lifestyle and genetic risk factors may be at considerable risk of developing several other genetically and environmentally related diseases.

Most hospitals today employ sort of hospital information systems to manage their healthcare or patient data. These systems typically generate huge amounts of data. There is a wealth of hidden information in these data that is largely untapped. How data is turned into useful information that can enable healthcare to make intelligent clinical decisions.



International Journal of Innovative Research in Computer and Communication Engineering

(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

II. PROBLEM STATEMENT

Many hospital information systems are designed to support patient billing, inventory management and generation of simple statistics. Some hospitals use decision support systems, but they are largely limited. They can answer simple queries like “What is the average age of patients who have heart disease?”, “How many surgeries had resulted in hospital stays longer than 10 days?”, “Identify the female patients who are single, above 30 years old, and who have been treated for cancer.” However, they cannot answer complex queries like “Identify the important Preoperative predictors that increase the length of hospital stay”, “Given patient records on cancer, should treatment include chemotherapy alone, radiation alone, or both chemotherapy and radiation?”, and “Given patient records, predict the probability of patients getting a heart disease.”.

III. DATA EXTRACTION AND PREPROCESSING USING BIG DATA FRAMEWORK

3.1. Data Extraction

Real world clinical data is noisy and heterogeneous in nature, severely skewed, and contains hundreds of relevant yet sometimes correlated attributes. This data resides in multiple databases such as individual EMRs, lab and imaging systems, physician notes, medical correspondences, claims, CRM systems, and hospital finance department servers. The collection, integration, and analysis of such big, complex, and noisy data healthcare are a challenging task. For this reason, healthcare information systems can be considered as a form of big data not only for its sheer volume, but also for its complexity and diversity which makes traditional data warehousing solutions prohibitively cumbersome and ill-suited for large scale data exploration and modeling. In this section, we study how a big data framework can be leveraged to extract and preprocess data.

The focus of the next section will be subsequent predictive modeling. We will leverage Hadoop as our big data framework to archive performance, scalability and fault tolerance for our task at hand. Hadoop is a popular open-source map-reduce implementation, which is being used as an alternative to store and process extremely data sets on commodity hardware. Hadoop is designed to scale up from single servers to hundreds of compute nodes, each offering local computation and storage capabilities within Hadoop.

However, Hadoop provides no query functionality. In addition, selection methods in Hadoop are comparatively slower than in most DBMS. Thus a processing framework on top of MapReduce solution is also needed to simulate a scalable data warehouse. To achieve this goal, we use Hive as an open-source data warehousing solution built on top of Hadoop.

Hive supports queries expressed in a SQL-like declarative language - HiveQL, which are compiled into map-reduce jobs that are executed using Hadoop. In addition, HiveQL enables users to plug in custom map-reduce scripts into queries. Hive has 2 main user interfaces of CLI (command line) and Web UI for access to the data using a SQL-like construct. The process is as follows: first the healthcare data such as raw patient event logs, or structured electronic medical records can be stored as flat files on various nodes. These will then become accessible (i.e. loaded) into HDFS (Hadoop File System).

Then one has to manually invoke Hive commands to create appropriate tables and develop the schema so that data can be structured and appropriately queried.

3.2. Data Integration

Many measures of healthcare delivery or quality are not publicly available at the individual patient or hospital level largely due to privacy restrictions, legal issues or reporting norms. Instead, such measures are provided at aggregate level with varying granularity such as state-level, county-level or city-level. For example, average income is typically available by zip-code, whereas death ratio is available by city, or average smoking rate by country, through a variety of

International Journal of Innovative Research in Computer and Communication Engineering

(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

publicly available datasets. Although these aggregated statistics cannot reconstruct the underlying individual-level data, these aggregated data can be combined with individual data to produce more informative models. To integrate such data from different sources, in this paper we propose a simple but effective clustering based technique. For example suppose we have two datasets A and B. The dataset A contains income data based on the zip-code, and we want to add this factor to dataset B. To achieve this, the dataset A (including income data based on the zip-code) is divided into a set of clusters using clustering method based on some common features between dataset A and B. Then, the average income is calculated for each cluster. In the next step, each record of B dataset is assigned to a cluster that is most similar to it (based on distance function on common set of features). Finally, income values of the records in B are patched up with the plausible value generated from its respective cluster (Average value).

