Introduction

We are attempting to leverage statistical and Machine Learning methods to predict patient survival. The idea is to create a model that helps the provider in better risk assessment. Which in turn can provide better intensive care facilities, provide personalized treatment, allocate resources for patients efficiently like getting the right doctors at the right time, timely change of medication or treatment, movement of patient to another facility etc.

Considering our team's work experience, past projects and interest in healthcare, we are participating in the datathon which focuses on patient survival prediction.

Related Work

Apache System

The APACHE system was first published long ago and provided predictions for patient mortality based upon data collected in the ICU. While the initial system was based on expert rules, later updates used data driven methods. In the kaggle competition we are provided all the fields that the apache system utilizes and therefore the models built are expected to perform better than the apache system.

Past models have been limited by technical and practical considerations, often using summary data from an entire day of a patient's ICU stay which was manually documented by trained personnel [1]. There have also been models that leverage Multivariable logistic regression modelling to evaluate information from history, physical examination (for example, blood pressure), drug use, and quality of life questionnaires that independently contributed to the prediction of death [2].

It is worth noting that the models mostly used purely physiology, laboratory measurements, and minimal demographic variables available on admission, whereas the APACHE system utilized over 100 diagnostic categories, comorbid burden, and treatment. These additional features can often require manual collection which can complicate automatic application of the model.

Other Methods

Apart from the apache system other methods that have gained momentum include models based on Gradient Boosting , Lasso. There have also been models for specific conditions which instead of being generally applicable, find their use in certain specific situations like for patients with acute renal failure [3] or for traumatically injured patients [4]

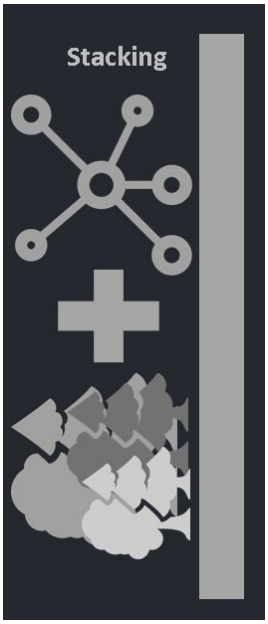
Project Topic and Proposed Solution

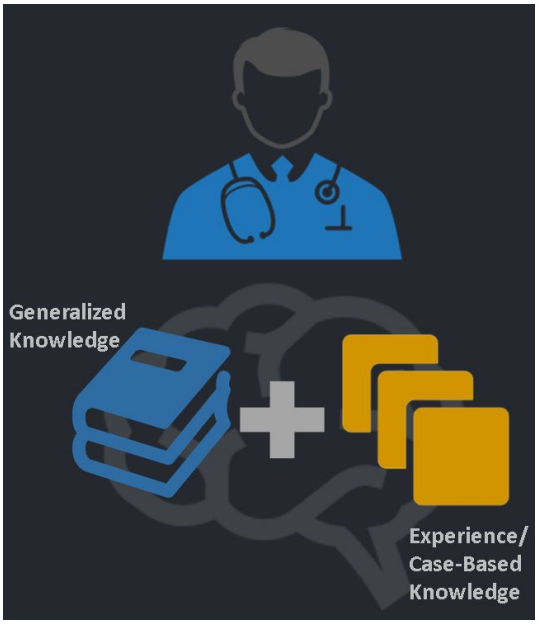
Project Topic : Patient Survival Prediction using Machine Learning and Statistical Methods

Dataset: Primary Dataset to be used is intensive care unit data from hospitals in multiple geographic regions, hosted on Kaggle.

Proposed Solution : Based on the initial research we are planning to use an ensemble method by combining Machine learning and traditional statistical methods. The choice of methods and algorithms would be driven by the EDA and Feature engineering results, as well as our choice of handling missing data.

Our initial intuition suggests **a stacking approach.** Trying to model after how a doctor or a nurse would approach the problem. Considering that a doctor not only has a vast knowledge that was gained from medical school but an even greater knowledge based on experience which allows them to begin investigation from the generalized knowledge but then being able to map out and fit the current patient to any existing case that they had previously handled gives the doctors a great advantage. What this means for us is that we should **not just try generalizing the patterns in medica data but try and use neighborhood based approach** to be able to use the most similar case that we know about as a reference in predicting patient mortality.





Research Question

What are the right features to be used to predict the patient survival.

Project Timeline

	Date	Milestones
1	Feb 7th	EDA
2	Feb 14th	Feature Engineering
3	Feb 20th	Model Selection
4	Feb 24th	Model Evaluation and Submission
5	Mar 7th	Check possibility for addition of external data ,try infuse domain knowledge similar to APACHE scores
6	Mar 20th	Feature Reduction/Selection/Extraction to beat AUC ROC of 0.914
7	Apr 20	Project Complete, final report due

Data And Domain Description

The data has been taken from Kaggle Competition where the challenge is to create a model that uses data from the first 24 hours of intensive care to predict patient survival. This dataset has data for more than 130,000 hospital Intensive Care Unit (ICU) visits from patients spanning one year time frame.

Dataset Link: https://www.kaggle.com/c/widsdatathon2020/datas

Github Link: https://github.com/abhijeetdtu/Datathon

EDA

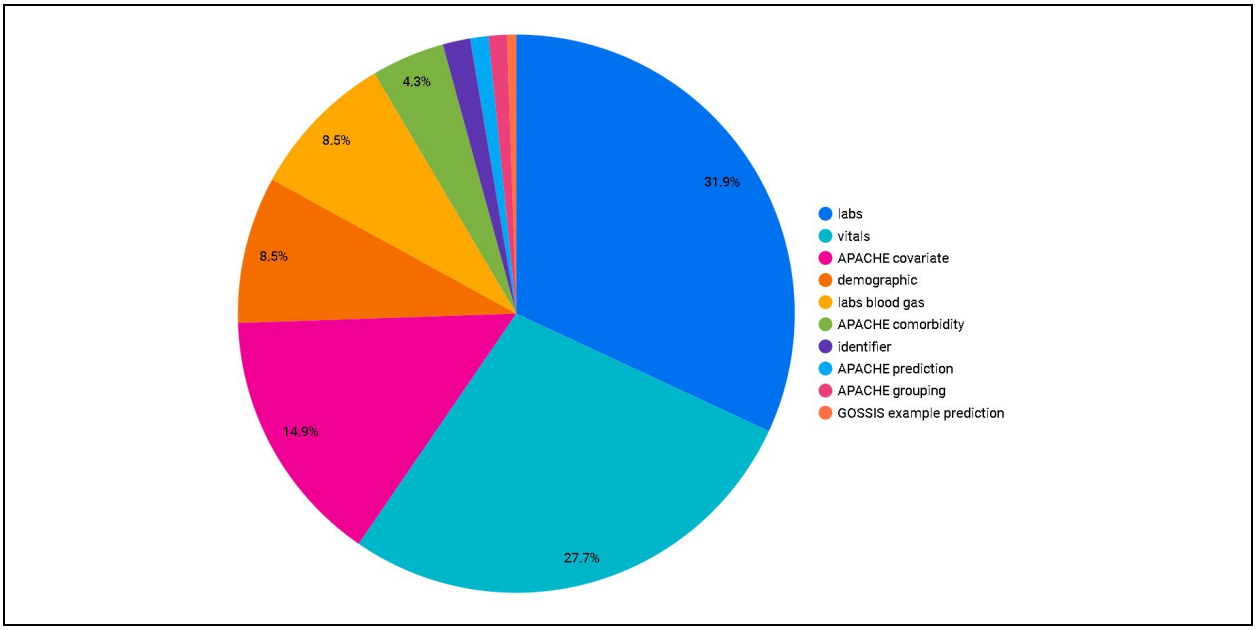
The dataset has a total 186 variables including the dependent variable. The dependent variable is **hospital_death**.

We performed initial exploratory data analysis of the dataset in order to understand the data better by visualizing on Google Cloud Studio.

Following are some of the insights from the visualization.

