Juxtaposition on Classifiers Modeling Hepatitis Diagnosis Data

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A Presentation by

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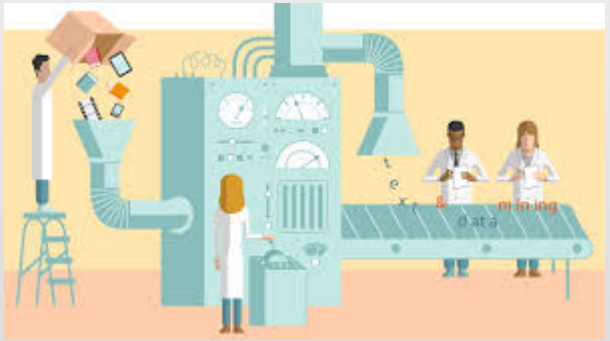
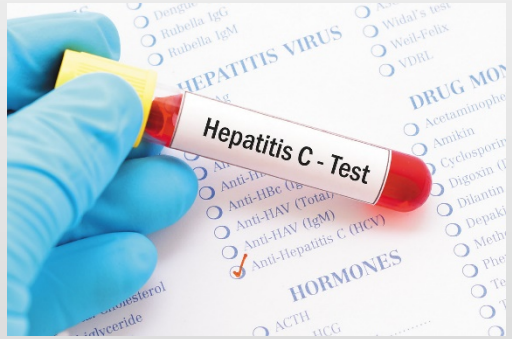
Introduction

- Machine Learning plays a crucial role in predicting unforeseeable parameters in different domains which has always been difficult for human prediction
- Data Mining plays a crucial role in mining the necessary features for prediction as the medical datasets has loads of information
- Hepatitis C, an acute or chronic disease that causes infection in the liver has approximately affected 130 – 170 million people in the world [1]





Motivation

- Hepatitis C is found worldwide
- Globally estimated 71 million people have chronic hepatitis C infection
- A serious number of those who chronically infected develop cirrhosis or liver cancer
- Antiviral medicines can cure more than 95% of people with the infection but access to diagnosis and treatment is low [2]
- Currently there is no vaccine for Hepatitis C

Motivation

- Hepatitis C can transmitted sexually and can be passed from an infected mother to her baby
- Estimated obtained from modeling suggest that worldwide, in 2015 there were 1.75 million new HCV infections [2]
- Globally 23.7 new HCV infections per 100,000 people [2]

