Mortality Aggregation

Benjamin Frost 2022

In [ ]:
```
import pandas as pd
import numpy as np
import torch.multiprocessing as mp
from sklearn.preprocessing import KBinsDiscretizer, OneHotEncoder, MinMaxScaler
from matplotlib import pyplot as plt
from sklearn.cluster import AgglomerativeClustering
from sklearn.metrics import silhouette_score
from sklearn.metrics import f1_score
from sklearn.metrics import recall_score
from sklearn.metrics import precision_score
from sklearn.cluster import KMeans
from sklearn.preprocessing import PolynomialFeatures
from tqdm import tqdm
from concurrent.futures import ThreadPoolExecutor, as_completed
from scipy.interpolate import interp1d
from Categorization import Categorizer
import torch
import copy
from torch.nn.functional import one_hot
import imblearn
from collections import Counter
from tslearn.clustering import TimeSeriesKMeans
from tslearn.utils import to_time_series_dataset
from tslearn.preprocessing import TimeSeriesScalerMeanVariance
from sklearn.metrics import silhouette_score
from tsfresh import extract_features, select_features
from tsfresh.utilities.dataframe_functions import impute
from dask.dataframe import from_pandas
from tsfresh.utilities.distribution import MultiprocessingDistributor
import hashlib
from sklearn.metrics import precision_recall_fscore_support
from importlib import reload
from temporalHelper import TemporalHelper as TH
```

Loading in the mimic dataset

In [ ]:
```
th = TH()

mimicDF = th.get_mimic()

mimicDF
```

Out[ ]:

	PatientID	Mortality14Days	ALT	AST	Admit Ht	Albumin	Arterial BP Mean	Arterial BP [Diastolic]	Arterial BP [Systolic]	Arterial PaCO2	...	SVI	SVR	SVRI	SaO2	Sodi
0	178177	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
1	178177	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
2	178177	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
3	178177	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
4	178177	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
47083	159740	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
47084	159740	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
47085	159740	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
47086	159740	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N
47087	159740	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	N

47088 rows × 44 columns

In [ ]:
```
mimicDF.describe()
```

Out[ ]:

	PatientID	Mortality14Days	ALT	AST	Admit Ht	Albumin	Arterial BP Mean	Arterial BP [Diastolic]	Arterial BP [Systolic]	A

	PatientID	Mortality14Days	ALT	AST	Admit Ht	Albumin	Arterial BP Mean	Arterial BP [Diastolic]	Arterial BP [Systolic]	A
count	47088.000000	47088.000000	484.000000	481.000000	705.000000	245.000000	31415.000000	31503.000000	31504.000000	8601.(
mean	151079.910805	0.039755	630.123967	954.301455	67.382553	2.721633	77.058157	57.226709	117.544502	40.5
std	29378.613191	0.195386	1245.805613	2384.326867	5.448469	0.584693	14.324177	11.197415	21.311674	7.(
min	100059.000000	0.000000	3.000000	3.000000	48.000000	1.400000	0.000000	0.000000	0.000000	15.(
25%	126241.000000	0.000000	25.000000	49.000000	64.000000	2.400000	68.000000	50.000000	103.000000	36.(
50%	151857.000000	0.000000	97.000000	137.000000	68.000000	2.700000	75.000000	56.000000	115.000000	40.(
75%	176484.000000	0.000000	554.750000	797.000000	70.000000	3.000000	84.000000	63.000000	129.000000	44.(
max	199998.000000	1.000000	8100.000000	23060.000000	160.000000	4.400000	287.000000	191.000000	255.000000	91.(

8 rows × 44 columns

In [ ]:
```
print(f"There are {mimicDF['PatientID'].nunique()} unique patients in the dataset")
```

```
There are 1126 unique patients in the dataset
```

In [ ]:
```
patients = th.get_patients()

print(len(patients))
```

```
100%|██████████| 1126/1126 [00:01<00:00, 945.96it/s]
1126
```