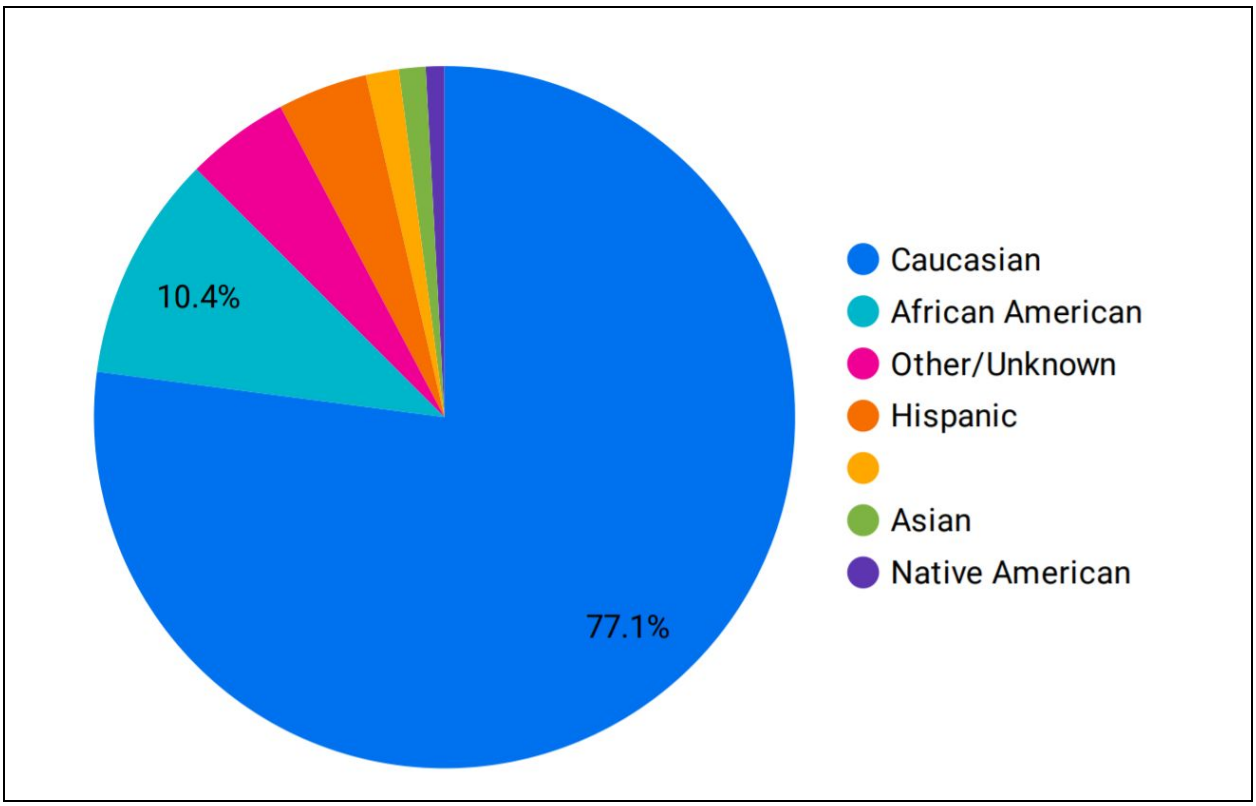
We tried to follow a line of thought as to what type of data we have at hand, who are the patients, what are the demographics , what are the main conditions because of which patients are being admitted etc.

What Data/Features do we have?

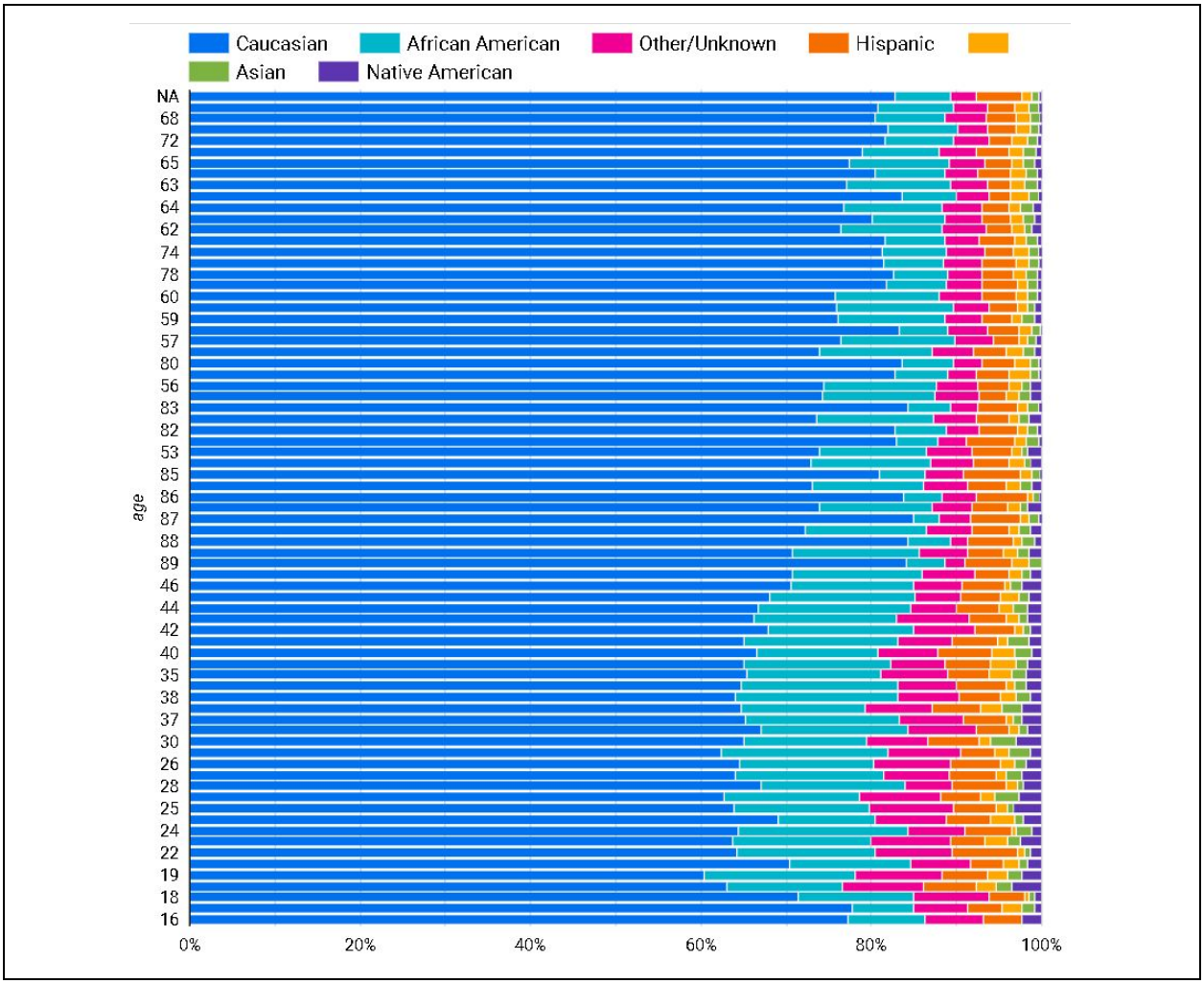


We began by examining what kind of data we have. For this we looked into the data dictionary. We see that **labs and vital readings** account for more than 50% of the data. i.e most of the columns in the dataset belong to these categories. Add to that **APACHE covariates** and we can account for almost 75% of the data. Apache Grouping and Prediction categories have very few columns compared to others.

Who is getting admitted?