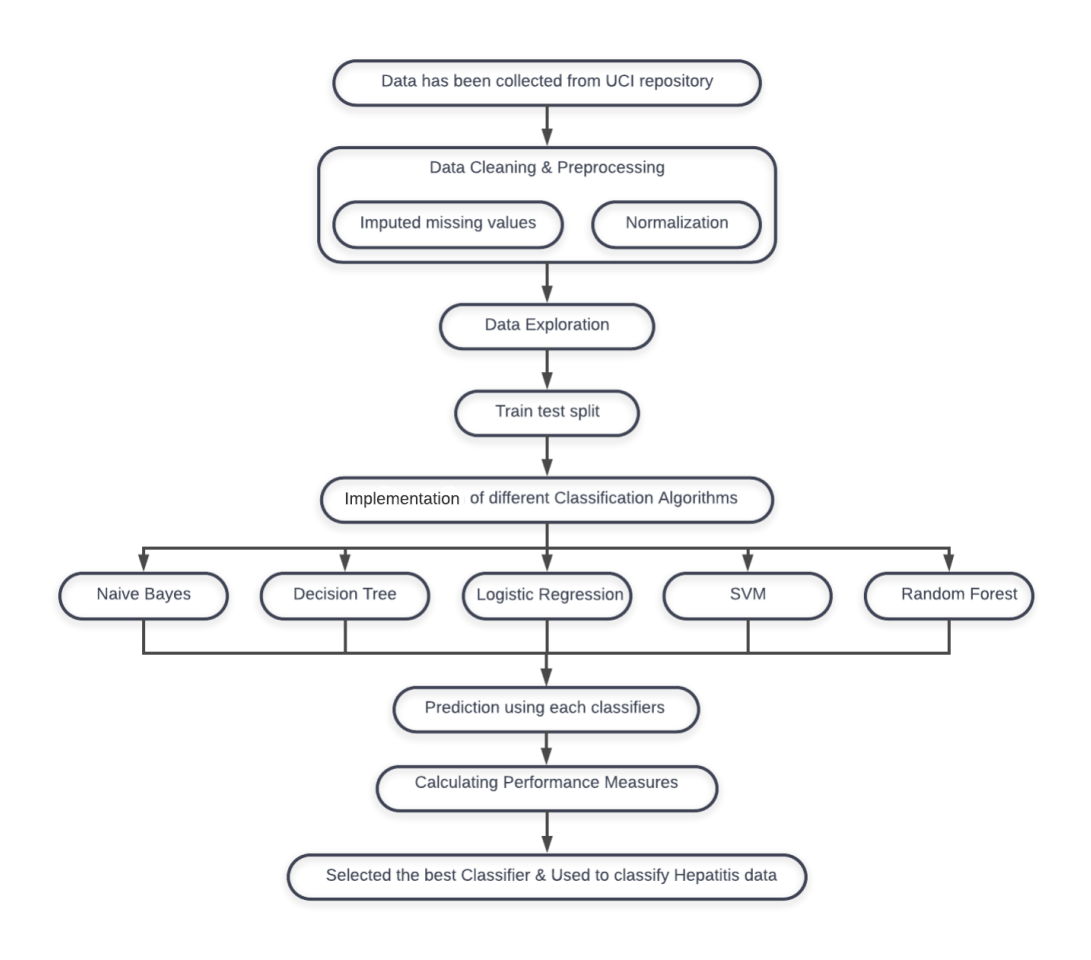
Related Works

Paper Name	Models Used	Performance Measures Used	Result
Ramaswamy et al [3]	Decision Stump, Random Forest, etc	Accuracy, Precision, Recall and F1-Measure	• Random Forest • Accuracy 87.5%
A. H. Roslina et al [4]	SVM (with & without feature selection)	Accuracy	• Feature selected • Accuracy 74.55%
S.Ekiz et al [5] (Heart Disease Dataset)	Decision Tree, SVM and Ensemble Learning in Weka and MATLAB	Accuracy	• Decision Tree (WEKA) • Accuracy 67.7%
K. Santhosh Bhargav et al [12]	SVM, Decision Tree, Logistic Regression, Naïve Bayes	Accuracy, Precision, Recall, and F-Measure	• Logistic Regression • Accuracy 87.17%

Methodology – Dataset Description

- Dataset is collected from UCI repository
- 155 tuples, 19 self-dependent attributes and label named “Class”
- **Numerical Attributes:**
  - Age, Bilirubin, Alk Phosphate, SGOT, Albumin & Protime
- **Categorical Attributes:**
  - Sex, Steroid, Antivirals, Fatigue, Malaise, Anorexia, Liver Big, Liver Firm, Spleen Palpable, Spiders, Ascites, Varices, Histology, **Class**

