Multiclass Classification -Predicting Disease given Symptoms

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Introduction - Problem Statement

- September 2023 Census Bureau report: 26 million Americans lack health facility access or insurance affordability.
- Machine learning in healthcare is increasing in popularity due to improved prediction technology.
- Growing availability of healthcare data provides a foundation for accurate prediction models.

Data sourced from the 'Disease Prediction Using Machine Learning' dataset on Kaggle, offering a symptom-diagnosis data frame.

Our goal

Construct a model that can forecast the disease associated with a patient's symptoms.



Exploratory Data Analysis

Exploratory Data Analysis

Number of Symptoms/Features	132
Number of Observations	4692
Number of Diseases	42

Top 10 symptoms:

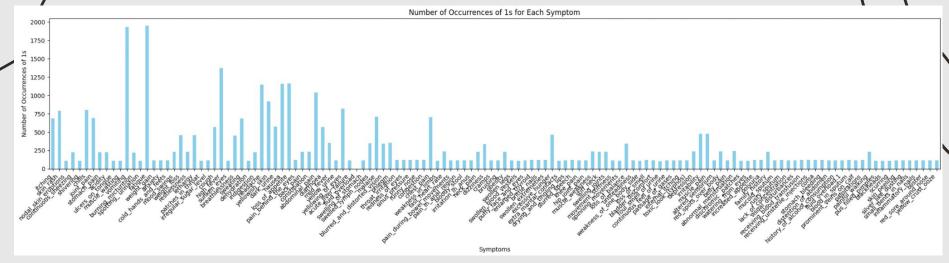
Fatigue, vomiting, high_fever, loss_of_appetite, nausea, headache, abdominal_pain, yellowish_skin yellowing_of_eyes, chills

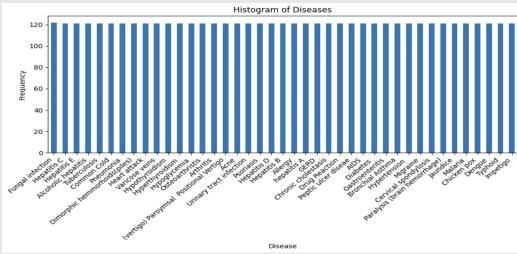
Top 10 diseases:

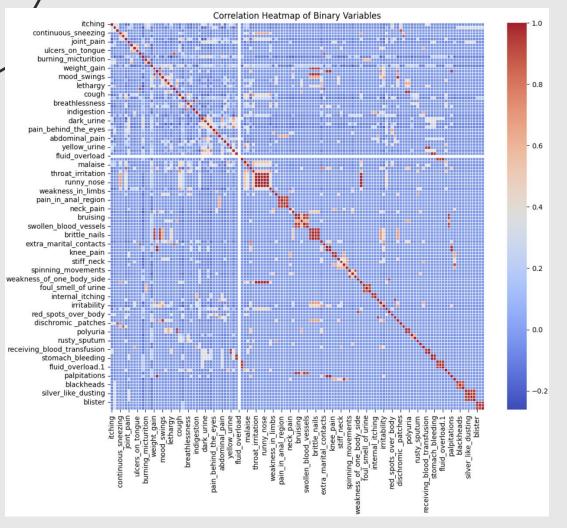
Fungal infection, Hepatitis C, Hepatitis E, Alcoholic hepatitis, Tuberculosis, Common Cold, Pneumonia, Dimorphic hemmorhoids(piles), Heart attack, Varicose veins

small_dents_in_nails	inflammatory_nails	blister	red_sore_around_nose	yellow_crust_ooze	prognosis
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Fungal infection
0	0	0	0	0	Allergy
0	0	0	0	0	Allergy
0	0	0	0	0	Allergy
0	0	0	0	0	Allergy
0	0	0	0	0	Allergy
0	0	0	0	0	Allergy
0	0	0	0	0	Allergy

STA 141C//Final Project







Correlation heatmap: we calculated the correlation matrix and created a heatmap to visualize the numbers.

With so many predictor variables, it is hard to see the specific correlations. However, we see that a majority of the predictor variables are not correlated with each other.

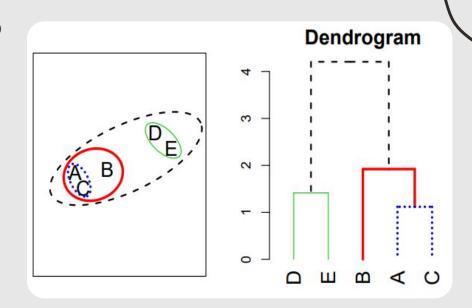
We looked at the top predictor variables that are correlated with each other. Redness_of_eyes, throat_irritation, sinus_pressure, loss_of_smell, congestion, runny_nose, phlegm, blurred_and_distorted_vision, malaise

