

Project: (K-) Nearest Neighbors & SVD

Programming project: probability of death

In this project, you have to predict the probability of death of a patient that is entering an ICU (Intensive Care Unit).

The dataset comes from MIMIC project (<https://mimic.physionet.org/>). MIMIC-III (Medical Information Mart for Intensive Care III) is a large, freely-available database comprising deidentified health-related data associated with over forty thousand patients who stayed in critical care units of the Beth Israel Deaconess Medical Center between 2001 and 2012.

Each row of *mimic_train.csv* corresponds to one ICU stay (*hadm_id+icustay_id*) of one patient (*subject_id*). Column *HOSPITAL_EXPIRE_FLAG* is the indicator of death (=1) as a result of the current hospital stay; this is the outcome to predict in our modelling exercise. The remaining columns correspond to vitals of each patient (when entering the ICU), plus some general characteristics (age, gender, etc.), and their explanation can be found at *mimic_patient_metadata.csv*.

Please don't use any feature that you infer you don't know the first day of a patient in an ICU.

Note that the main cause/disease of patient condition is embedded as a code at *ICD9_diagnosis* column. The meaning of this code can be found at *MIMIC_metadata_diagnose.csv*. **But** this is only the main one; a patient can have co-occurrent diseases (comorbidities). These secondary codes can be found at *extra_data/MIMIC_diagnoses.csv*.

As performance metric, you can use *AUC* for the binary classification case, but feel free to report as well any other metric if you can justify that is particularly suitable for this case.

Main tasks are:

- Using *mimic_train.csv* file build a predictive model for *HOSPITAL_EXPIRE_FLAG*.
- For this analysis there is an extra test dataset, *mimic_test_death.csv*. Apply your final model to this extra dataset and generate predictions following the same format as *mimic_kaggle_death_sample_submission.csv*. Once ready, you can submit to our Kaggle competition and iterate to improve the accuracy.

As a *bonus*, try different algorithms for neighbor search and for distance, and justify final selection. Try also different weights to cope with class imbalance and also to balance neighbor proximity. Try to assess somehow confidence interval of predictions.

You can follow those **steps** in your first implementation:

1. *Explore* and understand the dataset.
2. Manage missing data.
3. Manage categorial features. E.g. create *dummy variables* for relevant categorical features, or build an ad hoc distance function.
4. Build a prediction model. Try to improve it using methods to tackle class imbalance.
5. Assess expected accuracy of previous models using *cross-validation*.
6. Test the performance on the test file and report accuracy, following same preparation steps (missing data, dummies, etc). Remember that you should be able to yield a prediction for all the rows of the test dataset.

Feel free to reduce the training dataset if you experience computational constraints.

```
In [ ]: # Mount google drive if running from Google Collab
        from google.colab import drive
        drive.mount('/content/drive')
```

Mounted at /content/drive

```
In [ ]: ## Set current directory if running from Google Collab

        import os
        #os.chdir('/content/drive/My Drive/ComputationalML/nearest_neighbors/Pyth
        os.chdir('/content/drive/My Drive/CM1_CM2_learning/2021_2022_classes/CM1_
```

```
In [ ]: !pip install category_encoders
```

Generally useful packages

```
In [ ]: # Imports
        import pandas as pd
        import numpy as np
        %matplotlib inline
        import matplotlib.pyplot as plt
        import seaborn as sns
        import sklearn
```

Loading the data

```
In [ ]: # Training dataset
        train = pd.read_csv('bgse-svm-death/mimic_train.csv')
        train.head()
```

```
Out[ ]:
```

	HOSPITAL_EXPIRE_FLAG	subject_id	hadm_id	icustay_id	HeartRate_Min	HeartRate_M
0	0	55440	195768	228357	89.0	1.
1	0	76908	126136	221004	63.0	1
2	0	95798	136645	296315	81.0	!
3	0	40708	102505	245557	76.0	1.
4	0	28424	127337	225281	NaN	

5 rows x 41 columns

```
In [ ]:
```

```
# Test dataset (to produce predictions)
test = pd.read_csv('bgse-svm-death/mimic_test_death.csv')
test.sort_values('icustay_id').head()
```

```
Out[ ]:
```

	subject_id	hadm_id	icustay_id	HeartRate_Min	HeartRate_Max	HeartRate_Mean
4930	93535	121562	200011	56.0	82.0	71.205128
1052	30375	177945	200044	NaN	NaN	NaN
3412	73241	149216	200049	54.0	76.0	64.833333
1725	99052	129142	200063	85.0	102.0	92.560976
981	51698	190004	200081	82.0	133.0	94.323529

5 rows x 39 columns

```
In [ ]:
```

```
# Obtaining list of features - train
train.columns
```

```
Out[ ]:
```

```
Index(['HOSPITAL_EXPIRE_FLAG', 'subject_id', 'hadm_id', 'icustay_id',
       'HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_Min',
       'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'DiasBP_Mea
n',
       'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
       'RespRate_Max', 'RespRate_Mean', 'TempC_Min', 'TempC_Max', 'TempC_
Mean',
       'SpO2_Min', 'SpO2_Max', 'SpO2_Mean', 'Glucose_Min', 'Glucose_Max',
       'Glucose_Mean', 'GENDER', 'DOB', 'ADMITTIME', 'Diff', 'ADMISSION_T
YPE',
       'INSURANCE', 'RELIGION', 'MARITAL_STATUS', 'ETHNICITY', 'DIAGNOSIS
',
       'ICD9_diagnosis', 'FIRST_CAREUNIT', 'LOS'],
      dtype='object')
```

```
In [ ]: # Obtaining list of features - test  
test.columns
```

```
Out[ ]: Index(['subject_id', 'hadm_id', 'icustay_id', 'HeartRate_Min', 'HeartRate_Max',  
             'HeartRate_Mean', 'SysBP_Min', 'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min',  
             'DiasBP_Max', 'DiasBP_Mean', 'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean',  
             'RespRate_Min', 'RespRate_Max', 'RespRate_Mean', 'TempC_Min',  
             'TempC_Max', 'TempC_Mean', 'SpO2_Min', 'SpO2_Max', 'SpO2_Mean',  
             'Glucose_Min', 'Glucose_Max', 'Glucose_Mean', 'GENDER', 'DOB',  
             'ADMITTIME', 'Diff', 'ADMISSION_TYPE', 'INSURANCE', 'RELIGION',  
             'MARITAL_STATUS', 'ETHNICITY', 'DIAGNOSIS', 'ICD9_diagnosis',  
             'FIRST_CAREUNIT'],  
          dtype='object')
```