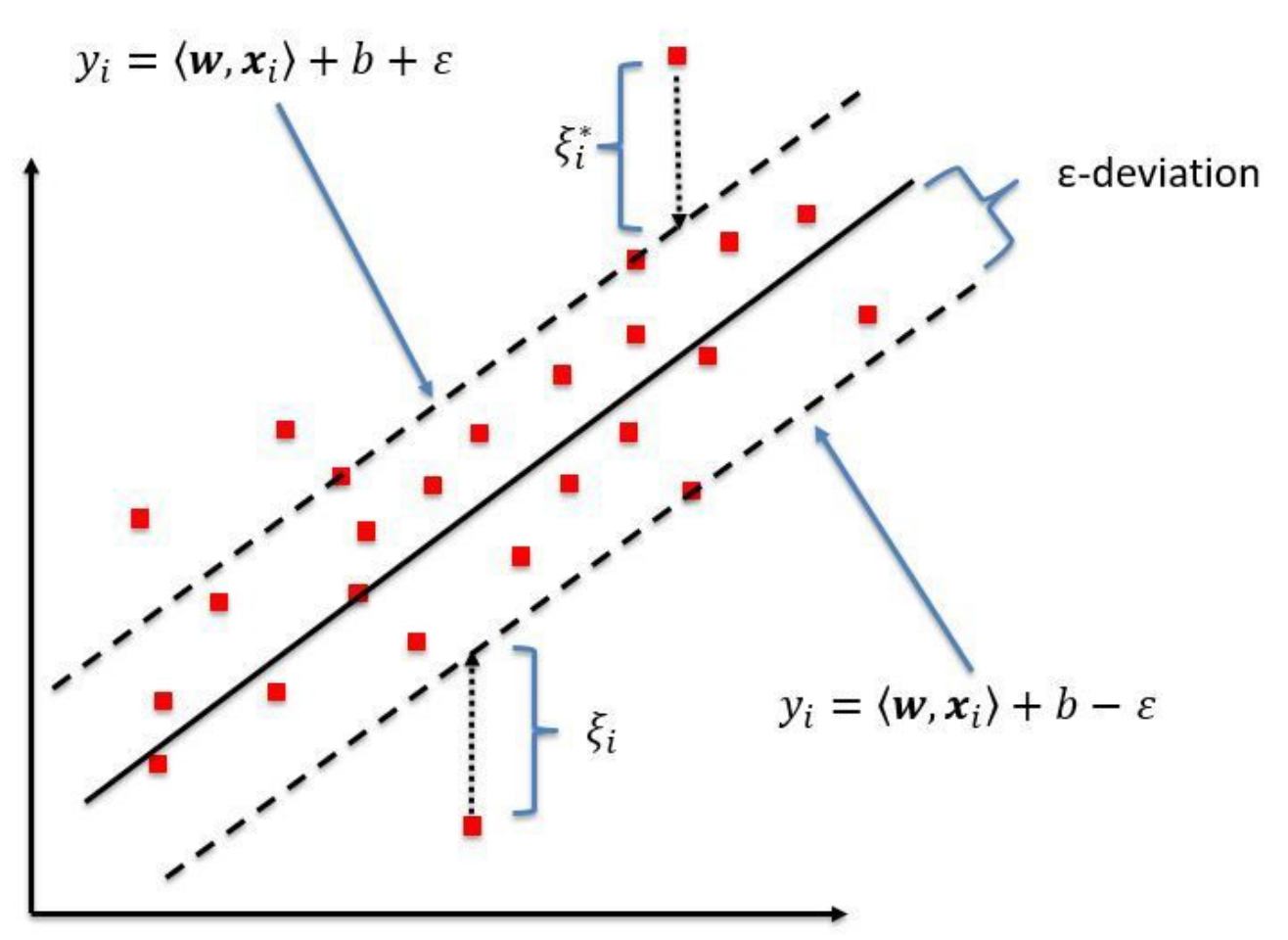
Methodology – Process Flow



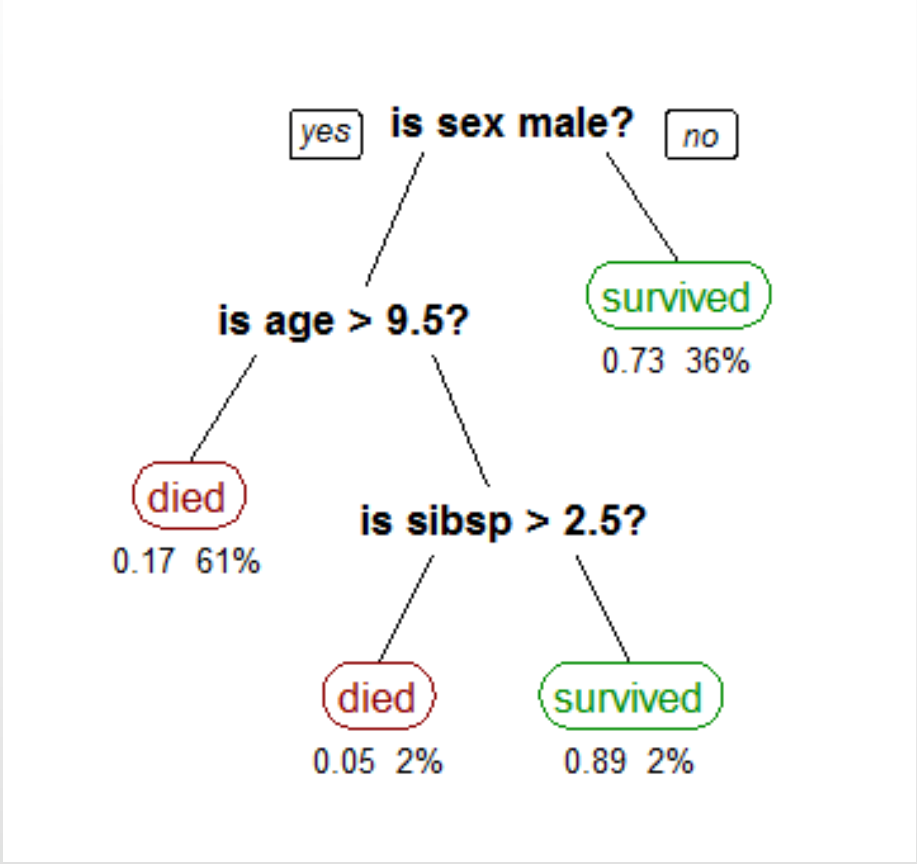
Methodology – Classifier Models

Support Vector Machine (SVM):	Naïve Bayes:	Decision Tree	Random Forest	Logistic Regression
• Classifies instances with high efficiency if they are in the form of vector [4] • Used to find optimal dividing hyperplane between classes [4]	• Based on implementation of Bayes Theorem [8] • Works on the assumption that attributes are independent of each other	• Structure similar to flowchart [9] • Consists of Decision Nodes, Chances Nodes and End Nodes [9]	• Ensemble learning method [10] • Builds swarm of decision trees during training • Overfit the model to training set [10]	• Logistic function used to model binary class variable • Label should be numerical (0/1) [11]