IV. BIG DATA FRAMEWORK FOR RISK OF READMISSION PREDICTIVE MODELING

Predictive models are appropriate for various kinds of clinical risk assessments in health care domain. Clinical risk calculators and risk assessment tools provide information about a person's chance of having a disease or encountering a clinical event. Such tools are useful to educate patients as well as healthcare providers to monitor the development of health conditions. Risk calculators are commonly used for diseases like cancer, diabetes, heart disease, and stroke etc. Developing predictive modelling solutions for such disease related risk of readmissions is extremely challenging in healthcare informatics due to high dimensionality and large volume of the data that is increasingly becoming available within hospital systems. In this paper, the focus is on demonstrating how clinical risk calculator tools can be augmented and scaled using a big data infrastructure implementation.

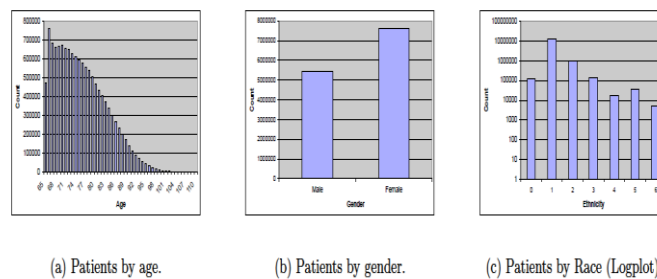


Figure 1: Data Statistics.

V. ALGORITHMS

5.1. Naive Bayes:

1. Each data sample is represented by an n dimensional feature vector, $X = (x_1, x_2, \dots, x_n)$, depicting n measurements made on the sample from n attributes, respectively A_1, A_2, \dots, A_n .
2. Suppose that there are m classes, C_1, C_2, \dots, C_m . Given an unknown data sample, X (i.e., having no class label), the classifier will predict that X belongs to the class having the highest posterior probability, conditioned on X. That is, the naive probability assigns an unknown sample X to the class C_i

if and only if:

$$P(C_i/X) > P(C_j/X) \text{ for all } 1 <= j <= m \text{ and } j \neq i$$

Thus we maximize $P(C_i/X)$. The class C_i for which $P(C_i/X)$ is maximized is called the maximum posteriori hypothesis. By Bayes theorem,



International Journal of Innovative Research in Computer and Communication Engineering

(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

$$P(C_i|X) = (P(X|C_i)P(C_i))/P(X)$$

3. As $P(X)$ is constant for all classes, only $P(X|C_i)P(C_i)$ need be maximized. If the class prior probabilities are not known, then it is commonly assumed that the classes are equally likely, i.e. $P(C_1) = P(C_2) = \dots = P(C_m)$, and we would therefore maximize $P(X|C_i)$. Otherwise, we maximize $P(X|C_i)P(C_i)$. Note that the class prior probabilities may be estimated by $P(C_i) = s_i/s$, where S_i is the number of training samples of class C_i , and s is the total number of training samples.

5.2. Pseudo code:

Calculate diagnosis="yes", diagnosis="no" probabilities P_{yes} , P_{no} from training input.

For Each Test Input Record

For Each Attribute

Calculate Category of Attribute Based On Categorical Division

Calculate Probabilities Of Diagnosis="Yes", Diagnosis="No" Corresponds To That Category $P(\text{Attr}, \text{Yes})$, $P(\text{Attr}, \text{No})$ From Training Input .