Dropping columns = 'DOD', 'DISCHTIME', 'DEATHTIME', 'LOS'

```
In [ ]: # Dropping the different columns from the training data  
#extra = ['DOD', 'DISCHTIME', 'DEATHTIME', 'LOS']  
extra = ['LOS']  
train = train.drop(extra, axis=1)  
train.shape
```

```
Out[ ]: (20885, 40)
```

Do we have missing data?

```
In [ ]: # Checking for Nulls - train  
train.isnull().sum()
```

```
Out[ ]: HOSPITAL_EXPIRE_FLAG      0
        subject_id            0
        hadm_id               0
        icustay_id            0
        HeartRate_Min         2187
        HeartRate_Max         2187
        HeartRate_Mean        2187
        SysBP_Min             2208
        SysBP_Max             2208
        SysBP_Mean            2208
        DiasBP_Min            2209
        DiasBP_Max            2209
        DiasBP_Mean           2209
        MeanBP_Min            2186
        MeanBP_Max            2186
        MeanBP_Mean           2186
        RespRate_Min          2189
        RespRate_Max          2189
        RespRate_Mean         2189
        TempC_Min             2497
        TempC_Max             2497
        TempC_Mean            2497
        SpO2_Min              2203
        SpO2_Max              2203
        SpO2_Mean             2203
        Glucose_Min           253
        Glucose_Max           253
        Glucose_Mean          253
        GENDER                0
        DOB                   0
        ADMITTIME             0
        Diff                   0
        ADMISSION_TYPE        0
        INSURANCE              0
        RELIGION               0
        MARITAL_STATUS        722
        ETHNICITY              0
        DIAGNOSIS              0
        ICD9_diagnosis         0
        FIRST_CAREUNIT         0
        dtype: int64
```

```
In [ ]: # Checking for Nulls - test
        test.isnull().sum()
```

```
Out[ ]: subject_id      0
        hadm_id        0
        icustay_id     0
        HeartRate_Min  545
        HeartRate_Max  545
        HeartRate_Mean 545
        SysBP_Min      551
        SysBP_Max      551
        SysBP_Mean     551
        DiasBP_Min     552
        DiasBP_Max     552
        DiasBP_Mean    552
        MeanBP_Min     547
        MeanBP_Max     547
        MeanBP_Mean    547
        RespRate_Min   546
        RespRate_Max   546
        RespRate_Mean  546
        TempC_Min      638
        TempC_Max      638
        TempC_Mean     638
        SpO2_Min       551
        SpO2_Max       551
        SpO2_Mean      551
        Glucose_Min    58
        Glucose_Max    58
        Glucose_Mean   58
        GENDER         0
        DOB            0
        ADMITTIME      0
        Diff           0
        ADMISSION_TYPE 0
        INSURANCE      0
        RELIGION       0
        MARITAL_STATUS 180
        ETHNICITY      0
        DIAGNOSIS      0
        ICD9_diagnosis 0
        FIRST_CAREUNIT 0
        dtype: int64
```

Do we have class imbalance?

```
In [ ]: # Checking for class imbalance
        train['HOSPITAL_EXPIRE_FLAG'].value_counts()
```

```
Out[ ]: 0    18540
        1     2345
        Name: HOSPITAL_EXPIRE_FLAG, dtype: int64
```

Pre-Processing

Age Variable

Using ADMITTIME , DOB and Diff to create an age variable

```
In [ ]: import datetime as dt

for my_df in [train, test]:
    # Convert admittance to date, adding "Diff" to make the dates realistic
    my_df['ADMITTIME'] = (pd.to_datetime(my_df['ADMITTIME']) + my_df["Diff"]
    # Convert dob to date, adding "Diff" to make the dates realistic
    my_df['DOB'] = (pd.to_datetime(my_df['DOB']) + my_df["Diff"].apply(lambda
    # Convert to age in years
    my_df['age'] = my_df.apply(lambda e: (e['ADMITTIME'] - e['DOB']).days
```

For patients who are older than 89 years old, we impute the values to be 90 years old.