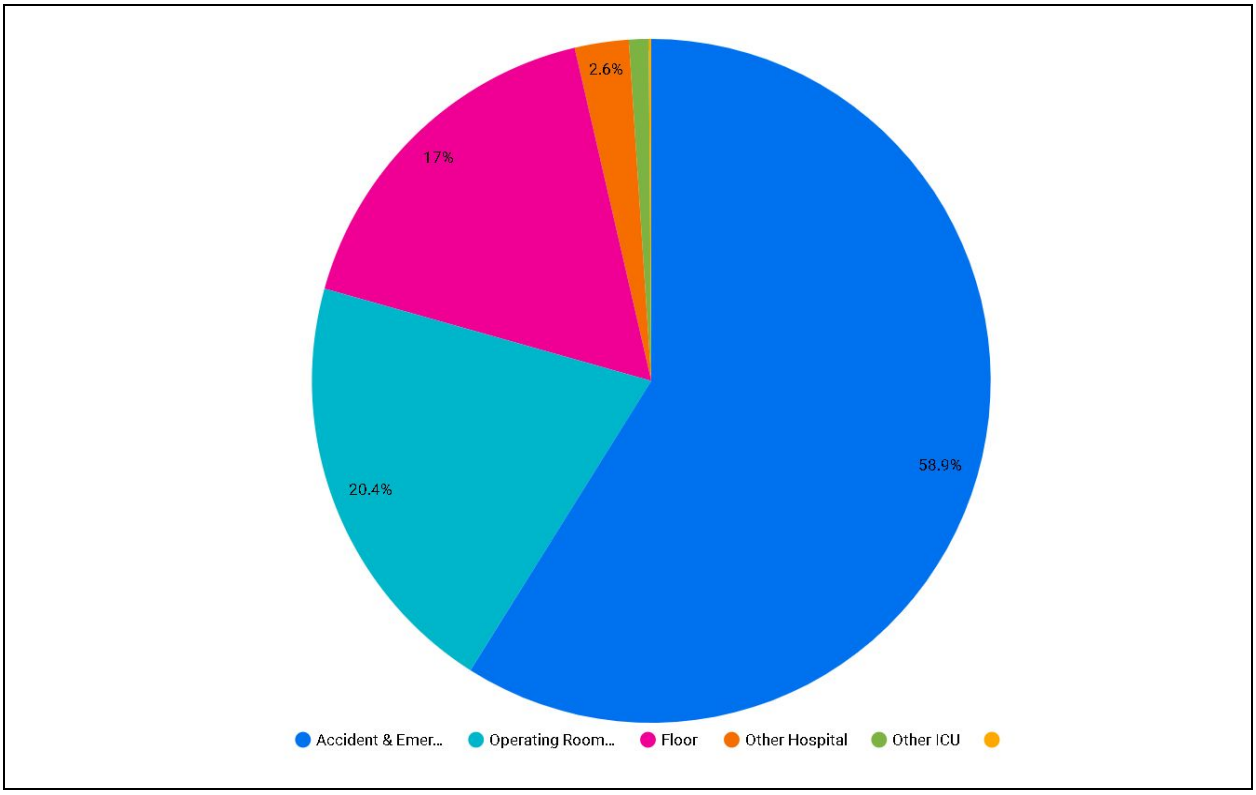


To understand whose data we actually have, we try to drill down along demographic lines.
We use **Ethnicity and Age** to drill into the data. From the Ethnicity Pie Chart, we see that most of the individuals in our dataset are **Caucasians** followed by African Americans.



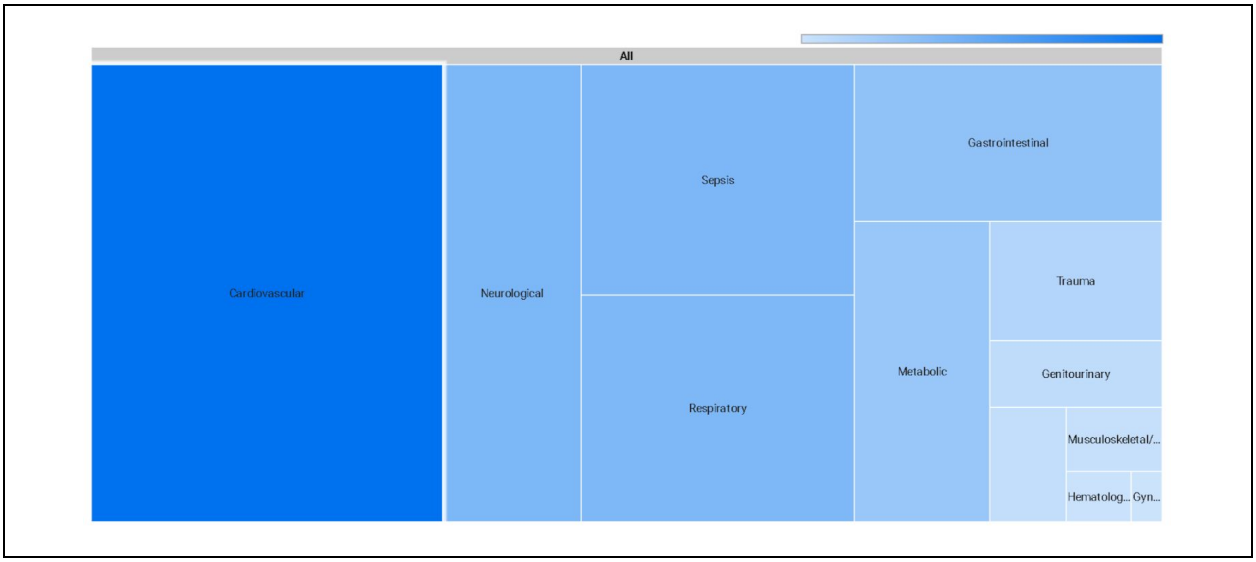
If We add another dimension - Age to the mix - we see an interesting pattern in the bar chart. We see that for African Americans in particular, the **proportion of patients declines with age.** We see that there are a number of young african american patients accounting for around 25-30% of total young patients but as we go upward in the chart to the older population we can see that the proportion drops to an average of around 10%.

Where did they come from?



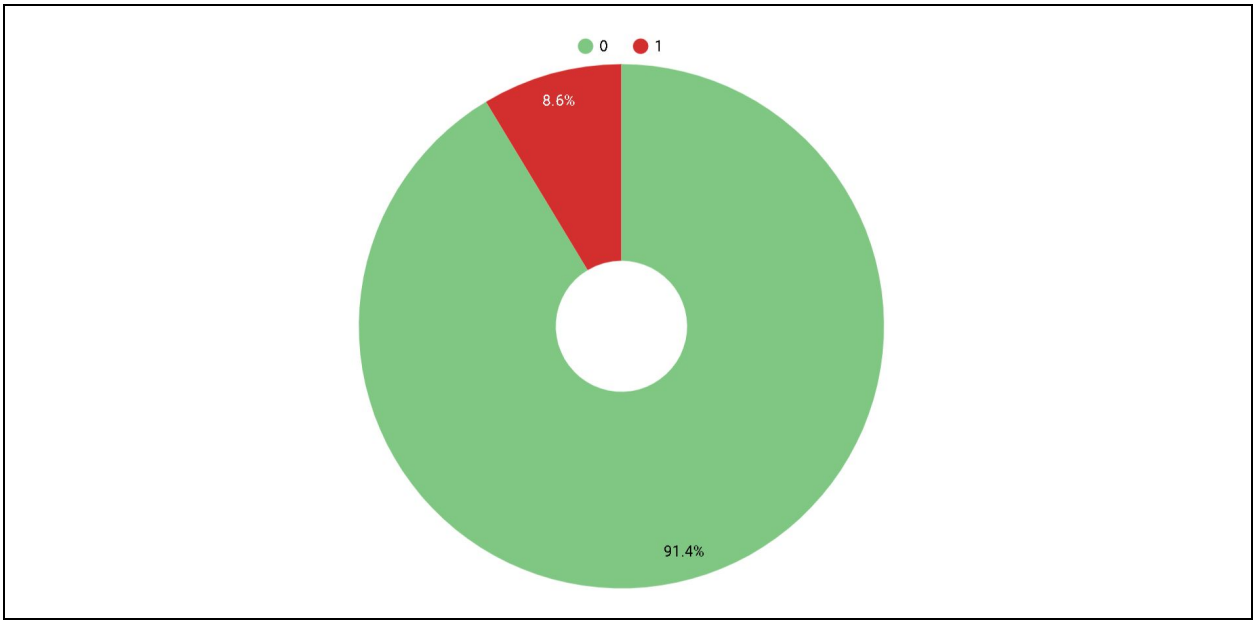
Next step is to explore how people ended up in the ICU. We can see that **Accident & Emergency** account for most of the ICU admissions which is 58.9% of the total admissions. Followed by Movement from the Operating room and then from the hospital wards.

Why are patients getting admitted?



Having seen that most of the people end up in ICU because of accident or emergency. We would like to see what kind of cases are usually seen in the ICU. For that we make a tree map of the diagnosis column. As it turns out most of the cases are Cardiovascular - heart attacks. We see that neurological cases , which might be from car crashes or other accidents , Respiratory and Sepsis cases also account for a large chunk of cases

