Assignment2_tofill

December 20, 2024

1 Assignment 2

To be delivered until 2024/12/23 23:59:59.

1.1 1) Arduino

You will start by setting up a series of connections in order to extract some data with the Arduino. First make the connections as shown below. **Mind the direction of the temperature sensor. If you have an incorrect position, you will be connection the power to the ground and vice-versa and you will damage the sensor.** The photoresistor sensor on the other hand has no polarity.

On this problem, you will read temperature and luminance from the sensors and print them on the serial.

1) Code an Arduino sketch, where the value of temperature and luminance are printed to the serial. For each serial print that you make, print the value of temperature, then a semicolon, then the value of luminance with a new line (use no whitespaces). You can do this by using three separate `Serial.print`, with the last one being a `Serial.println`. Print values 5 times per second (use the delay function to control this). Manually influence the readings of the sensors, by covering the photoresistor or shining light on it, and by lightly and carefully touching the temperature sensor to increase its temperature readings.

Note that the temperature sensor appears not to be very reliable. Since the objective of this exercise is just to plot the results, this should not be an issue.

Copy and paste your arduino code below. You may use a python code cell, even though the code can not be run.

Hint: for the temperature value to be in celsius, divide the read value by 1024 and multiply it by 500. The luminance does not have to be converted

[ ]:
```
const int tempPin = A1;  // Pin for temperature sensor
const int lightPin = A0; // Pin for photoresistor

int temp = 0;
int light = 0;

void setup() {
  Serial.begin(9600);
}
```

```
void loop() {
  temp = analogRead(tempPin);
  light = analogRead(lightPin);

  Serial.print((temp/1024.0)*500.0);
  Serial.print(";");
  Serial.println(light);

  delay(200);
}
```

To import the data into Arduino, keep it running (the Serial Monitor must be closed in Arduino) and run the following code. Change the COM port to your own. This block of code will read 1000 values from the Serial. Given that each observation is taken every 0.2 seconds, it should take a minute and a half.

[2]:
```python
import serial
import time

ser = serial.Serial('COM3', 9600, timeout=1)
time.sleep(2)

data = []
for i in range(500):
    line = ser.readline()
    if line:
        string = line.decode()
        data.append(string)

ser.close()
```

Convert the data into a pandas dataframe and save it in a csv file. Besides the value of temperature and luminance, also include the time, considering the first observation at $t = 0$ and every observation 0.2 seconds after the previous one. **The file must be submitted in Fenix and included in your Github repo**.

[20]:
```python
type(data)
import pandas as pd
time_values = [round(i * 0.2,2) for i in range(len(data))]
temperature = []
luminance = []

for entry in data:
    temp, lum = entry.split(';')
    temperature.append(round(float(temp),2))
    luminance.append(int(lum))
```

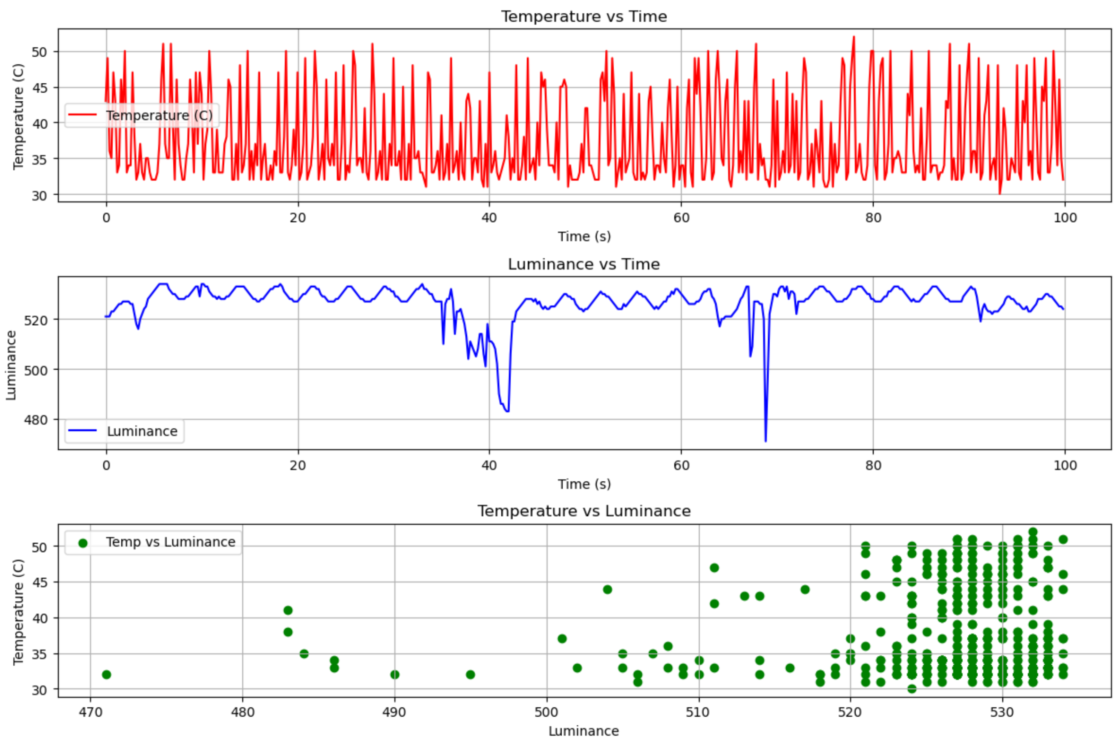
```python
df = pd.DataFrame({
    'Time (s)': time_values[:len(temperature)],
    'Temperature (C)': temperature,
    'Luminance': luminance
})

csv_filename = "sensor_data.csv"
df.to_csv(csv_filename, index=False)

print(f"Data saved to {csv_filename}")
print(df.head())
```

```
Data saved to sensor_data.csv
   Time (s)  Temperature (C)  Luminance
0       0.0             43.0        521
1       0.2             49.0        521
2       0.4             36.0        521
3       0.6             35.0        523
4       0.8             47.0        523
```

Plot the Temperature against time, the luminance against time and the temperature against the luminance.

[5]:
```python
import matplotlib.pyplot as plt
import pandas as pd

df = pd.read_csv("sensor_data.csv");

plt.figure(figsize=(12, 8))

# Plot 1: Temperature vs. Time
plt.subplot(3, 1, 1)
plt.plot(df['Time (s)'], df['Temperature (C)'], color='red', label='Temperature␣
 ↪(C)')
plt.xlabel('Time (s)')
plt.ylabel('Temperature (C)')
plt.title('Temperature vs Time')
plt.grid(True)
plt.legend()

# Plot 2: Luminance vs. Time
plt.subplot(3, 1, 2)
plt.plot(df['Time (s)'], df['Luminance'], color='blue', label='Luminance')
plt.xlabel('Time (s)')
plt.ylabel('Luminance')
plt.title('Luminance vs Time')
plt.grid(True)
```

```
plt.legend()

# Plot 3: Temperature vs. Luminance
plt.subplot(3, 1, 3)
plt.scatter(df['Luminance'], df['Temperature (C)'], color='green', label='Temp␣
    ↪vs Luminance')
plt.xlabel('Luminance')
plt.ylabel('Temperature (C)')
plt.title('Temperature vs Luminance')
plt.grid(True)
plt.legend()

plt.tight_layout()
plt.show()
```



1.2 2) Databases

For the databases part of this assignment, you will use the mimic-iii database from the laboratory session. Start by adding a few new tables to the database, using the SQL files included in the assignment's files. Open PGAdmin and connect to your mimic-iii database. **To properly load these tables, load the following files exactly and by the order presented.**

1) Run demographic.sql

2) Run lab_firstday.sql

You will now have to answer a few SQL questions.

1. Open the connection to your mimic-iii database. If you want, you can delete your credentials before submitting the assignment, but if you do so, please run the notebook first, for the results to be displayed.

[1]:
```
!pip install psycopg2
import pandas as pd
import numpy as np
import psycopg2 as psql
import matplotlib.pyplot as plt

conn = psql.connect(host='localhost',
                    database='mimic-iii',
                    user='postgres',
                    password='',
                    port=5432)

cursor = conn.cursor()


cursor.execute("select version()")


data = cursor.fetchone()
print("Connection established to: ", data)
```

```
Requirement already satisfied: psycopg2 in c:\users\marti\anaconda3\lib\site-
packages (2.9.10)
Connection established to:  ('PostgreSQL 17.2 on x86_64-windows, compiled by
msvc-19.42.34433, 64-bit',)
```

2. Create a function that receives an SQL query and automatically opens a cursor, queries the database, extracts the columns, creates a pandas database, and closes the connections.