<https://github.com/MIT-LCP/mimic-code/issues/637>

```
In [ ]: train['age'] = train.age.where(test['age'] < 89, 90)
test['age'] = test.age.where(test['age'] < 89, 90)
```

```
In [ ]: train = train.drop(['DOB', 'Diff'], axis = 1)
test = test.drop(['DOB', 'Diff'], axis = 1)
```

Combining ethnicities and religion

These are high cardinality categories with very few observations in some. We can logically combine them to reduce the number of dummy variables we have to produce

```
In [ ]: train['ETHNICITY'].value_counts()
```

```

Out[ ]: WHITE 15112
        BLACK/AFRICAN AMERICAN 1977
        UNABLE TO OBTAIN 577
        UNKNOWN/NOT SPECIFIED 568
        HISPANIC OR LATINO 562
        OTHER 489
        ASIAN 265
        PATIENT DECLINED TO ANSWER 175
        HISPANIC/LATINO - PUERTO RICAN 155
        ASIAN - CHINESE 146
        BLACK/CAPE VERDEAN 126
        WHITE - RUSSIAN 117
        BLACK/HAITIAN 72
        HISPANIC/LATINO - DOMINICAN 59
        ASIAN - ASIAN INDIAN 58
        WHITE - OTHER EUROPEAN 50
        MULTI RACE ETHNICITY 50
        PORTUGUESE 40
        WHITE - BRAZILIAN 33
        ASIAN - VIETNAMESE 28
        BLACK/AFRICAN 26
        MIDDLE EASTERN 24
        HISPANIC/LATINO - GUATEMALAN 24
        WHITE - EASTERN EUROPEAN 18
        HISPANIC/LATINO - CUBAN 17
        ASIAN - FILIPINO 16
        ASIAN - CAMBODIAN 14
        AMERICAN INDIAN/ALASKA NATIVE 13
        HISPANIC/LATINO - SALVADORAN 13
        HISPANIC/LATINO - MEXICAN 8
        HISPANIC/LATINO - CENTRAL AMERICAN (OTHER) 7
        SOUTH AMERICAN 7
        CARIBBEAN ISLAND 6
        ASIAN - KOREAN 6
        NATIVE HAWAIIAN OR OTHER PACIFIC ISLANDER 6
        ASIAN - JAPANESE 6
        HISPANIC/LATINO - COLOMBIAN 5
        ASIAN - OTHER 3
        ASIAN - THAI 3
        HISPANIC/LATINO - HONDURAN 2
        AMERICAN INDIAN/ALASKA NATIVE FEDERALLY RECOGNIZED TRIBE 2
        Name: ETHNICITY, dtype: int64

```

```

In [ ]: train['RELIGION'].value_counts()

```



```
In [ ]: test['ETHNICITY'] = test['ETHNICITY'].replace(['ASIAN', 'ASIAN - CHINESE',
                                                    'ASIAN - JAPANESE',
                                                    ], 'ASIAN')

test['ETHNICITY'] = test['ETHNICITY'].replace(['HISPANIC OR LATINO', 'HIS
                                                    'HISPANIC/LATINO - C
                                                    'HISPANIC/LATINO - M
                                                    'HISPANIC/LATINO - F
                                                    ], 'HISPANIC OR LATI

test['ETHNICITY'] = test['ETHNICITY'].replace(['WHITE', 'WHITE - RUSSIAN',
                                                    'WHITE - BRAZILIAN'
                                                    ], 'WHITE')

test['ETHNICITY'] = test['ETHNICITY'].replace(['BLACK/AFRICAN', 'BLACK/AF
                                                    ], 'BLACK')

test['ETHNICITY'] = test['ETHNICITY'].replace(['UNABLE TO OBTAIN', 'UNKNO
                                                    ], 'UNKNOWN')

test['ETHNICITY'] = test['ETHNICITY'].replace(['AMERICAN INDIAN/ALASKA NA
                                                    'CARIBBEAN ISLAND',
                                                    'MULTI RACE ethnici
                                                    ], 'OTHER')
```

```
In [ ]: religion_other = ['HEBREW', 'UNITARIAN-UNIVERSALIST', 'HINDU', 'GREEK OR
train['RELIGION'] = train['RELIGION'].replace(reigion_other, 'OTHER')
test['RELIGION'] = test['RELIGION'].replace(reigion_other, 'OTHER')
```

Or using some string operations

e.g.

```
# Ethnicities list
ethnicities = ["WHITE", "ASIAN", "BLACK", "HISPANIC"]

# Check if the category value contains the word "WHITE",
"ASIAN", "BLACK" or "HISPANIC"
for ethnicity in ethnicities:
    df_train[ethnicity] =
df_train.ETHNICITY.str.contains(ethnicity, regex=False)*1
    df_test[ethnicity] =
df_test.ETHNICITY.str.contains(ethnicity, regex=False)*1
```

Repeat Visits to the ICU

Some patients visited the ICU more than once, we can add the number of previous visits they have had as a variable

```
In [ ]: train["visits_ICU"] = train.sort_values(['subject_id', 'ADMITTIME']).groupby
test["visits_ICU"] = test.sort_values(['subject_id', 'ADMITTIME']).groupby
```

```
In [ ]: # Print some part of the output
train[["subject_id", "ADMITTIME", "visits_ICU"]].sort_values(["subject_id", "ADMITTIME"])
```

```
Out [ ]:
```

	subject_id	ADMITTIME	visits_ICU
18310	23	2011-05-02	1
17908	34	2012-07-03	1
9591	36	2011-03-01	1
727	85	2008-09-27	1
16007	109	2008-03-03	1
13738	109	2008-04-30	2
4002	109	2008-08-12	3
12883	109	2008-08-18	4
17983	109	2008-08-25	5
8222	109	2008-09-20	6
1283	109	2008-10-25	7
6733	109	2008-10-31	8
13431	109	2008-11-14	9

```
In [ ]: train = train.drop(['ADMITTIME'], axis = 1)
test = test.drop(['ADMITTIME'], axis = 1)
```

Diagnoses

- We remove the text fields
- We will target encode (with smoothing) in the pipeline
- Could do something more complicated aggregating the severity of each diagnosis with comorbidities e.g. max, mean, median ect. but for simplicity I stick to this

```
In [ ]: train = train.drop(['DIAGNOSIS'], axis = 1)
test = test.drop(['DIAGNOSIS'], axis = 1)
```

