30-Day Diabetes Readmission

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1

TABLE OF CONTENTS

01.

02.

03.

04.

05.

Project Scope

Overview of project charter and

Introduction

of diabetes, dataset and Infrastructure Project

Overview of infrastructure

Python Project

Overview of data cleaning and ML models

Visualization Project

Overview of Tableau dashboard

01.

Project Scope



3



Project name:

Reducing 30-day Readmission Rate for diabetic patients

Project Objective:

To reduce the 30-day readmission rate for diabetic patients by analyzing a large dataset of diabetic patient records and designing a predictive model using machine learning algorithms to identify patients at high risk of readmission.

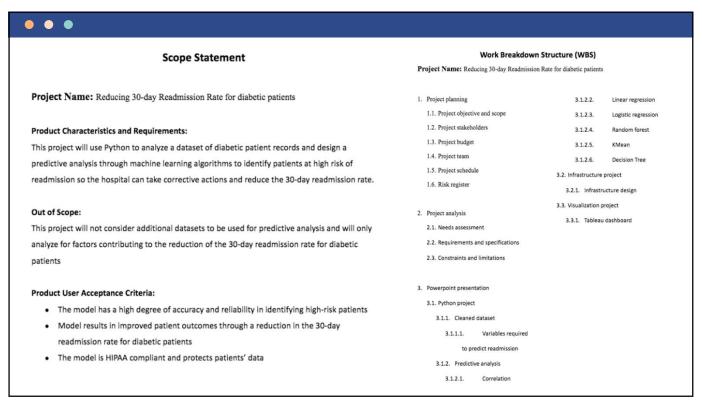
Success Criteria:

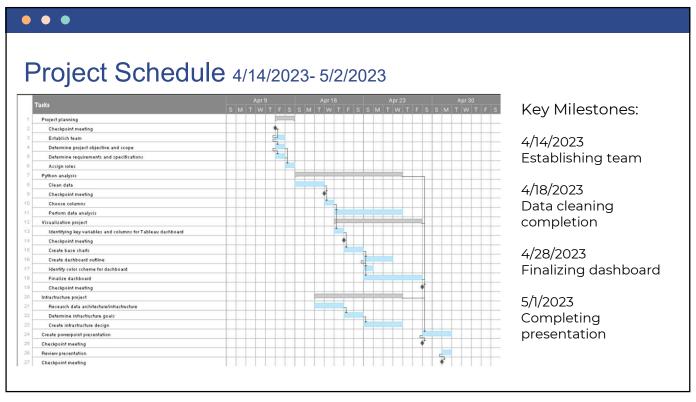
- Identifies leading variables of readmission
- Predictive model is accurate and reliable
- Project milestones are met on time
- Successful integration of predictive models into hospital's workflow
- Stakeholders are satisfied

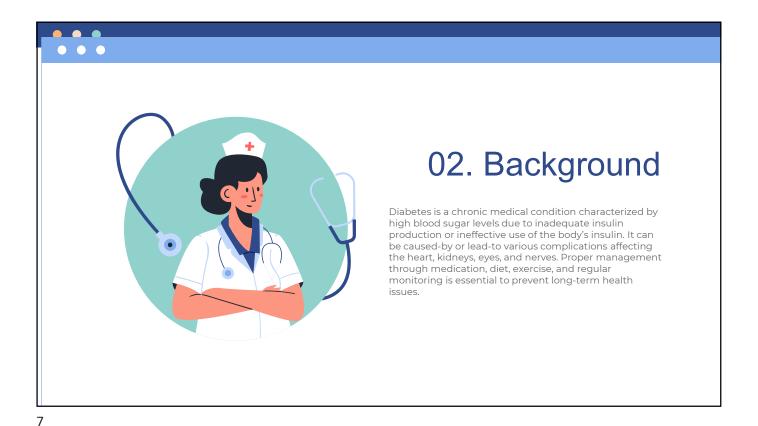
Approach:

Python program will be used to analyze the dataset of diabetic patient records to determine the leading variables of readmission. A predictive model that identifies high risk patients will be designed and deployed. Tableau program will be used to visualize the work done in building the diabetes remission predictive model.