[5]:
```
query = "SELECT * FROM public.admissions "

cursor.execute(query)

colnames = [desc[0] for desc in cursor.description]
data = cursor.fetchall()

#Closing the connection
conn.close()

admission_table = pd.DataFrame(data, columns = colnames)
admission_table
```

[5]:

```
     row_id  subject_id  hadm_id           admittime           dischtime  \
0     12258       10006   142345 2164-10-23 21:09:00 2164-11-01 17:15:00
1     12263       10011   105331 2126-08-14 22:32:00 2126-08-28 18:59:00
2     12265       10013   165520 2125-10-04 23:36:00 2125-10-07 15:13:00
3     12269       10017   199207 2149-05-26 17:19:00 2149-06-03 18:42:00
4     12270       10019   177759 2163-05-14 20:43:00 2163-05-15 12:00:00
..      …           …        …                   …                   …
124   41055       44083   198330 2112-05-28 15:45:00 2112-06-07 16:50:00
125   41070       44154   174245 2178-05-14 20:29:00 2178-05-15 09:45:00
126   41087       44212   163189 2123-11-24 14:14:00 2123-12-30 14:31:00
127   41090       44222   192189 2180-07-19 06:55:00 2180-07-20 13:00:00
128   41092       44228   103379 2170-12-15 03:14:00 2170-12-24 18:00:00

              deathtime admission_type         admission_location  \
0                   NaT      EMERGENCY       EMERGENCY ROOM ADMIT
1   2126-08-28 18:59:00      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
2   2125-10-07 15:13:00      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
3                   NaT      EMERGENCY       EMERGENCY ROOM ADMIT
4   2163-05-15 12:00:00      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
..                    …            …                          …
124                 NaT      EMERGENCY       EMERGENCY ROOM ADMIT
125 2178-05-15 09:45:00      EMERGENCY       EMERGENCY ROOM ADMIT
126                 NaT      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
127                 NaT      EMERGENCY       EMERGENCY ROOM ADMIT
128                 NaT      EMERGENCY       EMERGENCY ROOM ADMIT

           discharge_location insurance language           religion  \
0            HOME HEALTH CARE  Medicare     None           CATHOLIC
1                DEAD/EXPIRED   Private     None           CATHOLIC
2                DEAD/EXPIRED  Medicare     None           CATHOLIC
3                         SNF  Medicare     None           CATHOLIC
4                DEAD/EXPIRED  Medicare     None           CATHOLIC
..                          …       …       …                 …
124                      HOME   Private     ENGL           CATHOLIC
125              DEAD/EXPIRED  Medicare     ENGL  PROTESTANT QUAKER
126   REHAB/DISTINCT PART HOSP  Medicare     ENGL       UNOBTAINABLE
127                      HOME  Medicare     ENGL           CATHOLIC
128          HOME HEALTH CARE   Private     ENGL      NOT SPECIFIED

    marital_status               ethnicity           edregtime  \
0        SEPARATED  BLACK/AFRICAN AMERICAN 2164-10-23 16:43:00
1           SINGLE   UNKNOWN/NOT SPECIFIED                 NaT
2             None   UNKNOWN/NOT SPECIFIED                 NaT
3         DIVORCED                   WHITE 2149-05-26 12:08:00
4         DIVORCED                   WHITE                 NaT
..             …                      …                   …
124         SINGLE                   WHITE 2112-05-28 13:16:00
```

```
125        MARRIED                   WHITE 2178-05-14 17:37:00
126         SINGLE  BLACK/AFRICAN AMERICAN                 NaT
127         SINGLE                   WHITE 2180-07-19 04:50:00
128         SINGLE                   WHITE 2170-12-15 02:22:00

              edouttime                                          diagnosis  \
0   2164-10-23 23:00:00                                             SEPSIS
1                   NaT                                        HEPATITIS B
2                   NaT                                             SEPSIS
3   2149-05-26 19:45:00                                    HUMERAL FRACTURE
4                   NaT                                ALCOHOLIC HEPATITIS
..                  …                                                  …
124 2112-05-28 17:30:00                                PERICARDIAL EFFUSION
125 2178-05-14 22:08:00                               ALTERED MENTAL STATUS
126                 NaT  ACUTE RESPIRATORY DISTRESS SYNDROME;ACUTE RENA…
127 2180-07-19 08:23:00                                        BRADYCARDIA
128 2170-12-15 05:25:00                                        CHOLANGITIS

     hospital_expire_flag  has_chartevents_data
0                       0                     1
1                       1                     1
2                       1                     1
3                       0                     1
4                       1                     1
..                    …                   …
124                     0                     1
125                     1                     1
126                     0                     1
127                     0                     1
128                     0                     1

[129 rows x 19 columns]
```

3. Query the table admissions filtering for admission type as emergency and insurance as private.

[10]:
```
newquery = "SELECT * FROM public.admissions WHERE admission_type = 'EMERGENCY'␣
 ↪AND insurance = 'Private' "

conn = psql.connect(host='localhost',
                    database='mimic-iii',
                    user='postgres',
                    password='',
                    port=5432)
cursor = conn.cursor()


cursor.execute("select version()")
```

```python
data = cursor.fetchone()
print("Connection established to: ", data)

cursor.execute(newquery)

colnames = [desc[0] for desc in cursor.description]
data = cursor.fetchall()

#Closing the connection
conn.close()

admission_table = pd.DataFrame(data, columns = colnames)
admission_table
```

```
Connection established to:  ('PostgreSQL 17.2 on x86_64-windows, compiled by
msvc-19.42.34433, 64-bit',)
```

[10]:

	row_id	subject_id	hadm_id	admittime	dischtime
0	12263	10011	105331	2126-08-14 22:32:00	2126-08-28 18:59:00
1	12317	10067	160442	2130-10-06 01:34:00	2130-10-06 02:29:00
2	12339	10088	149044	2107-05-12 18:00:00	2107-05-18 13:30:00
3	12341	10090	176805	2124-01-12 14:26:00	2124-01-14 19:00:00
4	12349	10098	180685	2170-12-02 23:24:00	2170-12-03 15:55:00
5	12357	10106	133283	2161-09-14 22:22:00	2161-09-19 17:00:00
6	12368	10117	187023	2138-06-05 17:23:00	2138-06-11 10:16:00
7	12369	10117	105150	2138-11-09 18:08:00	2138-11-18 23:13:00
8	12381	10126	160445	2171-07-12 06:02:00	2171-08-16 12:00:00
9	12382	10127	182839	2198-06-28 05:34:00	2198-07-20 14:56:00
10	12385	10130	156668	2161-01-30 16:26:00	2161-02-19 14:05:00
11	39869	40310	186361	2144-07-11 15:02:00	2144-11-12 14:40:00
12	39962	40601	182879	2184-08-04 05:44:00	2184-08-10 15:30:00
13	40440	42066	171628	2112-02-04 14:49:00	2112-02-11 12:00:00
14	40512	42292	138503	2162-01-16 13:56:00	2162-01-19 13:45:00
15	40993	43881	172454	2104-09-24 17:31:00	2104-09-30 16:17:00
16	40994	43881	167021	2104-10-24 09:44:00	2104-11-01 11:59:00
17	41054	44083	131048	2112-05-22 15:37:00	2112-05-25 13:30:00
18	41055	44083	198330	2112-05-28 15:45:00	2112-06-07 16:50:00
19	41092	44228	103379	2170-12-15 03:14:00	2170-12-24 18:00:00