Number of Comorbidities

A simple way to include the comorbidities is to simply count how many comorbidities each patient had. One could do more complicated things also (see above)

```
In [ ]: # Reading comorbidities dataset
comorbidities = pd.read_csv("bgse-svm-death/extra_data/MIMIC_diagnoses.csv")
comorbidities.head()
```

```
Out[ ]:
```

	SUBJECT_ID	HADM_ID	SEQ_NUM	ICD9_CODE
0	256	108811	1.0	53240
1	256	108811	2.0	41071
2	256	108811	3.0	53560
3	256	108811	4.0	40390
4	256	108811	5.0	5859

```
In [ ]:
```

```
# Computing the number of comorbidities in each of the ICU stays
number_comorbidities_patient = comorbidities.groupby(["SUBJECT_ID", "HADM_ID"]).agg({"ICD9_CODE": "count", "SEQ_NUM": "count"})
number_comorbidities_patient = number_comorbidities_patient.rename({"SEQ_NUM": "number_comorbidities_patient"})
```

```
Out[ ]:
```

	SUBJECT_ID	HADM_ID	number_comorbidities
0	2	163353	3.0
1	3	145834	9.0
2	4	185777	9.0
3	5	178980	3.0
4	6	107064	8.0
...
58971	99985	176670	13.0
58972	99991	151118	17.0
58973	99992	197084	12.0
58974	99995	137810	17.0
58975	99999	113369	5.0

58976 rows x 3 columns

```
In [ ]:
```

```
# Join with training set
train = pd.merge(train, number_comorbidities_patient, left_on=["subject_id", "hadm_id"], right_on=["SUBJECT_ID", "HADM_ID"])

# Join with test set
test = pd.merge(test, number_comorbidities_patient, left_on=["subject_id", "hadm_id"], right_on=["SUBJECT_ID", "HADM_ID"])
```

Handling Missing Values

```
In [ ]:
```

```
# Checking for Nulls - train
train.isnull().sum()
```

```

Out[ ]: HOSPITAL_EXPIRE_FLAG      0
        subject_id          0
        hadm_id             0
        icustay_id          0
        HeartRate_Min       2187
        HeartRate_Max       2187
        HeartRate_Mean      2187
        SysBP_Min           2208
        SysBP_Max           2208
        SysBP_Mean          2208
        DiasBP_Min          2209
        DiasBP_Max          2209
        DiasBP_Mean         2209
        MeanBP_Min          2186
        MeanBP_Max          2186
        MeanBP_Mean         2186
        RespRate_Min        2189
        RespRate_Max        2189
        RespRate_Mean       2189
        TempC_Min           2497
        TempC_Max           2497
        TempC_Mean          2497
        SpO2_Min            2203
        SpO2_Max            2203
        SpO2_Mean           2203
        Glucose_Min         253
        Glucose_Max         253
        Glucose_Mean        253
        GENDER              0
        ADMISSION_TYPE      0
        INSURANCE           0
        RELIGION            0
        MARITAL_STATUS      722
        ETHNICITY           0
        ICD9_diagnosis      0
        FIRST_CAREUNIT      0
        age                 0
        visits_ICU          0
        number_comorbidities 0
        dtype: int64

```

Marital Status

We can logically combine `nan` values for marital status with the `UNKNOWN (DEFAULT)` class. If there were not this class already you could add a 'missing' class

```

In [ ]: train["MARITAL_STATUS"].unique()

```

```

Out[ ]: array(['SINGLE', 'MARRIED', 'SEPARATED', 'WIDOWED', 'DIVORCED', nan,
              'UNKNOWN (DEFAULT)', 'LIFE PARTNER'], dtype=object)

```

```

In [ ]: #first we deal with marital status missing
        # there is a category of unknown, so i'll fill the missing values with t
        train['MARITAL_STATUS'] = train['MARITAL_STATUS'].fillna('UNKNOWN (DEFAULT)')
        test['MARITAL_STATUS'] = test['MARITAL_STATUS'].fillna('UNKNOWN (DEFAULT)')

```

Forward/Backward filling from previous visits

We can use repeat visits to forward and backward fill missing data

```
In [ ]: train = train.groupby(['subject_id'], as_index = False).apply(lambda group:
test = test.groupby(['subject_id'], as_index = False).apply(lambda group:
```

```
In [ ]: # Checking for Nulls - train
train.isnull().sum()
```

```
Out[ ]: HOSPITAL_EXPIRE_FLAG      0
subject_id                    0
hadm_id                       0
icustay_id                    0
HeartRate_Min                 1937
HeartRate_Max                 1937
HeartRate_Mean                1937
SysBP_Min                     1957
SysBP_Max                     1957
SysBP_Mean                    1957
DiasBP_Min                    1958
DiasBP_Max                    1958
DiasBP_Mean                   1958
MeanBP_Min                    1937
MeanBP_Max                    1937
MeanBP_Mean                   1937
RespRate_Min                  1938
RespRate_Max                  1938
RespRate_Mean                 1938
TempC_Min                     2207
TempC_Max                     2207
TempC_Mean                    2207
SpO2_Min                      1952
SpO2_Max                      1952
SpO2_Mean                     1952
Glucose_Min                   214
Glucose_Max                   214
Glucose_Mean                   214
GENDER                        0
ADMISSION_TYPE                0
INSURANCE                     0
RELIGION                      0
MARITAL_STATUS                0
ETHNICITY                     0
ICD9_diagnosis                0
FIRST_CAREUNIT                 0
age                           0
visits_ICU                     0
number_comorbidities          0
dtype: int64
```

```
In [ ]: train = train.groupby(['subject_id'], as_index = False).apply(lambda group:
test = test.groupby(['subject_id'], as_index = False).apply(lambda group:
```

```
In [ ]: # Checking for Nulls - train  
train.isnull().sum()
```

```
Out[ ]: HOSPITAL_EXPIRE_FLAG      0  
subject_id                  0  
hadm_id                    0  
icustay_id                  0  
HeartRate_Min              1787  
HeartRate_Max              1787  
HeartRate_Mean             1787  
SysBP_Min                  1804  
SysBP_Max                  1804  
SysBP_Mean                 1804  
DiasBP_Min                 1805  
DiasBP_Max                 1805  
DiasBP_Mean                1805  
MeanBP_Min                 1788  
MeanBP_Max                 1788  
MeanBP_Mean                1788  
RespRate_Min              1787  
RespRate_Max              1787  
RespRate_Mean             1787  
TempC_Min                 2028  
TempC_Max                 2028  
TempC_Mean                2028  
SpO2_Min                  1800  
SpO2_Max                  1800  
SpO2_Mean                 1800  
Glucose_Min                191  
Glucose_Max                191  
Glucose_Mean               191  
GENDER                    0  
ADMISSION_TYPE            0  
INSURANCE                  0  
RELIGION                   0  
MARITAL_STATUS            0  
ETHNICITY                  0  
ICD9_diagnosis            0  
FIRST_CAREUNIT            0  
age                        0  
visits_ICU                0  
number_comorbidities      0  
dtype: int64
```