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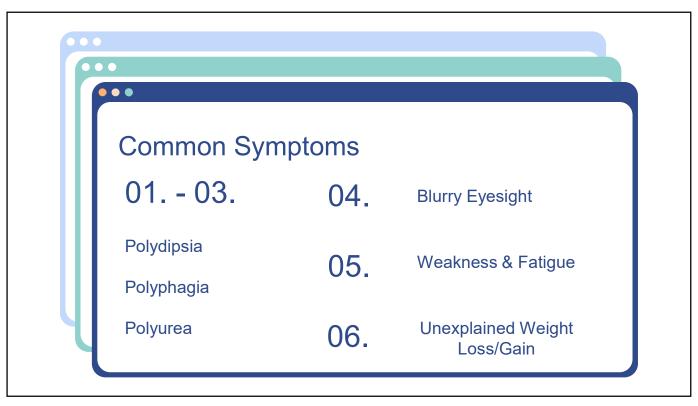


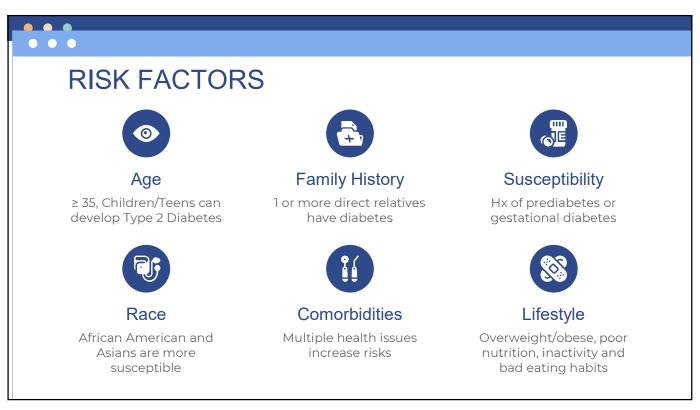


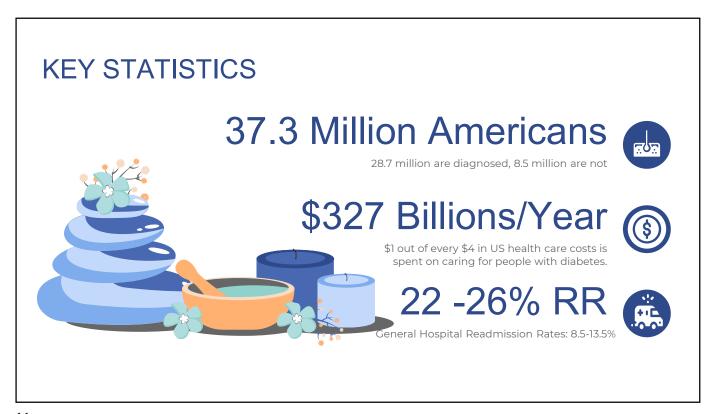
Type 1

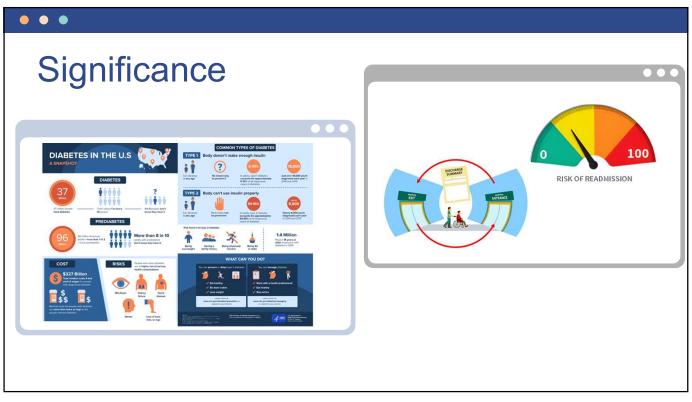
(Hereditary) Immune system attacks the cells that produce insulin, so the body is unable to make insulin

