Code_Appendix

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1 Machine Learning Applications for Health (COMP90089_2022_SM2)

2 Group Assignment: Digital Phenotype of Diabetes Mellitus.

2.0.1 Group members

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This notebook assumes that you have access to MIMIC-IV on Google BigQuery.

2.0.2 Goals

Propose a digital pheonotype for **diabetes mellitus**, describe ways to identify a patient cohort with MIMIC-IV using the diagnosis criteria, apply different machine learning approaches, and compare and contrast the metrics.

2.0.3 Definitions

Disease: Diabetes mellitus.

According to UpToDate, diabetes mellitus refers to 'diseases of abnormal carbohydrate metabolism that are characterized by hyperglycemia.' It is related to impaired insulin secretion and peripheral resistance to insulin action.

Disease criteria source: Diabetes: Diagnosis of diabetes mellitus or prediabetes in non-pregnant adults

2.0.4 Install necessary libraries: Google Colab does not have the InterpretML library installed, so the following command needs to be run.

[ ]:
```
pip install interpret
```

2.0.5 Load libraries and set up the environment

[ ]:
```
# Import libraries
from sklearn import neighbors
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.neural_network import MLPClassifier

from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.preprocessing import OrdinalEncoder, StandardScaler
from sklearn.metrics import balanced_accuracy_score, matthews_corrcoef,␣
↪roc_curve, auc, roc_auc_score, classification_report

from interpret import set_visualize_provider, show
from interpret.glassbox import ExplainableBoostingClassifier
from interpret.provider import InlineProvider

import os
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

%matplotlib inline
import warnings
warnings.filterwarnings("ignore")

# Access data with Google BigQuery
from google.colab import auth
from google.cloud import bigquery
```

To query MIMIC-IV, authenticate this notebook with the Google Cloud Platform using a Google account that has been granted access to MIMIC-IV via PhysioNet.

[ ]:
```
# Authenticate
auth.authenticate_user()
```

Set up the project ID by pasting the one you have from BigQuery into the code below.

[ ]:
```
# Set up environment variables
project_id = "clinical-entity-extraction"
```

```
os.environ["GOOGLE_CLOUD_PROJECT"] = project_id

# Read data from BigQuery into pandas dataframes
def run_query(query, project_id = project_id):
    return pd.io.gbq.read_gbq(query, project_id = project_id, dialect = "standard")
```

2.1 Diagnosis for diabetes mellitus

Patients with diabetes mellitus have either symptomatic or asymptomatic hyperglycemia. The diagnosis criteria for the two kinds of hyperglycemia are listed as follows:

Symptomatic hyperglycemia

1. Exhibition of thirst, polyuria, weight loss, or blurry vision → **Not applicable**: MIMIC-IV does not contain any information regarding these symptoms.

2. Random blood glucose values $\geq$ 200 mg/dL → **Not applicable**: MIMIC-IV does not contain items related to random blood glucose values.

Asymptomatic hyperglycemia

1. FPG values $\geq$ 126 mg/dL → **Not applicable**: MIMIC-IV does not contain any information regarding FPG values.
2. Two-hour plasma glucose values $\geq$ 200 mg/dL during a 75g OGTT → **Indirectly applicable**: MIMIC-IV does not contain items directly related to plasma glucose, but it does contain items for blood glucose.
3. A1C values $\geq$ 6.5% → **Applicable**: MIMIC-IV contains items for A1C values.

2.2 Items for finalized diagnosis criteria

Given that MIMIC-IV could not be used to determine whether a patient has symptomatic hyperglycemia, only asymptomatic hyperglycemia should be considered. Blood glucose and A1C values would be used to perform digital phenotyping. The items that would be used from MIMIC-IV for doing so are listed below:

2.2.1 Blood glucose values:

1. Table: d_labitems

- Glucose: itemid = 50809
- Glucose: itemid = 50931

2. Table: d_items

- Glucose (whole blood): itemid = 226537

2.2.2 A1C values:

1. Table: d_labitems

- % Hemoglobin A1c: itemid = 50852

2.3 MIMIC-IV exploration: Number of occurrences of each selected item

[ ]:
```
query = """SELECT itemid, COUNT(*) AS Frequency FROM `physionet-data.
↪mimiciv_hosp.labevents`
WHERE itemid IN (50809, 50931, 50852)
GROUP BY itemid
UNION ALL
SELECT itemid, COUNT(*) AS Frequency FROM `physionet-data.mimiciv_icu.
↪chartevents`
WHERE itemid = 226537
GROUP BY itemid;"""

result = run_query(query)
result
```

[ ]:

	itemid	Frequency
0	226537	156736
1	50852	235348
2	50809	221767
3	50931	2893059

2.4 MIMIC-IV exploration: Number of unique patients from each selected item

[ ]:
```
query = """SELECT itemid, COUNT(DISTINCT(subject_id)) AS Patients FROM␣
↪`physionet-data.mimiciv_hosp.labevents`
WHERE ((itemid = 50809 OR itemid = 50931) AND (valuenum >= 200)) OR ((itemid =␣
↪50852) AND (valuenum >= 6.5))
GROUP BY itemid
UNION ALL
SELECT itemid, COUNT(DISTINCT(subject_id)) AS Patients FROM `physionet-data.
↪mimiciv_icu.chartevents`
WHERE (itemid = 226537) AND (valuenum >= 200)
GROUP BY itemid;"""

result = run_query(query)
result
```

[ ]:

	itemid	Patients
0	226537	5571

```
1    50852      22013
2    50931      40232
3    50809      10444
```

2.5 Data collection

```
[ ]: # Module: mimiciv_hosp
     # Table: labevents

     query = """SELECT subject_id, valuenum AS glucose_amount FROM `physionet-data.
      ↪mimiciv_hosp.labevents`
     WHERE (itemid = 50809 OR itemid = 50931) AND (valuenum >= 200);"""

     glucose_hosp = run_query(query)
     glucose_hosp
```

```
[ ]:         subject_id  glucose_amount
     0         10108480           316.0
     1         10128111           270.0
     2         10227155           350.0
     3         10270064           303.0
     4         10297774           289.0
     …             …              …
     268226    18434727           255.0
     268227    18754359           255.0
     268228    18852216           255.0
     268229    18962557           255.0
     268230    19056923           255.0

     [268231 rows x 2 columns]
```

```
[ ]: # Module: mimiciv_hosp
     # Table: labevents

     query = """SELECT subject_id, valuenum AS a1c_amount FROM `physionet-data.
      ↪mimiciv_hosp.labevents`
     WHERE (itemid = 50852) AND (valuenum >= 6.5);"""

     a1c_hosp = run_query(query)
     a1c_hosp
```

```
[ ]:        subject_id  a1c_amount
     0        10030753        11.6
     1        10030753        10.8
     2        10152997        10.9
     3        10250304        14.9
```

```
4        10367718        15.4
…            …          …
90201    17090246        10.4
90202    18646253        10.4
90203    18902344        10.4
90204    11042045        10.4
90205    15848938        10.4

[90206 rows x 2 columns]
```

[ ]:
```python
# Module: mimiciv_icu
# Table: chartevents

query = """SELECT subject_id, valuenum AS glucose_amount FROM `physionet-data.
 ↪mimiciv_icu.chartevents`
WHERE (itemid = 226537) AND (valuenum >= 200);"""

glucose_icu = run_query(query)
glucose_icu
```

[ ]:
```
       subject_id  glucose_amount
0        17455762           228.0
1        18118203           225.0
2        16785014           203.0
3        17536222           200.0
4        10538657           291.0
…            …               …
13917    11151240           320.0
13918    11917664           217.0
13919    14901524           207.0
13920    12003679           241.0
13921    12279131           210.0

[13922 rows x 2 columns]
```

[ ]:
```python
glucose = pd.concat([glucose_icu, glucose_hosp])
glucose
```

[ ]:
```
        subject_id  glucose_amount
0         17455762           228.0
1         18118203           225.0
2         16785014           203.0
3         17536222           200.0
4         10538657           291.0
…             …               …
268226    18434727           255.0
268227    18754359           255.0
```

```
268228    18852216          255.0
268229    18962557          255.0
268230    19056923          255.0

[282153 rows x 2 columns]
```

[ ]:
```
patient_cohort = pd.merge(glucose, a1c_hosp, how = "inner", left_on =␣
↪"subject_id", right_on = "subject_id")
patient_cohort
```

[ ]:
```
          subject_id  glucose_amount  a1c_amount
0           17455762           228.0        11.4
1           17455762           244.0        11.4
2           17455762           390.0        11.4
3           17455762           332.0        11.4
4           17455762           277.0        11.4
…              …              …          …
1210400     16985138           255.0         6.7
1210401     16985138           255.0         7.2
1210402     16985138           255.0         7.7
1210403     18303020           255.0         7.2
1210404     15305021           255.0         8.1

[1210405 rows x 3 columns]
```

2.6 Feature engineering

Create the following features:

1. Mean blood glucose value
2. Mean A1C value

[ ]:
```
patient_cohort_gb = patient_cohort.groupby(by = "subject_id")

patient_id = [i for i, g in patient_cohort_gb]
patient_glucose_mean = [g["glucose_amount"].mean() for i, g in␣
↪patient_cohort_gb]
patient_a1c_mean = [g["a1c_amount"].mean() for i, g in patient_cohort_gb]

patient_cohort_mean = pd.DataFrame({"patient_id": patient_id, "mean_glucose":␣
↪patient_glucose_mean, "mean_a1c": patient_a1c_mean})
patient_cohort_mean.head()
```

[ ]:
```
   patient_id  mean_glucose   mean_a1c
0    10000980    266.222222   7.180000
1    10001122    247.500000   8.500000
2    10001877    205.000000   7.700000
```

```
3     10002013     313.573770    8.857895
4     10002976     278.333333   10.400000
```

2.7 Obtain information on the mortality rate

[ ]:
```
query = "SELECT * FROM `physionet-data.mimiciv_hosp.patients`;"

death = run_query(query)
death
```

[ ]:
```
        subject_id gender  anchor_age  anchor_year anchor_year_group dod
0         10078138      F          18         2110       2017 - 2019 NaT
1         10180372      M          18         2110       2008 - 2010 NaT
2         10686175      M          18         2110       2011 - 2013 NaT
3         10851602      F          18         2110       2014 - 2016 NaT
4         10902424      F          18         2110       2017 - 2019 NaT
…              …     …          …            …                 …   ..
315455    11965764      F          59         2208       2014 - 2016 NaT
315456    14476240      F          64         2208       2014 - 2016 NaT
315457    17217407      F          68         2208       2014 - 2016 NaT
315458    18539655      M          69         2208       2014 - 2016 NaT
315459    15211528      F          77         2208       2014 - 2016 NaT

[315460 rows x 6 columns]
```

[ ]:
```
# Obtain a dataset containing information on patient mortality, mean blood␣
↪glucose values and mean A1C values
merged_death = pd.merge(death, patient_cohort_mean, how = "inner", left_on =␣
↪"subject_id", right_on = "patient_id")
merged_death
```