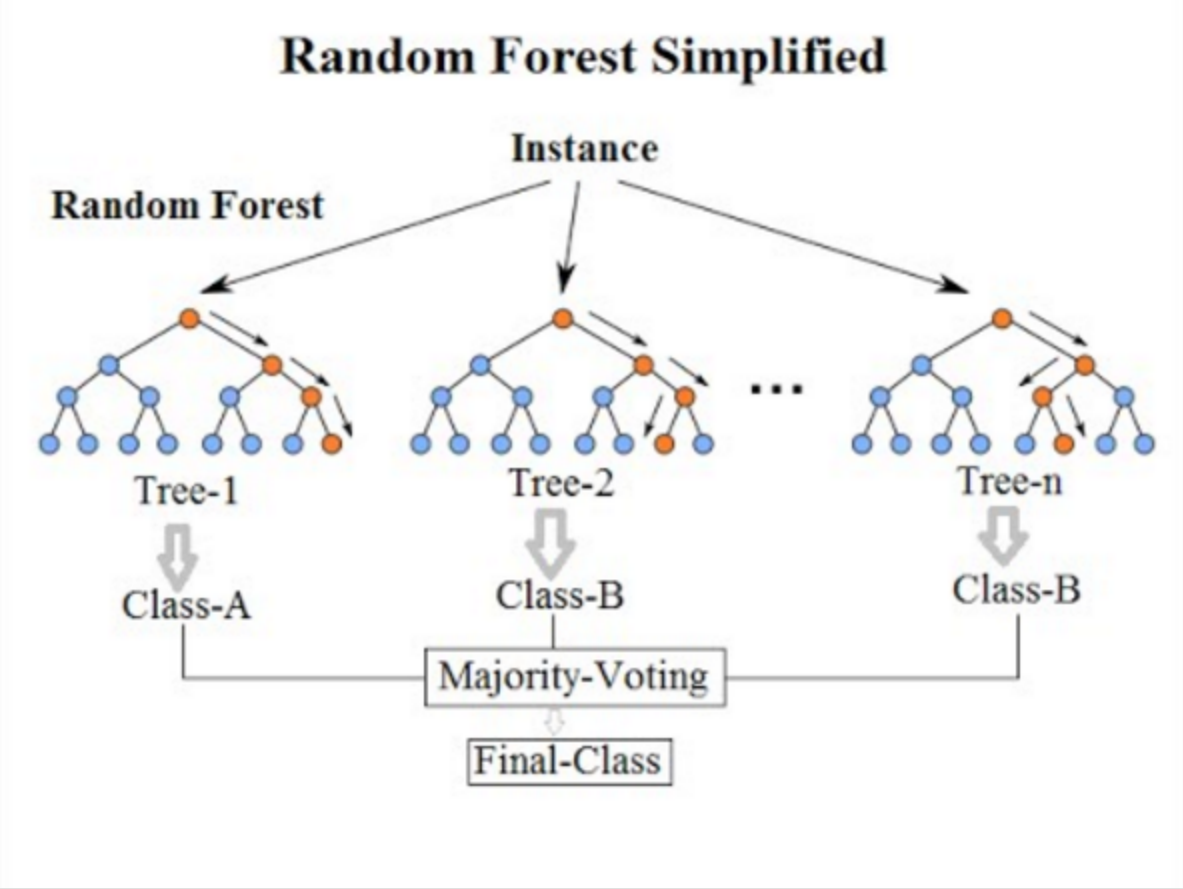
Methodology - SVM



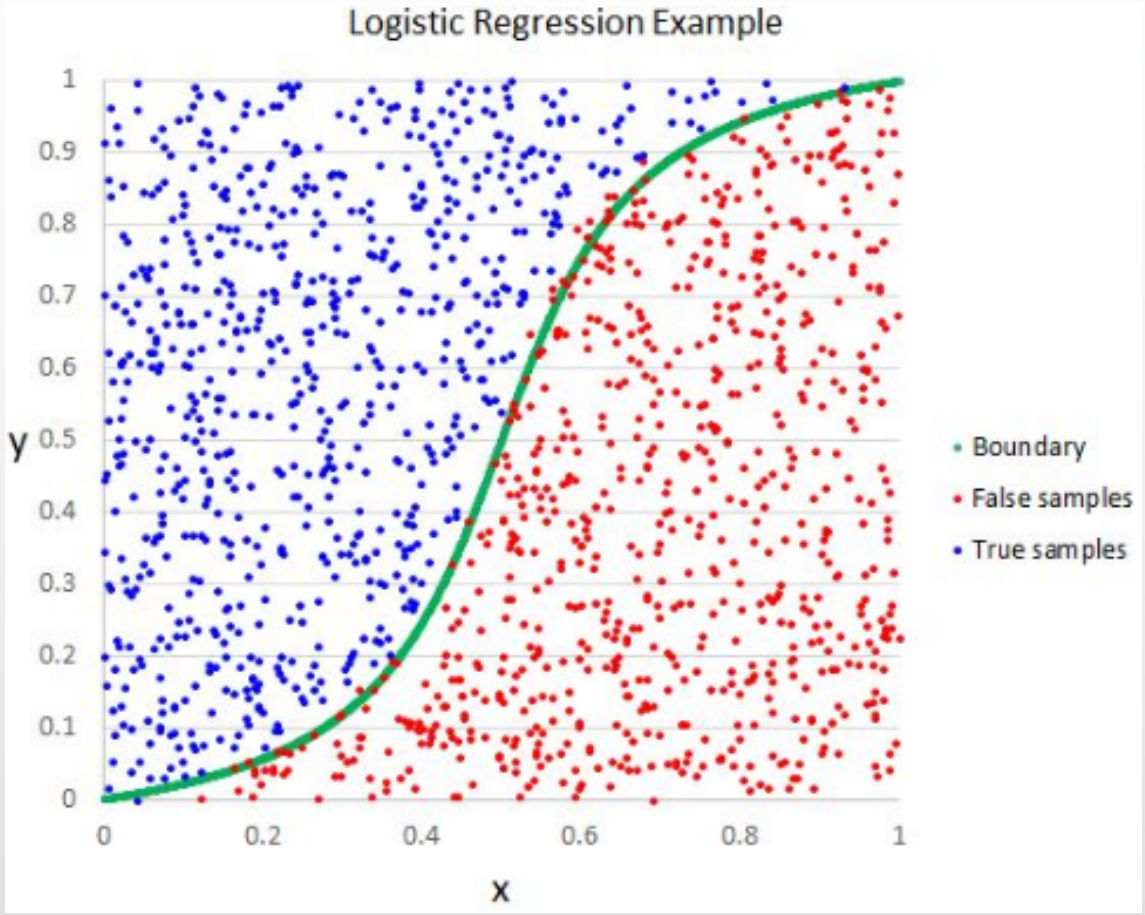
Methodology – Decision Tree



Methodology – Random Forest



Methodology – Logistic Regression



Methodology – Performance Measures

- Confusion Matrix / Contingency Table:

Confusion Matrix	Actual Class		
Predicted Class	Class	Class A	Class B
	Class A	True Positive (TP)	False Positive (FP)
	Class B	False Negative (FN)	True Negative (TN)

Methodology – Performance Measures

Accuracy	(TP + TN) / (TP + TN + FP + FN)
Balanced Accuracy	((TP / P) + (TN + N)) / 2
Recall (R) / Sensitivity (SN)	TP / (FP + TN)
Specificity (SP)	TN / (TN + FP)
Precision (P)	TP / (TP + FP)
Negative Predictive Value (NPV)	TN / (TN + FN) [6]
Fall-out	FP / (FP + TN)