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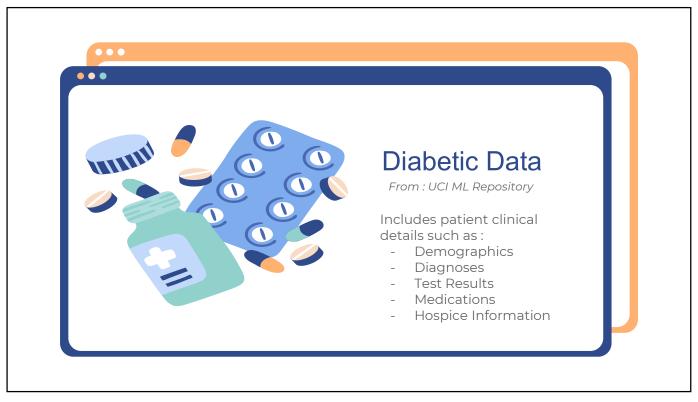
Diabetic Data

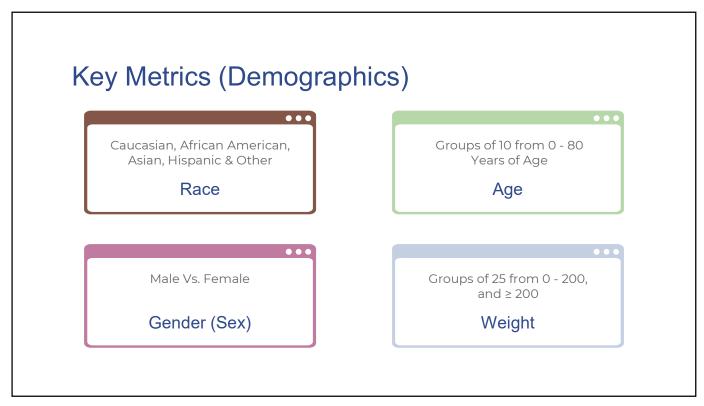
From: UCI ML Repository

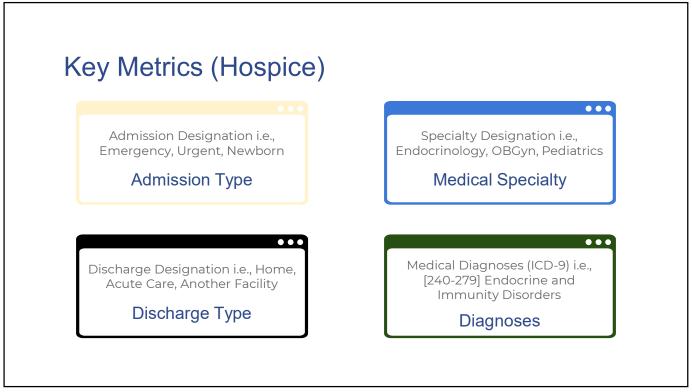
10 Years (1999 - 2008) of Clinical Diabetic Data from 130 US Hospitals. To be used to construct (test, train, and deploy) a ML Model for 30-Day Diabetic Based Readmissions Prediction



13









Blood Sugar Level (mg/dl) i.e., Normal [150], Prediabetic [≥ 200], Diabetic [≥ 300]