[ ]:
```
       subject_id gender  anchor_age  anchor_year anchor_year_group  \
0        15689743      M          21         2110       2011 - 2013
1        14456100      M          22         2110       2011 - 2013
2        10008454      F          26         2110       2011 - 2013
3        12343415      M          28         2110       2011 - 2013
4        10950807      M          29         2110       2017 - 2019
…             …     …          …            …                 …
16346    11973788      F          71         2206       2011 - 2013
16347    18802748      M          46         2207       2014 - 2016
16348    13774741      F          91         2207       2014 - 2016
16349    13899008      F          91         2207       2014 - 2016
16350    14476240      F          64         2208       2014 - 2016

             dod  patient_id  mean_glucose  mean_a1c
```

```
0            NaT    15689743    237.000000     10.90
1            NaT    14456100    333.000000      9.60
2            NaT    10008454    223.625000      7.10
3            NaT    12343415    242.000000      7.70
4            NaT    10950807    299.000000      9.00
…          …         …           …          …
16346        NaT    11973788    278.666667      7.92
16347        NaT    18802748    269.125000      8.80
16348 2211-02-27    13774741    224.000000      6.90
16349 2207-08-09    13899008    203.000000      6.90
16350        NaT    14476240    274.000000      7.20

[16351 rows x 9 columns]
```

[ ]:
```
dead_patient = merged_death[merged_death["dod"].notna()]
print(f"Mortality rate: {100 * dead_patient.shape[0] / merged_death.shape[0]}%")
```

```
Mortality rate: 24.022995535441257%
```

[ ]:
```
# Create an indicator that lists each patient as alive (0) or dead (1)
merged_death["label"] = merged_death["dod"].where(merged_death["dod"].isnull(),
 ↪1).fillna(0).astype(int)
merged_death
```

[ ]:
```
       subject_id gender  anchor_age  anchor_year anchor_year_group  \
0        15689743      M          21         2110       2011 - 2013
1        14456100      M          22         2110       2011 - 2013
2        10008454      F          26         2110       2011 - 2013
3        12343415      M          28         2110       2011 - 2013
4        10950807      M          29         2110       2017 - 2019
…             …     …           …           …               …
16346    11973788      F          71         2206       2011 - 2013
16347    18802748      M          46         2207       2014 - 2016
16348    13774741      F          91         2207       2014 - 2016
16349    13899008      F          91         2207       2014 - 2016
16350    14476240      F          64         2208       2014 - 2016

             dod  patient_id  mean_glucose  mean_a1c  label
0            NaT    15689743    237.000000     10.90      0
1            NaT    14456100    333.000000      9.60      0
2            NaT    10008454    223.625000      7.10      0
3            NaT    12343415    242.000000      7.70      0
4            NaT    10950807    299.000000      9.00      0
…          …         …           …          …       …
16346        NaT    11973788    278.666667      7.92      0
16347        NaT    18802748    269.125000      8.80      0
16348 2211-02-27    13774741    224.000000      6.90      1
```

```
16349 2207-08-09    13899008    203.000000      6.90      1
16350         NaT    14476240    274.000000      7.20      0

[16351 rows x 10 columns]
```

2.8 Feature extraction

[ ]:
```
query = "SELECT * FROM `physionet-data.mimiciv_hosp.admissions`;"

admissions = run_query(query)
admissions
```

[ ]:
```
        subject_id   hadm_id           admittime           dischtime  \
0         10006053  22942076 2111-11-13 23:39:00 2111-11-15 17:20:00
1         10017531  20668418 2158-01-20 16:52:00 2158-01-30 14:30:00
2         10017531  21095812 2159-12-26 20:14:00 2160-02-04 16:00:00
3         10017531  22580355 2159-09-22 19:30:00 2159-10-24 13:40:00
4         10021312  25020332 2113-08-16 00:32:00 2113-08-18 17:35:00
…              …         …                   …                   …
454319    19979081  25032257 2179-02-20 07:15:00 2179-02-27 16:45:00
454320    19991135  28088185 2124-02-17 08:30:00 2124-02-20 08:50:00
454321    19995012  29185936 2153-04-11 13:00:00 2153-04-14 13:51:00
454322    19995790  22970553 2185-02-02 12:00:00 2185-02-06 17:08:00
454323    19999303  27034282 2161-03-20 08:00:00 2161-03-28 13:24:00

                 deathtime                admission_type  \
0      2111-11-15 17:20:00                        URGENT
1                      NaT                        URGENT
2                      NaT                        URGENT
3                      NaT                        URGENT
4                      NaT                        URGENT
…                      …                           …
454319                 NaT  SURGICAL SAME DAY ADMISSION
454320                 NaT  SURGICAL SAME DAY ADMISSION
454321                 NaT  SURGICAL SAME DAY ADMISSION
454322                 NaT  SURGICAL SAME DAY ADMISSION
454323                 NaT  SURGICAL SAME DAY ADMISSION

            admission_location            discharge_location insurance  \
0       TRANSFER FROM HOSPITAL                          DIED  Medicaid
1       TRANSFER FROM HOSPITAL              HOME HEALTH CARE     Other
2       TRANSFER FROM HOSPITAL                         REHAB     Other
3       TRANSFER FROM HOSPITAL  CHRONIC/LONG TERM ACUTE CARE     Other
4       TRANSFER FROM HOSPITAL                          HOME     Other
…                          …                             …        …
454319      PHYSICIAN REFERRAL      SKILLED NURSING FACILITY  Medicare
```

```
454320      PHYSICIAN REFERRAL              HOME HEALTH CARE  Medicare
454321      PHYSICIAN REFERRAL      SKILLED NURSING FACILITY     Other
454322      PHYSICIAN REFERRAL      SKILLED NURSING FACILITY  Medicare
454323      PHYSICIAN REFERRAL              HOME HEALTH CARE     Other

       language marital_status                   race edregtime edouttime  \
0       ENGLISH           None                UNKNOWN       NaT       NaT
1       ENGLISH           None                  WHITE       NaT       NaT
2       ENGLISH           None                  WHITE       NaT       NaT
3       ENGLISH           None                  WHITE       NaT       NaT
4       ENGLISH           None                UNKNOWN       NaT       NaT
…         …           …                …       …       …
454319  ENGLISH       DIVORCED        ASIAN - CHINESE       NaT       NaT
454320  ENGLISH       DIVORCED                  WHITE       NaT       NaT
454321  ENGLISH       DIVORCED BLACK/AFRICAN AMERICAN       NaT       NaT
454322  ENGLISH       DIVORCED                  WHITE       NaT       NaT
454323  ENGLISH       DIVORCED                  WHITE       NaT       NaT

        hospital_expire_flag
0                          1
1                          0
2                          0
3                          0
4                          0
…                        …
454319                     0
454320                     0
454321                     0
454322                     0
454323                     0

[454324 rows x 15 columns]
```

2.9 Feature engineering

Create the following features:

1. Average number of hours per hospital stay
2. Total number of admissions

```
[ ]: # Average number of hours per hospital stay
admissions["hospital_stay_h"] = (admissions["dischtime"] -␣
↪admissions["admittime"]).astype("timedelta64[h]")
```

```
[ ]: admissions_gb = admissions.groupby(by = "subject_id")

patient_id = [i for i, g in admissions_gb]
```

```python
patient_mean_stay = [g["hospital_stay_h"].mean() for i, g in admissions_gb]
patient_total_admissions = [len(g) for i, g in admissions_gb]

patient_cohort_info = pd.DataFrame({"patient_id": patient_id, "mean_stay":␣
↪patient_mean_stay, "total_admissions": patient_total_admissions})
patient_cohort_info.head()
```

[ ]:

```
   patient_id  mean_stay  total_admissions
0    10000032      34.25                 4
1    10000068       7.00                 1
2    10000084      59.00                 2
3    10000108       9.00                 1
4    10000117      41.00                 2
```

[ ]:

```python
admissions_additional = pd.merge(admissions, patient_cohort_info, how =␣
↪"inner", left_on = "subject_id", right_on = "patient_id")
admissions_additional.head()
```

[ ]:

```
   subject_id   hadm_id           admittime           dischtime  \
0    10006053  22942076 2111-11-13 23:39:00 2111-11-15 17:20:00
1    10017531  20668418 2158-01-20 16:52:00 2158-01-30 14:30:00
2    10017531  21095812 2159-12-26 20:14:00 2160-02-04 16:00:00
3    10017531  22580355 2159-09-22 19:30:00 2159-10-24 13:40:00
4    10017531  27635105 2160-02-15 20:54:00 2160-02-22 18:00:00

            deathtime admission_type      admission_location  \
0 2111-11-15 17:20:00         URGENT  TRANSFER FROM HOSPITAL
1                 NaT         URGENT  TRANSFER FROM HOSPITAL
2                 NaT         URGENT  TRANSFER FROM HOSPITAL
3                 NaT         URGENT  TRANSFER FROM HOSPITAL
4                 NaT       EW EMER.          EMERGENCY ROOM

             discharge_location insurance language marital_status     race  \
0                          DIED  Medicaid  ENGLISH           None  UNKNOWN
1              HOME HEALTH CARE     Other  ENGLISH           None    WHITE
2                         REHAB     Other  ENGLISH           None    WHITE
3  CHRONIC/LONG TERM ACUTE CARE     Other  ENGLISH           None    WHITE
4       SKILLED NURSING FACILITY     Other  ENGLISH           None    WHITE

            edregtime           edouttime  hospital_expire_flag  \
0                 NaT                 NaT                     1
1                 NaT                 NaT                     0
2                 NaT                 NaT                     0
3                 NaT                 NaT                     0
4 2160-02-15 12:48:00 2160-02-15 22:40:00                     0

   hospital_stay_h  patient_id   mean_stay  total_admissions
```

```
0          41.0   10006053   41.000000              1
1         237.0   10017531  380.666667              6
2         955.0   10017531  380.666667              6
3         762.0   10017531  380.666667              6
4         165.0   10017531  380.666667              6
```

[ ]:
```
# Merge the new features and mortality data together into one dataset
full_feature = pd.merge(admissions_additional, merged_death, how = "inner",␣
 ↪left_on = "subject_id", right_on = "subject_id")
full_feature
```