How Bad is it? : Hospital Deaths

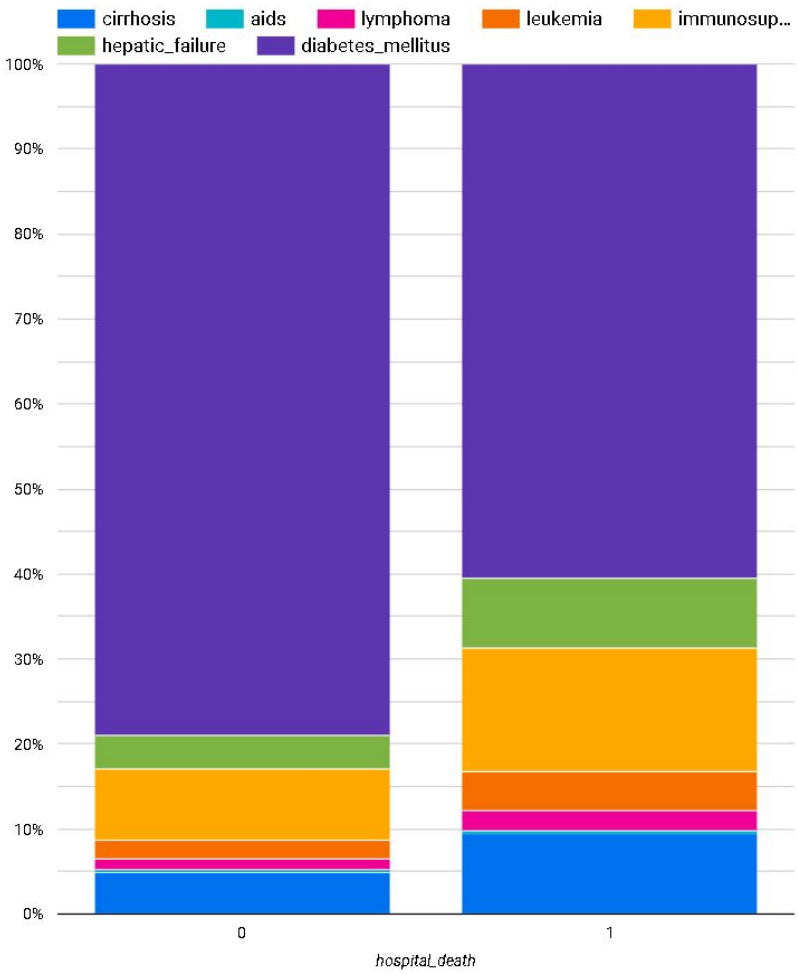


Here we wanted to explore how often these ICU admissions are fatal. The pie Chart shows that the picture is not that grim with only 8.6% cases being fatal.

Value count of number of hospital deaths

0	83798
1	7915

There are 7915 not survived in the training set and 83798 patients survived from the analysis.

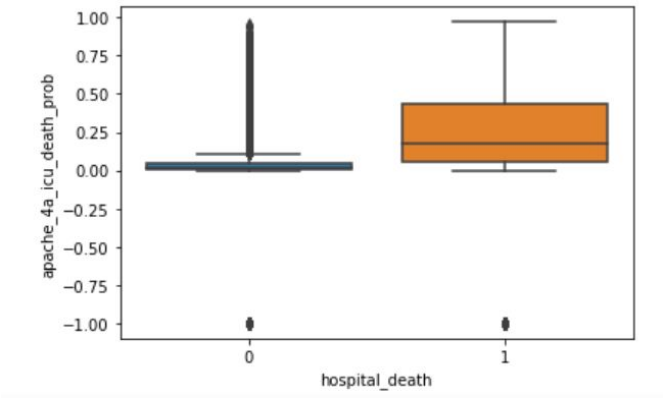


If we further split the data based on different conditions, we see that most of the patients had diabetes. Comparing fatal cases to non fatal cases, we see an interesting pattern - there are different proportions for diseases in the two cases. Even though diabetes accounts for almost 80% of the non-fatal cases, it comprises only 60% for the fatal ones. Proportion for Hepatic Failures almost doubles from 5% to around 10% and for immunosuppression they go from around 10% to 15%.

Box Plots

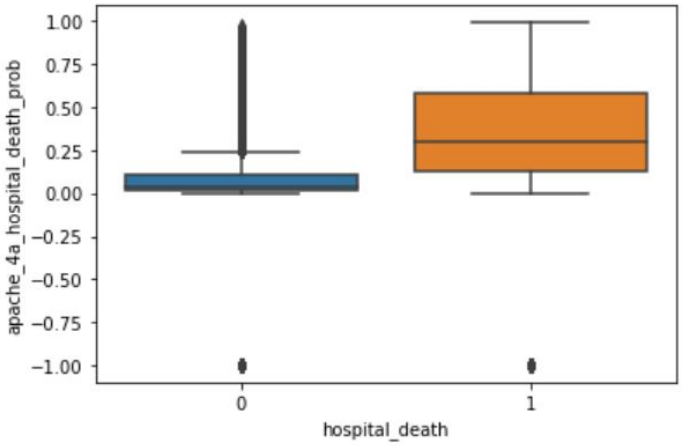
Using the graph, we can compare the range and distribution of various attributes for Survived patients(Hospital_death=0) and Not survived patients(Hospital_death=1).

apache_4a_icu_death_prob



From the above box plot, we can see that the median of apache_4a_icu_death_prob for Survived and Not Survived patients differ which means that hospital death may be dependent on apache_4a_icu_death_prob

Apache_4a_hospital_death_prob

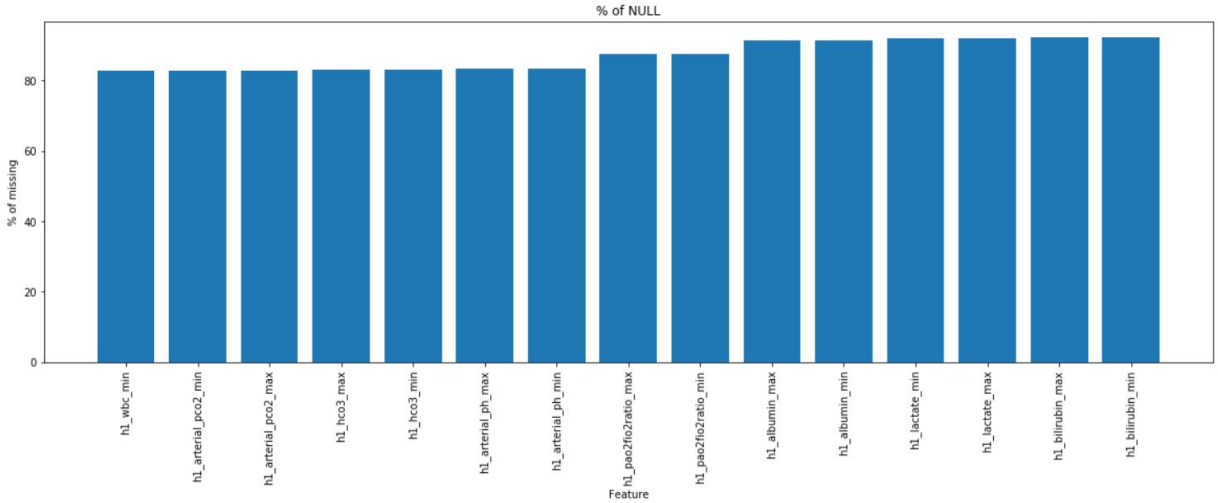


From the above box plot, we can see that the median of apache_4a_hospital_death_prob for Survived and Not Survived patients differ which means that hospital death may be dependent on apache_4a_hospital_death_prob

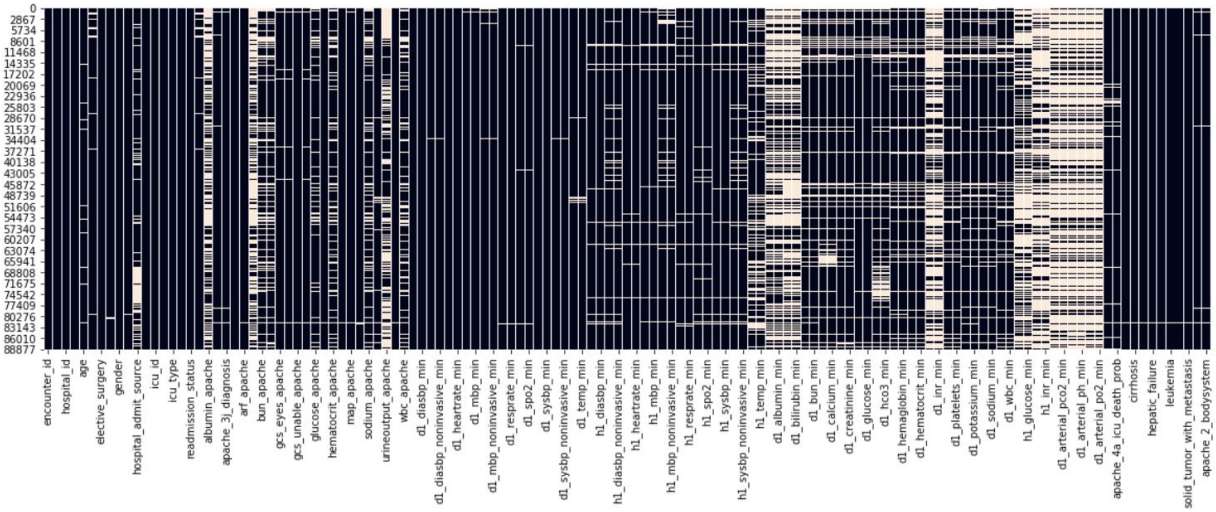
Missing values:

Around 160 variables have missing values out of which 74 variables have more than 50% of missing values.