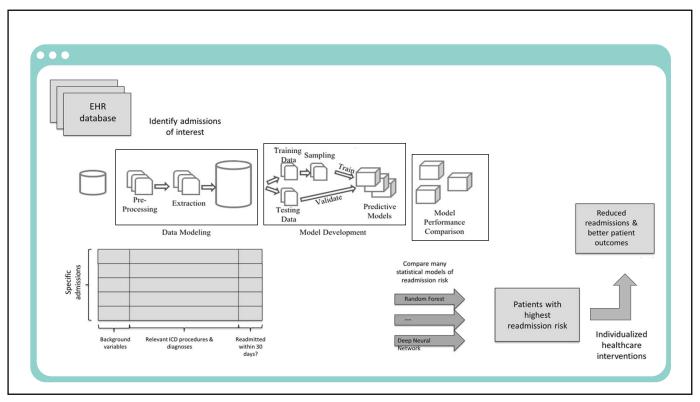
MAX GLU SERUM

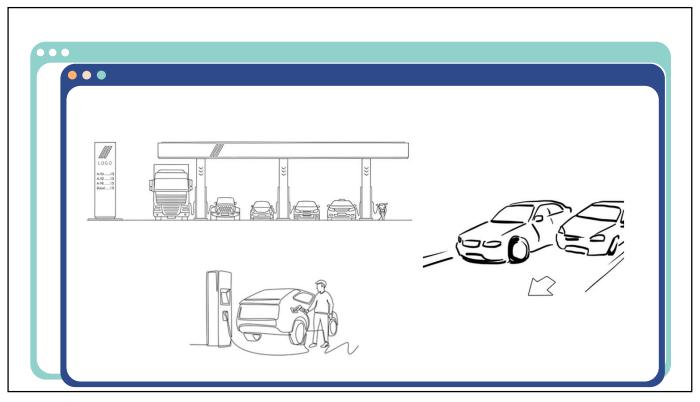
Hemoglobin A1C Level i.e., Normal [150], Prediabetic [≥ 7], Diabetic [≥ 8]

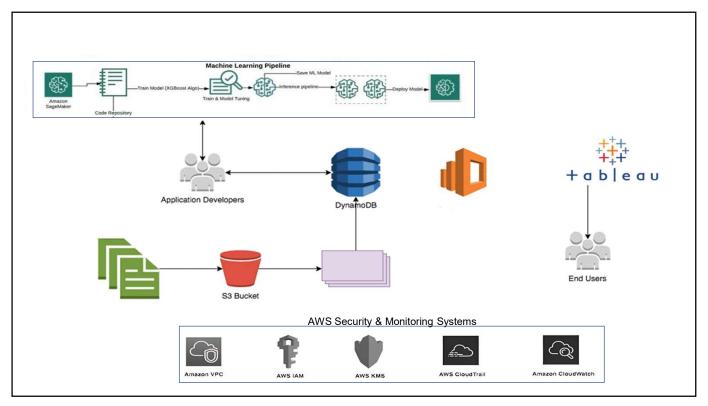
A1CRESULT

17











Python Project Overview

Data Cleaning

Grouping Data, Missing Data, etc.

Feature Selection

Feature Importance, Correlation Heat Map, Recursive Feature Elimination



Exploratory Analysis

Review Missing Data, Categorical Data, Numerical Data

ML + Hyperparameter Tuning

Logistic Regression, Random Forest, etc.

23

Data Cleaning

Re-Admitted



Final Variables: 'YES' and 'NO'

Admission Source ID

'Physician Referral'
'Emergency Room' 'Clinic Referral' 'Transfer from a hospital' 'Transfer from a Skilled Nursing Facility (SNF)', 'Transfer from another health care facility' nan 'HMO Referral' 'Court/Law Enforcement' 'childbirth', 'Transfer from critical access hospital' 'Transfer from hospital inpt/same fac reslt in a sep claim', 'Transfer from Ambulatory Surgery Center'

Admission Type ID



Final Variables: NULL 'Emergency' 'Urgent' 'Elective' 'Newborn' 'Trauma Center'



Data Cleaning

discharge disposition ID

nan
'home'
'acute_care'
'expired'
'left_AMA'
'hospice'
'other_healthcare_facility'

Medical Specialities

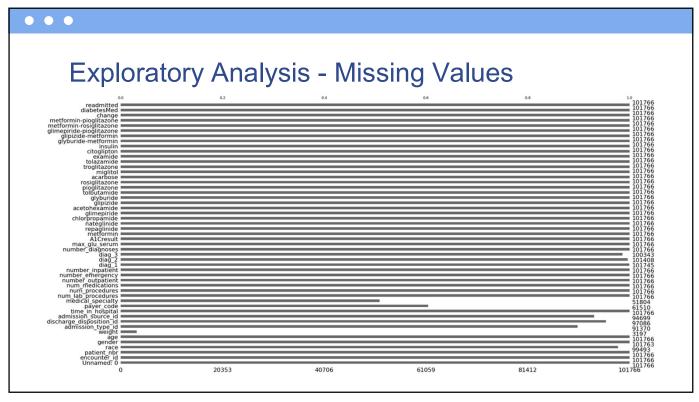
'surgery'
'pediatrics'
'orthopedics'
'ob_gyn'
'psychiatry'
'primary_care'
'cardiology'
'oncology'
'endocrinology'
'neurology'
'anesthesiology'
'radiology'