[ ]:
```
       subject_id   hadm_id           admittime           dischtime deathtime  \
0        10017531  20668418 2158-01-20 16:52:00 2158-01-30 14:30:00       NaT
1        10017531  21095812 2159-12-26 20:14:00 2160-02-04 16:00:00       NaT
2        10017531  22580355 2159-09-22 19:30:00 2159-10-24 13:40:00       NaT
3        10017531  27635105 2160-02-15 20:54:00 2160-02-22 18:00:00       NaT
4        10017531  29771935 2160-03-06 21:37:00 2160-03-07 15:09:00       NaT
…             …        …                   …                   …       …
74558    19212133  21662307 2156-05-14 00:00:00 2156-05-22 17:22:00       NaT
74559    19212133  26107723 2156-02-24 00:00:00 2156-03-03 20:50:00       NaT
74560    19466197  26157727 2189-03-07 00:00:00 2189-03-14 13:00:00       NaT
74561    19521410  26296290 2177-11-23 07:15:00 2177-11-27 14:15:00       NaT
74562    19623396  24187699 2169-02-28 00:00:00 2169-03-05 17:05:00       NaT

                   admission_type      admission_location  \
0                          URGENT  TRANSFER FROM HOSPITAL
1                          URGENT  TRANSFER FROM HOSPITAL
2                          URGENT  TRANSFER FROM HOSPITAL
3                        EW EMER.          EMERGENCY ROOM
4          AMBULATORY OBSERVATION          PROCEDURE SITE
…                             …                     …
74558  SURGICAL SAME DAY ADMISSION      PHYSICIAN REFERRAL
74559  SURGICAL SAME DAY ADMISSION      PHYSICIAN REFERRAL
74560  SURGICAL SAME DAY ADMISSION      PHYSICIAN REFERRAL
74561  SURGICAL SAME DAY ADMISSION      PHYSICIAN REFERRAL
74562  SURGICAL SAME DAY ADMISSION      PHYSICIAN REFERRAL

                discharge_location insurance language  … total_admissions  \
0                 HOME HEALTH CARE     Other  ENGLISH  …                6
1                            REHAB     Other  ENGLISH  …                6
2       CHRONIC/LONG TERM ACUTE CARE     Other  ENGLISH  …                6
3          SKILLED NURSING FACILITY     Other  ENGLISH  …                6
4                             None     Other  ENGLISH  …                6
…                               …       …      …  …              …
74558             HOME HEALTH CARE     Other  ENGLISH  …                2
74559     SKILLED NURSING FACILITY     Other  ENGLISH  …                2
74560                        REHAB     Other  ENGLISH  …                1
```

```
74561               HOME HEALTH CARE     Other  ENGLISH  …               1
74562               HOME HEALTH CARE     Other  ENGLISH  …               1

      gender anchor_age anchor_year  anchor_year_group  dod  patient_id_y  \
0          M         63        2158        2008 - 2010  NaT      10017531
1          M         63        2158        2008 - 2010  NaT      10017531
2          M         63        2158        2008 - 2010  NaT      10017531
3          M         63        2158        2008 - 2010  NaT      10017531
4          M         63        2158        2008 - 2010  NaT      10017531
…        …          …           …                …   …             …
74558      M         67        2156        2017 - 2019  NaT      19212133
74559      M         67        2156        2017 - 2019  NaT      19212133
74560      M         49        2183        2011 - 2013  NaT      19466197
74561      M         61        2177        2014 - 2016  NaT      19521410
74562      M         57        2169        2017 - 2019  NaT      19623396

       mean_glucose   mean_a1c label
0        252.636364   7.250000     0
1        252.636364   7.250000     0
2        252.636364   7.250000     0
3        252.636364   7.250000     0
4        252.636364   7.250000     0
…               …         …    …
74558    267.619048   7.500000     0
74559    267.619048   7.500000     0
74560    259.055556  10.566667     0
74561    286.500000   9.800000     0
74562    222.000000   7.400000     0

[74563 rows x 28 columns]
```

2.10 Feature analysis

[ ]:
```
full_feature.describe()
```

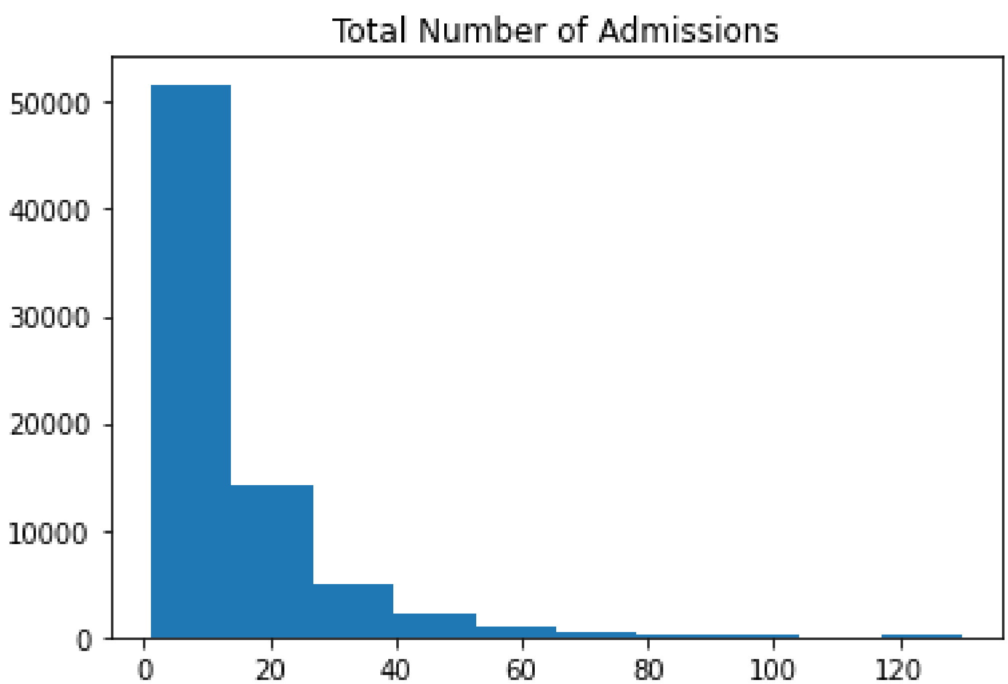
[ ]:
```
         subject_id       hadm_id  hospital_expire_flag  hospital_stay_h  \
count  7.456300e+04  7.456300e+04          74563.000000     74563.000000
mean   1.501880e+07  2.501067e+07              0.016067       121.758245
std    2.884809e+06  2.888772e+06              0.125734       165.307006
min    1.000098e+07  2.000004e+07              0.000000       -17.000000
25%    1.250758e+07  2.251152e+07              0.000000        36.000000
50%    1.504929e+07  2.502319e+07              0.000000        74.000000
75%    1.752249e+07  2.751472e+07              0.000000       145.000000
max    1.999983e+07  2.999957e+07              1.000000      7103.000000

       patient_id_x     mean_stay  total_admissions    anchor_age  \
```

count	7.456300e+04	74563.000000	74563.000000	74563.000000
mean	1.501880e+07	121.758245	12.836863	61.189571
std	2.884809e+06	95.072908	14.149795	14.663825
min	1.000098e+07	0.000000	1.000000	18.000000
25%	1.250758e+07	68.000000	4.000000	52.000000
50%	1.504929e+07	101.600000	8.000000	62.000000
75%	1.752249e+07	147.250000	16.000000	72.000000
max	1.999983e+07	2677.000000	130.000000	91.000000

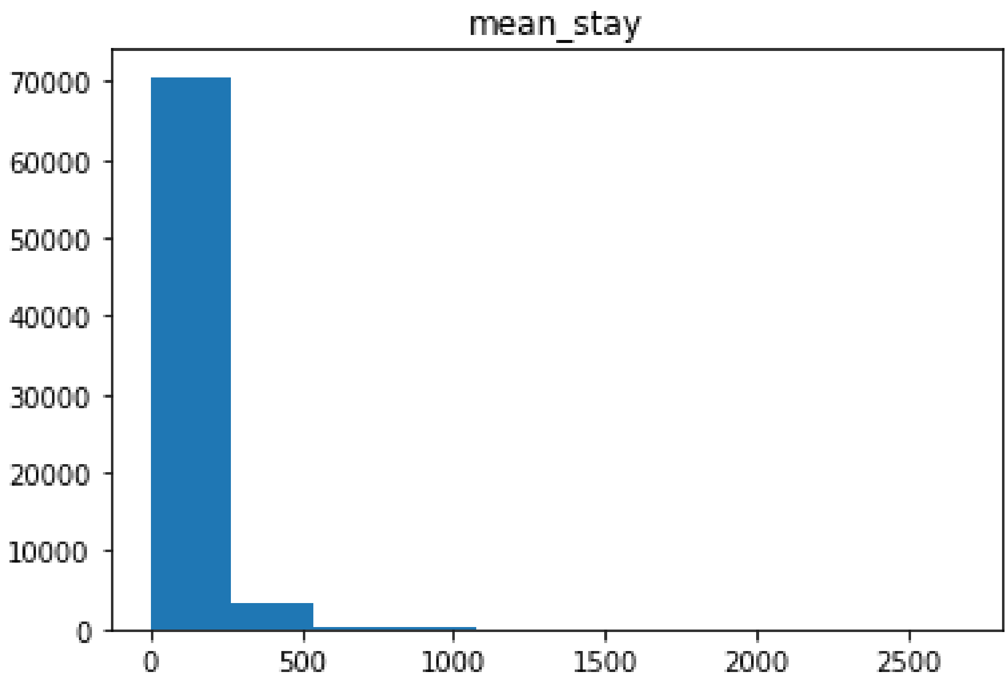
	anchor_year	patient_id_y	mean_glucose	mean_a1c	label
count	74563.000000	7.456300e+04	74563.000000	74563.000000	74563.000000
mean	2154.798171	1.501880e+07	323.140747	8.135586	0.375816
std	23.964974	2.884809e+06	6394.365862	1.441035	0.484336
min	2110.000000	1.000098e+07	200.000000	6.500000	0.000000
25%	2135.000000	1.250758e+07	238.467742	7.075000	0.000000
50%	2154.000000	1.504929e+07	260.352941	7.750000	0.000000
75%	2175.000000	1.752249e+07	287.625000	8.800000	1.000000
max	2208.000000	1.999983e+07	999999.000000	22.000000	1.000000

2.10.1 Preliminary analysis on numerical features

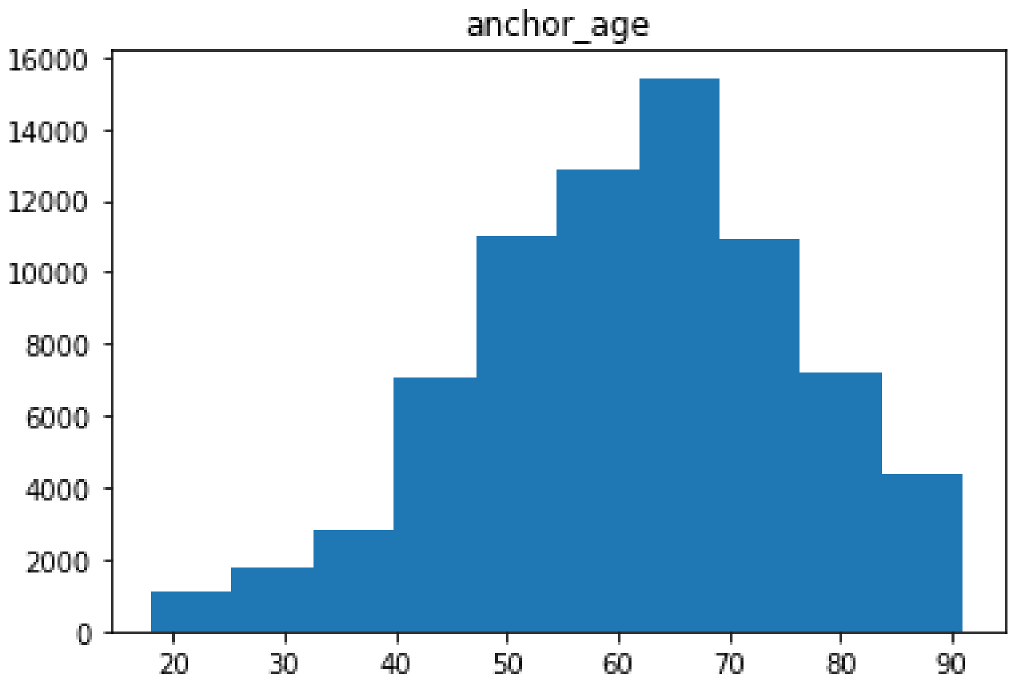
[ ]:
```
plt.hist(full_feature["total_admissions"])
plt.title("Total Number of Admissions")
plt.show()
```