Some of the variables with highest number of missing values:



We would need to check if these values are missing at random or if there is a pattern associated with it.



It was observed that most of the values which are missing are min and max of the same variable. Most of the missing values are across vitals, lab gas and lab reports. On further analysis it is seen that most of the missing values taken under the initial hour of admission (h1). Most of the values are available for d1 (24 hours).

Number of missing values more than 50% in the case of initial hour(h1) is 44 while for 24 hrs(d1) is 21.

To check if the missing values are pertaining to some particular disease:

Disease	No of records	Missing values
aids	78	40
cirrhosis	1428	903
diabetes_mellitus	20492	12793
hepatic_failure	1182	766
immunosuppression	2381	1488
leukemia	643	418
lymphoma	376	226
solid_tumor_with_metastasis	1878	1267

The missing values are spread across all the diseases and not biased over a disease

To check if there is any missing pattern across diseases, the variables were grouped based on the category as described in the data dictionary. It is observed that for all the diseases, the vitals and lab records were missing at random.

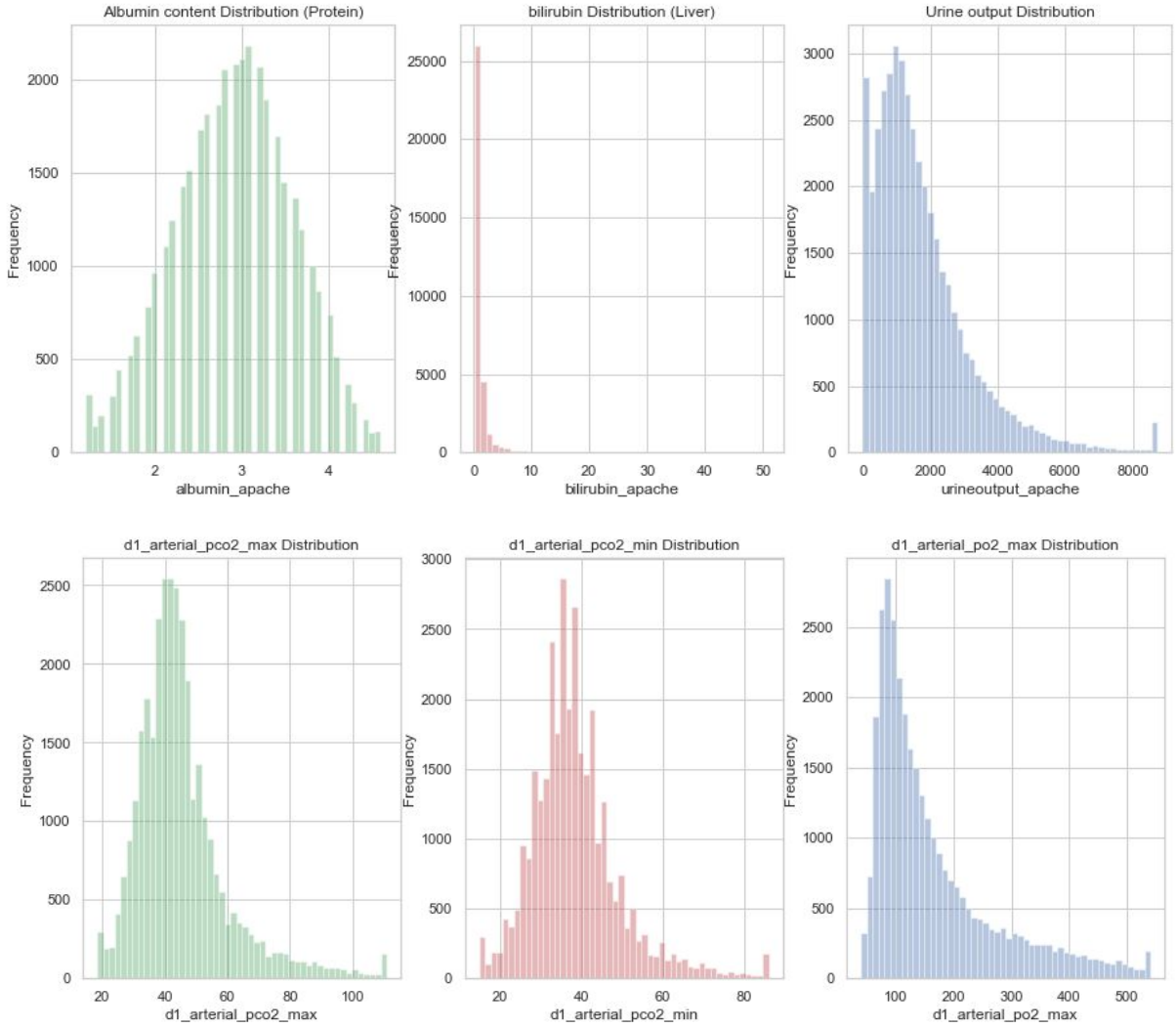
apache_3j_bodysystem	aids	Labs_missing	Vital_missing	Lab_gas_missing
Cardiovascular	5	0	4	3
Gastrointestinal	4	1	3	3
Genitourinary	4	0	4	3
Hematological	1	0	1	1
Metabolic	6	2	6	3
Musculoskeletal/Skin	1	0	1	1
Neurological	9	2	8	5
Respiratory	16	4	13	6
Sepsis	30	2	23	13
Trauma	1	1	1	1

apache_3j_bodysystem	cirrhosis	Labs_missing	Vital_missing	Lab_gas_missing
Cardiovascular	165	26	101	100
Gastrointestinal	534	26	445	388
Genitourinary	38	1	32	20
Hematological	17	1	14	11
Metabolic	94	7	92	72
Musculoskeletal/Skin	13	0	7	8
Neurological	103	18	83	68
Respiratory	111	10	85	53
Sepsis	318	11	220	155
Trauma	26	9	21	22

Imputation:

Since most of the missing values were falling under the initial hour observation(h1) and these values were explained by the values present in d1, the variables missing more than 50% in h1_variables were dropped.

Other variables such as albumin_apache, bilirubin_apache, Distribution of variables were checked before imputation:



For the initial model Random forest was used for variable imputation.

Other imputation Approaches that were tried were

- **Clustering Imputation**
    - Idea was to cluster observations and then use cluster means to impute the observations

-

clusters = KMeans(n_clusters = 50).fit(ndf)

```
@numba.jit
def imputeRow(row):
    #row = kdf.loc[1:1,]
    i = row.name
    naCols = row.index[row.isna()]
    meanVals = meansDf.loc[row["clusterId"] ,naCols ].astype("float")
    row.update(meanVals[naCols])
    return row
```

- **Neighbor based Imputation**
  - Following similar line of thought as with clustering we tried to implement K-nn Implementation
  - Since Sklearn's base implementation is all in memory therefore it needed 13.7 gb of space which was prohibitive - therefore we tried a number custom implementation using Dask (parallelization) , Numba (compilation) and KD Trees (approximation)