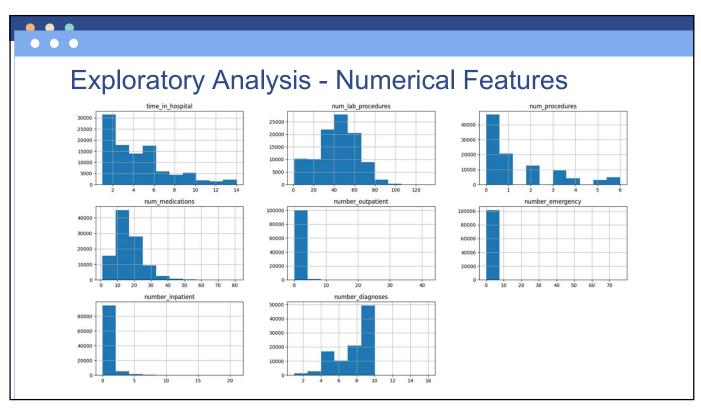
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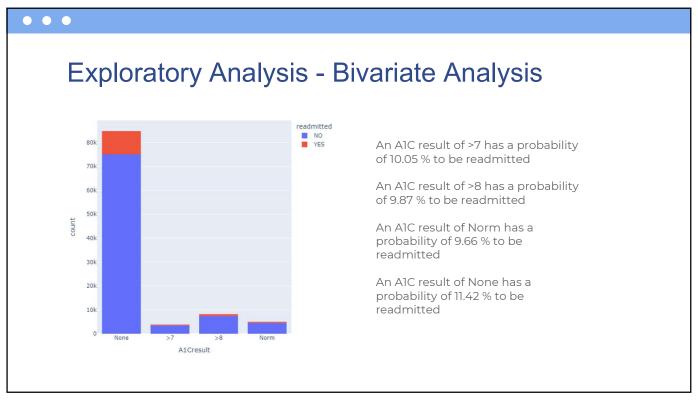


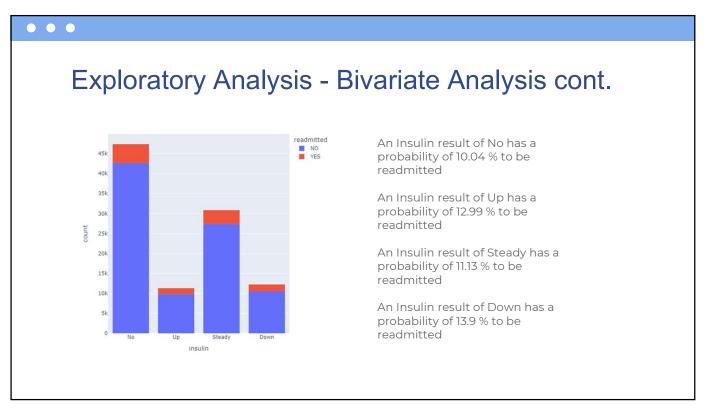
Data Cleaning - Diagnostic 1, 2, 3 Columns