	deathtime	admission_type	admission_location
0	2126-08-28 18:59:00	EMERGENCY	TRANSFER FROM HOSP/EXTRAM
1	2130-10-06 02:29:00	EMERGENCY	EMERGENCY ROOM ADMIT
2	NaT	EMERGENCY	TRANSFER FROM HOSP/EXTRAM
3	NaT	EMERGENCY	EMERGENCY ROOM ADMIT
4	2170-12-03 15:55:00	EMERGENCY	EMERGENCY ROOM ADMIT
5	NaT	EMERGENCY	EMERGENCY ROOM ADMIT

```
6                   NaT      EMERGENCY       EMERGENCY ROOM ADMIT
7   2138-11-18 23:13:00      EMERGENCY       EMERGENCY ROOM ADMIT
8   2171-08-16 12:00:00      EMERGENCY  PHYS REFERRAL/NORMAL DELI
9                   NaT      EMERGENCY       EMERGENCY ROOM ADMIT
10                  NaT      EMERGENCY       EMERGENCY ROOM ADMIT
11                  NaT      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
12                  NaT      EMERGENCY       EMERGENCY ROOM ADMIT
13  2112-02-11 12:00:00      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
14                  NaT      EMERGENCY       EMERGENCY ROOM ADMIT
15                  NaT      EMERGENCY       EMERGENCY ROOM ADMIT
16                  NaT      EMERGENCY       EMERGENCY ROOM ADMIT
17                  NaT      EMERGENCY       EMERGENCY ROOM ADMIT
18                  NaT      EMERGENCY       EMERGENCY ROOM ADMIT
19                  NaT      EMERGENCY       EMERGENCY ROOM ADMIT

             discharge_location insurance language           religion  \
0                  DEAD/EXPIRED   Private     None           CATHOLIC
1                  DEAD/EXPIRED   Private     None       UNOBTAINABLE
2                           SNF   Private     None       UNOBTAINABLE
3        DISCH-TRAN TO PSYCH HOSP   Private     ENGL      NOT SPECIFIED
4                  DEAD/EXPIRED   Private     None       UNOBTAINABLE
5      HOME WITH HOME IV PROVIDR   Private     None           CATHOLIC
6                          HOME   Private     None           CATHOLIC
7                  DEAD/EXPIRED   Private     None           CATHOLIC
8                  DEAD/EXPIRED   Private     None       UNOBTAINABLE
9      REHAB/DISTINCT PART HOSP   Private     None      NOT SPECIFIED
10             HOME HEALTH CARE   Private     None           CATHOLIC
11     REHAB/DISTINCT PART HOSP   Private     ENGL           CATHOLIC
12                          SNF   Private     ENGL  PROTESTANT QUAKER
13                 DEAD/EXPIRED   Private     ENGL           CATHOLIC
14                         HOME   Private     ENGL           CATHOLIC
15             HOME HEALTH CARE   Private     ENGL      NOT SPECIFIED
16                         HOME   Private     ENGL      NOT SPECIFIED
17             HOME HEALTH CARE   Private     ENGL           CATHOLIC
18                         HOME   Private     ENGL           CATHOLIC
19             HOME HEALTH CARE   Private     ENGL      NOT SPECIFIED

        marital_status             ethnicity           edregtime  \
0               SINGLE  UNKNOWN/NOT SPECIFIED                 NaT
1                 None                  OTHER 2130-10-06 00:12:00
2    UNKNOWN (DEFAULT)                  WHITE                 NaT
3               SINGLE                  WHITE 2124-01-12 11:56:00
4                 None                  OTHER 2170-12-02 22:45:00
5              MARRIED                  WHITE 2161-09-14 14:45:00
6               SINGLE  UNKNOWN/NOT SPECIFIED 2138-06-05 11:42:00
7               SINGLE  UNKNOWN/NOT SPECIFIED 2138-11-09 15:42:00
8               SINGLE                  WHITE                 NaT
```

```
9              None                    WHITE 2198-06-28 04:28:00
10          MARRIED  UNKNOWN/NOT SPECIFIED 2161-01-30 10:35:00
11           SINGLE                    WHITE                 NaT
12          MARRIED                    WHITE 2184-08-04 01:35:00
13           SINGLE                    WHITE                 NaT
14           SINGLE                    WHITE 2162-01-16 11:28:00
15          MARRIED                    WHITE 2104-09-24 12:07:00
16          MARRIED                    WHITE 2104-10-24 07:17:00
17           SINGLE                    WHITE 2112-05-22 09:25:00
18           SINGLE                    WHITE 2112-05-28 13:16:00
19           SINGLE                    WHITE 2170-12-15 02:22:00

             edouttime                                       diagnosis  \
0                  NaT                                     HEPATITIS B
1  2130-10-06 01:30:00                         S/P MOTORCYCLE ACCIDENT
2                  NaT                                       UROSEPSIS
3  2124-01-12 16:09:00                                        OVERDOSE
4  2170-12-03 00:56:00  STATUS POST MOTOR VEHICLE ACCIDENT WITH INJURIES
5  2161-09-15 01:30:00                                        HEADACHE
6  2138-06-05 21:20:00                                           FEVER
7  2138-11-09 20:42:00                                           FEVER
8                  NaT                                   LIVER FAILURE
9  2198-06-28 05:52:00                      S/P MOTOR VEHICLE ACCIDENT
10 2161-01-30 20:25:00                                         ABSCESS
11                 NaT                                 FACIAL NUMBNESS
12 2184-08-04 06:47:00                                          SEPSIS
13                 NaT                               TRACHEAL STENOSIS
14 2162-01-16 16:12:00                  PNEUMONIA/HYPOGLCEMIA/SYNCOPE
15 2104-09-24 18:50:00                        ACUTE PULMONARY EMBOLISM
16 2104-10-24 11:10:00                                  UPPER GI BLEED
17 2112-05-22 17:04:00                             SHORTNESS OF BREATH
18 2112-05-28 17:30:00                             PERICARDIAL EFFUSION
19 2170-12-15 05:25:00                                     CHOLANGITIS

    hospital_expire_flag  has_chartevents_data
0                      1                     1
1                      1                     1
2                      0                     1
3                      0                     1
4                      1                     1
5                      0                     1
6                      0                     1
7                      1                     1
8                      1                     1
9                      0                     1
10                     0                     1
11                     0                     1
```

```
12                      0                      1
13                      1                      1
14                      0                      1
15                      0                      1
16                      0                      1
17                      0                      1
18                      0                      1
19                      0                      1
```

4. Query the table admissions, filtering for the same conditions as the previous exercise (admission type as emergency and insurance as private). Join the "drgcodes" table on the admission ID. Display only the columns regarding the subject id, admission id, time of death, and description of the drug.

[13]:

```
newquery = "SELECT * FROM public.admissions LEFT JOIN public.prescriptions ON␣
↪public.admissions.subject_id = public.prescriptions.subject_id AND public.
↪admissions.hadm_id = public.prescriptions.hadm_id WHERE admission_type =␣
↪'EMERGENCY' AND insurance = 'Private' "

conn = psql.connect(host='localhost',
                    database='mimic-iii',
                    user='postgres',
                    password='',
                    port=5432)
cursor = conn.cursor()


cursor.execute("select version()")

data = cursor.fetchone()
print("Connection established to: ", data)

cursor.execute(newquery)

colnames = [desc[0] for desc in cursor.description]
data = cursor.fetchall()

conn.close()

admission_table = pd.DataFrame(data, columns = colnames)
admission_table
```

```
Connection established to:  ('PostgreSQL 17.2 on x86_64-windows, compiled by
msvc-19.42.34433, 64-bit',)
```

[13]:

```
   row_id  subject_id  hadm_id           admittime           dischtime  \
0   12263       10011   105331 2126-08-14 22:32:00 2126-08-28 18:59:00
1   12317       10067   160442 2130-10-06 01:34:00 2130-10-06 02:29:00
```

```
2       12339        10088   149044 2107-05-12 18:00:00 2107-05-18 13:30:00
3       12339        10088   149044 2107-05-12 18:00:00 2107-05-18 13:30:00
4       12339        10088   149044 2107-05-12 18:00:00 2107-05-18 13:30:00
…       …          …      …                 …                  …
2086    41092        44228   103379 2170-12-15 03:14:00 2170-12-24 18:00:00
2087    41092        44228   103379 2170-12-15 03:14:00 2170-12-24 18:00:00
2088    41092        44228   103379 2170-12-15 03:14:00 2170-12-24 18:00:00
2089    41092        44228   103379 2170-12-15 03:14:00 2170-12-24 18:00:00
2090    41092        44228   103379 2170-12-15 03:14:00 2170-12-24 18:00:00

               deathtime admission_type        admission_location  \
0    2126-08-28 18:59:00      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
1    2130-10-06 02:29:00      EMERGENCY       EMERGENCY ROOM ADMIT
2                    NaT      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
3                    NaT      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
4                    NaT      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
…                  …              …                         …
2086                 NaT      EMERGENCY       EMERGENCY ROOM ADMIT
2087                 NaT      EMERGENCY       EMERGENCY ROOM ADMIT
2088                 NaT      EMERGENCY       EMERGENCY ROOM ADMIT
2089                 NaT      EMERGENCY       EMERGENCY ROOM ADMIT
2090                 NaT      EMERGENCY       EMERGENCY ROOM ADMIT

     discharge_location insurance  …            drug_name_generic  \
0          DEAD/EXPIRED   Private  …                         None
1          DEAD/EXPIRED   Private  …                         None
2                   SNF   Private  …  Sodium Chloride 0.9%  Flush
3                   SNF   Private  …                   Lisinopril
4                   SNF   Private  …     Docusate Sodium (Liquid)
…                 …         …   …                          …
2086   HOME HEALTH CARE   Private  …                         None
2087   HOME HEALTH CARE   Private  …                         None
2088   HOME HEALTH CARE   Private  …                         None
2089   HOME HEALTH CARE   Private  …                         None
2090   HOME HEALTH CARE   Private  …                         None

     formulary_drug_cd     gsn          ndc      prod_strength dose_val_rx  \
0                 None    None         None               None        None
1                 None    None         None               None        None
2            NACLFLUSH    None            0            Syringe           3
3                LISI5  000393  00310013039            5MG TAB           5
4             DOCU100L  003017  51079033530       100MG UD CUP         100
…                  …      …          …                  …        …
2086         CIPR400PM  015921  00085174102   400mg Premix Bag         400
2087            CALG1I  001356  63323031110       1g/10mL Vial           4
2088           KCL20PM  045309  00338070341  20mEq/50mL Premix       20-60
2089         METR500PM  009588  00409781124   500mg Premix Bag         500
```

```
2090            CEFX1F  059424  00338500241      1g Frozen Bag           1

     dose_unit_rx  form_val_disp  form_unit_disp  route
0            None           None            None   None
1            None           None            None   None
2              ml            0.6             SYR     IV
3              mg              1             TAB     NG
4              mg              1           UDCUP     NG
…             …              …              …     …
2086           mg              1             BAG     IV
2087           gm              4            VIAL     IV
2088          mEq              1             BAG     IV
2089           mg              1             BAG     IV
2090            g              1             BAG     IV

[2091 rows x 38 columns]
```