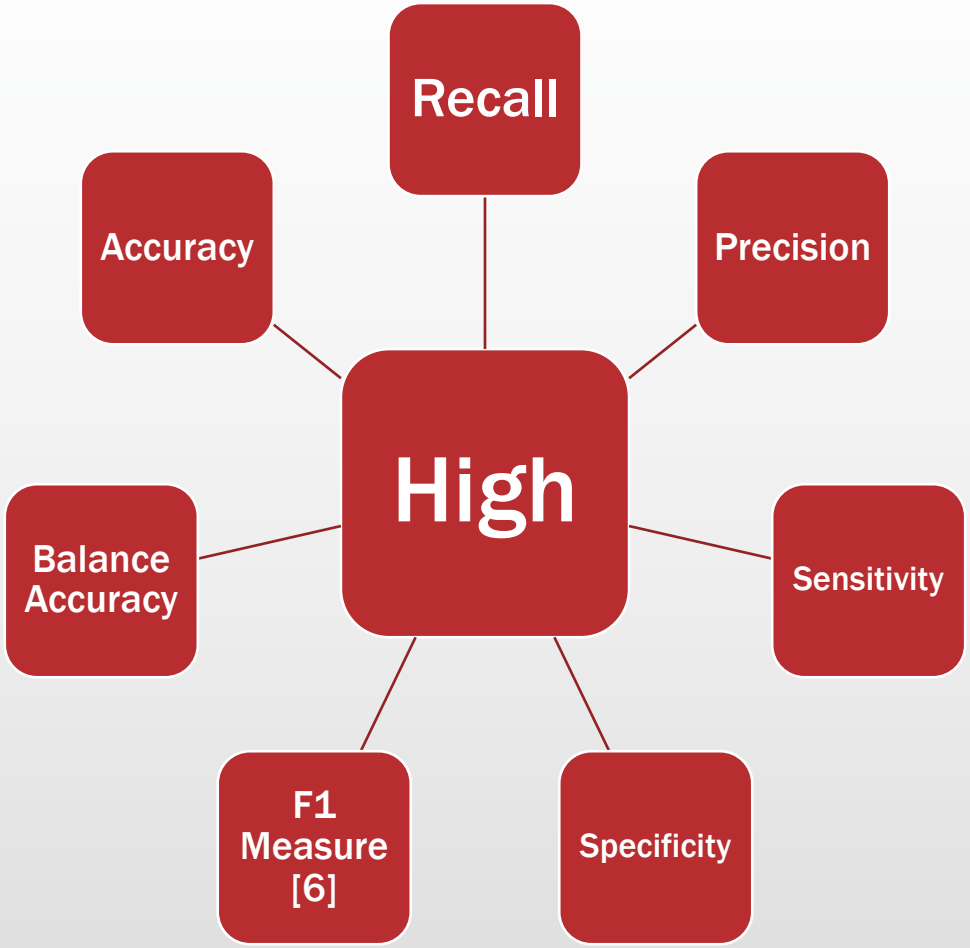
Methodology – Performance Measures

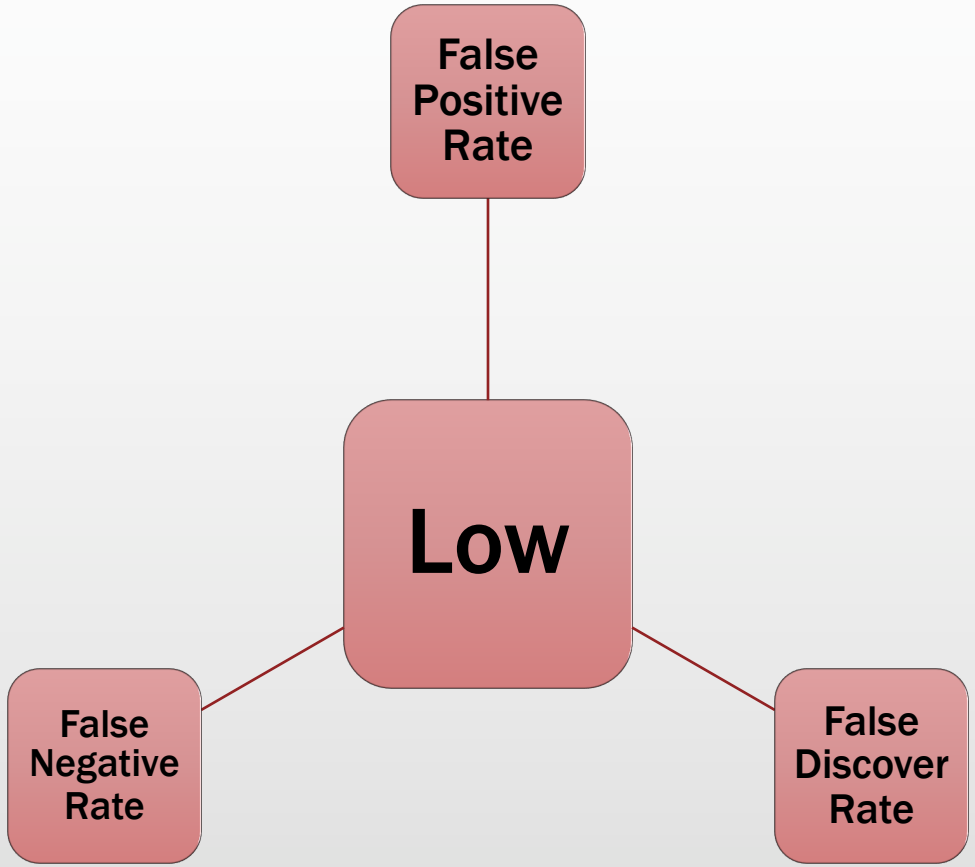
False Discovery Rate	FP / (FP + TP)
False Negative Rate	FN / (FN + TP)
F-Measure	2 * P * R / (P + R) [6]
Mathews Correlation Coefficient	((TP * TN) – (FP * FN)) / sqrt((TP + FP) * (TP + FN) * (TN + FP) * (TN + FN))
Informedness [7]	SP + SN - 1
Markedness	P + NPV - 1