Dask Based

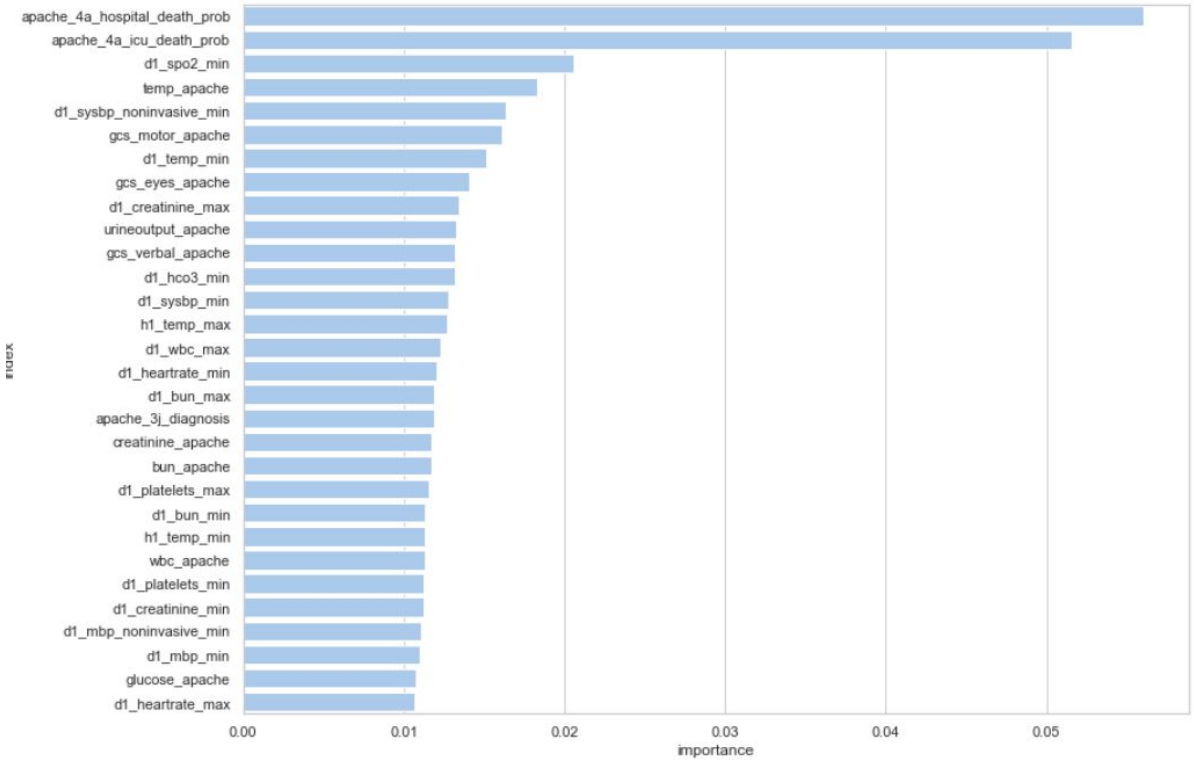
```
def KNN(kdf):
    #dist = euclidean_distances(kdf , distSample)
    dist = pairwise_distances(kdf, distSample, metric='nan_euclidean', force_all_finite=False)
    indices =  dist.argsort(axis=1)[:,:knnk]
    #kdf = kdf[].fillna()
    return indices

chunk_size = (int(kdf.shape[0]/30) , kdf.shape[1])

distMat = dd.from_pandas(kdf , chunksize=chunk_size[0]).\
            map_partitions(KNN).compute(scheduler = "processes")
```

Numba Based

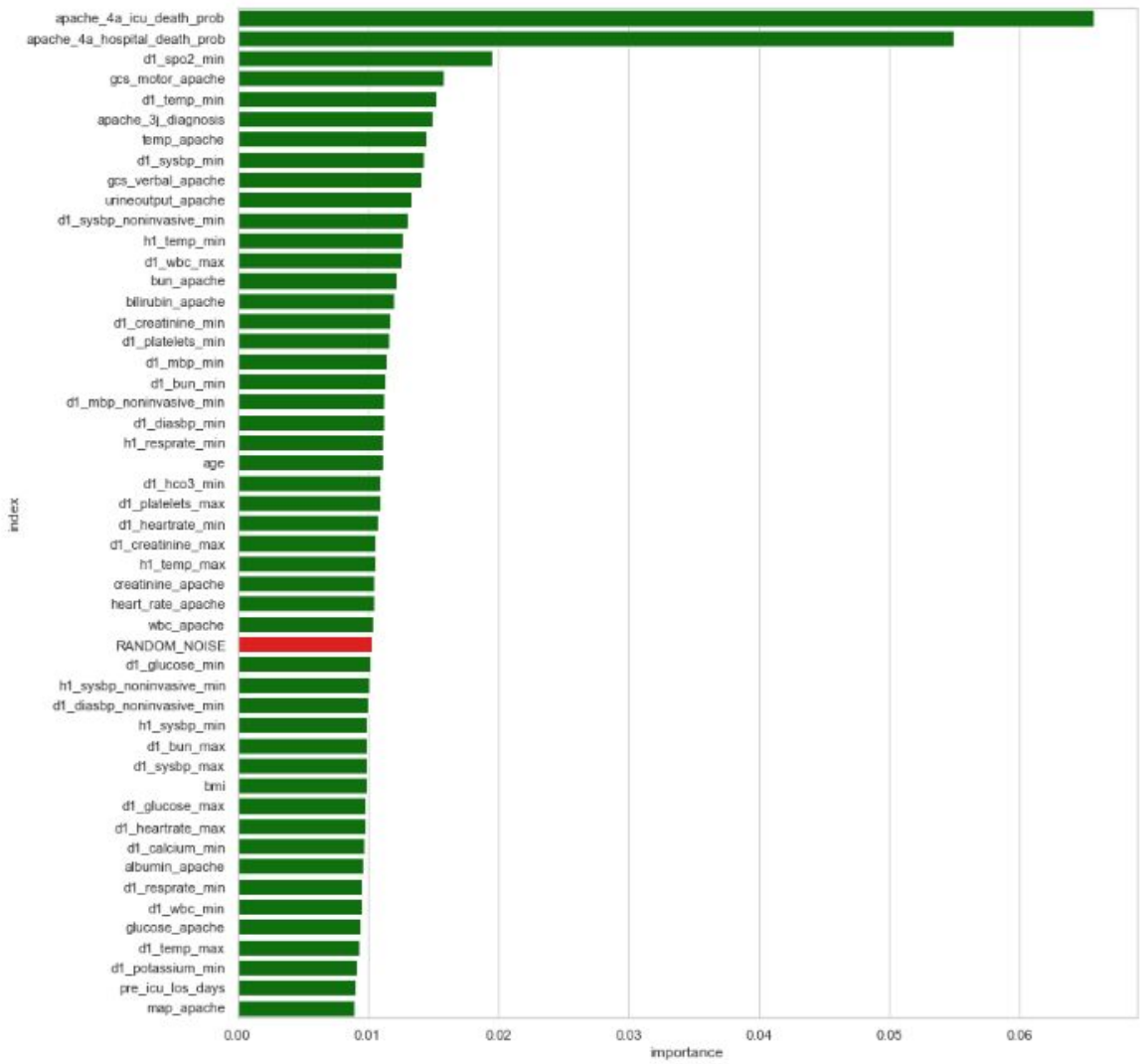
```
import numba

@numba.jit(parallel = True)
def imputeRow(row):
    #row = kdf.loc[1:1,]
    i = row.name
    dist , neighbors = tree.query([row.fillna(0)], 5)
    meanVals = kdf.loc[neighbors[0] , ].astype("float").mean(skipna= Tr
    naCols = row.index[row.isna()]
    meanVals = meanVals[naCols]
    #naCols = list(naCols)[0]
    #print(naCols)
    #row.update( pd.Series(meanVals[naCols] , index=naCols) )
```

Feature selection:

Since there are many variables, Random forest was used to check the importance of features:



The most important features were apache_4a_hospital_death_prob and apache_4a_hospital_icu_prob.Since most of the feature importance was falling in the range of 1-2%, a random noise was introduced to see how its effect is different from the other variables



From the above chart,It was observed that most of the features have less importance as random noise introduced has more explanatory power than the other features following it.

To check if there is any variation in the feature importances if other techniques were used, ANOVA feature selection was used to compare the results:

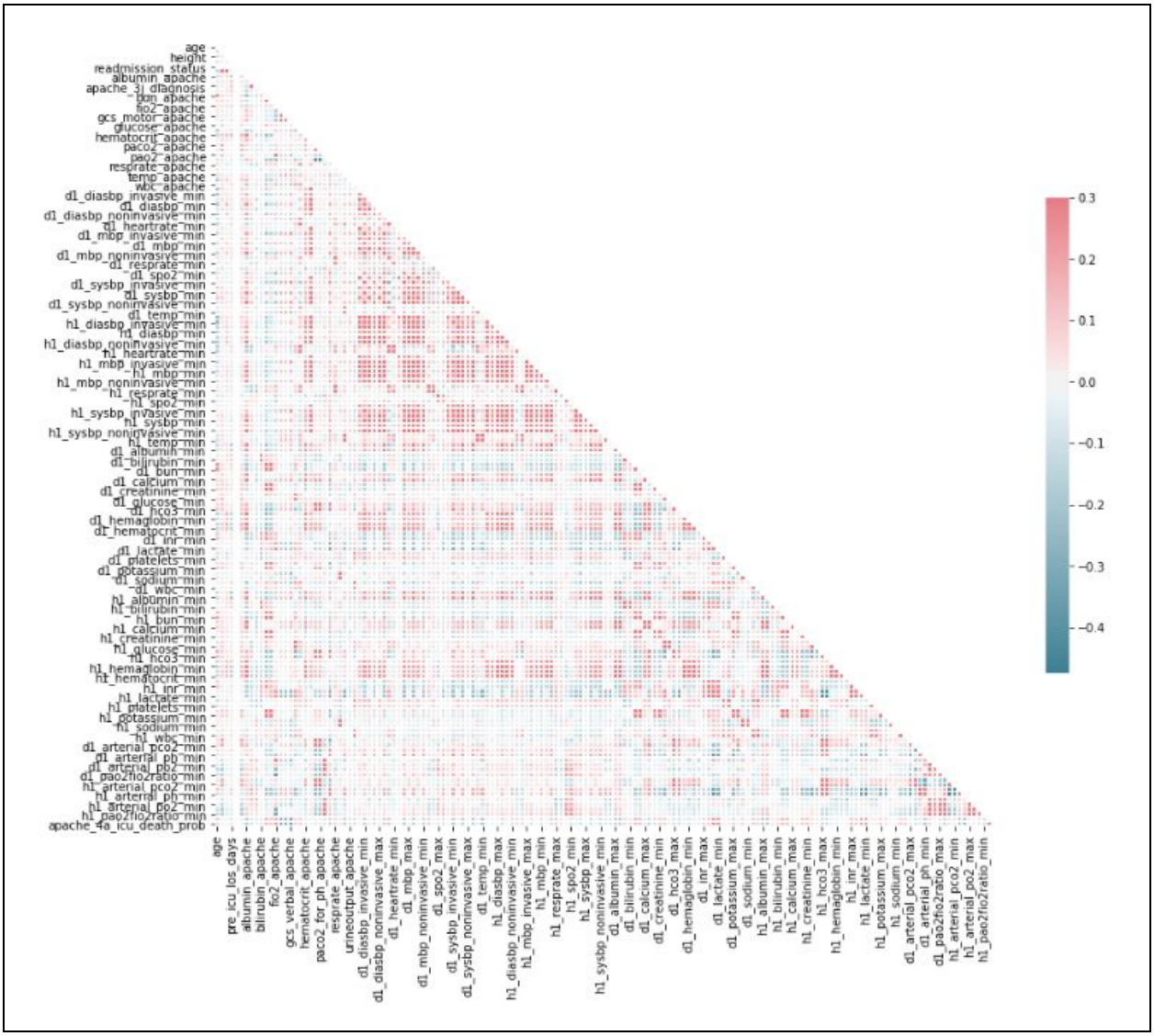
Feat_names	F_Scores
apache_4a_hospital_death_prob	423.084286
apache_4a_icu_death_prob	406.968435
gcs_motor_apache	213.574976
d1_temp_min	157.863302
d1_spo2_min	137.346796
gcs_eyes_apache	130.379405
d1_mbp_min	129.216005
d1_mbp_noninvasive_min	129.131079
d1_sysbp_noninvasive_min	123.885647

d1_sysbp_min	123.866523
d1_diasbp_noninvasive_min	111.915857
d1_diasbp_min	111.165977
temp_apache	101.275252
d1_hco3_min	101.127909
gcs_verbal_apache	82.110157
d1_bun_max	80.980113
bun_apache	72.677319
d1_bun_min	71.930350
d1_wbc_max	69.510020
albumin_apache	67.943430

d1_pao2fio2ratio_min	64.357691
h1_temp_min	63.999678
wbc_apache	58.892790
h1_temp_max	58.812908
d1_hco3_max	58.307062
d1_calcium_min	49.393117
d1_creatinine_max	40.545137
d1_arterial_pco2_min	40.062660
age	40.034508
creatinine_apache	38.644913

The results were quite similar.

Correlation heatmap



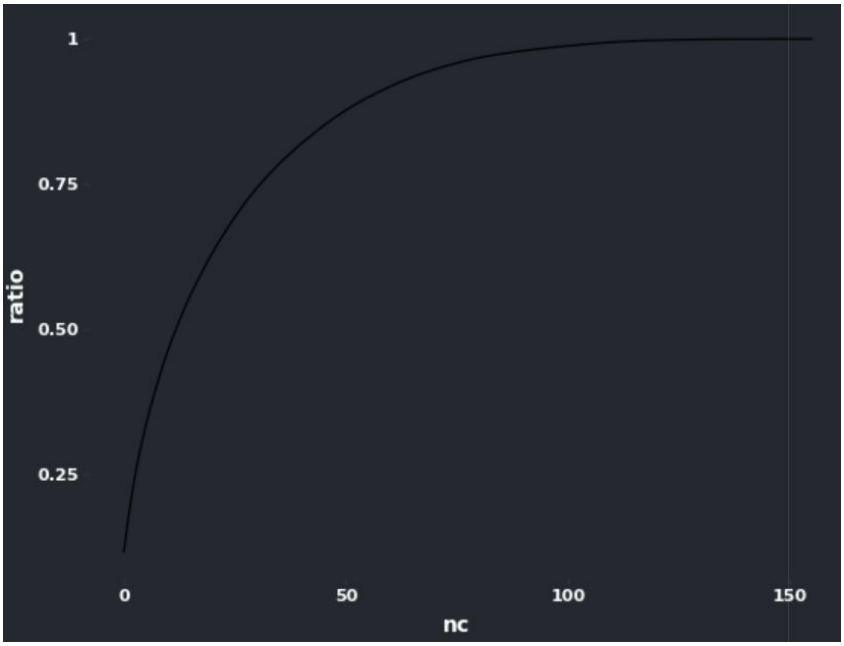
Recursive Feature Elimination

We used RFE with the logistic regression algorithm to select the top 90 features.

```
Index(['age', 'elective_surgery', 'albumin_apache', 'apache_post_operative',
       'arf_apache', 'creatinine_apache', 'gcs_eyes_apache',
       'gcs_motor_apache', 'gcs_unable_apache', 'intubated_apache',
       'ventilated_apache', 'd1_spo2_min', 'd1_temp_max', 'd1_temp_min',
       'h1_resprate_min', 'h1_temp_max', 'h1_temp_min', 'd1_albumin_max',
       'd1_albumin_min', 'd1_bilirubin_max', 'd1_bilirubin_min',
       'd1_calcium_max', 'd1_creatinine_max', 'd1_creatinine_min',
       'd1_hco3_max', 'd1_hco3_min', 'd1_hemaglobin_max', 'd1_hemaglobin_min',
       'd1_hematocrit_max', 'd1_hematocrit_min', 'd1_potassium_max',
       'd1_wbc_min', 'apache_4a_hospital_death_prob',
       'apache_4a_icu_death_prob', 'aids', 'diabetes_mellitus',
       'hepatic_failure', 'immunosuppression', 'leukemia', 'lymphoma',
       'solid_tumor_with_metastasis', 'ethnicity_Asian', 'ethnicity_Caucasian',
       'ethnicity_Hispanic', 'ethnicity_Other/Unknown', 'gender_F', 'gender_M',
       'hospital_admit_source_Acute Care/Floor',
       'hospital_admit_source_Chest Pain Center',
       'hospital_admit_source_Direct Admit', 'hospital_admit_source_ICU',
       'hospital_admit_source_Observation',
       'hospital_admit_source_Operating Room', 'hospital_admit_source_Other',
       'hospital_admit_source_Other Hospital',
       'hospital_admit_source_Other ICU', 'hospital_admit_source_PACU',
       'hospital_admit_source_Recovery Room',
       'hospital_admit_source_Step-Down Unit (SDU)',
       'icu_admit_source_Accident & Emergency',
       'icu_admit_source_Operating Room / Recovery',
       'icu_admit_source_Other Hospital', 'icu_admit_source_Other ICU',
       'icu_stay_type_admit', 'icu_stay_type_readmit', 'icu_type_CCU-CTICU',
       'icu_type_CSICU', 'icu_type_Cardiac ICU', 'icu_type_MICU',
       'icu_type_Med-Surg ICU', 'icu_type_Neuro ICU', 'icu_type_SICU',
       'apache_3j_bodysystem_Gynecological',
       'apache_3j_bodysystem_Hematological', 'apache_3j_bodysystem_Metabolic',
       'apache_3j_bodysystem_Musculoskeletal/Skin',
       'apache_3j_bodysystem_Neurological', 'apache_3j_bodysystem_Respiratory',
       'apache_3j_bodysystem_Sepsis', 'apache_3j_bodysystem_Trauma',
       'apache_2_bodysystem_Cardiovascular',
       'apache_2_bodysystem_Gastrointestinal',
       'apache_2_bodysystem_Haematologic', 'apache_2_bodysystem_Metabolic',
       'apache_2_bodysystem_Neurologic',
       'apache_2_bodysystem_Renal/Genitourinary',
       'apache_2_bodysystem_Respiratory', 'apache_2_bodysystem_Trauma',
       'apache_2_bodysystem_Undefined Diagnoses',
       'apache_2_bodysystem_Undefined diagnoses'],
      dtype='object')
```

PCA

We also applied PCA to reduce dimensionality. After having imputed and Standard Scaling the numerical features we ran PCA only on the numerical features and the results showed that 100 features out of 157 could explain 100% of the variance.