5.1. Obtain the dataset for this problem, by running the SQL query below.

[2]:
```python
newquery = "SELECT pivoted_lab.*," +\
                "gender as gender," +\
                "admission_age," +\
                "ethnicity_grouped as eth_grp," +\
                "hospital_expire_flag," +\
                "los_icu " +\
        "FROM demographics " +\
        "LEFT JOIN pivoted_lab " +\
        "ON demographics.icustay_id = pivoted_lab.icustay_id " +\
        "WHERE first_icu_stay = true"


conn = psql.connect(host='localhost',
                    database='mimic-iii',
                    user='postgres',
                    password='',
                    port=5432)
cursor = conn.cursor()


cursor.execute("select version()")

data = cursor.fetchone()
print("Connection established to: ", data)

cursor.execute(newquery)

colnames = [desc[0] for desc in cursor.description]
```

```
data = cursor.fetchall()



df = pd.DataFrame(data, columns = colnames)
df
```

```
Connection established to:  ('PostgreSQL 17.2 on x86_64-windows, compiled by
msvc-19.42.34433, 64-bit',)
```

[2]:

```
     subject_id  hadm_id  icustay_id  aniongap_min  aniongap_max  albumin_min  \
0         10006   142345      206504          12.0          20.0          2.7
1         10011   105331      232110          12.0          12.0          2.6
2         10013   165520      264446          13.0          13.0          NaN
3         10017   199207      204881          13.0          13.0          2.8
4         10019   177759      228977          20.0          46.0          3.2
..          …        …          …            …            …           …
123       44083   198330      286428          16.0          16.0          NaN
124       44154   174245      217724          15.0          15.0          NaN
125       44212   163189      239396          15.0          21.0          2.9
126       44222   192189      238186          11.0          15.0          NaN
127       44228   103379      217992          12.0          18.0          2.2

     albumin_max  bands_min  bands_max  bicarbonate_min  …  sodium_max  \
0            3.4        NaN        NaN             29.0  …       139.0
1            2.6        2.0        2.0             23.0  …       136.0
2            NaN       13.0       13.0             29.0  …       138.0
3            2.8        NaN        NaN             29.0  …       139.0
4            3.2        NaN        NaN             10.0  …       141.0
..           …          …          …               …  …         …
123          NaN        NaN        NaN             21.0  …       142.0
124          NaN        NaN        NaN             19.0  …       142.0
125          3.0        NaN        NaN             18.0  …       150.0
126          NaN        NaN        NaN             22.0  …       135.0
127          2.7        NaN        NaN             15.0  …       142.0

     bun_min  bun_max  wbc_min  wbc_max  gender  admission_age  eth_grp  \
0        9.0     11.0      4.6      7.8       F           70.0    black
1        3.0      3.0     10.6     10.6       F           36.0  unknown
2       32.0     32.0     13.8     16.2       F           87.0  unknown
3        3.0      3.0     15.8     15.8       F           74.0    white
4       31.0     53.0      3.7      6.8       M           49.0    white
..        …        …        …        …     …             …      …
123     12.0     12.0     12.3     14.9       M           55.0    white
124     16.0     21.0     12.2     17.1       M          300.0    white
125     37.0     57.0      8.8     11.4       F           45.0    black
126     21.0     24.0      9.3      9.9       M           73.0    white
```

```
127     10.0     11.0      7.0     41.9       F            58.0     white

     hospital_expire_flag  los_icu
0                       0      1.0
1                       1     13.0
2                       1      2.0
3                       0      2.0
4                       1      1.0
..                    …      …
123                     0      3.0
124                     1      0.0
125                     0     31.0
126                     0      1.0
127                     0      4.0

[128 rows x 46 columns]
```

5.2. Close the connection to your SQL server.

[3]:
```python
conn.close()
```

5.3. Prepare your dataset:

- Drop the ID columns of subject, admission and ICU stay.
- Drop columns with at least one NA value.
- Encode the categorical columns, the ethnicity and gender ('eth_grp', 'gender'). *Suggestion: use pd.get_dummies*
- Consider the column 'hospital_expire_flag' as the response and all remaining columns as the predictors.

[4]:
```python
from sklearn import preprocessing


df = df.drop(["subject_id", 'hadm_id', 'icustay_id'], axis='columns')
df = df.dropna(axis = 1)

le = preprocessing.LabelEncoder()

df['gender'] = le.fit_transform(df['gender'])
df['eth_grp'] = le.fit_transform(df['eth_grp'])

df
```

[4]:
```
     bicarbonate_min  bicarbonate_max  creatinine_min  creatinine_max  \
0               29.0             31.0             3.0             3.5
1               23.0             23.0             0.7             0.7
2               29.0             29.0             1.7             1.7
3               29.0             29.0             0.3             0.3
4               10.0             18.0             4.0             7.2
```

```
..              …               …               …               …
123          21.0            21.0             0.7             0.7
124          19.0            19.0             0.9             0.9
125          18.0            23.0             3.0             4.8
126          22.0            27.0             1.2             1.7
127          15.0            24.0             0.6             0.8

     chloride_min  chloride_max  glucose_min  glucose_max  hematocrit_min  \
0            96.0         100.0         84.0        217.0            36.9
1           107.0         107.0         79.0         79.0            33.9
2            98.0         100.0        134.0        165.0            28.1
3           100.0         100.0        137.0        137.0            27.5
4            83.0         104.0         80.0        360.0            30.6
..            …             …            …            …             …
123         108.0         108.0        151.0        151.0            26.0
124         107.0         113.0        164.0        177.0            40.8
125         108.0         115.0         99.0        122.0            23.8
126         100.0         101.0         56.0        268.0            37.8
127         103.0         115.0         91.0        132.0            22.6

     hematocrit_max  …  sodium_max  bun_min  bun_max  wbc_min  wbc_max  \
0              42.4  …       139.0      9.0     11.0      4.6      7.8
1              34.0  …       136.0      3.0      3.0     10.6     10.6
2              29.2  …       138.0     32.0     32.0     13.8     16.2
3              27.5  …       139.0      3.0      3.0     15.8     15.8
4              36.0  …       141.0     31.0     53.0      3.7      6.8
..              …  …          …        …       …        …        …
123            29.0  …       142.0     12.0     12.0     12.3     14.9
124            41.8  …       142.0     16.0     21.0     12.2     17.1
125            25.9  …       150.0     37.0     57.0      8.8     11.4
126            39.0  …       135.0     21.0     24.0      9.3      9.9
127            27.6  …       142.0     10.0     11.0      7.0     41.9

     gender  admission_age  eth_grp  hospital_expire_flag  los_icu
0         0           70.0        1                     0      1.0
1         0           36.0        5                     1     13.0
2         0           87.0        5                     1      2.0
3         0           74.0        6                     0      2.0
4         1           49.0        6                     1      1.0
..      …            …      …                   …      …
123       1           55.0        6                     0      3.0
124       1          300.0        6                     1      0.0
125       0           45.0        1                     0     31.0
126       1           73.0        6                     0      1.0
127       0           58.0        6                     0      4.0

[128 rows x 25 columns]
```

6. Fit the following tree-based classifiers to the dataset. For each method:

- Perform k-fold cross validation to evaluate the models. Consider 10 folds.
- Plot the ROC curves for each fold, along with the mean ROC curve.
- Calculate the mean AUC.

a. Decision tree.

[5]:
```python
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import KFold
from sklearn.metrics import roc_curve, auc, RocCurveDisplay
from sklearn.model_selection import StratifiedKFold





X = df.drop('hospital_expire_flag', axis = 1)
y = df['hospital_expire_flag']

X, y
```