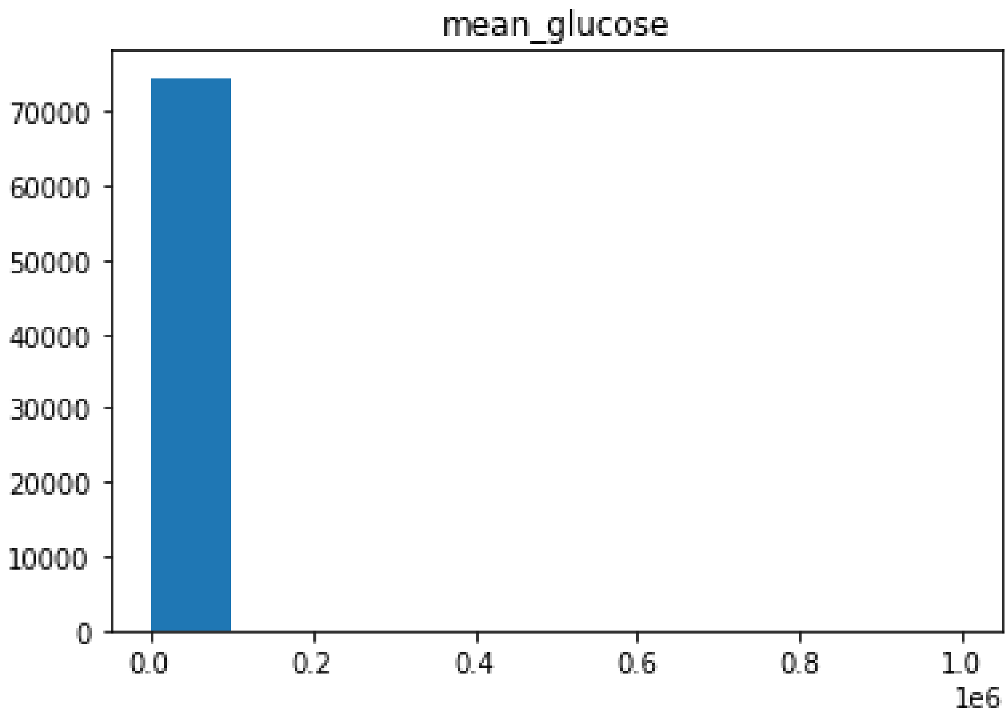
[ ]:
```
plt.hist(full_feature["mean_stay"].sort_values())
plt.title("mean_stay")
plt.show()
```



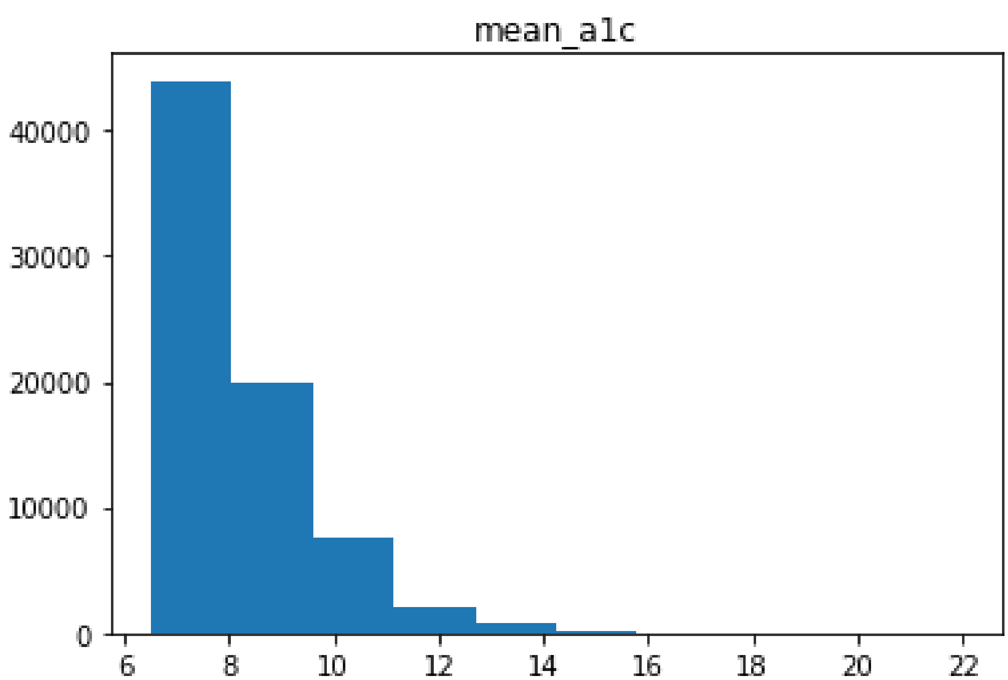
[ ]:
```
plt.hist(full_feature["anchor_age"])
plt.title("anchor_age")
plt.show()
```



[ ]:
```
# This graph contains outliers but is not used in our analysis.
plt.hist(full_feature["mean_glucose"])
plt.title("mean_glucose")
plt.show()
```

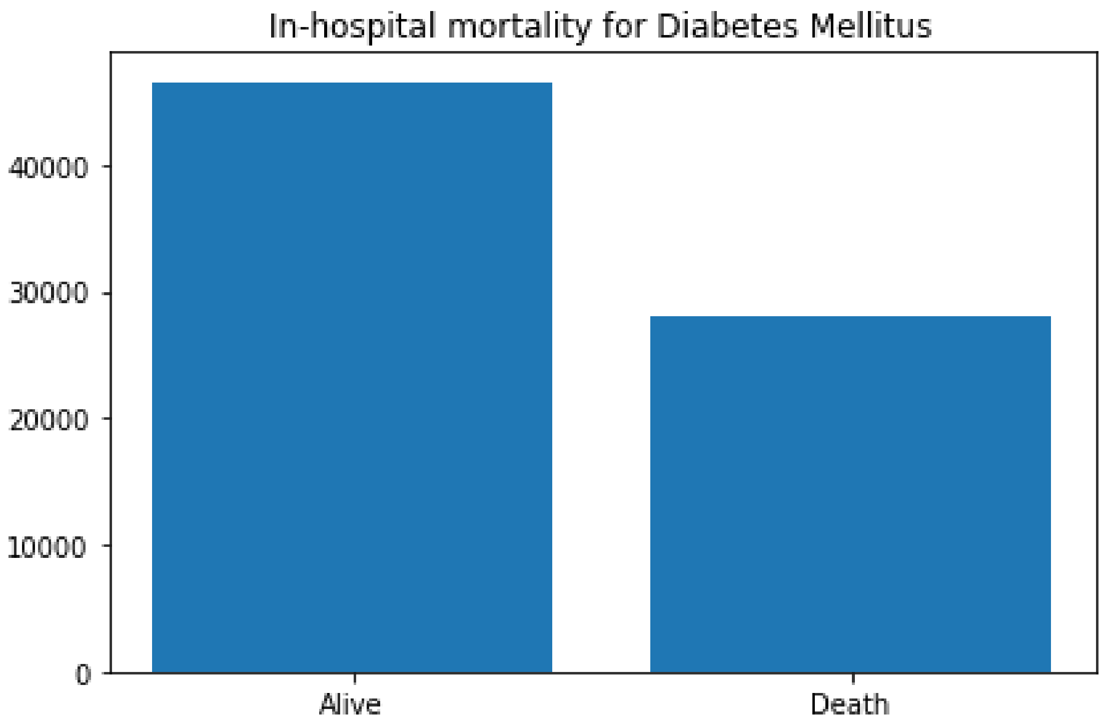


[ ]:
```
plt.hist(full_feature["mean_a1c"])
plt.title("mean_a1c")
plt.show()
```



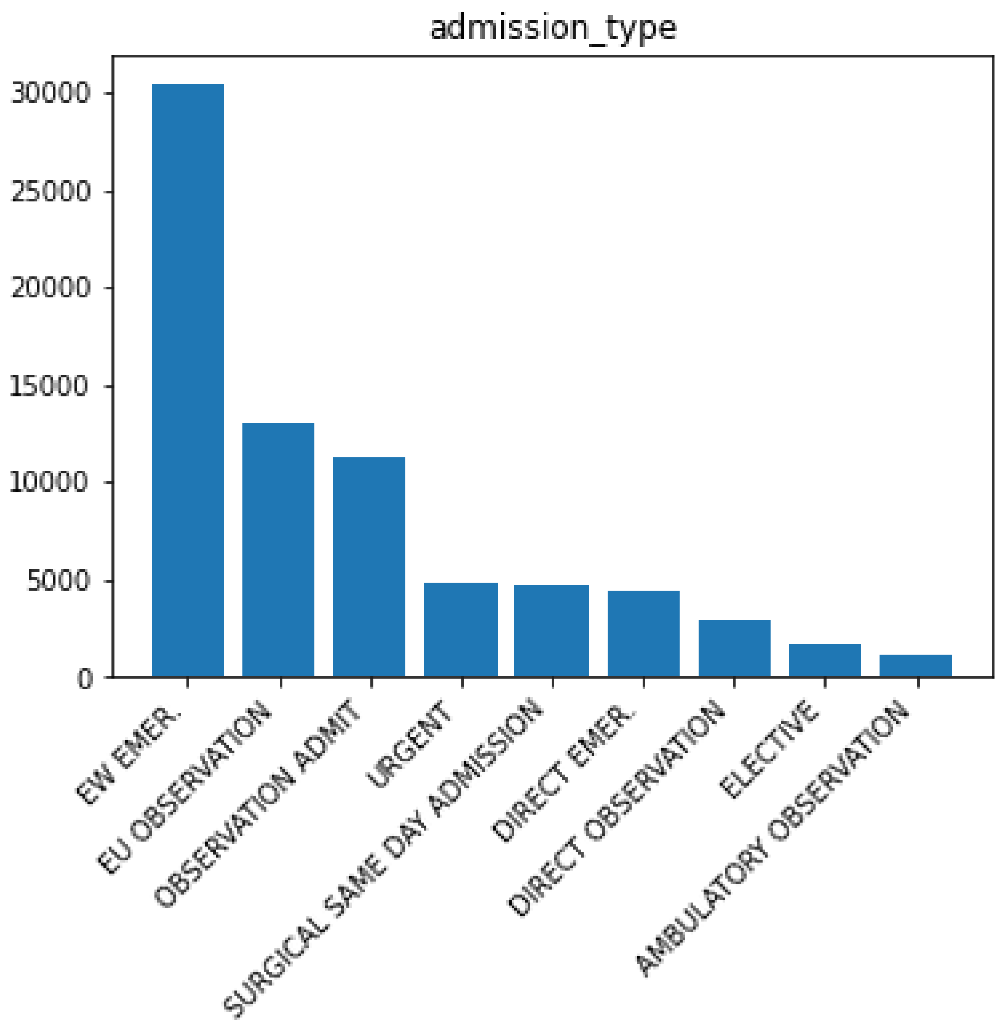
2.10.2 Preliminary analysis on categorical features