Aggregating the dataset using expert values

In [ ]:
```
# Aggregating the dataset

staticPatients = []

target = []

for patient in patients:

    curr = {}

    df = patient.data

    curr['PatientID'] = patient.patientID
    target.append(patient.label)
    curr['ALT'] = df['ALT'].max()
    curr['AST'] = df['AST'].max()
    curr['Admit_Ht'] = df['Admit Ht'].max()
    curr['Albumin'] = df['Albumin'].min()
    curr['Arterial_BP_Mean'] = df['Arterial BP Mean'].min()
    curr['Arterial_BP_Diastolic'] = df['Arterial BP [Diastolic]'].min()
    curr['Arterial_BP_Systolic'] = df['Arterial BP [Systolic]'].min()
    curr['Arterial_PaCO2'] = df['Arterial PaCO2'].min()
    curr['Arterial_PaO2'] = df['Arterial PaO2'].min()
    curr['Arterial_pH_Max'] = df['Arterial pH'].max()
    curr['Arterial_pH_Min'] = df['Arterial pH'].min()
    curr['Urea'] = df['BUN'].min() * 0.357
    curr['CVP_Min'] = df['CVP'].min()
    curr['CVP_Max'] = df['CVP'].max()
    curr['CaO2'] = df['CaO2'].min()
    curr['Chloride'] = df['Chloride'].min()
    curr['Creatinine'] = df['Creatinine'].min()
    curr['Daily_Weight'] = df['Daily Weight'].loc[df['Daily Weight'].first_valid_index()] / 2.205 if df['Daily Weight
    curr['Fibrinogen'] = df['Fibrinogen'].max()
    curr['Glucose_Max'] = df['Glucose'].max()
    curr['Glucose_Min'] = df['Glucose'].min()
    curr['Heart_Rate_Min'] = df['Heart Rate'].min()
    curr['Heart_Rate_Max'] = df['Heart Rate'].max()
    curr['Hamoglobin'] = df['Hemoglobin'].min()
    curr['INR'] = df['INR'].max()
    curr['Ionized_Calcium'] = df['Ionized Calcium'].min()
    curr['LDH'] = df['LDH'].max()
    curr['Magnesium'] = df['Magnesium'].min()
    curr['NBP_Mean'] = df['NBP Mean'].min()
    curr['NBP_Diastolic'] = df['NBP [Diastolic]'].min()
    curr['NBP_Systolic'] = df['NBP [Systolic]'].min()
    curr['PTT'] = df['PTT'].max()
    curr['Platelets'] = df['Platelets'].min()
```

```
    curr['Potassium_Max'] = df['Potassium'].max()
    curr['Potassium_Min'] = df['Potassium'].min()
    curr['Resp_Rate_(Spont)_Min'] = df['Resp Rate (Spont)'].min()
    curr['Resp_Rate_(Spont)_Max'] = df['Resp Rate (Spont)'].max()
    curr['SVI'] = df['SVI'].min()
    curr['SVRI_Max'] = df['SVRI'].max()
    curr['SVRI_Min'] = df['SVRI'].min()
    curr['SaO2'] = df['SaO2'].min()
    curr['Sodium_Max'] = df['Sodium'].max()
    curr['Sodium_Min'] = df['Sodium'].min()
    curr['SpO2'] = df['SpO2'].min()
    curr['SvO2_Max'] = df['SvO2'].max()
    curr['SvO2_Min'] = df['SvO2'].min()
    curr['Temperature_C_Max'] = df['Temperature C'].max()
    curr['Temperature_C_Min'] = df['Temperature C'].min()
    curr['Bilirubin'] = df['Total Bili'].max()
    curr['White_Blood_Cells_Max'] = df['WBC'].max()
    curr['White_Blood_Cells_Min'] = df['WBC'].min()

    staticPatients.append(curr)


staticPatientsDF = pd.DataFrame([x.values() for x in staticPatients], columns=curr.keys())

staticPatientsDF = staticPatientsDF.set_index('PatientID')

targetSeries = pd.Series(data=target)
```

In [ ]:
```
staticPatientsDF.describe()
```

Out[ ]:

	ALT	AST	Admit_Ht	Albumin	Arterial_BP_Mean	Arterial_BP_Diastolic	Arterial_BP_Systolic	Arterial_PaCO2	Arte
count	253.000000	250.000000	663.000000	143.000000	1096.000000	1097.000000	1097.000000	1075.000000	107
mean	388.296443	652.108000	67.376471	2.613287	60.073905	43.779398	87.995442	34.494884	9
std	1014.823729	2053.610608	5.529188	0.584451	9.878763	11.453517	21.175211	5.266344	3
min	3.000000	3.000000	48.000000	1.400000	0.000000	0.000000	0.000000	15.000000	
25%	19.000000	40.000000	64.000000	2.200000	55.000000	40.000000	82.000000	31.000000	7
50%	40.000000	79.500000	68.000000	2.600000	60.000000	45.000000	90.000000	35.000000	8
75%	220.000000	359.000000	70.000000	3.000000	65.000000	50.000000	98.000000	38.000000	10
max	8100.000000	23060.000000	160.000000	4.400000	106.000000	77.000000	170.000000	66.000000	38

8 rows × 51 columns

In [ ]:
```
rowsWithNaN = sum(staticPatientsDF.isnull().any(axis=1))
print(f"{staticPatientsDF.shape[0]} rows in df, {rowsWithNaN} containing NaN values")
```

```
1126 rows in df, 1124 containing NaN values
```

Filling the missing values from aggregated data

In [ ]:
```
fillNaModeDF = staticPatientsDF.copy()

for col in fillNaModeDF:
    fillNaModeDF[col] = fillNaModeDF[col].fillna(fillNaModeDF[col].mean())

fillNaModeDF['Admit_Ht'][fillNaModeDF["Admit_Ht"] > 100] = fillNaModeDF["Admit_Ht"].mean()

display(fillNaModeDF)
```

PatientID	ALT	AST	Admit_Ht	Albumin	Arterial_BP_Mean	Arterial_BP_Diastolic	Arterial_BP_Systolic	Arterial_PaCO2	Arterial_Pa
100059	388.296443	652.108	66.000000	2.613287	60.0	43.0	106.0	39.0	8
100298	388.296443	652.108	68.000000	2.613287	62.0	48.0	81.0	33.0	7
100321	388.296443	652.108	59.000000	2.613287	59.0	41.0	86.0	32.0	12
100336	304.000000	780.000	72.000000	2.100000	63.0	53.0	80.0	26.0	2
100392	388.296443	652.108	69.000000	2.613287	56.0	45.0	80.0	43.0	6
...	...	...	...	...	...	...	...	...	

PatientID	ALT	AST	Admit_Ht	Albumin	Arterial_BP_Mean	Arterial_BP_Diastolic	Arterial_BP_Systolic	Arterial_PaCO2	Arterial_Pa
199876	388.296443	652.108	67.376471	2.613287	57.0	37.0	93.0	38.0	7
199877	388.296443	652.108	67.376471	2.613287	63.0	51.0	134.0	38.0	12
199963	388.296443	652.108	72.000000	2.613287	56.0	42.0	82.0	30.0	10
199993	388.296443	652.108	67.376471	2.613287	63.0	52.0	81.0	38.0	8
199998	388.296443	652.108	69.500000	2.613287	58.0	40.0	100.0	27.0	10

1126 rows × 51 columns

Binning with K-Bins

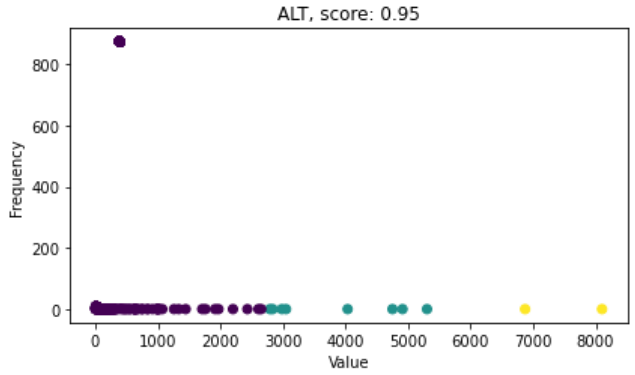
In [ ]:

```
import Categorization

reload(Categorization)

cat = Categorization.Categorizer(fillNaModeDF)

cat.kBins(bins = 3)

boundaries = cat.getBoundaries()

display(boundaries['kBins'])

cat.display(num=6)
```