For Each Attribute

Calculate The $\text{Result}_{yes} = \text{Result}_{yes} * P(\text{Attr}, \text{Yes})$, $\text{Result}_{no} = \text{Result}_{no} * P(\text{Attr}, \text{No})$;

Calculate $\text{Result}_{yes} = \text{Result}_{yes} * P_{yes}$ $\text{Result}_{no} = \text{Result}_{no} * P_{no}$;

If($\text{Result}_{yes} > \text{Result}_{no}$) Then Diagnosis="Yes";

Else Then Diagnosis ="No";

5.3. Formulae:

1. P_{yes} =total number of yes/total number of records;
2. P_{no} =total number of no/total number of records;
3. $P(\text{attr}, \text{yes})$ =total number of yes in corresponding category/total number of yes;
4. $P(\text{attr}, \text{no})$ =total number of no in corresponding category/total number of no;

5.4. Data source

A total of 2268 records with 15 medical attributes (factors) were obtained from the Cleveland Heart Disease database. Figure 2 lists the attributes. The records were split equally into two datasets: training dataset (1857 records) and testing dataset (411 records).

The attribute "Diagnosis" was identified as the predictable attribute with value "1" for patients with heart disease and value "0" for patients with no heart disease.

5.5. Predictable attribute

1. Diagnosis (value 0: < 50% diameter narrowing (no heart disease); value 1: > 50% diameter narrowing (has heart disease))

Key attribute

1. Patientid – Patient's identification number

International Journal of Innovative Research in Computer and Communication Engineering

(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

Input attributes

Table3: Heart attack parameters with corresponding values and their weightages

Parameters	Weightage	
Male and Female	Age < 30	0.1
	>30 to <50	0.3
	Age>50 and Age <70	0.7
	Age>70	0.8
Smoking	Never	0.1
	Past	0.3
	Current	0.6
Overweight	Yes	0.8
	No	0.1
Alcohol Intake	Never	0.1
	Past	0.3
	Current	0.6
High salt diet	Yes	0.9
	No	0.1
High saturated fat diet	Yes	0.9
	No	0.1
Exercise	Never	0.6
	Regular	0.1
	High If age < 30	0.1
	High If age > 50	0.6
Sedentary Lifestyle/inactivity	Yes	0.7
	No	0.1
Hereditary	Yes	0.7
	No	0.1
Bad cholesterol	Very High >200	0.9
	High 160 to 200	0.8
	Normal <160	0.1
Blood Pressure	Normal (130/89)	0.1
	Low (<119/79)	0.8
	High (>200/160)	0.9

1. Sex (value 1: Male; value 0 : Female)

2. Chest Pain Type (value 1: typical type 1 angina, value 2: typical type angina, value 3: non-angina pain; value 4: asymptomatic)

3. Fasting Blood Sugar (value 1: > 120 mg/dl; value 0: < 120 mg/dl)

4. Restecg – resting electrographic results (value 0: normal; value 1: 1 having ST-T wave abnormality; value2:showing probable or definite left ventricular hypertrophy)

5. Exang – exercise induced angina (value 1: yes; value 0: no)

6. Slope – the slope of the peak exercise ST segment (value1: unsloping; value 2: flat; value 3: downsloping)

7. CA – number of major vessels colored by fluoroscopy (value 0 – 3)

8. Thal (value 3: normal; value 6: fixed defect; value7:reversible defect)

9. Trest Blood Pressure (mm Hg on admission to the hospital)

10. Serum Cholesterol (mg/dl)

International Journal of Innovative Research in Computer and Communication Engineering