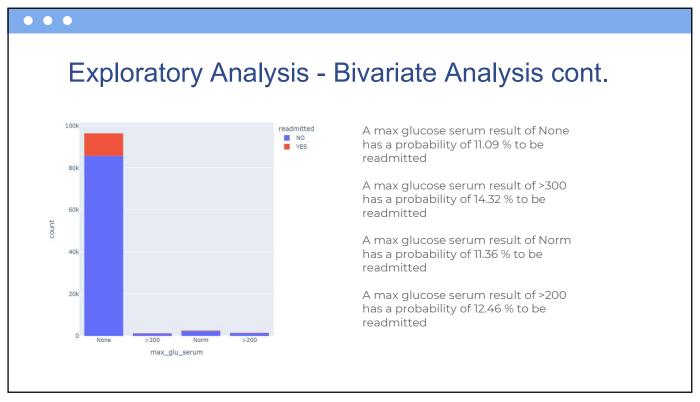
'ENDOCRINE, NUTRITIONAL AND METABOLIC DISEASES, AND IMMUNITY DISORDERS' 'COMPLICATIONS OF PREGNANCY, CHILDBIRTH, AND THE PUERPERIUM' 'INFECTIOUS AND PARASITIC DISEASES' 'NEOPLASMS' 'DISEASES OF THE CIRCULATORY SYSTEM' 'DISEASES OF THE RESPIRATORY SYSTEM' 'INJURY AND POISONING' 'DISEASES OF THE SKIN AND SUBCUTANEOUS TISSUE' 'DISEASES OF THE MUSCULOSKELETAL SYSTEM AND CONNECTIVE TISSUE' 'DISEASES OF THE DIGESTIVE SYSTEM' 'SUPPLEMENTARY CLASSIFICATION OF FACTORS INFLUENCING HEALTH STATUS AND CONTACT WITH HEALTH SERVICES' 'SYMPTOMS, SIGNS, AND ILL-DEFINED CONDITIONS' 'DISEASES OF THE GENITOURINARY SYSTEM' 'MENTAL, BEHAVIORAL AND NEURODEVELOPMENTAL DISORDERS' 'DISEASES OF THE NERVOUS SYSTEM AND SENSE ORGANS' 'DISEASES OF THE BLOOD AND BLOOD-FORMING ORGANS' nan 'CONGENITAL ANOMALIES' 'SUPPLEMENTARYCLASSIFICATION OF EXTERNAL CAUSES OF INJURY AND POISONING'