Results & Discussion

- Missing values in the dataset has been imputed using Predictive Mean Matching
- Numerical attributes normalized using Z-score Normalization
- Holdout method used iteratively to split data into Train and Test where each iteration has different set of instances

Results & Discussion – Good Classifier





Results & Discussion

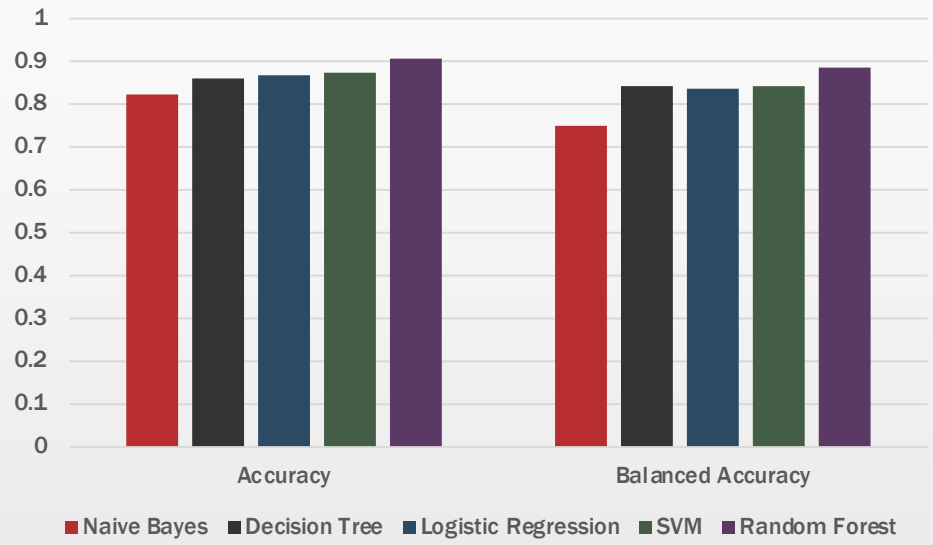
Performance Measure	Naïve Bayes	Decision Tree	Logistic Regression	SVM	Random Forest
Accuracy	0.823	0.86	0.867	0.873	**0.907**
Balanced Accuracy	0.749	0.843	0.836	0.842	**0.885**
Recall	0.536	0.808	0.702	0.788	**0.845**
Specificity	**0.962**	0.878	0.904	0.896	0.926
Precision	**0.867**	0.45	0.717	0.55	0.683
Negative Predictive Value [6]	0.813	**0.963**	0.904	0.954	**0.963**
Fall-out	**0.038**	0.122	0.096	0.104	0.074
False Discovery Rate [6]	**0.133**	0.55	0.283	0.45	0.317
False Negative Rate	0.464	0.192	0.298	0.212	**0.155**
F-Measure [6]	0.66	0.535	0.68	0.622	**0.734**

Results & Discussion

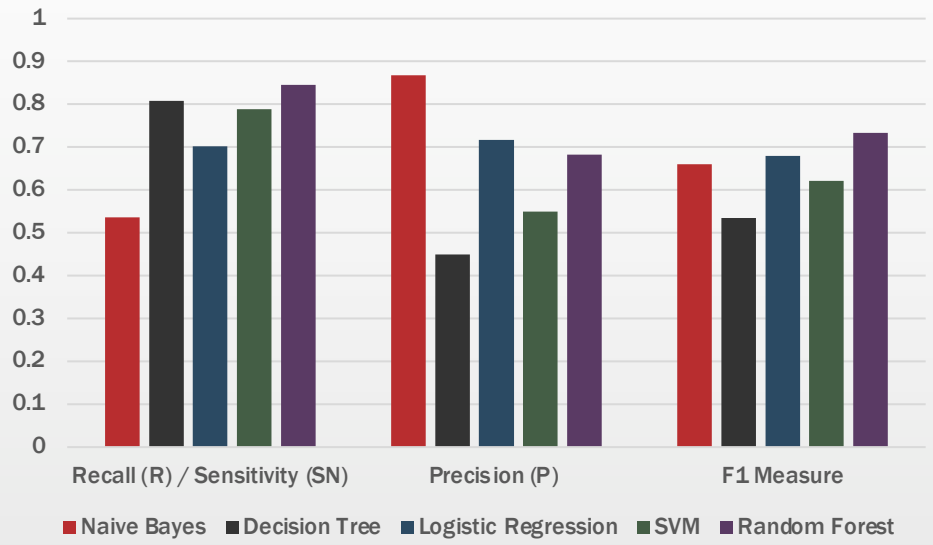
Performance Measure	Naïve Bayes	Decision Tree	Logistic Regression	SVM	Random Forest
Matthews Correlation Coefficient	0.116	**0.206**	0.158	0.189	0.189
Informedness [7]	0.499	0.687	0.606	0.684	**0.771**
Markedness	**0.679**	0.413	0.621	0.504	0.646