(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

VI. PERFORMANCE EVALUATION

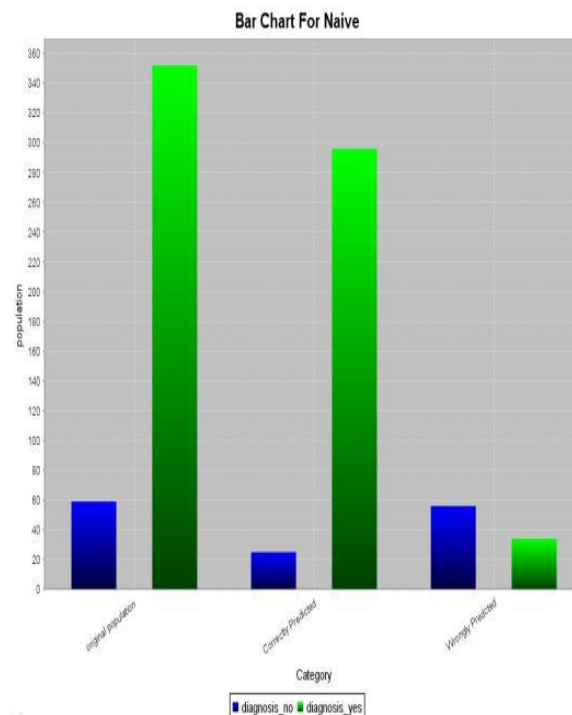
The effectiveness of models was tested using two methods: Classification Matrix. The purpose was to determine which model gave the highest percentage of correct predictions for diagnosing patients with a heart disease.

Classification Matrix: Classification Matrix displays the frequency of correct and incorrect predictions. It compares the actual values in the test dataset with the predicted values in the trained model. In this example, the test dataset contained 208 patients with heart disease and 246 patients without heart disease. Figure 4 shows the results of the Classification Matrix for all the three models. The rows represent predicted values while the columns represent actual values (1 for patients with heart disease, „0” for patients with no heart disease). The left-most columns show values predicted by the models. The diagonal values show correct predictions.

Predicted	0(actual)	1(actual)
0	25	56
1	34	296

The steps for producing Lift Chart are similar to the above except that the state of the predictable

6.1. Bar Charts: Bar charts as shown in the figure5 actually how many records are taken for testing and out of those how many are with diagnosis “yes” and how many are with diagnosis “no” and after testing the result analysis in the same manner as shown in below figure5 . From the bar charts below we can say that out of 411 testing records for naive bayes 321 predicted correctly.

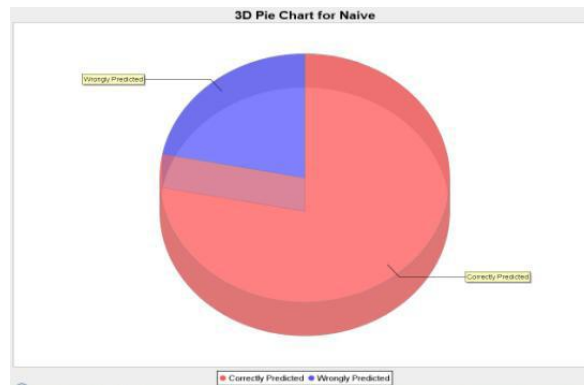


International Journal of Innovative Research in Computer and Communication Engineering

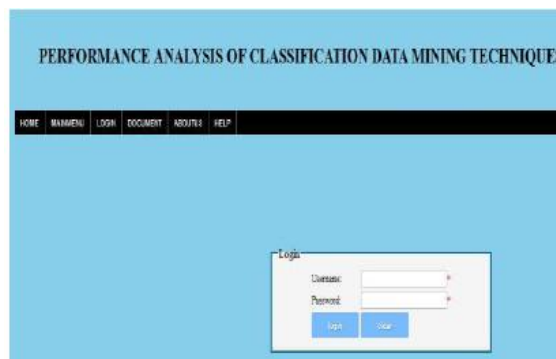
(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

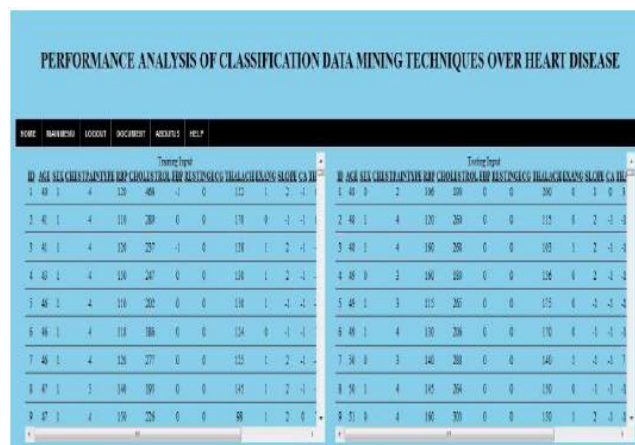
6.2. Pie charts: The pie chart is perhaps the most widely used statistical chart in the business world and the mass media. Pie charts presented here can explain clearly what the performance level of each technique is. fig 7 shows pie charts for both Naïve Bayes.