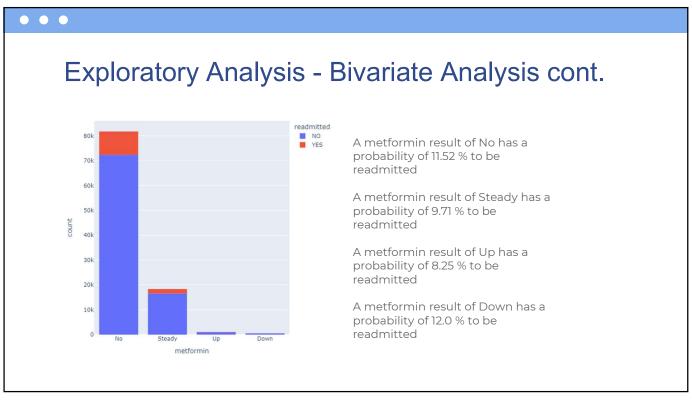


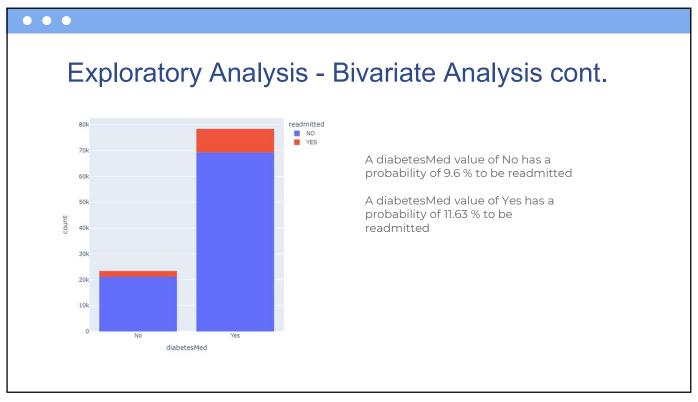


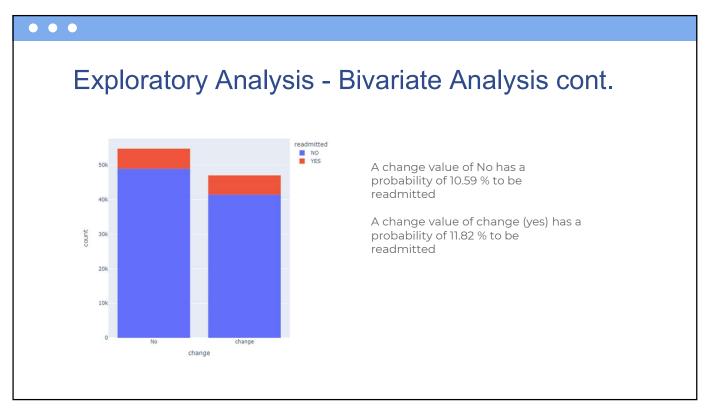


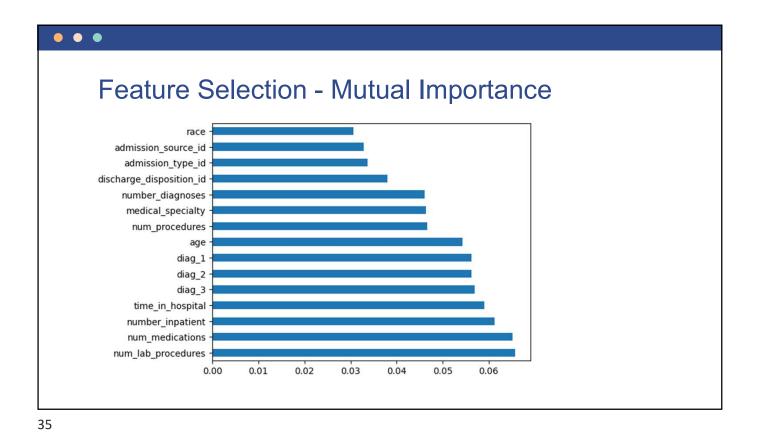












Feature Selection - Recursive Feature Elimination

```
1 y = y_train
2 X = X_train
3
4 from sklearn.feature_selection import RFE
5 from sklearn.linear_model import LogisticRegression
6
7 logreg = LogisticRegression()
8 rfe = RFE(estimator=LogisticRegression(), n_features_to_select=15)
9 rfe = rfe.fit(X, y)
10 print(rfe.support_)
11 print(rfe.ranking_)

[False False False False True False True False Fa
```

[8 18 7 15 1 12 1 19 23 10 9 17 3 1 14 20 21 1 1 4 1 1 1 1

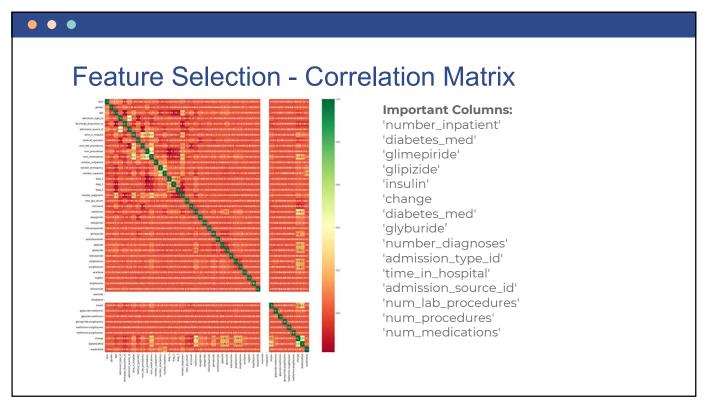
1 26 2 11 1 6 16 1 1 31 1 25 28 5 13 24 29 30 27 22 1]

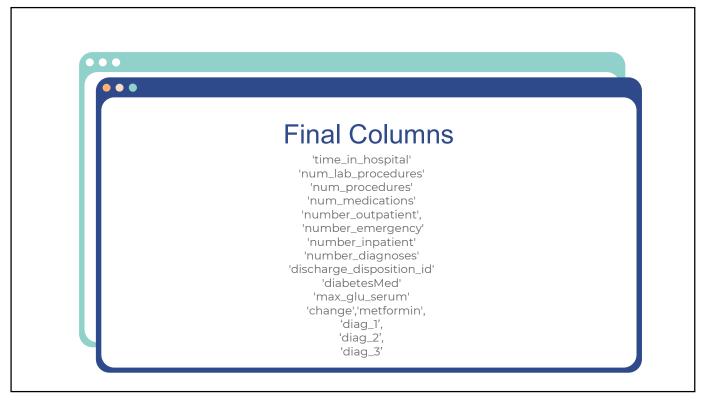
False False False False False False False True]

Important Columns: 'diabetesMed' 'tolazamide' 'miglitol' 'acarbose' 'tolbutamide' 'glimepiride' 'chlorpropamide' 'nateglinide' 'repaglinide' 'metformin ,'max_glu_serum' 'number_diagnoses' 'number_inpatient' 'time_in_hospital' 'discharge_disposition_id'