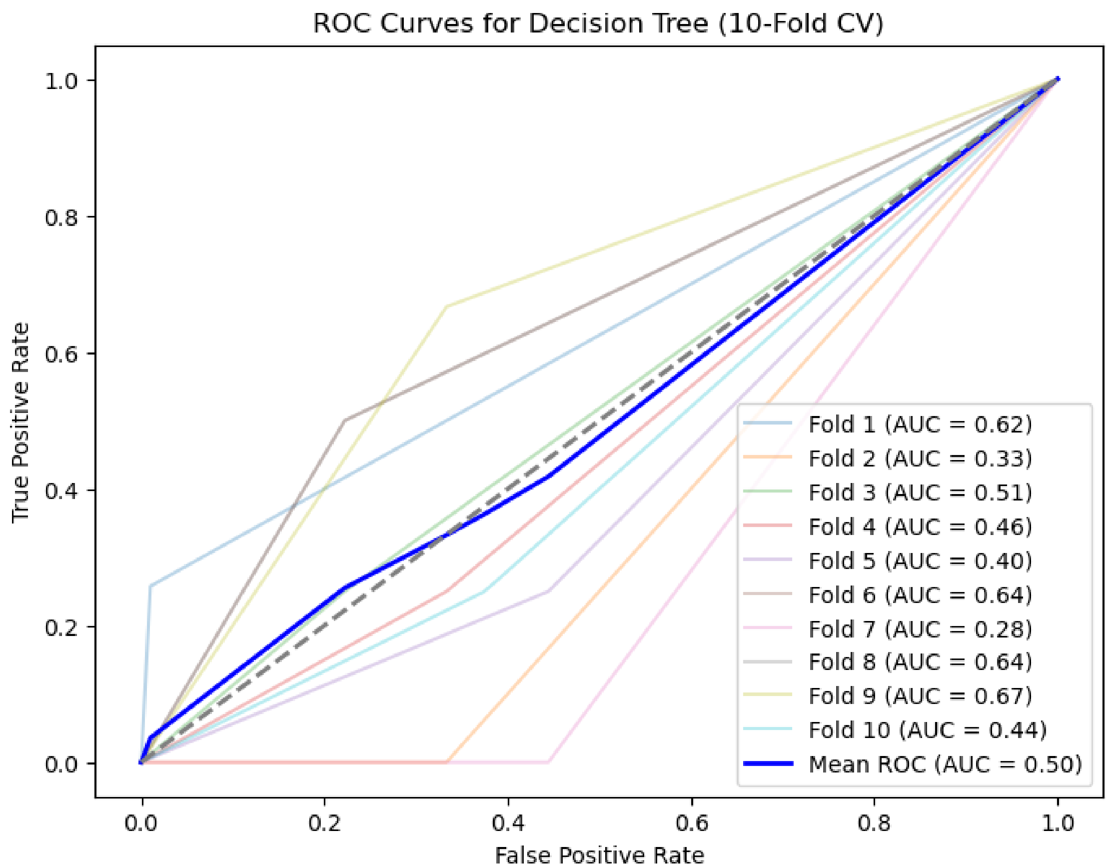
[5]:
```
(     bicarbonate_min  bicarbonate_max  creatinine_min  creatinine_max  \
 0               29.0             31.0             3.0             3.5
 1               23.0             23.0             0.7             0.7
 2               29.0             29.0             1.7             1.7
 3               29.0             29.0             0.3             0.3
 4               10.0             18.0             4.0             7.2
 ..               …                …               …               …
 123             21.0             21.0             0.7             0.7
 124             19.0             19.0             0.9             0.9
 125             18.0             23.0             3.0             4.8
 126             22.0             27.0             1.2             1.7
 127             15.0             24.0             0.6             0.8

      chloride_min  chloride_max  glucose_min  glucose_max  hematocrit_min  \
 0            96.0         100.0         84.0        217.0            36.9
 1           107.0         107.0         79.0         79.0            33.9
 2            98.0         100.0        134.0        165.0            28.1
 3           100.0         100.0        137.0        137.0            27.5
 4            83.0         104.0         80.0        360.0            30.6
 ..            …             …            …            …               …
 123         108.0         108.0        151.0        151.0            26.0
 124         107.0         113.0        164.0        177.0            40.8
 125         108.0         115.0         99.0        122.0            23.8
 126         100.0         101.0         56.0        268.0            37.8
 127         103.0         115.0         91.0        132.0            22.6
```

```
     hematocrit_max  …  sodium_min  sodium_max  bun_min  bun_max  wbc_min  \
0              42.4  …       139.0       139.0      9.0     11.0      4.6
1              34.0  …       136.0       136.0      3.0      3.0     10.6
2              29.2  …       136.0       138.0     32.0     32.0     13.8
3              27.5  …       139.0       139.0      3.0      3.0     15.8
4              36.0  …       136.0       141.0     31.0     53.0      3.7
..              …  …         …         …      …      …      …
123            29.0  …       142.0       142.0     12.0     12.0     12.3
124            41.8  …       141.0       142.0     16.0     21.0     12.2
125            25.9  …       141.0       150.0     37.0     57.0      8.8
126            39.0  …       132.0       135.0     21.0     24.0      9.3
127            27.6  …       138.0       142.0     10.0     11.0      7.0

     wbc_max  gender  admission_age  eth_grp  los_icu
0        7.8       0           70.0        1      1.0
1       10.6       0           36.0        5     13.0
2       16.2       0           87.0        5      2.0
3       15.8       0           74.0        6      2.0
4        6.8       1           49.0        6      1.0
..       …     …             …      …      …
123     14.9       1           55.0        6      3.0
124     17.1       1          300.0        6      0.0
125     11.4       0           45.0        1     31.0
126      9.9       1           73.0        6      1.0
127     41.9       0           58.0        6      4.0

[128 rows x 24 columns],
0      0
1      1
2      1
3      0
4      1
      ..
123    0
124    1
125    0
126    0
127    0
Name: hospital_expire_flag, Length: 128, dtype: int64)
```

[34]:
```python
X = X.reset_index(drop=True)
y = y.reset_index(drop=True)


dt_model = DecisionTreeClassifier(random_state=42)
```

```
kf = StratifiedKFold(n_splits=10, shuffle=True, random_state=42)


tprs = []
mean_fpr = np.linspace(0, 1, 100)
aucs = []


for train_idx, test_idx in kf.split(X, y):

    X_train, X_test = X.iloc[train_idx], X.iloc[test_idx]
    y_train, y_test = y.iloc[train_idx], y.iloc[test_idx]


    dt_model.fit(X_train, y_train)

    y_proba = dt_model.predict_proba(X_test)[:, 1]


    fpr, tpr, _ = roc_curve(y_test, y_proba)
    roc_auc = auc(fpr, tpr)
    aucs.append(roc_auc)


    tprs.append(np.interp(mean_fpr, fpr, tpr))
    tprs[-1][0] = 0.0


mean_tpr = np.mean(tprs, axis=0)
mean_tpr[-1] = 1.0
mean_auc = auc(mean_fpr, mean_tpr)


plt.figure(figsize=(8, 6))
for i, tpr in enumerate(tprs):
    plt.plot(mean_fpr, tpr, alpha=0.3, label=f"Fold {i+1} (AUC = {aucs[i]:.
 ↪2f})")

plt.plot(mean_fpr, mean_tpr, color="blue", label=f"Mean ROC (AUC = {mean_auc:.
 ↪2f})", lw=2)


plt.plot([0, 1], [0, 1], color="gray", linestyle="--", lw=2)

plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("ROC Curves for Decision Tree (10-Fold CV)")
```

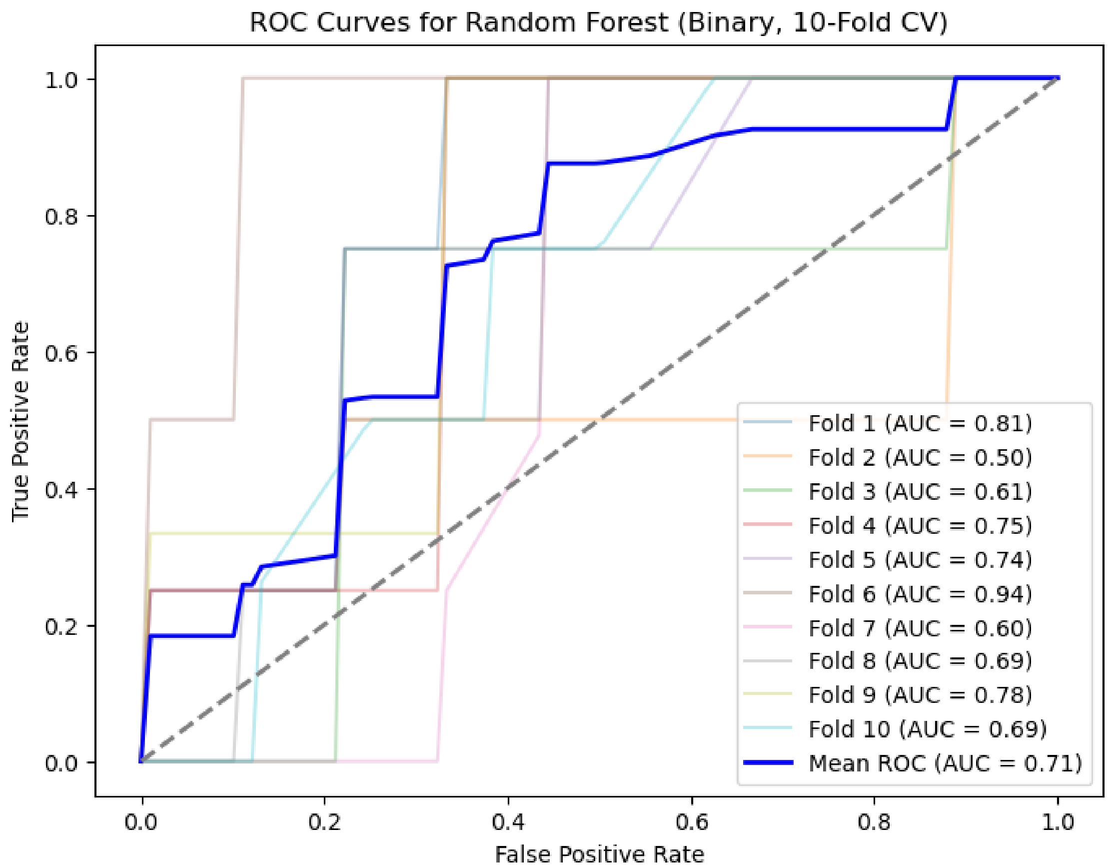
```
plt.legend(loc="lower right")
plt.show()
```



b. Random forest

[36]:
```
from sklearn.ensemble import RandomForestClassifier

rf_model = RandomForestClassifier(random_state=42, n_estimators=100)

kf = StratifiedKFold(n_splits=10, shuffle=True, random_state=42)


tprs = []
mean_fpr = np.linspace(0, 1, 100)
aucs = []


for train_idx, test_idx in kf.split(X, y):

    X_train, X_test = X.iloc[train_idx], X.iloc[test_idx]
```