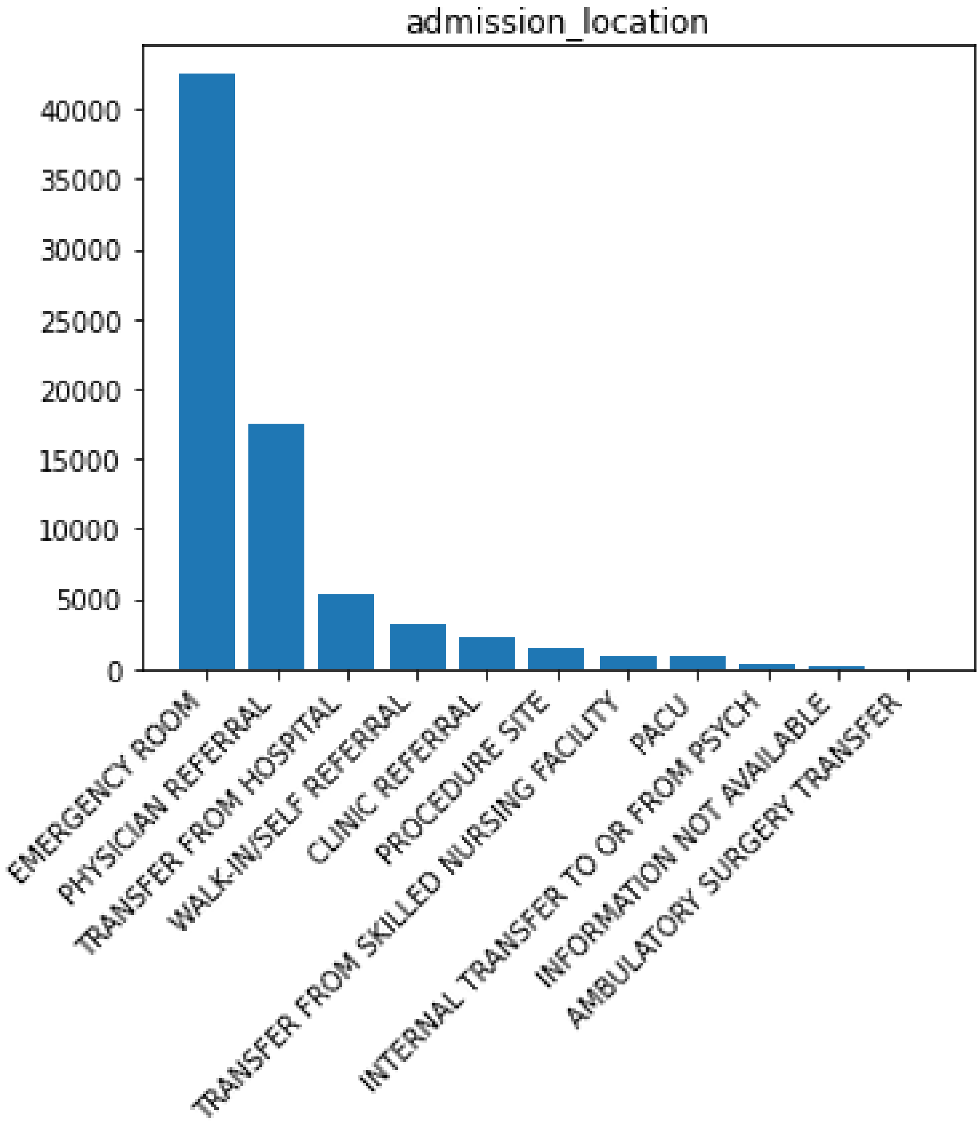
[ ]:
```
plt.bar(["Alive", "Death"], full_feature["label"].value_counts())
plt.title("In-hospital mortality for Diabetes Mellitus")
plt.tight_layout()

plt.savefig("In-hospital mortality for Diabetes Mellitus.png")
plt.show()
```

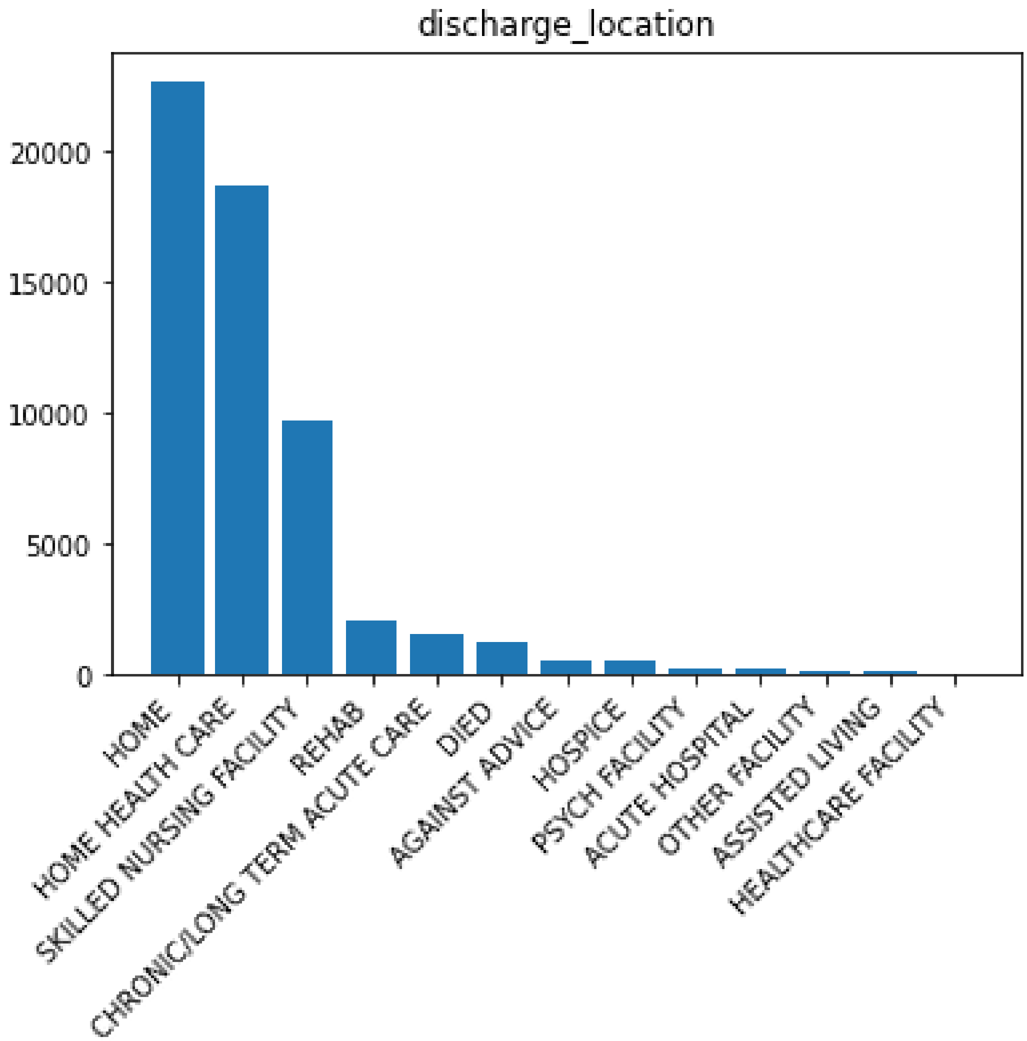


[ ]:
```
plt.bar(full_feature["admission_type"].value_counts().index,␣
 ↪full_feature["admission_type"].value_counts())
plt.title("admission_type")
plt.tight_layout()
plt.xticks(rotation = 45, ha = "right")
plt.show()

plt.bar(full_feature["admission_location"].value_counts().index,␣
 ↪full_feature["admission_location"].value_counts())
plt.title("admission_location")
```

```
plt.tight_layout()
plt.xticks(rotation = 45, ha = "right")
plt.show()

# Died indicate death, so this feature dropped
plt.bar(full_feature["discharge_location"].value_counts().index,␣
 ↪full_feature["discharge_location"].value_counts())
plt.title("discharge_location")
plt.tight_layout()
plt.xticks(rotation = 45, ha = "right")
plt.show()
```

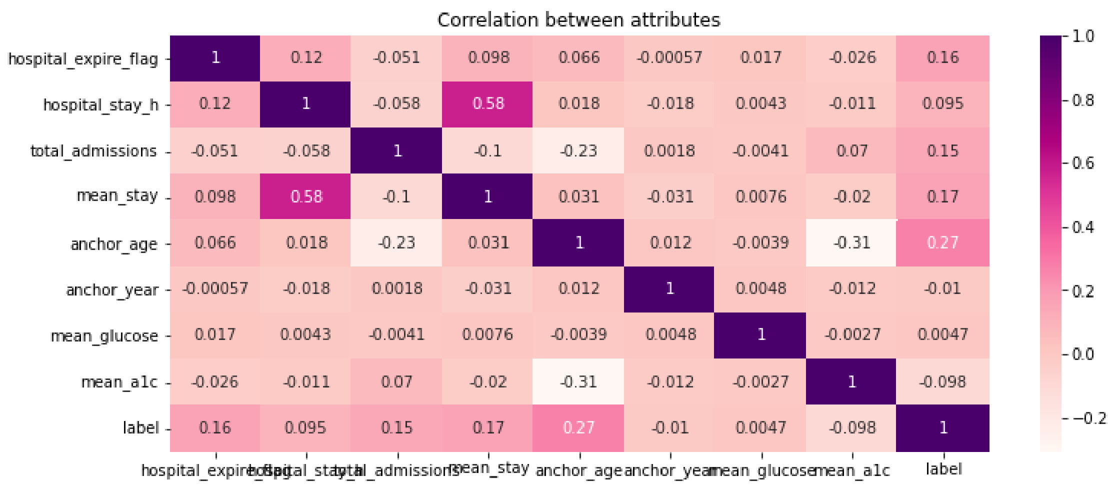



admission_location
40000
35000
30000
25000
20000
15000
10000
5000
0
EMERGENCY ROOM
PHYSICIAN REFERRAL
TRANSFER FROM HOSPITAL
WALK-IN/SELF REFERRAL
CLINIC REFERRAL
PROCEDURE SITE
TRANSFER FROM SKILLED NURSING FACILITY
PACU
INTERNAL TRANSFER TO OR FROM PSYCH
INFORMATION NOT AVAILABLE
AMBULATORY SURGERY TRANSFER