kNN imputation

We will impute the remaining continuous values of missing data using kNN as part of the pipeline.

You could be smarter than this, e.g. presumably age will have a greater impact on vitals than religion will

```
In [ ]:
from sklearn.impute import KNNImputer
from sklearn.impute import SimpleImputer

#cont_imputer = KNNImputer()
cont_imputer = SimpleImputer(strategy="mean")
```

Category Encoding

We will use the pipeline to encode our unordered categorical variables

OneHotEncoding/Dummy variables

OneHotEncoder is a slightly nicer alternative to `pd.get_dummies`

`sparse=False` prevents OneHotEncoder from outputting a sparse matrix and allowing compatibility later down the pipeline.

```
In [ ]:
from sklearn.preprocessing import OneHotEncoder

cat_encoder = OneHotEncoder(handle_unknown="ignore", sparse=False)
```

Target Encoding (Smoothed)

We encode each disease by it's death rate. Smoothing can help deal with cases where very few observations had a certain disease.

$$X_{ICD9-TE,j} = \lambda \frac{\# \text{ died with disease } j}{\# \text{ with disease } j} + (1 - \lambda) \frac{\# \text{ died}}{\# \text{ patients}}$$

```
In [ ]:
import category_encoders as ce

icd9_encoder = ce.TargetEncoder(smoothing = 1.0)
```

```
/usr/local/lib/python3.7/dist-packages/statsmodels/tools/_testing.py:19:
FutureWarning: pandas.util.testing is deprecated. Use the functions in the
public API at pandas.testing instead.
import pandas.util.testing as tm
```

Scaling

I am going to use a RobustScaler for the continuous variables and StandardScaler for the discrete ones

```
In [ ]:
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import RobustScaler

cont_scaler = RobustScaler()
cat_scaler = StandardScaler()
```



```
In [ ]: x_train = train.drop(["HOSPITAL_EXPIRE_FLAG", "subject_id", "hadm_id",
y_train = train["HOSPITAL_EXPIRE_FLAG"]
```

```
In [ ]: x_train
```

```
Out[ ]:
```

	HeartRate_Min	HeartRate_Max	HeartRate_Mean	SysBP_Min	SysBP_Max	SysBP
0	89.0	145.0	121.043478	74.0	127.0	106.5
1	63.0	110.0	79.117647	89.0	121.0	106.7
2	81.0	98.0	91.689655	88.0	138.0	112.0
3	76.0	128.0	98.857143	84.0	135.0	106.9
4	58.0	64.0	60.324324	78.0	118.0	99.0
...
20880	65.0	92.0	78.500000	60.0	160.0	110.0
20881	74.0	112.0	89.156250	100.0	150.0	123.0
20882	58.0	97.0	76.933333	94.0	131.0	112.0
20883	59.0	102.0	81.844444	96.0	150.0	123.8
20884	59.0	97.0	77.526316	82.0	139.0	106.0

20885 rows x 35 columns

```
In [ ]: y_train
```

```
Out[ ]:
```

0	0
1	0
2	0
3	0
4	0
...	...
20880	0
20881	0
20882	0
20883	0
20884	0

Name: HOSPITAL_EXPIRE_FLAG, Length: 20885, dtype: int64

Preprocessing Pipeline

We will use the `ColumnTransformer` to allow for different data preprocessing for different types of columns

- Numerical values - `RobustScaler()` and `KNNImputer()`
- Categoricals (not ICD9) - `OneHotEncoder()` and `StandardScaler()`
- ICD9 - `TargetEncoder()` and `StandardScaler()`

In []:

```
# Update list of numerical and categorical features
num_feat = X_train.select_dtypes(exclude=['object', 'category']).columns
print(num_feat)

cat_feat = X_train.select_dtypes(include=['object', 'category']).columns

# make own category for preprocessing 'ICD9_diagnosis'
icd9_feat = ['ICD9_diagnosis']
cat_feat = cat_feat.drop(['ICD9_diagnosis'])
print(icd9_feat)
print(cat_feat)
```

```
Index(['HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_Min',
      'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'DiasBP_Mea
n',
      'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
      'RespRate_Max', 'RespRate_Mean', 'TempC_Min', 'TempC_Max', 'TempC_
Mean',
      'SpO2_Min', 'SpO2_Max', 'SpO2_Mean', 'Glucose_Min', 'Glucose_Max',
      'Glucose_Mean', 'age', 'visits_ICU', 'number_comorbidities'],
      dtype='object')
['ICD9_diagnosis']
Index(['GENDER', 'ADMISSION_TYPE', 'INSURANCE', 'RELIGION', 'MARITAL_STAT
US',
      'ETHNICITY', 'FIRST_CAREUNIT'],
      dtype='object')
```