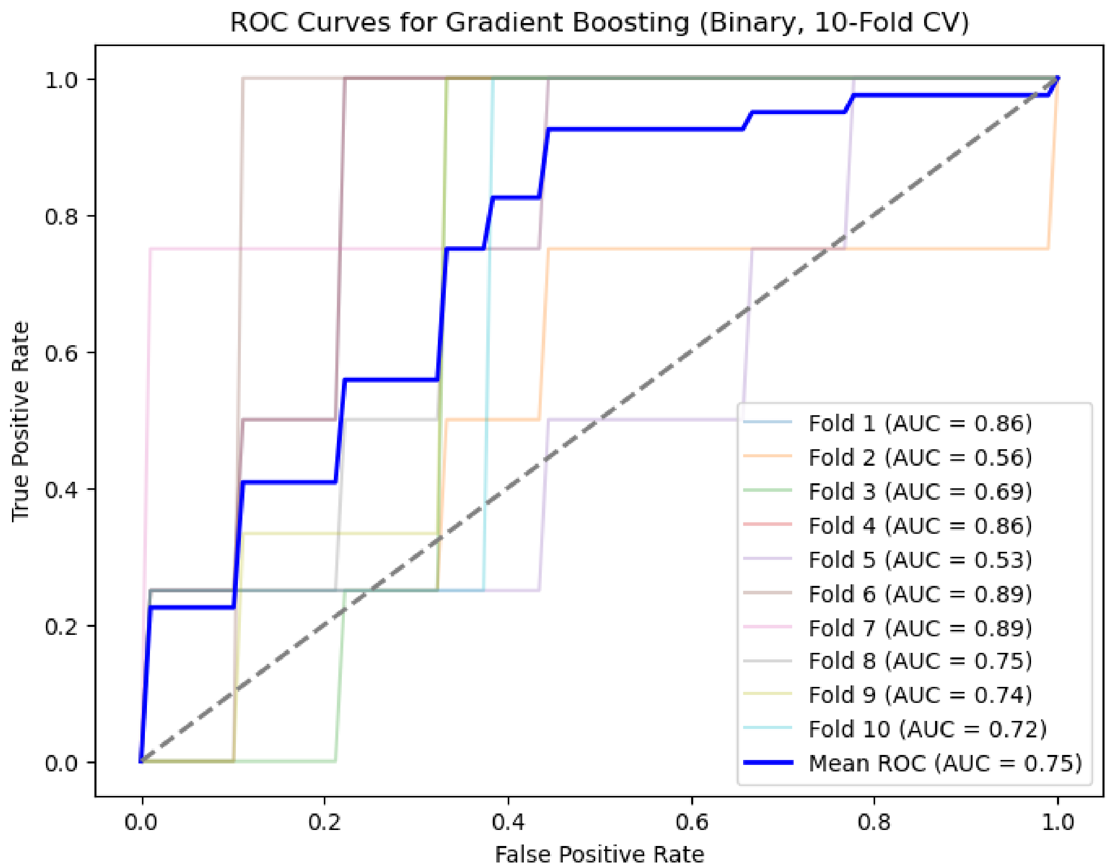
```python
    y_train, y_test = y.iloc[train_idx], y.iloc[test_idx]


    rf_model.fit(X_train, y_train)


    y_proba = rf_model.predict_proba(X_test)[:, 1]


    fpr, tpr, _ = roc_curve(y_test, y_proba)
    roc_auc = auc(fpr, tpr)
    aucs.append(roc_auc)


    tprs.append(np.interp(mean_fpr, fpr, tpr))
    tprs[-1][0] = 0.0


mean_tpr = np.mean(tprs, axis=0)
mean_tpr[-1] = 1.0
mean_auc = auc(mean_fpr, mean_tpr)


plt.figure(figsize=(8, 6))
for i, tpr in enumerate(tprs):
    plt.plot(mean_fpr, tpr, alpha=0.3, label=f"Fold {i+1} (AUC = {aucs[i]:.
 ↪2f})")


plt.plot(mean_fpr, mean_tpr, color="blue", label=f"Mean ROC (AUC = {mean_auc:.
 ↪2f})", lw=2)


plt.plot([0, 1], [0, 1], color="gray", linestyle="--", lw=2)

plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("ROC Curves for Random Forest (Binary, 10-Fold CV)")
plt.legend(loc="lower right")
plt.show()
```



c. Gradient Boosting

[37]:
```
from sklearn.ensemble import GradientBoostingClassifier


gb_model = GradientBoostingClassifier(random_state=42, n_estimators=100,␣
↪learning_rate=0.1)


kf = StratifiedKFold(n_splits=10, shuffle=True, random_state=42)


tprs = []
mean_fpr = np.linspace(0, 1, 100)
aucs = []

for train_idx, test_idx in kf.split(X, y):

    X_train, X_test = X.iloc[train_idx], X.iloc[test_idx]
    y_train, y_test = y.iloc[train_idx], y.iloc[test_idx]
```

```
    gb_model.fit(X_train, y_train)


    y_proba = gb_model.predict_proba(X_test)[:, 1]


    fpr, tpr, _ = roc_curve(y_test, y_proba)
    roc_auc = auc(fpr, tpr)
    aucs.append(roc_auc)


    tprs.append(np.interp(mean_fpr, fpr, tpr))
    tprs[-1][0] = 0.0


mean_tpr = np.mean(tprs, axis=0)
mean_tpr[-1] = 1.0
mean_auc = auc(mean_fpr, mean_tpr)


plt.figure(figsize=(8, 6))
for i, tpr in enumerate(tprs):
    plt.plot(mean_fpr, tpr, alpha=0.3, label=f"Fold {i+1} (AUC = {aucs[i]:.
 ↪2f})")


plt.plot(mean_fpr, mean_tpr, color="blue", label=f"Mean ROC (AUC = {mean_auc:.
 ↪2f})", lw=2)


plt.plot([0, 1], [0, 1], color="gray", linestyle="--", lw=2)

plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("ROC Curves for Gradient Boosting (Binary, 10-Fold CV)")
plt.legend(loc="lower right")
plt.show()
```



7.1. Perform a grid search cross-validation on the Gradient boosting methods, changing the value of the learning rate (0.01 to 0.5) and the number of estimators (50-500). Consider the mean AUC of the folds as the performance measure.

[39]:
```
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import roc_auc_score, make_scorer

gb_model = GradientBoostingClassifier(random_state=42)


param_grid = {
    "learning_rate": np.linspace(0.01, 0.5, 5),
    "n_estimators": [50, 100, 200, 300, 400, 500]
}


cv = StratifiedKFold(n_splits=10, shuffle=True, random_state=42)

auc_scorer = make_scorer(roc_auc_score, needs_proba=True)
```

```
grid_search = GridSearchCV(
    estimator=gb_model,
    param_grid=param_grid,
    scoring=auc_scorer,
    cv=cv,
    verbose=1,
    n_jobs=-1
)


grid_search.fit(X, y)


best_params = grid_search.best_params_
best_auc = grid_search.best_score_

print("Best Parameters:", best_params)
print("Best Mean AUC:", best_auc)
```