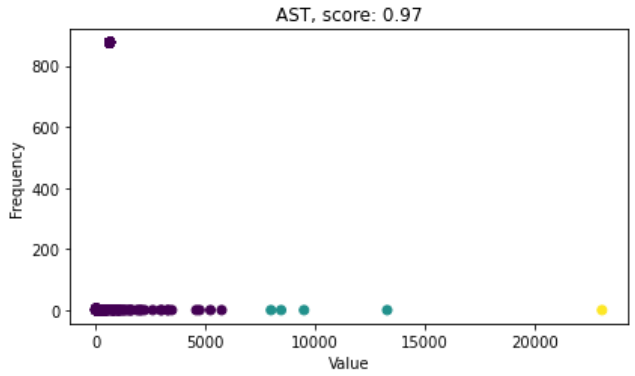
```
{'ALT': [2791.0, 6870.0],
 'AST': [7989.0, 23060.0],
 'Admit_Ht': [58.0, 68.0],
 'Albumin': [2.5, 3.5],
 'Arterial_BP_Mean': [36.0, 71.0],
 'Arterial_BP_Diastolic': [26.0, 52.0],
 'Arterial_BP_Systolic': [57.0, 114.0],
 'Arterial_PaCO2': [32.0, 49.0],
 'Arterial_PaO2': [135.0, 281.0],
 'Arterial_pH_Max': [187.0],
 'Arterial_pH_Min': [7.11, 7.3],
 'Urea': [14.994, 29.988],
 'CVP_Min': [8.0, 15.0],
 'CVP_Max': [18.0, 34.0],
 'CaO2': [7.688059807, 14.1566],
 'Chloride': [99.0, 111.0],
 'Creatinine': [3.9, 8.3],
 'Daily_Weight': [40.27211022675737, 67.57369614512471],
 'Fibrinogen': [358.0, 645.0],
 'Glucose_Max': [261.0, 467.0],
 'Glucose_Min': [148.0, 270.0],
 'Heart_Rate_Min': [46.0, 92.0],
 'Heart_Rate_Max': [108.0, 166.0],
 'Hamoglobin': [6.0, 11.5],
 'INR': [27.0],
 'Ionized_Calcium': [0.76, 1.03],
 'LDH': [4412.0, 9830.0],
 'Magnesium': [2.1, 3.3],
 'NBP_Mean': [37.66669846, 75.66670227],
 'NBP_Diastolic': [33.0, 66.0],
 'NBP_Systolic': [78.0, 158.0],
 'PTT': [64.4, 107.9],
 'Platelets': [216.0, 443.0],
 'Potassium_Max': [61259.0],
 'Potassium_Min': [3.3, 4.3],
 'Resp_Rate_(Spont)_Min': [9.0, 20.0],
 'Resp_Rate_(Spont)_Max': [13.0, 26.0],
 'SVI': [27.12770081, 55.24860001],
 'SVRI_Max': [2589.0, 4339.620117],
 'SVRI_Min': [1052.630005, 2105.26001],
 'SaO2': [62.0, 80.0],
 'Sodium_Max': [139.7587601078167, 153.0],
 'Sodium_Min': [120.0],
 'SpO2': [42.0, 67.0],
 'SvO2_Max': [64.0, 89.0],
 'SvO2_Min': [63.0, 80.0],
 'Temperature_C_Max': [33.70000076],
 'Temperature_C_Min': [29.60000038],
 'Bilirubin': [5.8, 12.2],
```

```
'White_Blood_Cells_Max': [17.7, 33.2],
'White_Blood_Cells_Min': [17.4, 38.6]}
```