In []:

```
from sklearn.pipeline import make_pipeline, Pipeline
from sklearn.compose import ColumnTransformer

# pipeline for numerical data
num_preprocessing = make_pipeline(
    cont_scaler,
    cont_imputer
)

# pipeline for categorical data
cat_preprocessing = make_pipeline(
    #SimpleImputer(strategy="most_frequent"), # we only have missing data
    cat_encoder,
    cat_scaler)

icd9_preprocessing = make_pipeline(
    icd9_encoder,
    cat_scaler)

# combine preprocessing pipelines using a columnTransformer
preprocessing = ColumnTransformer(
    [ ("num", num_preprocessing, num_feat),
      ("cat", cat_preprocessing, cat_feat),
      ("icd9", icd9_preprocessing, icd9_feat)
    ],
    #,remainder='passthrough'
    , remainder='drop'
)
```



In []:

```
from sklearn import set_config
set_config(display="diagram")
preprocessing
```

Out []:

```
ColumnTransformer(transformers=[('num',
                                Pipeline(steps=[('robustscaler',
                                                    RobustScaler()),
                                                    ('simpleimputer',
                                                    SimpleImputer())
                                                    ])),
                                Index(['HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_Min',
                                        'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'DiasBP_Mean',
                                        'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
                                        'RespRate_Max', 'RespRate_Mean', 'TempC_M...
                                Pipeline(steps=[('onehotencoder',
                                                    OneHotEncoder(handle_unknown='ignore',
                                                                    sparse=False)),
                                ('standardscaler'
```

```

StandardScaler()
    ])),
    Index(['GENDER', 'ADMISSION_TYPE',
, 'INSURANCE', 'RELIGION', 'MARITAL_STATUS',
    'ETHNICITY', 'FIRST_CAREUNIT'],
    dtype='object')),
    ('icd9',
    Pipeline(steps=[('targetencoder',
    TargetEncoder())
,
    ('standardscaler'
,
    StandardScaler()
    ])),
    ['ICD9_diagnosis'])))

```

Please rerun this cell to show the HTML repr or trust the notebook.

ColumnTransformer

```

ColumnTransformer(transformers=[('num',
    Pipeline(steps=[('robustscaler',
    RobustScaler()),
    ('simpleimputer',
    SimpleImputer())
    ])),
    Index(['HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_Min',
    'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'DiasBP_Mean',
    'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
    'RespRate_Max', 'RespRate_Mean', 'TempC_M...
    Pipeline(steps=[('onehotencoder',
    OneHotEncoder(ha
ndle_unknown='ignore',
    sparse=False)),
    ('standardscaler'
,
    StandardScaler()
    ])),
    Index(['GENDER', 'ADMISSION_TYPE',
, 'INSURANCE', 'RELIGION', 'MARITAL_STATUS',
    'ETHNICITY', 'FIRST_CAREUNIT'],
    dtype='object')),
    ('icd9',
    Pipeline(steps=[('targetencoder',
    TargetEncoder())
,
    ('standardscaler'
,
    StandardScaler()
    ])),
    ['ICD9_diagnosis'])))
num
Index(['HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_

```

```

Min',
    'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'Dia
sBP_Mean',
    'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
    'RespRate_Max', 'RespRate_Mean', 'TempC_Min', 'TempC_Max',
    'TempC_Mean',
    'SpO2_Min', 'SpO2_Max', 'SpO2_Mean', 'Glucose_Min', 'Glucos
e_Max',
    'Glucose_Mean', 'age', 'visits_ICU', 'number_comorbidities'
],
    dtype='object')
RobustScaler
RobustScaler()
SimpleImputer
SimpleImputer()
cat
Index(['GENDER', 'ADMISSION_TYPE', 'INSURANCE', 'RELIGION', 'MARIT
AL_STATUS',
      'ETHNICITY', 'FIRST_CAREUNIT'],
      dtype='object')
OneHotEncoder
OneHotEncoder(handle_unknown='ignore', sparse=False)
StandardScaler
StandardScaler()
icd9
['ICD9_diagnosis']
TargetEncoder
TargetEncoder()
StandardScaler
StandardScaler()

```

```

In [ ]: #X_train_pp = preprocessing.fit_transform(X_train, y_train)

```

```

In [ ]: preprocessing.fit(X_train, y_train)
        X_train_pp = preprocessing.transform(X_train)

```

```

In [ ]: X_train_pp.shape

```

```

Out[ ]: (20885, 63)

```

Class Imbalance

- The SVC offers the `class_weight = 'balanced'`, this conducts RandomOverSampling of the minority class till the classes are balanced.
- KNeighborsClassifier has no such option
- and in any case randomly repeating minority observations is not necessarily the best you can do

SMOTEing

SMOTE = Synthetic Minority Oversampling Technique. The idea is to create synthetic observations that lie in between two close members of the minority class

- Sample minority observation at random
- Sample one of k nearest neighbours (default $k = 5$)
- Draw a line between the point and the chosen neighbour
- Generate a new observation on this line

Tomek links

Tomek links is a method for undersampling. This removes majority class observations that are close to minority class observations.

x_i and x_j are Tomek links if

- x_i is x_j 's nearest neighbour
- x_j is x_i 's nearest neighbour
- $y_i \neq y_j$