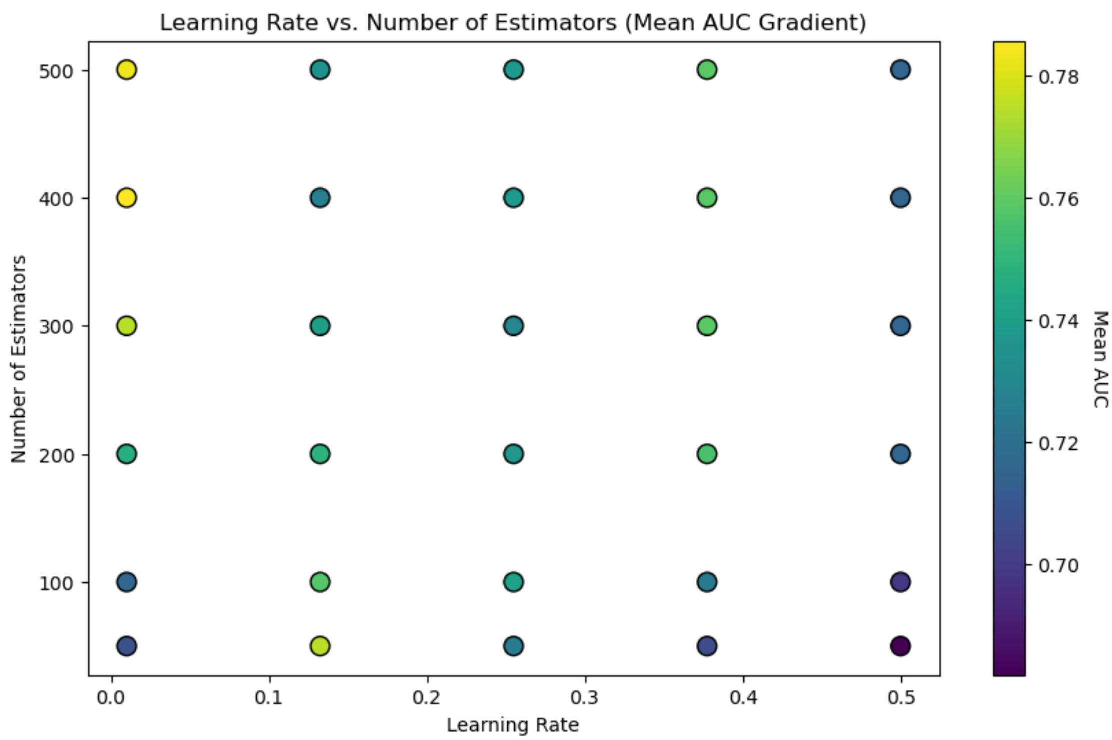
```
C:\Users\marti\anaconda3\Lib\site-packages\sklearn\metrics\_scorer.py:548:
FutureWarning: The `needs_threshold` and `needs_proba` parameter are deprecated
in version 1.4 and will be removed in 1.6. You can either let `response_method`
be `None` or set it to `predict` to preserve the same behaviour.
  warnings.warn(
```

```
Fitting 10 folds for each of 30 candidates, totalling 300 fits
Best Parameters: {'learning_rate': 0.01, 'n_estimators': 400}
Best Mean AUC: 0.7857638888888888
```

7.2. Plot a scatterplot of the learning rate versus the number of estimators, with the mean AUC as the color gradient.

[40]:
```
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd

results = grid_search.cv_results_


results_df = pd.DataFrame({
    "learning_rate": results["param_learning_rate"].data.astype(float),
    "n_estimators": results["param_n_estimators"].data.astype(int),
    "mean_auc": results["mean_test_score"]
})


plt.figure(figsize=(10, 6))
```

```
scatter = plt.scatter(
    results_df["learning_rate"],
    results_df["n_estimators"],
    c=results_df["mean_auc"],
    cmap="viridis",
    s=100,
    edgecolor="k",
)


cbar = plt.colorbar(scatter)
cbar.set_label("Mean AUC", rotation=270, labelpad=15)


plt.xlabel("Learning Rate")
plt.ylabel("Number of Estimators")
plt.title("Learning Rate vs. Number of Estimators (Mean AUC Gradient)")


plt.show()
```



8.1. Perform forward stepwise selection on the dataset. Use the best parameters of the gradient boosting method obtained in **7.1.**.

[41]:
```
from sklearn.model_selection import cross_val_score
from sklearn.ensemble import GradientBoostingClassifier
import numpy as np


best_params = grid_search.best_params_
print("Best Parameters from Grid Search:", best_params)


remaining_features = list(X.columns)
selected_features = []
best_auc = 0
feature_scores = []

while remaining_features:
    print(f"\nRemaining features: {remaining_features}")
    auc_scores = []

    for feature in remaining_features:

        temp_features = selected_features + [feature]


        gb_model = GradientBoostingClassifier(**best_params, random_state=42)
        auc = np.mean(
            cross_val_score(gb_model, X[temp_features], y, scoring="roc_auc",␣
 ↪cv=5)
        )
        auc_scores.append((feature, auc))
        print(f"Feature: {feature}, AUC: {auc:.4f}")

    best_feature, best_feature_auc = max(auc_scores, key=lambda x: x[1])
    print(f"\nBest feature this step: {best_feature}, AUC: {best_feature_auc:.
 ↪4f}")


    if best_feature_auc > best_auc:
        best_auc = best_feature_auc
        selected_features.append(best_feature)
        remaining_features.remove(best_feature)
        feature_scores.append((best_feature, best_auc))
        print(f"Selected Features: {selected_features}")
    else:
        print("No improvement. Stopping selection.")
        break

# Final Results
```

```python
print("\nForward Stepwise Selection Complete.")
print("Selected Features:", selected_features)
print("Feature Scores (Step-by-Step AUC):", feature_scores)
```

```
Best Parameters from Grid Search: {'learning_rate': 0.01, 'n_estimators': 400}

Remaining features: ['bicarbonate_min', 'bicarbonate_max', 'creatinine_min',
'creatinine_max', 'chloride_min', 'chloride_max', 'glucose_min', 'glucose_max',
'hematocrit_min', 'hematocrit_max', 'platelet_min', 'platelet_max',
'potassium_min', 'potassium_max', 'sodium_min', 'sodium_max', 'bun_min',
'bun_max', 'wbc_min', 'wbc_max', 'gender', 'admission_age', 'eth_grp',
'los_icu']
Feature: bicarbonate_min, AUC: 0.6210
Feature: bicarbonate_max, AUC: 0.6234
Feature: creatinine_min, AUC: 0.3644
Feature: creatinine_max, AUC: 0.4189
Feature: chloride_min, AUC: 0.3975
Feature: chloride_max, AUC: 0.5221
Feature: glucose_min, AUC: 0.4932
Feature: glucose_max, AUC: 0.4343
Feature: hematocrit_min, AUC: 0.4650
Feature: hematocrit_max, AUC: 0.4198
Feature: platelet_min, AUC: 0.4857
Feature: platelet_max, AUC: 0.5031
Feature: potassium_min, AUC: 0.4460
Feature: potassium_max, AUC: 0.5042
Feature: sodium_min, AUC: 0.5629
Feature: sodium_max, AUC: 0.5418
Feature: bun_min, AUC: 0.5449
Feature: bun_max, AUC: 0.5248
Feature: wbc_min, AUC: 0.3417
Feature: wbc_max, AUC: 0.5070
Feature: gender, AUC: 0.5566
Feature: admission_age, AUC: 0.7299
Feature: eth_grp, AUC: 0.5746
Feature: los_icu, AUC: 0.5870

Best feature this step: admission_age, AUC: 0.7299
Selected Features: ['admission_age']

Remaining features: ['bicarbonate_min', 'bicarbonate_max', 'creatinine_min',
'creatinine_max', 'chloride_min', 'chloride_max', 'glucose_min', 'glucose_max',
'hematocrit_min', 'hematocrit_max', 'platelet_min', 'platelet_max',
'potassium_min', 'potassium_max', 'sodium_min', 'sodium_max', 'bun_min',
'bun_max', 'wbc_min', 'wbc_max', 'gender', 'eth_grp', 'los_icu']
Feature: bicarbonate_min, AUC: 0.6892
Feature: bicarbonate_max, AUC: 0.7144
Feature: creatinine_min, AUC: 0.6631
```

```
Feature: creatinine_max, AUC: 0.7524
Feature: chloride_min, AUC: 0.6473
Feature: chloride_max, AUC: 0.7414
Feature: glucose_min, AUC: 0.6869
Feature: glucose_max, AUC: 0.7075
Feature: hematocrit_min, AUC: 0.7008
Feature: hematocrit_max, AUC: 0.6277
Feature: platelet_min, AUC: 0.7340
Feature: platelet_max, AUC: 0.6853
Feature: potassium_min, AUC: 0.6454
Feature: potassium_max, AUC: 0.6559
Feature: sodium_min, AUC: 0.7402
Feature: sodium_max, AUC: 0.7191
Feature: bun_min, AUC: 0.6766
Feature: bun_max, AUC: 0.7116
Feature: wbc_min, AUC: 0.6601
Feature: wbc_max, AUC: 0.7748
Feature: gender, AUC: 0.7147
Feature: eth_grp, AUC: 0.7512
Feature: los_icu, AUC: 0.7151

Best feature this step: wbc_max, AUC: 0.7748
Selected Features: ['admission_age', 'wbc_max']

Remaining features: ['bicarbonate_min', 'bicarbonate_max', 'creatinine_min',
'creatinine_max', 'chloride_min', 'chloride_max', 'glucose_min', 'glucose_max',
'hematocrit_min', 'hematocrit_max', 'platelet_min', 'platelet_max',
'potassium_min', 'potassium_max', 'sodium_min', 'sodium_max', 'bun_min',
'bun_max', 'wbc_min', 'gender', 'eth_grp', 'los_icu']
Feature: bicarbonate_min, AUC: 0.7328
Feature: bicarbonate_max, AUC: 0.7440
Feature: creatinine_min, AUC: 0.7382
Feature: creatinine_max, AUC: 0.7392
Feature: chloride_min, AUC: 0.7506
Feature: chloride_max, AUC: 0.7227
Feature: glucose_min, AUC: 0.6593
Feature: glucose_max, AUC: 0.7130
Feature: hematocrit_min, AUC: 0.7138
Feature: hematocrit_max, AUC: 0.6838
Feature: platelet_min, AUC: 0.7399
Feature: platelet_max, AUC: 0.6672
Feature: potassium_min, AUC: 0.7006
Feature: potassium_max, AUC: 0.6862
Feature: sodium_min, AUC: 0.7718
Feature: sodium_max, AUC: 0.7505
Feature: bun_min, AUC: 0.6744
Feature: bun_max, AUC: 0.7280
Feature: wbc_min, AUC: 0.7068
```

```
Feature: gender, AUC: 0.7621
Feature: eth_grp, AUC: 0.7689
Feature: los_icu, AUC: 0.7275

Best feature this step: sodium_min, AUC: 0.7718
No improvement. Stopping selection.

Forward Stepwise Selection Complete.
Selected Features: ['admission_age', 'wbc_max']
Feature Scores (Step-by-Step AUC): [('admission_age', 0.7298786181139122),
('wbc_max', 0.7748190943043884)]
```

8.2. Compare and comment the results from **8.1.** with the features importance obtained through the grid search of queastion **7.1.**.