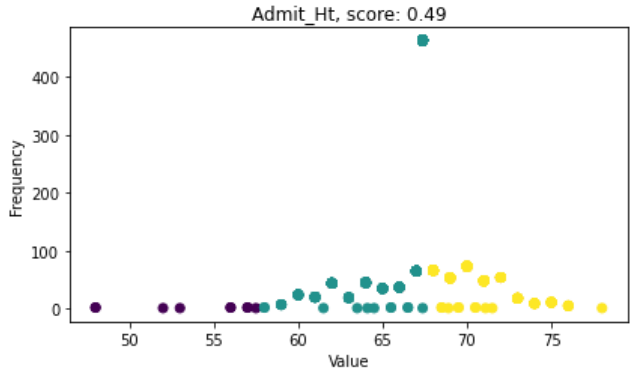
kBins



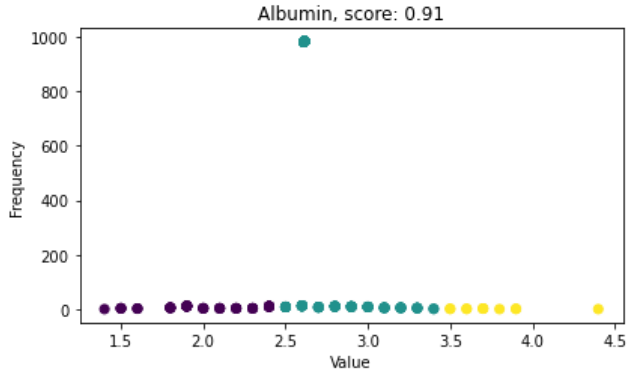
kBins

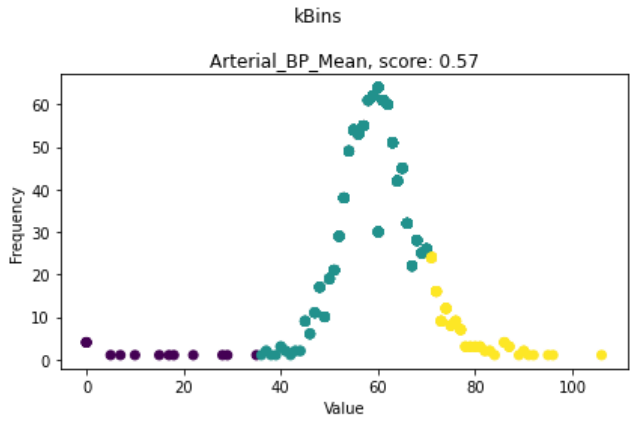


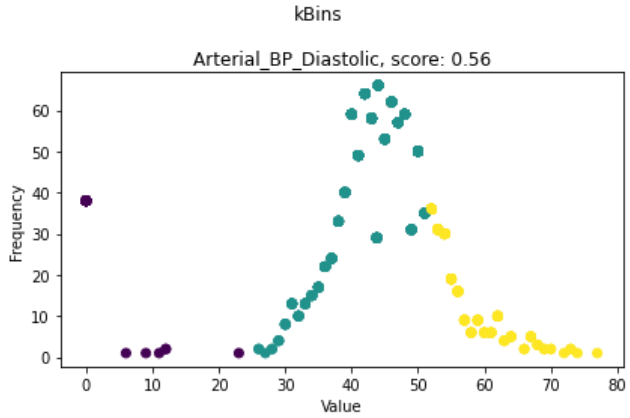
kBins



kBins







Labelling high to low

In [ ]:
```
categories = {0: 'very_low', 1: 'low', 2: 'medium', 3: 'high', 4: 'very_high'}

cat.map_types(mapping=categories)

mapped = cat.mappedTypes['kBins']

mapped
```

Out[ ]:

	ALT_high	ALT_low	ALT_medium	AST_high	AST_low	AST_medium	Admit_Ht_high	Admit_Ht_low	Admit_Ht_medium	Albumin_high
0	0	1	0	0	1	0	0	0	1	0
1	0	1	0	0	1	0	1	0	0	0
2	0	1	0	0	1	0	0	0	1	0
3	0	1	0	0	1	0	1	0	0	0
4	0	1	0	0	1	0	1	0	0	0
...	...	...	...	...	...	...	...	...	...	...
1121	0	1	0	0	1	0	0	0	1	0
1122	0	1	0	0	1	0	0	0	1	0
1123	0	1	0	0	1	0	1	0	0	0
1124	0	1	0	0	1	0	0	0	1	0
1125	0	1	0	0	1	0	1	0	0	0

1126 rows × 141 columns

In [ ]:
```
targetSeries.value_counts()
```

Out[ ]:
```
0    1077
1      49
dtype: int64
```

In [ ]:
```
mapped['Mortality14Days'] = targetSeries.values

mapped.to_csv("./categorisedData/expertLabelledData.csv")
```