<https://imbalanced-learn.org/stable/references/generated/imblearn.combine.SMOTETomek.html>

In []:

```
from imblearn.under_sampling import RandomUnderSampler
from imblearn.over_sampling import SMOTE
from imblearn.combine import SMOTETomek
from imblearn.under_sampling import TomekLinks
```

kNN

In []:

```
from sklearn.neighbors import KNeighborsClassifier
from imblearn.pipeline import Pipeline as imbPipe

kNN_pipe = imbPipe([
    ('preprocess', preprocessing),
    #('oversampling', SMOTE()),
    #('undersampling', RandomUnderSampler()),
    #('resampling', SMOTETomek(tomek=TomekLinks(sampling_strategy='majority')),
    #('features', fs.RFECV(estimator = DecisionTreeClassifier(class_weight='balanced',
    # step = 10, cv = 5, scoring = 'roc_auc')))
    ('kNN', KNeighborsClassifier(algorithm = 'auto'))
])
```

In []:

```
from sklearn import set_config
set_config(display="diagram")
kNN_pipe
```

Out []:

```
Pipeline(steps=[('preprocess',
                  ColumnTransformer(transformers=[('num',
                                                    Pipeline(steps=[
('robustscaler',
RobustScaler()),
('simpleimputer',
SimpleImputer())])),
Index(['HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_Min',
'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'DiasBP_Mean',
'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
'RespRate...'],
OneHotEncoder(handle_unknown='ignore',
sparse=False)),
('standardscaler',
StandardScaler())]),
Index(['GENDER',
'ADMISSION_TYPE', 'INSURANCE', 'RELIGION', 'MARITAL_STATUS',
'ETHNICITY', 'FIRST_CAREUNIT'],
dtype='object')),
('icd9',
Pipeline(steps=[
('targetencoder',
TargetEncoder()),
('standardscaler',
```

```
StandardScaler()))],
                                                                    ['ICD9_diagnosis
']])),
                ('kNN', KNeighborsClassifier()))
Please rerun this cell to show the HTML repr or trust the notebook.
Pipeline
Pipeline(steps=[('preprocess',
                  ColumnTransformer(transformers=[('num',
                                                  Pipeline(steps=[
('robustscaler',
RobustScaler()),
('simpleimputer',
SimpleImputer())])),
                  Index(['HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_Min',
                        'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'Dia
sBP_Mean',
                        'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
                        'RespRate...
OneHotEncoder(handle_unknown='ignore',
sparse=False)),
('standardscaler',
StandardScaler()))],
                                                                    Index(['GENDER',
'ADMISSION_TYPE', 'INSURANCE', 'RELIGION', 'MARITAL_STATUS',
'ETHNICITY', 'FIRST_CAREUNIT'],
dtype='object')),
                                                                    ('icd9',
                                                                    Pipeline(steps=[
('targetencoder',
TargetEncoder()),
('standardscaler',
StandardScaler()))],
                                                                    ['ICD9_diagnosis
']])),
                ('kNN', KNeighborsClassifier()))
preprocess: ColumnTransformer
ColumnTransformer(transformers=[('num',
                                Pipeline(steps=[('robustscaler',
                                                    RobustScaler()),
('simpleimputer',
SimpleImputer())
]),
```



```

Index(['HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_Min',
      'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'DiasBP_Mean',
      'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
      'RespRate_Max', 'RespRate_Mean', 'TempC_Min', 'TempC_Max',
      'TempC_Mean', 'SpO2_Min', 'SpO2_Max', 'SpO2_Mean', 'Glucose_Min', 'Glucose_Max',
      'Glucose_Mean', 'age', 'visits_ICU', 'number_comorbidities'],
      dtype='object'))
Pipeline(steps=[('onehotencoder', OneHotEncoder(handle_unknown='ignore', sparse=False)),
                 ('standardscaler', StandardScaler())]),
Index(['GENDER', 'ADMISSION_TYPE', 'INSURANCE', 'RELIGION', 'MARITAL_STATUS',
      'ETHNICITY', 'FIRST_CAREUNIT'],
      dtype='object')),
('icd9',
 Pipeline(steps=[('targetencoder', TargetEncoder())
                 ('standardscaler', StandardScaler())]),
 ['ICD9_diagnosis'])))
num
Index(['HeartRate_Min', 'HeartRate_Max', 'HeartRate_Mean', 'SysBP_Min',
      'SysBP_Max', 'SysBP_Mean', 'DiasBP_Min', 'DiasBP_Max', 'DiasBP_Mean',
      'MeanBP_Min', 'MeanBP_Max', 'MeanBP_Mean', 'RespRate_Min',
      'RespRate_Max', 'RespRate_Mean', 'TempC_Min', 'TempC_Max',
      'TempC_Mean', 'SpO2_Min', 'SpO2_Max', 'SpO2_Mean', 'Glucose_Min', 'Glucose_Max',
      'Glucose_Mean', 'age', 'visits_ICU', 'number_comorbidities'],
      dtype='object')
RobustScaler
RobustScaler()
SimpleImputer
SimpleImputer()
cat
Index(['GENDER', 'ADMISSION_TYPE', 'INSURANCE', 'RELIGION', 'MARITAL_STATUS',
      'ETHNICITY', 'FIRST_CAREUNIT'],
      dtype='object')
OneHotEncoder
OneHotEncoder(handle_unknown='ignore', sparse=False)
StandardScaler

```

```
StandardScaler()
icd9
['ICD9_diagnosis']
TargetEncoder
TargetEncoder()
StandardScaler
StandardScaler()
KNeighborsClassifier
KNeighborsClassifier()
```

GridSearch

The minimum I wanted to see you grid search over were the number of neighbours, the 'weights' and the parameter of the distance.