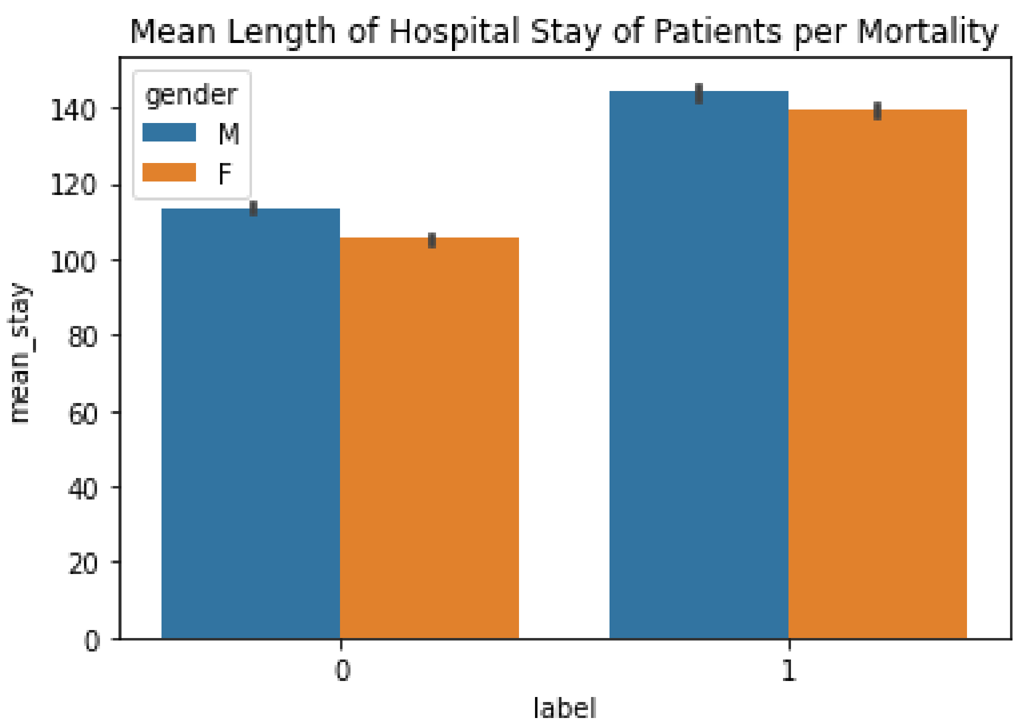


Examine correlations betweeen features

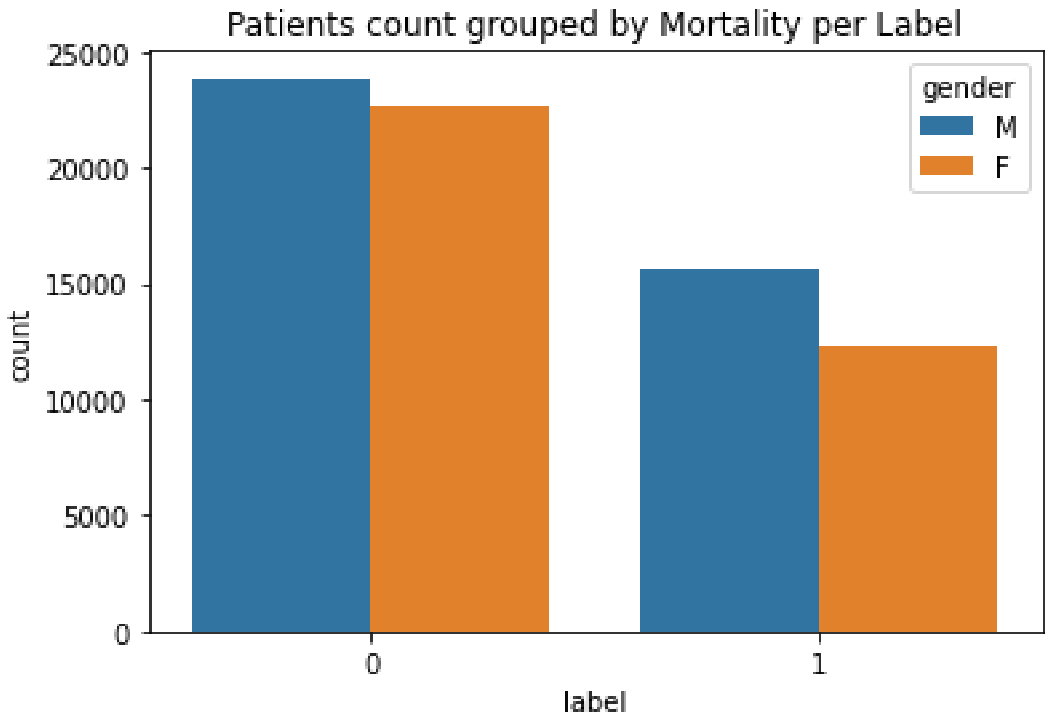
[ ]:
```
dataset = full_feature[["admittime", "dischtime", "deathtime",␣
↪"admission_type", "admission_location", "discharge_location",
       "insurance", "language", "marital_status", "race", "edregtime",␣
↪"edouttime", "hospital_expire_flag", "hospital_stay_h",
       "total_admissions", "mean_stay", "gender", "anchor_age", "anchor_year",␣
↪"anchor_year_group", "dod", "mean_glucose", "mean_a1c",
       "label"]]
plt.subplots(figsize = (12, 5))
sns.heatmap(dataset.corr(), annot = True, cmap = "RdPu")
plt.title("Correlation between attributes")
plt.xticks(rotation = 0);
```




```
[ ]: ax = sns.barplot(data = dataset, x = "label", y = "mean_stay", hue = "gender")
     ax.set_title("Mean Length of Hospital Stay of Patients per Mortality");
     plt.show()
```




```
[ ]: ax = sns.countplot(data = dataset, x = "label", hue = "gender")
     ax.set_title("Patients count grouped by Mortality per Label");
     plt.show()
```



2.11 Select the target features

```
[ ]: full_feature.columns
```

```
[ ]: Index(['subject_id', 'hadm_id', 'admittime', 'dischtime', 'deathtime',
            'admission_type', 'admission_location', 'discharge_location',
            'insurance', 'language', 'marital_status', 'race', 'edregtime',
            'edouttime', 'hospital_expire_flag', 'hospital_stay_h', 'patient_id_x',
            'mean_stay', 'total_admissions', 'gender', 'anchor_age', 'anchor_year',
            'anchor_year_group', 'dod', 'patient_id_y', 'mean_glucose', 'mean_a1c',
            'label'],
           dtype='object')
```

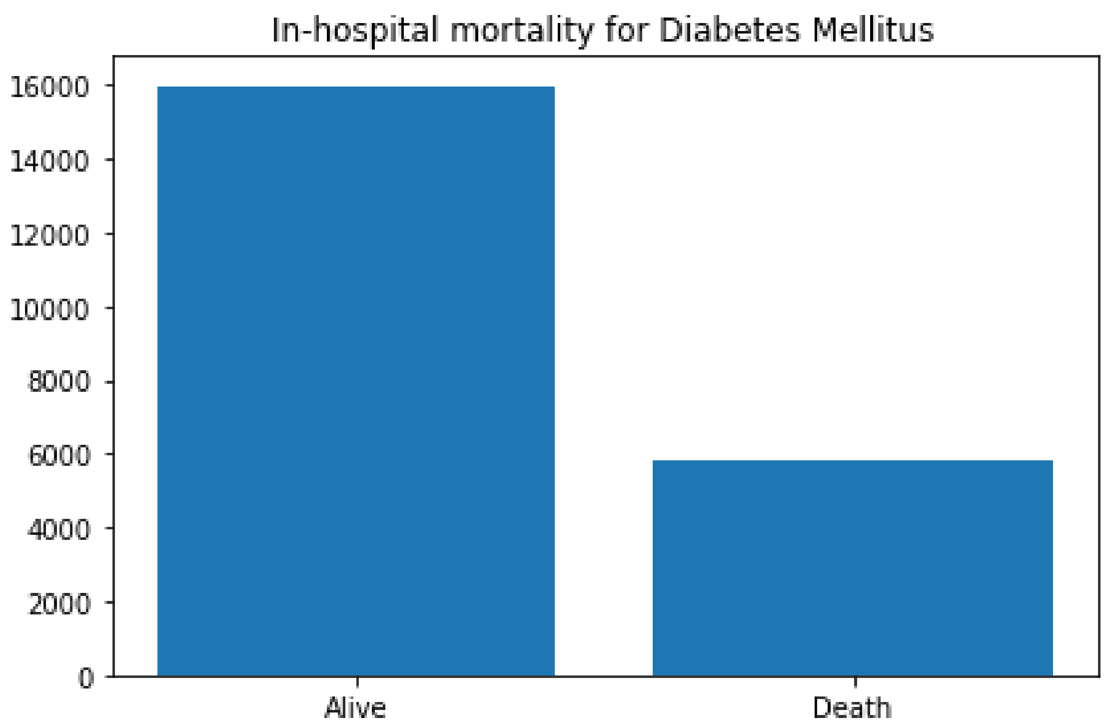
```
[ ]: ## Remove features that would not be used for the machine learning models, such␣
     ↪as hospital_expire_flag

     cleaned_feature = full_feature[["subject_id",
             "insurance", "language", "marital_status", "race",
             "total_admissions", "mean_stay", "gender", "anchor_age", "anchor_year",
             "anchor_year_group", "mean_glucose", "mean_a1c", "label"]]
```

```
[ ]: # Each patient may contain multiply admissions; keep all of those admissions
     cleaned_feature = cleaned_feature.drop_duplicates()
```

```
[ ]: cleaned_feature["label"].value_counts() / cleaned_feature["label"].
     ↪value_counts().sum()
```

```
[ ]: 0    0.733254
     1    0.266746
     Name: label, dtype: float64
```

```
[ ]: plt.bar(["Alive", "Death"], cleaned_feature["label"].value_counts())
     plt.title("In-hospital mortality for Diabetes Mellitus")
     plt.tight_layout()

     plt.savefig("In-hospital mortality for Diabetes Mellitus.png")
     plt.show()
```




```
[ ]: cleaned_feature.to_csv("patient_data.csv", index = False)
```

2.12 Split training features and labels

[ ]:
```
X = cleaned_feature.drop(columns = ["subject_id", "label"])
col_name = X.columns
Y = cleaned_feature["label"]
X.head()
```

[ ]:
```
  insurance language marital_status     race  total_admissions   mean_stay  \
0     Other  ENGLISH           None    WHITE                 6  380.666667
6     Other  ENGLISH           None  UNKNOWN                 1  210.000000
7  Medicare  ENGLISH           None  UNKNOWN                 1  118.000000
8     Other  ENGLISH           None  UNKNOWN                 8  126.625000
9     Other  ENGLISH        MARRIED    WHITE                 8  126.625000

  gender  anchor_age  anchor_year anchor_year_group  mean_glucose  mean_a1c
0      M          63         2158       2008 - 2010    252.636364      7.25
6      M          61         2136       2014 - 2016    253.833333      7.65
7      M          77         2160       2017 - 2019    209.666667      7.80
8      M          55         2171       2017 - 2019    242.100000      8.80
9      M          55         2171       2017 - 2019    242.100000      8.80
```

2.13 Feature encoding

[ ]:
```
# Ordinal encoding for all features
enc = OrdinalEncoder()
X = pd.DataFrame(enc.fit_transform(X), columns = X.columns)
X
```

[ ]:
```
       insurance  language  marital_status  race  total_admissions  mean_stay  \
0            2.0       1.0             4.0  28.0               5.0     4383.0
1            2.0       1.0             4.0  27.0               0.0     3638.0
2            1.0       1.0             4.0  27.0               0.0     2238.0
3            2.0       1.0             4.0  27.0               7.0     2443.0
4            2.0       1.0             1.0  28.0               7.0     2443.0
…              …         …               …     …                 …          …
21791        1.0       0.0             0.0  18.0               0.0     3344.0
21792        2.0       1.0             0.0  28.0               1.0     3642.0
21793        2.0       1.0             0.0  28.0               0.0     3356.0
21794        2.0       1.0             0.0  31.0               0.0     1862.0
21795        2.0       1.0             0.0  28.0               0.0     2663.0

       gender  anchor_age  anchor_year  anchor_year_group  mean_glucose  \
0         1.0        45.0         48.0                0.0        1801.0
1         1.0        43.0         26.0                2.0        1869.0
2         1.0        59.0         50.0                3.0          63.0
```

```
3          1.0        37.0         61.0                  3.0        1152.0
4          1.0        37.0         61.0                  3.0        1152.0
…        …         …          …                 …          …
21791      1.0        55.0         69.0                  2.0         154.0
21792      1.0        49.0         46.0                  3.0        2760.0
21793      1.0        31.0         73.0                  1.0        2207.0
21794      1.0        43.0         67.0                  2.0        3790.0
21795      1.0        39.0         59.0                  3.0         293.0

       mean_a1c
0         720.0
1        1265.0
2        1454.0
3        2388.0
4        2388.0
…          …
21791      26.0
21792    1059.0
21793    3184.0
21794    2931.0
21795     925.0

[21796 rows x 12 columns]
```