36

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• • • Results - Without Feature Selection AUC Accuracy Recall Precision Specificity Prevalence Logistic 0.663 0.646 0.573 0.172 0.655 0.111 Regression KNN 0.644 0.646 0.544 0.166 0.619 0.111 0.654 0.655 0.556 0.173 0.667 0.111 Stochastic Gradient Descent 0.594 0.631 0.111 Decision Tree 0.632 0.628 0.168 Random Forest 0.669 0.640 0.618 0.178 0.643 0.111 Linear SVC 0.662 0.879 0.094 0.340 0.977 0.111 0.111 0.649 0.609 0.614 0.164 0.609 Gradient Boosting XG Boost 0.657 0.613 0.617 0.166 0.613 0.111 Cat Boost 0.648 0.602 0.610 0.161 0.601 0.111



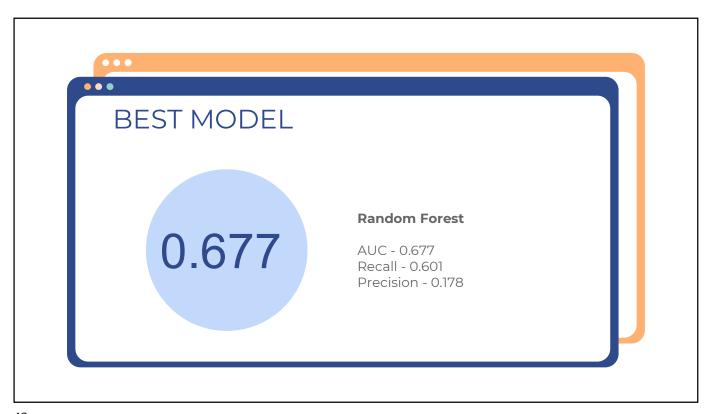
Results - Feature Selection

	AUC	Accuracy	Recall	Precision	Specificity	Prevalence
Logistic Regression	0.663	0.660	0.569	0.178	0.671	0.111
KNN	0.652	0.658	0.535	0.170	0.640	0.111
Stochastic Gradient Descent	0.653	0.661	0.546	0.174	0.671	0.111
Decision Tree	0.633	0.628	0.584	0.166	0.613	0.111
Random Forest	0.673	0.650	0.591	0.179	0.661	0.111
Linear SVC	0.664	0.880	0.077	0.335	0.981	0.111
Gradient Boosting	0.646	0.611	0.590	0.161	0.614	0.111
XG Boost	0.650	0.612	0.612	0.165	0.612	0.111
Cat Boost	0.646	0.605	0.608	0.161	0.605	0.111

41

Hyper-Parameter Tuning

	AUC	RECALL	PRECISION
DECISION TREE	0.62901127267603	0.6301531213191991	0.15853211009174312
RANDOM FOREST	0.6773528020383	0.6095406360424	0.178171802375624
XGBOOST	0.6402066158071	0.598939929328622	0.1611216730038023



```
• • •
                           1 rf_grid = {'n_estimators':range(200,1000,200), # number of trees
                                          'max_features':['auto','sqrt'], # maximum number of features to use at each split
                                         'max_depth':range(1,11,1), # maximum depth of the tree
                                         'min_samples_split':range(2,10,2), # minimum number of samples to split a node
                                         'criterion':['gini', 'entropy']} # criterion for evaluating a split
                          7 rf_random = RandomizedSearchCV(estimator = rf_clf, param_distributions = rf_grid,
                                                               n_iter = 20, cv = 2, scoring=recall_score,
verbose = 1, random_state = 111)
                          11 rf_random.fit(X_train, y_train)
                          13 rf_random.best_params_
                         15 rf_hp_preds = rf_random.best_estimator_.predict(X_valid)
16 rf_hp_preds_proba = rf_random.best_estimator_.predict_proba(X_valid)[:,1]
                          17 roc_auc_score(y_valid, rf_hp_preds_proba)
                         Fitting 2 folds for each of 20 candidates, totalling 40 fits
                         0.6773528020382722
                          1 recall_score(y_valid, rf_hp_preds)
                         0.6095406360424028
                          1 precision_score(y_valid, rf_hp_preds)
                         0.17817180237562402
```