Baseline Models:

As a baseline model, the imputed data was split into test and train and Logistic Regression was applied to check the model performance.

```
  ---Logistic Regression Model---
Logistic Regression AUC = 0.57
              precision    recall  f1-score   support

           0       0.92      0.99      0.96     25139
           1       0.62      0.14      0.23      2375

    accuracy                           0.92     27514
   macro avg       0.77      0.57      0.59     27514
weighted avg       0.90      0.92      0.89     27514
```

The baseline models AUC is just 0.57 which is quite less.

Since the number of records for hospital_deaths in the dataset is quite less as compared to surviving patients, there is an imbalance in the data. So different sampling techniques were used to see if it improves the model performance.

```
The best AUC Score for Original data:
0.8317507863743032
The best AUC Score for Upsampled data:
0.8465680582401258
The best AUC Score for SMOTE data:
0.8592121473886737
The best AUC Score for Downsampled data:
0.8462038473067549
```

When different sampling techniques were used on the data, we can see drastic improvement in results.

Yet Another Baseline

We tried another baseline which

1. Imputed Based on Most Frequent Values
2. Converted Categorical Values to Dummy Variables
3. Dropped ID Columns like Hospital_Id , Encounter_Id
4. Used a Random Forest Classifier
5. This gave us Cross Validated AUC of 0.878 on average

```
DEPENDENT_VAR = getDependentVariable()
catcols = getCategorialColumns(df)
catcolsWoBogus = [c for c in catcols if c not in ["hospital_id" , "encounter_id" , "icu_id" , "patient_id"]]
catcolsWoBogusWoTarget = [c for c in catcolsWoBogus if c != DEPENDENT_VAR]
from sklearn.impute import SimpleImputer
si = SimpleImputer(strategy="most_frequent")
woTarget = df.drop([DEPENDENT_VAR] , axis=1)
df.loc[:,woTarget.columns] = si.fit_transform(woTarget)
ndf = pd.get_dummies(df , columns=catcolsWoBogusWoTarget , drop_first=True)
ndf.shape (91713, 668)
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier()
from sklearn.model_selection import cross_val_score
cross_val_score(rfc , ndf.drop(DEPENDENT_VAR,axis=1) , df[DEPENDENT_VAR] , scoring="roc_auc")
array([0.87833394, 0.89186543, 0.88231617, 0.8757929 , 0.87694405])
```

Another Baseline Model - RF and Logistic Regression

Imputation : Starting with handling missing values, we dropped columns that had more than 60% missing values, from 186 columns, 66 columns were dropped as they had more than 60% missing values, left with 120 columns.

Next, for the columns that had missing values, we imputed using average, max, backward filling and forward filling for different columns.
Since we were started by building a baseline model, we tried by imputing all the numerical columns with average value imputation, and other features with mode values.
Dummy Coding was used for Categorical variables.

We used Random Forest for feature importance, to use only the variables that were significant enough for the model.

Model 1 :

For modelling we first split the data into train and test , then build the model using Random Forest to check the performance however, did not give a good accuracy and AUC.

```
Accuracy: 92.44%

Random Forest Classifier: ROC AUC=0.610
```

Model 2:

Also, trying different models, we build Logistic Regression with similar imputation of average, mean and mode.
We used Random Forest for Feature Engineering i.e importance, below are the results for accuracy and AUC of Logistic Regression.

```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, l1_ratio=None, max_iter=10000,
                   multi_class='warn', n_jobs=None, penalty='l2',
                   random_state=None, solver='warn', tol=0.0001, verbose=0,
                   warm_start=False)

Accuracy for Logistic Regression : 0.9195746542383147

 Logistic Regression: ROC AUC=0.825
```

Final Kaggle Submission Model Summary

Pipeline >

- **Missing Values**
  - num_mean = **SimpleImputer**(strategy="mean")
  - cat_freq = **SimpleImputer**(strategy="most_frequent")
- **Add Apache Score column** - getAPACHEScore
- **Feature Transformations**
  - rs = **RobustScaler**()
    - Robust Scaler scales features using statistics that are robust to outliers.
  - pt = **PowerTransformer**()
    - Apply a power transform feature wise to make data more Gaussian-like
- **Feature Reduction**
  - We used Feature agglomeration/ clustering using correlation coefficient as the distance metric
  - fa = **FeatureAgglomeration**(n_clusters=None,affinity="precomputed",compute_full_tree=True, linkage="average" ,distance_threshold=1/corrcoefmin)
- **Categorical Columns**
  - ohe = **OneHotEncoder**(sparse=False , handle_unknown='ignore')
- **Modelling**
  - For the final model we used lightgbm
  - import lightgbm as lgb
  - The optimal parameters found using grid search were

```
params = {
  'max_depth': 10,
  'n_estimators ': 10,
  'objective': 'binary',
  'colsample_bytree': 0.8,
  "class_weight":{0:1 , 1:20},
  "base_score":0.2,
  "n_jobs":-1,
  "metric":"auc",
  "reg_alpha":0.4,
  "Reg_lambda":0.18,
}
```

The final Score we managed to get was 0.8978

7. What have you accomplished so far? What have you changed or updated with respect to your project proposal? Provide a clear description of any issues you faced and how you overcame them and how you changed your strategies. <15-20 sentences>

Milestones:

- Performed **data cleaning/preprocessing:** Handling Missing values, variable transformation, find correlation among variables
- Have predicted the top features impacting the patient death using various **feature engineering** techniques
- Tried **different imputation techniques**
- **Baseline model:** Have applied different modelling techniques to the imputed data to compare the performance of each model
    - Now we have a better sense of the challenges and how hard it's going to be to push forward the evaluation metric - AUC ROC to beyond 0.90
- Realised that throwing data and models won't work , we need to focus on extracting signal from the noise to better the model.

Issues:

- Since its healthcare data, **understanding most of the variables** needed spending some time going through the data dictionary.
- The data has many features which makes it **difficult to identify the important features.** Correlation among variables need to be considered while performing variable selection
- **Imbalance in the data** - we have a class imbalance where only 8% of the observations have the target class
- **Handling missing values**: Since there are multiple ways to handle missing data, the right way to handle it which goes in hand with the model selected is tricky.
- **Variable transformation:** Since there are multiple variables and each variable has problems of skewness and outliers associated with it, the right transformation technique would play a major role in model performance
- **Model execution and computational complexity**: Since the data is comparatively large with many features, few algorithms like SVM or grid search with Boosting algorithms would take a long time to execute

Strategies used

- Different Imputation and Feature selection techniques were tried by each member of the group and the results were compared to identify how its affects the model.
- Different models were tired to check its performance. Further hyperparameter tuning was performed manually to check if there is any improvement in model performance
- Data imbalance: Two approaches were used to handle this. One was upsampling of the data which showed significant improvement in results while the other method was to use Boosting and stacking algorithms which improves the performance by heavily penalizing the weak learners.

Team Roles and Contributions

	Team Member Name (800 id)	Responsible For
1	Abhijeet - 801155955	**EDA using Google Cloud Data Studio,Python** **Feature engineering -KNN , PCA, RandomForest,Clustering** **Exploring Dask and Numba for faster computation** **GridSearch and Hyperparameter Tuning** **Github Documentation**
2	Ridhi - 801151577	**EDA , Feature engineering - PCA,Model Selection, Model evaluation, Github Wiki Documentation**
3	Vivek - 801151371	**EDA , Feature engineering - ANOVA and Random Forest , Model Selection, Model evaluation, Github Wiki Documentation**
4	Mansi - 801136257	**EDA , Feature engineering - Recursive Feature Elimination, Model Selection - ML Models,Model evaluation, Github Wiki Documentation**

References

1. Johnson AEW, Mark RG. Real-time mortality prediction in the Intensive Care Unit. *AMIA Annu Symp Proc*. 2018;2017:994–1003. Published 2018 Apr 16.
2. Bouvy ML, Heerdink ER, Leufkens HGM*, et al*Predicting mortality in patients with heart failure: a pragmatic approach*Heart* 2003;**89:**605-609.
3. C E Douma, W K Redekop, J H van der Meulen, R W van Olden, J Haeck, D G Struijk and R T Krediet JASN January 1997, 8 (1) 111-117;
4. Cannon, Chad M., et al. "Utility of the shock index in predicting mortality in traumatically injured patients." *Journal of Trauma and Acute Care Surgery* 67.6 (2009): 1426-1430.
5. A clinical prediction model to identify patients at high risk of death in the emergency department : https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4477719/
6. Emergency department triage prediction of clinical outcomes using machine learning models:https://ccforum.biomedcentral.com/articles/10.1186/s13054-019-2351-7