2.14 Feature scaling

[ ]:
```
scaler = StandardScaler()
X = pd.DataFrame(scaler.fit_transform(X), columns = X.columns)
X
```

[ ]:
```
       insurance  language  marital_status      race  total_admissions  \
0       0.950533  0.463980        2.772749  0.753275         -0.025119
1       0.950533  0.463980        2.772749  0.649672         -0.699549
2      -0.559182  0.463980        2.772749  0.649672         -0.699549
3       0.950533  0.463980        2.772749  0.649672          0.244652
4       0.950533  0.463980       -0.605323  0.753275          0.244652
…          …        …              …        …                …
21791  -0.559182 -2.155266       -1.731347 -0.282748         -0.699549
21792   0.950533  0.463980       -1.731347  0.753275         -0.564663
21793   0.950533  0.463980       -1.731347  0.753275         -0.699549
21794   0.950533  0.463980       -1.731347  1.064081         -0.699549
21795   0.950533  0.463980       -1.731347  0.753275         -0.699549

       mean_stay    gender  anchor_age  anchor_year  anchor_year_group  \
0       1.884860  0.924139    0.083199     0.175430          -0.822369
1       1.318430  0.924139   -0.054154    -0.747018           1.065696
```

```
2        0.253999  0.924139    1.044671     0.259289           2.009729
3        0.409862  0.924139   -0.466214     0.720513           2.009729
4        0.409862  0.924139   -0.466214     0.720513           2.009729
…             …         …           …           …                  …
21791    1.094900  0.924139    0.769965     1.055949           1.065696
21792    1.321472  0.924139    0.357905     0.091571           2.009729
21793    1.104024  0.924139   -0.878273     1.223667           0.121664
21794   -0.031877  0.924139   -0.054154     0.972090           1.065696
21795    0.577130  0.924139   -0.328860     0.636654           2.009729

       mean_glucose  mean_a1c
0         -0.295053 -0.735112
1         -0.257327 -0.241128
2         -1.259293 -0.069819
3         -0.655117  0.776753
4         -0.655117  0.776753
…               …         …
21791     -1.208806 -1.364150
21792      0.236999 -0.427845
21793     -0.069805  1.498243
21794      0.808441  1.268925
21795     -1.131689 -0.549302

[21796 rows x 12 columns]
```

2.15 Split the training, testing and development sets

[ ]:
```
X_train, X_test, y_train, y_test = train_test_split(X, Y, test_size = 0.2,␣
↪random_state = 1)
```

2.15.1 Baseline model (KNN)

[ ]:
```
knn = neighbors.KNeighborsClassifier(3)
knn.fit(X_train, y_train)
```

[ ]:
```
KNeighborsClassifier(n_neighbors=3)
```

2.15.2 Logistic Regression

[ ]:
```
lr = LogisticRegression(random_state = 0).fit(X_train, y_train)
```

2.15.3 Random Forest

[ ]:
```
rf = RandomForestClassifier(random_state = 0)
rf.fit(X_train, y_train)
```

[ ]:
```
RandomForestClassifier(random_state=0)
```

MLP: The performance is not as high as expected and requires further review.

[ ]:
```
mlp = MLPClassifier(random_state = 0, max_iter = 1000).fit(X_train, y_train)
```

EBM: Explainable Boosting Machine

[ ]:
```
ebm = ExplainableBoostingClassifier(random_state = 0)
```

2.16 Parameter tuning

[ ]:
```
# Logistic Regression
parameters = {"penalty": ["l1", "l2"]}
lr = LogisticRegression(random_state = 0)
lr = GridSearchCV(lr, parameters)
lr.fit(X_train, y_train)

print("Final parameters:", lr.cv_results_["params"][0])
```

```
Final parameters: {'penalty': 'l1', 'solver': 'saga'}
```

[ ]:
```
# MLP
parameters = {"activation": ["logistic", "relu"]}
mlp = MLPClassifier(random_state = 0)
mlp = GridSearchCV(mlp, parameters)
mlp.fit(X_train, y_train)

print("Final parameters:",mlp.cv_results_["params"][0])
```

```
Final parameters: {'activation': 'logistic'}
```

[ ]:
```
# Random Forest
parameters = {"max_features": ["sqrt", "log2"], "criterion": ["gini",␣
 ↪"entropy"]}
rf = RandomForestClassifier(oob_score = True, random_state = 0)
rf = GridSearchCV(rf, parameters)
rf.fit(X_train, y_train)

print("Final parameters:", rf.cv_results_["params"][0])
```

```
Final parameters: {'criterion': 'gini', 'max_features': 'sqrt'}
```

2.16.1 Fit the models

```
[ ]: lr = LogisticRegression(max_iter = 1000, random_state = 0, penalty = "l1",␣
      ↪solver = "saga")
     lr.fit(X_train, y_train)
```

```
[ ]: LogisticRegression(max_iter=1000, penalty='l1', random_state=0, solver='saga')
```

```
[ ]: mlp = MLPClassifier(random_state = 0, activation = "logistic", max_iter = 1000)
     mlp.fit(X_train, y_train)
```

```
[ ]: MLPClassifier(activation='logistic', max_iter=1000, random_state=0)
```

```
[ ]: rf = RandomForestClassifier(oob_score = True, random_state = 0, criterion =␣
      ↪"gini", max_features = "sqrt")
     rf.fit(X_train, y_train)
```

```
[ ]: RandomForestClassifier(max_features='sqrt', oob_score=True, random_state=0)
```

```
[ ]: clf = ebm.fit(X_train, y_train)
     clf
```

```
WARNING:interpret.utils.all:Passing a numpy array to schema autogen when it
should be dataframe.
WARNING:interpret.utils.all:Passing a numpy array to schema autogen when it
should be dataframe.
```

```
[ ]: ExplainableBoostingClassifier(feature_names=['insurance', 'language',
                                                  'marital_status', 'race',
                                                  'total_admissions', 'mean_stay',
                                                  'gender', 'anchor_age',
                                                  'anchor_year', 'anchor_year_group',
                                                  'mean_glucose', 'mean_a1c',
                                                  'total_admissions x mean_a1c',
                                                  'mean_stay x anchor_age',
                                                  'total_admissions x mean_stay',
                                                  'race x mean_glucose',
                                                  'race x mean_stay',
                                                  'total_admissions x anchor_age…
                                                  'total_admissions x mean_glucose',
                                                  'race x mean_a1c'],
                                   feature_types=['continuous', 'continuous',
                                                  'continuous', 'continuous',
                                                  'continuous', 'continuous',
                                                  'continuous', 'continuous',
```

```
                                    'continuous', 'continuous',
                                    'continuous', 'continuous',
                                    'interaction', 'interaction',
                                    'interaction', 'interaction',
                                    'interaction', 'interaction',
                                    'interaction', 'interaction',
                                    'interaction', 'interaction'],
                      random_state=0)
```

2.16.2 Model evaluation

[ ]:
```
print("The train accuracy for KNN is: {}".format(knn.score(X_train, y_train)))
print("The test accuracy for KNN is: {}\n".format(knn.score(X_test, y_test)))

print("The train accuracy for Logistic Regression is: {}".format(lr.
 ↪score(X_train, y_train)))
print("The test accuracy for Logistic Regression is: {}\n".format(lr.
 ↪score(X_test, y_test)))

print("The train accuracy for MLP is: {}".format(mlp.score(X_train, y_train)))
print("The test accuracy for MLP is: {}\n".format(mlp.score(X_test, y_test)))

print("The train accuracy for Random Forest is: {}".format(rf.score(X_train,␣
 ↪y_train)))
print("The test accuracy for Random Forest is: {}\n".format(rf.score(X_test,␣
 ↪y_test)))

print("The train accuracy for EBM is: {}".format(ebm.score(X_train, y_train)))
print("The test accuracy for EBM is: {}".format(ebm.score(X_test, y_test)))
```

```
The train accuracy for KNN is: 0.8696948841477403
The test accuracy for KNN is: 0.7559633027522936

The train accuracy for Logistic Regression is: 0.766173434273916
The test accuracy for Logistic Regression is: 0.7786697247706422

The train accuracy for MLP is: 0.8230672172516632
The test accuracy for MLP is: 0.7834862385321101

The train accuracy for Random Forest is: 1.0
The test accuracy for Random Forest is: 0.8841743119266054

The train accuracy for EBM is: 0.8034526267492544
The test accuracy for EBM is: 0.8036697247706422
```

[ ]:
```python
# Classification Report
print("Classification Report for KNN")
print(classification_report(y_test, knn.predict(X_test)))

print("Classification Report for Logistic Regression")
print(classification_report(y_test, lr.predict(X_test)))

print("Classification Report for MLP")
print(classification_report(y_test, mlp.predict(X_test)))

print("Classification Report for Random Forest")
print(classification_report(y_test, rf.predict(X_test)))

print("Classification Report for Explainable Boosting Machine")
print(classification_report(y_test, ebm.predict(X_test)))
```

```
Classification Report for KNN
              precision    recall  f1-score   support

           0       0.81      0.87      0.84      3188
           1       0.56      0.45      0.50      1172

    accuracy                           0.76      4360
   macro avg       0.68      0.66      0.67      4360
weighted avg       0.74      0.76      0.75      4360

Classification Report for Logistic Regression
              precision    recall  f1-score   support

           0       0.80      0.93      0.86      3188
           1       0.66      0.36      0.47      1172

    accuracy                           0.78      4360
   macro avg       0.73      0.65      0.66      4360
weighted avg       0.76      0.78      0.75      4360

Classification Report for MLP
              precision    recall  f1-score   support

           0       0.82      0.89      0.86      3188
           1       0.63      0.48      0.55      1172

    accuracy                           0.78      4360
   macro avg       0.73      0.69      0.70      4360
weighted avg       0.77      0.78      0.77      4360

Classification Report for Random Forest
```

```
              precision    recall  f1-score   support

           0       0.88      0.97      0.92      3188
           1       0.89      0.65      0.75      1172

    accuracy                           0.88      4360
   macro avg       0.89      0.81      0.84      4360
weighted avg       0.89      0.88      0.88      4360

Classification Report for Explainable Boosting Machine
              precision    recall  f1-score   support

           0       0.82      0.93      0.87      3188
           1       0.71      0.45      0.55      1172

    accuracy                           0.80      4360
   macro avg       0.77      0.69      0.71      4360
weighted avg       0.79      0.80      0.79      4360
```

[ ]:
```
# Balanced accuracy
print("Balanced accuracy for KNN:", balanced_accuracy_score(y_test, knn.
 ↪predict(X_test)))
print("Balanced accuracy for Logistic Regression:",␣
 ↪balanced_accuracy_score(y_test, lr.predict(X_test)))
print("Balanced accuracy for MLP:", balanced_accuracy_score(y_test, mlp.
 ↪predict(X_test)))
print("Balanced accuracy for Random Forest:", balanced_accuracy_score(y_test,␣
 ↪rf.predict(X_test)))
print("Balanced accuracy for Explainable Boosting Machine:",␣
 ↪balanced_accuracy_score(y_test, ebm.predict(X_test)))
```

```
Balanced accuracy for KNN: 0.658844386586217
Balanced accuracy for Logistic Regression: 0.6460441459226365
Balanced accuracy for MLP: 0.6887260674628835
Balanced accuracy for Random Forest: 0.8085670025393862
Balanced accuracy for Explainable Boosting Machine: 0.6930854184420245
```