VII. OUTPUT SCREENS



LOGIN PAGE



The screenshot shows the "HOME PAGE" of the application. The page title is "PERFORMANCE ANALYSIS OF CLASSIFICATION DATA MINING TECHNIQUES OVER HEART DISEASE". There is a navigation menu with links for HOME, MAIN MENU, LOGIN, DOCUMENT, RESULTS, and HELP. The main content area displays two tables side-by-side, each showing performance metrics for various classification techniques. The tables have columns for ID, Accuracy, Precision, Recall, F1 Score, etc.

Technique 1											Technique 2										
ID	ACC	PREC	RECALL	F1	ROC	AUC	INFO	CONF	TIME	MEM	ID	ACC	PREC	RECALL	F1	ROC	AUC	INFO	CONF	TIME	MEM
1	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	1	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
2	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	2	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
3	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	3	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
4	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	4	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
5	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	5	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
6	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	6	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
7	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	7	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
9	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	9	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8

HOME PAGE

International Journal of Innovative Research in Computer and Communication Engineering

(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

Attributes	Values	Probability %
FastingBloodSugar	FastingBloodSugar = 0	86.179
Fxang	Fxang = 0	83.74
CA	ca = 0	80.488
Thal	thal = 3	79.268
Oldpeak	Oldpeak < 0.63	67.073
Slope	slope = 1	65.854
Restecg	Restecg = 0	57.724
Sex	Sex = 1	56.911
Sex	Sex = 0	43.089
Restecg	Restecg = 2	41.463
Chest	ChestPainType = 3	41.057
ThalachMaxHeartRate	ThalachMaxHeartRate >= 167.58	38.211

INPUT ATTRIBUTES

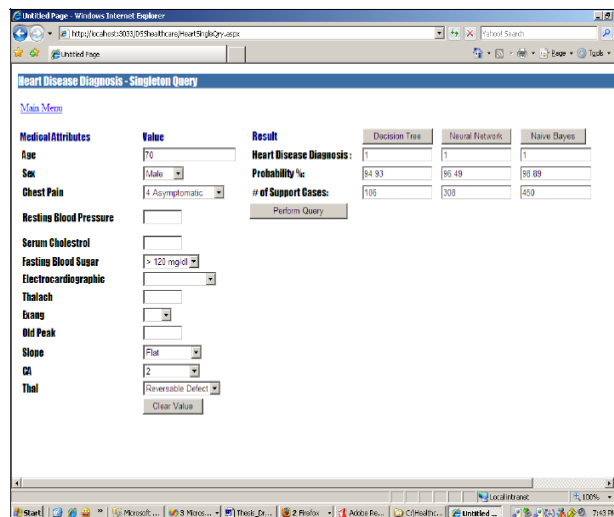


Figure 6. Output for singleton query module

VIII. CONCLUSION

In this work, we study the big data solution for predicting the risk of readmission for the patients. Our proposed solution leverages big data infrastructure for both information extraction and predictive and analysis modeling. We study the effectiveness of our proposed solution with a comprehensive set of experiment, considering quality and scalability. As ongoing work, we aim at leveraging big data infrastructure for our designed risk calculation tool, for designing more sophisticated predictive modeling and feature extraction techniques, and extending our proposed solutions to predict other clinical risks.

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International Journal of Innovative Research in Computer and Communication Engineering

(An ISO 3297: 2007 Certified Organization)

Vol. 3, Issue 6, June 2015

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