Some students also considered specifically defining the `metric`.

Once idea I particularly liked was deliberately scaling different columns differently to give them higher or lower importance

```
In [ ]: knn_params = {'preprocess_num_cont_imputer_n_neighbors':[10, 50, 100],
                    #'preprocess_num_cont_imputer_strategy':['mean', 'median'],
                    #'preprocess_icd9_icd9_encoder_smoothing':[0.5, 1, 2],
                    #'oversampling_sampling_strategy':[0.1,0.3,0.5],
                    #'undersampling_sampling_strategy':[0.5, 0.6, 0.7],
                    #'kNN_n_neighbors':[1, 2, 5, 10, 20, 50],
                    'kNN_n_neighbors':[300],
                    #'kNN_weights':['uniform', 'distance'],
                    'kNN_weights':['distance'],
                    #'kNN_p':[1, 2, 3]
                    'kNN_p':[3]
                    }
```

Here I consider `HalvingGridSearch()` to speed up my grid search.

```
In [ ]: from sklearn.experimental import enable_halving_search_cv
        from sklearn.model_selection import HalvingGridSearchCV
```

```
In [ ]: grid_knn = HalvingGridSearchCV(knn_pipe, knn_params, scoring='roc_auc', cv=5)
        grid_knn.fit(X_train, y_train)

        print("Best parameter (CV score=%0.3f):" % grid_knn.best_score_)
        print(grid_knn.best_params_)
```

```
Best parameter (CV score=0.770):
{'kNN_n_neighbors': 300, 'kNN_p': 3, 'kNN_weights': 'distance'}
```

Test set predictions

```
In [ ]: x_test = test.drop(["subject_id", "hadm_id", "icustay_id"], axis=1)
```

```
In [ ]: y_pred_kNN = grid_kNN.predict_proba(X_test)
```

Reweighting to adjust for class-imbalance

```
In [ ]: def reweight(pi,q1=0.5,r1=0.5):
    r0 = 1-r1
    q0 = 1-q1
    tot = pi*(q1/r1)+(1-pi)*(q0/r0)
    w = pi*(q1/r1)
    w /= tot
    return w
## assign q the proper reweight
q1 = y_test.sum()/len(y_test)
r1 = 0.5 ??? this will depend on what reweighting you did
## reweight probabilities
y_pred_kNN_reweighted = pd.Series(y_pred_kNN[:,1]).apply(reweight,args=(q1,r1))
```

or

Calibrating Probabilities

LogisticRegression() built a model for $P(Y|X, \beta)$ and then trained this model to

$$\max \sum_{i=1}^n \log P(Y = y_i | X_i, \beta)$$

this can be shown to trained the model to produce *calibrated* probabilities.

For a binary event A , the probability p_A is well calibrated if $p_A \times 100\%$ **of the time that you quote p_A , A happens**

CalibratedClassifierCV uses cross-validation both to fit the model and also to assess its calibration and recalibrate it.

<https://scikit-learn.org/stable/modules/calibration.html#calibration>

```
In [ ]: # Calibrated probabilities of the best model
kNN_calibrator = CalibratedClassifierCV(grid_kNN, cv = 5, method = 'isotonic')
kNN_calibrator.fit(X_train, y_train)
```

```
In [ ]: y_pred_kNN_recalibrated = kNN_calibrator.fit(X_test)
```

Comparing to the true y's

While you could submit to kaggle I can use the real y's

```
In [ ]: # Training dataset
y_test_true = pd.read_csv('mimic_test_death_true.csv')
```

```
In [ ]: y_test_true
```

```
In [ ]: from sklearn.metrics import roc_auc_score

roc_auc_score(y_test_true["HOSPITAL_EXPIRE_FLAG"], y_pred_kNN[:,1])
#roc_auc_score(y_test_true, y_pred_kNN_reweighted)
#roc_auc_score(y_test_true, y_pred_kNN_recalibrated[:,1])
```

SVM

```
In [ ]: from sklearn.neighbors import KNeighborsClassifier
from imblearn.pipeline import Pipeline as imbPipe

SVM_pipe = imbPipe([
    ('preprocess', preprocessing),
    #('oversampling', SMOTE()),
    #('undersampling', RandomUnderSampler()),
    #('resampling', SMOTETomek(tomek=TomekLinks(sampling_strategy='majority'),
    #('features', fs.RFECV(estimator = DecisionTreeClassifier(class_weight='balanced',
    # step = 10, cv = 5, scoring = 'roc_auc_max')))
    ('SVC', SVC())
])
```

```
In [ ]: from sklearn import set_config
set_config(display="diagram")
SVM_pipe
```

Gridsearch

```
In [ ]: SVM_params = {'preprocess__num__cont__imputer__n_neighbors':[10, 50, 100],
    #'preprocess__icd9__icd9_encoder__smoothing':[0.5, 1, 2],
    #'oversampling__sampling_strategy':[0.1,0.3,0.5],
    #'undersampling__sampling_strategy':[0.5, 0.6, 0.7],
    #'SVC__C':[0.1, 1, 10],
    #'SVC__C':[1],
    #'SVC__kernel':['linear', 'rbf', 'poly'],
    #'SVC__kernel':['rbf'],
    #'SVC__gamma':[0.25, 0.5, 0.75],
    #'SVC__gamma':[0.5]
}
```

In []:

```
grid_SVM = HalvingGridSearchCV(SVM_pipe, SVM_params, scoring='roc_auc', c

grid_SVM.fit(X_train, y_train)

print("--- %s seconds ---" % (time.time() - start_time))
print("Best parameter (CV score=%0.3f):" % grid_SVM.best_score_)
print(grid_SVM.best_params_)
```