[ ]:
```
# Matthews correlation coefficient
print("Matthews correlation coefficient for KNN:", matthews_corrcoef(y_test,␣
 ↪knn.predict(X_test)))
print("Matthews correlation coefficient for Logistic Regression:",␣
 ↪matthews_corrcoef(y_test, lr.predict(X_test)))
print("Matthews correlation coefficient for MLP:", matthews_corrcoef(y_test,␣
 ↪mlp.predict(X_test)))
print("Matthews correlation coefficient for Random Forest:",␣
 ↪matthews_corrcoef(y_test, rf.predict(X_test)))
```

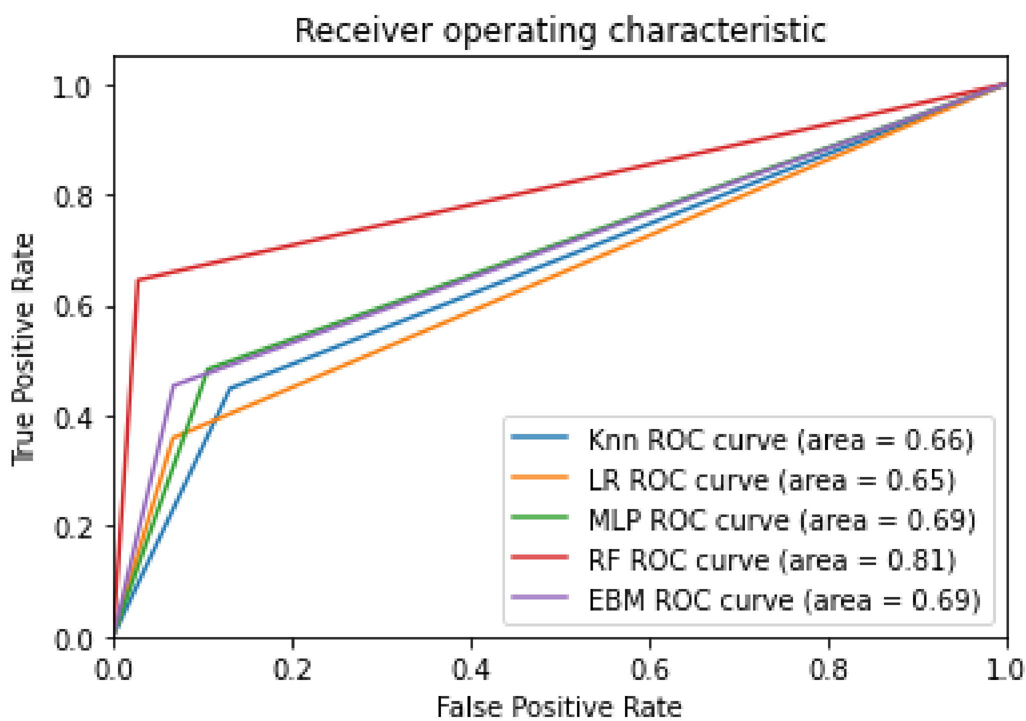
```
print("Matthews correlation coefficient for Explainable Boosting Machine:",␣
↪matthews_corrcoef(y_test, ebm.predict(X_test)))
```

```
Matthews correlation coefficient for KNN: 0.34196361664376296
Matthews correlation coefficient for Logistic Regression: 0.36710230376698677
Matthews correlation coefficient for MLP: 0.41243886486368886
Matthews correlation coefficient for Random Forest: 0.6921678456195637
Matthews correlation coefficient for Explainable Boosting Machine:
0.45412746244576185
```

2.16.3 AUC and ROC curve

[ ]:
```
fpr_knn = dict()
tpr_knn = dict()
roc_auc_knn = dict()
for i in range(2):
    fpr_knn[i], tpr_knn[i], _ = roc_curve(y_test, knn.predict(X_test))
    roc_auc_knn[i] = auc(fpr_knn[i], tpr_knn[i])

fpr_lr = dict()
tpr_lr = dict()
roc_auc_lr = dict()
for i in range(2):
    fpr_lr[i], tpr_lr[i], _ = roc_curve(y_test, lr.predict(X_test))
    roc_auc_lr[i] = auc(fpr_lr[i], tpr_lr[i])

fpr_mlp = dict()
tpr_mlp = dict()
roc_auc_mlp = dict()
for i in range(2):
    fpr_mlp[i], tpr_mlp[i], _ = roc_curve(y_test, mlp.predict(X_test))
    roc_auc_mlp[i] = auc(fpr_mlp[i], tpr_mlp[i])

fpr_rf = dict()
tpr_rf = dict()
roc_auc_rf = dict()
for i in range(2):
    fpr_rf[i], tpr_rf[i], _ = roc_curve(y_test, rf.predict(X_test))
    roc_auc_rf[i] = auc(fpr_rf[i], tpr_rf[i])

fpr_ebm = dict()
tpr_ebm = dict()
roc_auc_ebm = dict()
for i in range(2):
    fpr_ebm[i], tpr_ebm[i], _ = roc_curve(y_test, ebm.predict(X_test))
    roc_auc_ebm[i] = auc(fpr_ebm[i], tpr_ebm[i])
```

```
plt.figure()
plt.plot(fpr_knn[1], tpr_knn[1], label = "Knn ROC curve (area = %0.2f)" %␣
↪roc_auc_score(y_test, knn.predict(X_test)))
plt.plot(fpr_lr[1], tpr_lr[1], label = "LR ROC curve (area = %0.2f)" %␣
↪roc_auc_score(y_test, lr.predict(X_test)))
plt.plot(fpr_mlp[1], tpr_mlp[1], label = "MLP ROC curve (area = %0.2f)" %␣
↪roc_auc_score(y_test, mlp.predict(X_test)))
plt.plot(fpr_rf[1], tpr_rf[1], label = "RF ROC curve (area = %0.2f)" %␣
↪roc_auc_score(y_test, rf.predict(X_test)))
plt.plot(fpr_ebm[1], tpr_ebm[1], label = "EBM ROC curve (area = %0.2f)" %␣
↪roc_auc_score(y_test, ebm.predict(X_test)))
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Receiver operating characteristic")
plt.legend(loc = "lower right")
plt.savefig("AUC.png")
plt.show()
```



Visualise the global model behaviour with each feature

[ ]:
```
ebm_global = ebm.explain_global()
show(ebm_global)

# Please run the code in jupyter notebook to see the actual plot
```

```
<IPython.core.display.HTML object>
```

2.16.4 Visualise the local model behaviour with some unseen examples from the testing set

[ ]:
```
set_visualize_provider(InlineProvider()) # plot the output here
ebm_local = ebm.explain_local(X_test[:15], y_test[:15])
show(ebm_local)
# Please run the code in jupyter notebook to see the actual plot
```

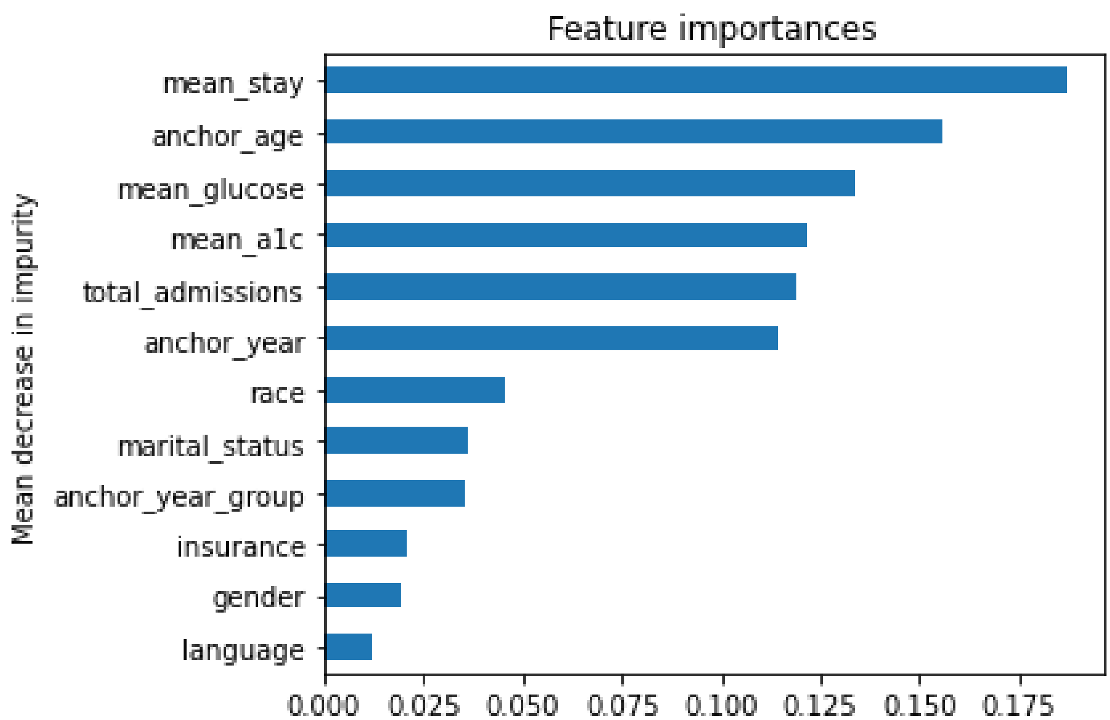
```
Output hidden; open in https://colab.research.google.com to view.
```

2.17 Final model: Random Forest

Feature analysis is performed on the Random Forest model.

[ ]:
```
forest_importances = pd.Series(rf.feature_importances_, index = col_name).
↪sort_values(ascending = True)
std = np.std([rf.feature_importances_ for tree in rf.estimators_], axis = 0)
```

[69]:
```
fig, ax = plt.subplots()
forest_importances.plot.barh(yerr = std, ax = ax)
ax.set_title("Feature importances")

ax.set_ylabel("Mean decrease in impurity")
fig.tight_layout()
plt.savefig("Featureimportances.png")
plt.show()
```



[ ]:
```
!apt-get install texlive texlive-xetex texlive-latex-extra pandoc
!pip install pypandoc
```

[ ]:
```
from google.colab import drive
drive.mount('/content/drive')
```

```
Mounted at /content/drive
```

[76]:
```
!jupyter nbconvert --to pdf --output "Code Appendix.pdf" --output-dir /content/
↪drive/MyDrive/COMP90089/ /content/drive/MyDrive/COMP90089/Code_Appendix.ipynb
```

```
[NbConvertApp] Converting notebook
/content/drive/MyDrive/COMP90089/Code_Appendix.ipynb to pdf
[NbConvertApp] Support files will be in Code Appendix_files/
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
```

```
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Making directory ./Code Appendix_files
[NbConvertApp] Writing 136055 bytes to ./notebook.tex
[NbConvertApp] Building PDF
[NbConvertApp] Running xelatex 3 times: ['xelatex', './notebook.tex', '-quiet']
[NbConvertApp] Running bibtex 1 time: ['bibtex', './notebook']
[NbConvertApp] WARNING | bibtex had problems, most likely because there were no
citations
[NbConvertApp] PDF successfully created
[NbConvertApp] Writing 327570 bytes to /content/drive/MyDrive/COMP90089/Code
Appendix.pdf
```