Results & Discussion

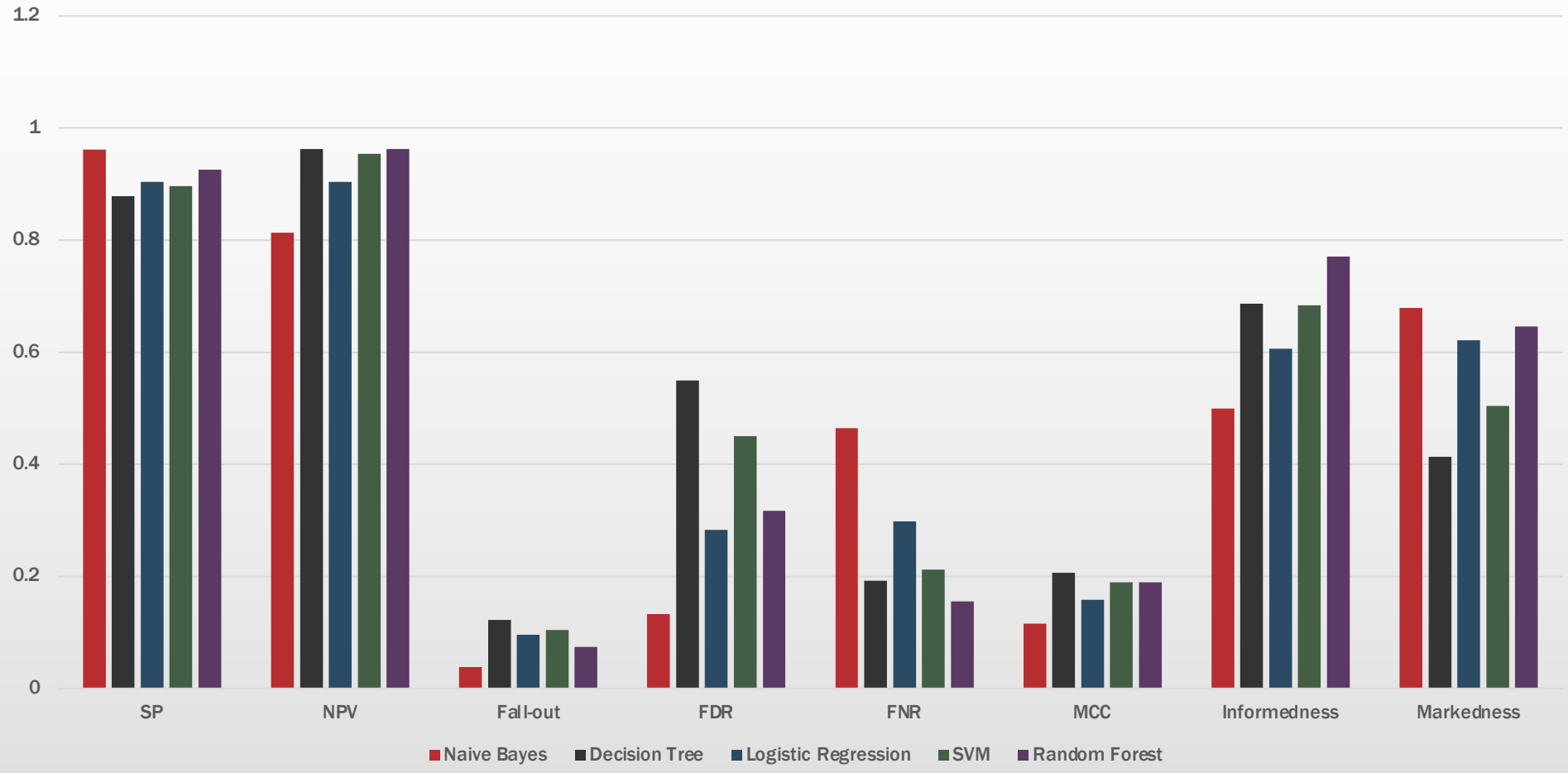
Accuracy & Balanced Accuracy



Recall, Precision & F1 Measure



Results & Discussion



Conclusion

- Inspected the performance of different classifiers modeled on the Hepatitis Data from UCI repository
- Random Forest works best with accuracy of 90.7%
- Also this model can be chosen because it worked well on the sparse data

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