The forward stepwise selection identified admission_age and wbc_max as the most impactful features based on their incremental improvement in AUC, while feature importance from the Gradient Boosting model provides a global ranking of all features based on their contribution to the model's performance. If these selected features align with highly ranked features in the feature importance analysis, it validates their significance.

1.3 3) Theoretical Questions

1. Consider a dataset where best subset, forward stepwise and backward stepwise selection will be performed. For each of the 3 approaches, we obtain $p + 1$ models, p being the total number of predictors. This means that each approach has a model with 0 predictors, one with 1 predictor, one with 2 predictor, up until one model with p predictors. Answer and justify the following questions:

a) Which of the three models with k, $\forall_{k\in[0,p]}$ predictors has the smallest training RSS?

The best subset selection model with predictors will have the smallest training RSS because it examines all possible combinations of predictors and selects the one that minimizes the training RSS, whereas forward and backward stepwise selection are constrained by their sequential selection processes and may not explore all combinations.

b) Which of the three models with k, $\forall_{k\in[0,p]}$ predictors has the smallest test RSS?

The model with predictors that has the smallest test RSS depends on the data, but generally, no approach consistently guarantees the smallest test RSS as it depends on the balance between bias and variance for each method.

c) Evaluate the following statements with *true* or *false*. Justify your answers.

`i. The predictors in the k-variable model identified by forward stepwise selection are a subse`

True. In forward stepwise selection, predictors are added sequentially at each step, meaning the -variable model is always a subset of the (k+1)-variable model, as no previously selected predictors are removed.

`ii. The predictors in the k-variable model identified by backward stepwise selection are a subs`

False. In backward stepwise selection, predictors are removed sequentially from the full model, so the k-variable model is not necessarily a subset of the (k+1)-variable model. A predictor excluded in the (k+1)-variable model could still remain in the k-variable model.

`iii. The predictors in the k-variable model identified by backward stepwise selection are a sul`

True. In forward stepwise selection, predictors are added sequentially, while in backward stepwise selection, predictors are removed from the full model. Consequently, the k-variable model from backward selection, which is derived by removing predictors, will always include predictors that are part of the (k+1)-variable model from forward selection.

`iv. The predictors in the k-variable model identified by forward stepwise selection are a subs`

False. Forward stepwise selection adds predictors sequentially to build the model, while backward stepwise selection removes predictors starting from the full model. As a result, the k-variable model from forward selection is not guaranteed to be a subset of the (k+1)-variable model from backward selection because the two methods may select different predictors based on their criteria.

`v. The predictors in the k-variable model identified by best subset selection are a subset of`

False. Best subset selection evaluates all possible combinations of predictors for each model size k. Therefore, the predictors in the k-variable model are not necessarily a subset of those in the (k+1)-variable model, as different combinations of predictors might minimize the RSS for different values of k.

2. Ridge regression tends to give similar coefficient values to correlated variables, whereas lasso regression may give substantially different coefficients to correlated variables. This questions explores this property in a simplified setting.

Suppose that $n = 2$, $p = 2$, $x_{11} = x_{12}$, $x_{21} = x_{22}$. Moreover, suppose that $y_1 + y_2 = 0$ and $x_{11} + x_{21} = 0$ and $x_{12} + x_{22} = 0$, meaning that the estimate for the intercept in a least squares, ridge regression, or lasso regression is zero: $\hat{\beta} = 0$.

a) Write the ridge regression optimization problem in this setting.

The ridge regression optimization problem in this setting minimizes the sum of the squared residuals from the least squares loss, along with a regularization term that penalizes the squared values of the coefficients. Specifically, the objective function to minimize is:

2 * (1 - -)^2 + * (^{2} + ^{2})

where the first term represents the squared differences between the observed values and the model predictions, and the second term is the ridge penalty that shrinks the coefficients and to prevent overfitting.

b) Prove that in this setting, the ridge regression coefficient estimates satisfy $\hat{\beta}_1 = \hat{\beta}_2$.

To prove that the ridge regression coefficient estimates satisfy $ _1 = _2 $, we start with the objective function $ J(_1, _2) = 2(1 - _1 - _2)^2 + (_1^2 + _2^2) $. By expanding and taking the partial derivatives with respect to $ _1 $ and $ _2 $, we obtain two symmetric equations:

$$\frac{\partial J}{\partial \beta_1} = -4 + 2(2 + \lambda)\beta_1 + 4\beta_2 = 0$$

and

$$\frac{\partial J}{\partial \beta_2} = -4 + 2(2 + \lambda)\beta_2 + 4\beta_1 = 0$$

Solving these equations shows that $ _1 = _2 $, as the system reduces to:

$$\lambda(\beta_1 - \beta_2) = 0$$

Since $ 0 $, it follows that $ _1 = _2 $, proving the desired result.

c) Write the lasso regression optimization problem in this setting.

The lasso regression optimization problem in this setting can be written as:

$$\min_{\beta_1,\beta_2} \left[2(1 - \beta_1 - \beta_2)^2 + \lambda(|\beta_1| + |\beta_2|)\right]$$

Here, the first term $ 2(1 - _1 - _2)^2 $ represents the sum of squared residuals (least squares loss), and the second term $ (| _1| + | _2|) $ is the lasso penalty that adds the absolute values of the coefficients $ _1 $ and $ _2 $, which encourages sparsity (i.e., setting some coefficients to zero). The parameter $ $ controls the strength of the penalty.

d) Prove that in this setting, the lasso regression coefficients $\hat{\beta}_1$ and $\hat{\beta}_2$ are not unique, meaning that there are many possible solutions to the optimization problem in (c). Describe these solutions.

To prove that in this setting, the lasso regression coefficients $ _1 $ and $ _2 $ are not unique, we analyze the lasso regression optimization problem:

$$\min_{\beta_1,\beta_2} \left[2(1 - \beta_1 - \beta_2)^2 + \lambda(|\beta_1| + |\beta_2|)\right]$$

The presence of the lasso penalty term $ (| _1| + | _2|) $ introduces a non-differentiable point at $ _1 = 0 $ and $ _2 = 0 $. This causes the optimization problem to have multiple solutions. Specifically, the solutions occur when $ _1 = _2 $, and both coefficients can be simultaneously zero, or both can take non-zero values while still satisfying the optimization condition.

For example, when $ _1 = _2 $, the objective function simplifies, and the solution can be obtained by solving for $ _1 $ (and $ _2 $), leading to the non-uniqueness of solutions. This is because the solution path can be constrained to a region where $ _1 $ and $ _2 $ move together, thus generating multiple equivalent solutions that satisfy the same objective function.

These solutions correspond to different values of $ _1 $ and $ _2 $ that are symmetric and fulfill the lasso penalty's constraint. As a result, the optimization problem has many possible solutions, where the coefficients can take different values while maintaining equivalence in terms of the overall penalty and loss.

3. Draw an example of a partition of two-dimensional feature space that could result from recursive binary splitting. Your example should contain at least six regions. Draw a decision tree corresponding to this partition. Be sure to label all aspects of your figures, including the regions R1, R2,…, the cutpoints t1, t2,…, and so forth.

If you prefer you can draw it by hand or in any software and use a scan of it.

4. In 2 dimensions, a linear decision boundary takes the form $\beta_0 + \beta_1 X_1 + \beta_2 X_2 = 0$. Consider a nn-linear decision boundary:

a) Sketch the curve

$$(1 + X_1)^2 + (2 - X_2)^2 = 4$$

Additionally, indicate on your sketch the set of points that verify the condition

$$(1 + X_1)^2 + (2 - X_2)^2 > 4$$

and the condition

$$(1 + X_1)^2 + (2 - X_2)^2 \leq 4$$

[ ]:

b) Suppose that a classifier assigns an observation to the blue class if $(1 + X_1)^2 + (2 - X_2)^2 > 4$ and to the red class otherwise. To what class are the following observations classified? (0,0), (-1,1), (2,2), (3,8)

c) Prove that while the decision boundary in (b) is not linear in terms of X_1 and X_2, it is linear in terms of X_1, X_1^2, X_2, and X_2^2.

2 4) Laboratory Questions

What are the advantages and disadvantages of relational dabases versus graph databases, and when should one type be preferred over the other?