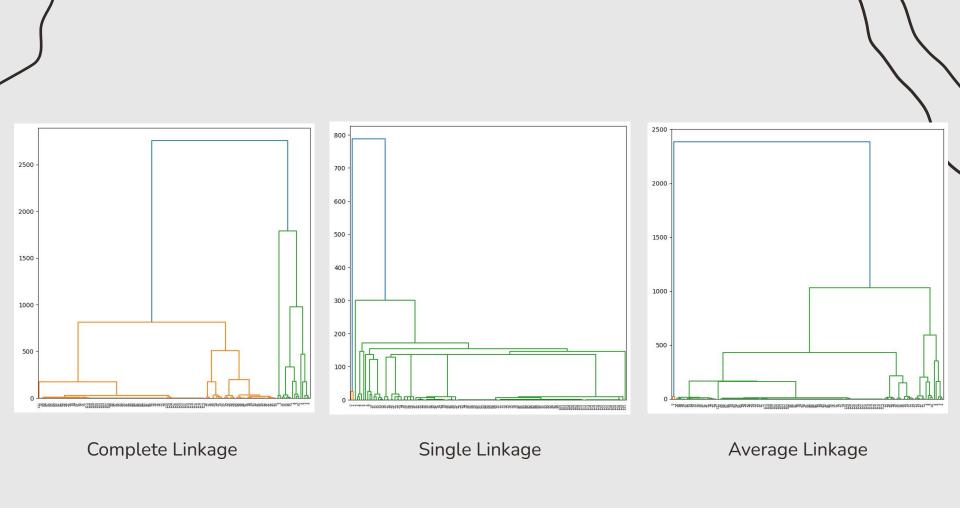
Clustering

Clustering can be used to see if we can group similar symptoms together.

Hierarchical Clustering: Doesn't need a predefined number of clusters, allows us to create dendrograms based on Euclidean distance.

Height of each fusion in dendrogram can indicate similarities/dissimilarities between symptoms.









Data Preprocessing:

NA/Missing values, Types, Label encoding, Correlated Features

Random Forest Model:

Bagging

Higher prediction accuracy than individual DTL, DTL are prone to overfitting

Error Calculation: Out of Bag

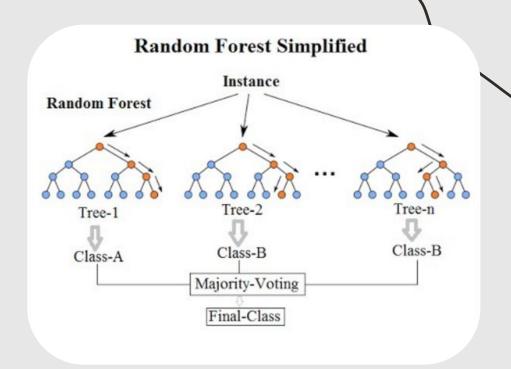
Observations not seen in bootstrapped samples.

Validity: ⅓ observations are unseen, unfitted data

Error: Measured through majority vote. Predictions obtained through passing observation -> RF Majority vote classification of aggregated individual trees

Random Forest

- Why RF?
 - Ensemble of trees using bootstrapped training samples
 - Binary data
- Why RF > DT?
 - Decision Tree
 - Interpretability, easier feature split, less complex
 - OVERFIT
 - Random Forest
 - Larger, complex
 - Aggregated trees lead to less overfitting, lower variance, decorrelation





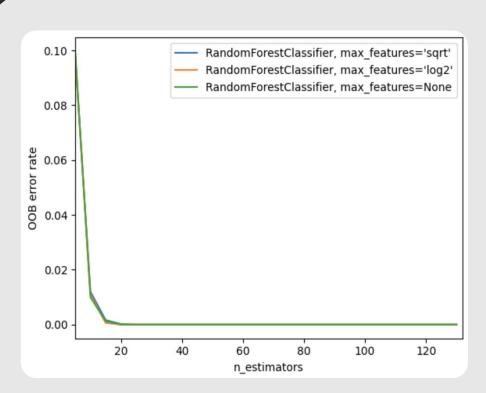
& Accuracy Measurements

	precision	recall	f1-score	support
accuracy	0.976190	0.976190	0.976190	0.97619
macro avg	0.987805	0.987805	0.983740	42.00000
weighted avg	0.988095	0.976190	0.976190	42.00000

SAME RESULTS FOR ALL FEATURE SIZES

[M = P, M = P/2, M = SQRT(P)]





How many trees is good?

Out of Bag: The out-of-bag (OOB) error represents the mean error of each observation, utilizing predictions from trees that exclude that observation in their bootstrap samples. This feature enables the RandomForestClassifier to be trained and validated simultaneously.

Discussion/ Outlook



- High accuracy
- Random Forest performed well given the binary data



- Compare other tree based methods
- Eliminate more variables
- Change the train/test split of the dataset

Conclusion



- Our fitted model turned out to perform really well in classifying the symptoms into diseases
- Clustering also helped in indicating similarities and dissimilarities between symptoms
- However, because our accuracy was so unusually high, this could be an indicator of bias present in our model
- This could be due to a poor split of between the training and testing data, or our model is insufficient in predicting symptoms with diseases in this particular dataset