Project_IAU

November 5, 2025

1 Import libraries

[750]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
import scipy.stats as stats
from scipy.stats import shapiro, ttest_ind, mannwhitneyu, levene, pearsonr
from statsmodels.stats.power import TTestIndPower
from sklearn.model_selection import train_test_split
from pandas.api.types import CategoricalDtype
from sklearn.preprocessing import StandardScaler , RobustScaler ,␣
↪PowerTransformer, QuantileTransformer

#preprocesing
from sklearn.feature_selection import mutual_info_classif, chi2
from sklearn.ensemble import RandomForestClassifier
from sklearn.preprocessing import MinMaxScaler
```

[751]:
```
#warnings fix
warnings.filterwarnings("ignore", category=UserWarning, module="IPython")
plt.rcParams['font.family'] = 'DejaVu Sans'   # Change the font globally
plt.tight_layout()  # Ensure layout adjustments
```

```
<Figure size 640x480 with 0 Axes>
```

2 Load datasets

[752]:
```
patient_df = pd.read_csv('132/patient.csv', sep = '\t')
station_df = pd.read_csv('132/station.csv', sep= '\t')
observation_df = pd.read_csv('132/observation.csv', sep = '\t')
```

[753]:
```
patient_df.head()
```

[753]:
```
                                company  \
0
```

```
1  Gray, Cunningham and Morales
2                        Walter
3
4                 Munari s.r.l.

                               current_location              ssn  \
0      (Decimal('32.168477'), Decimal('9.804478'))      302-73-9054
1     (Decimal('-80.289857'), Decimal('2.308813'))      499-92-6793
2   (Decimal('63.5169555'), Decimal('-48.876252'))      925-81-9055
3   (Decimal('-71.015803'), Decimal('140.978474'))      175-19-6965
4  (Decimal('-58.1525245'), Decimal('-120.099037'))  FRSMRL26C50L167Z

               name                  mail  user_id  residence  \
0                   takuma47@gmail.com     1770        NaN
1  Nicholas Campbell     curtis06@yahoo.com      946        NaN
2        Raissa Rose  junkgisbert@yahoo.de     2010        NaN
3                   morimomoko@gmail.com     1100        NaN
4  Eraldo Anguillara   bpergolesi@poste.it     1247        NaN

              username   birthdate  \
0            snakajima  1937-03-07
1           benjamin02  1993-05-15
2             jkoehler         NaN
3        yamaguchikana  2000-08-20
4  guglielmomicheletti         NaN

                                          address          registration  \
0                                       27 2 7            2020-08-15
1  0515 Angela Run\r\nPort Thomasberg, GU 35535            2018-11-30
2     Louise-Stey-Platz 79\r\n88420 Bremervörde  05/09/2025, 00:00:00
3                      26 5 4     985  10/21/2022, 00:00:00
4                                           NaN            2024-11-26

  blood_group  station_ID
0          B-         464
1          A-         109
2          O-         462
3          B-         191
4          B+         588
```

[754]:
```
station_df.head()
```

[754]:
```
            QoS code  latitude              revision  longitude      station
0          good   JP  36.00000            2020-11-25  139.55722      Okegawa
1     excellent   IN  11.93381  05/24/2021, 00:00:00   79.82979   Puducherry
2   maintenance   DE  52.21099            2022-05-10    7.02238       Gronau
3     excellent   CN  41.09822            2018-01-23  120.74792      Nanpiao
```

```
4         good   US  33.54428           08 Jun 2024  -84.23381  Stockbridge
```

[755]:
```
observation_df.head()
```

[755]:
```
         SpO          HR          PI          RR        EtCO         FiO  \
0  97.538229  87.194745  11.225419  14.812012  42.113735  33.852538
1  97.933271  80.787303  11.730935  14.964972  39.537692  65.326035
2  98.209983  79.733895  12.839449  14.840668  39.758706  53.925230
3  98.202790  86.156903  11.204152  14.523288  43.448577  35.227704
4  97.951933  78.966258  13.691758  14.992054  39.722280  35.005559

          PRV          BP  Skin Temperature  Motion/Activity index  …  \
0  144.504405  100.455727         35.961920              10.302567  …
1  110.615787  102.133386         36.274352               8.975704  …
2  107.208040  104.036654         35.583851               7.653790  …
3  143.282224  105.723603         36.463180               8.795732  …
4  118.524021   98.996494         35.080937               8.388887  …

         CO  Blood Flow Index  PPG waveform features  Signal Quality Index  \
0  4.022852         58.317397              49.143701             42.399816
1  4.002043         70.127865              15.557799             46.078137
2  4.001451         76.139163              53.879956             41.525607
3  4.015162         49.461570              58.701159             36.535021
4  4.001110         47.065823              52.338305             29.506008

   Respiratory effort  O  extraction ratio        SNR  oximetry   latitude  \
0           46.497869                 0.289012  39.334620       1.0  49.183239
1           53.351208                 0.290879  26.006709       0.0  33.544280
2           52.124182                 0.263171  31.890829       1.0 -27.505780
3           50.342830                 0.256780  30.721375       1.0  37.656390
4           39.480811                 0.276094  38.214856       0.0  51.202190

    longitude
0   15.454273
1  -84.233810
2  153.102360
3  126.835000
4    7.360270

[5 rows x 23 columns]
```

lets have a look at the attributes

[756]:
```
observation_df.columns
```

[756]:
```
Index(['SpO ', 'HR', 'PI', 'RR', 'EtCO ', 'FiO ', 'PRV', 'BP',
       'Skin Temperature', 'Motion/Activity index', 'PVI', 'Hb level', 'SV',
       'CO', 'Blood Flow Index', 'PPG waveform features',
       'Signal Quality Index', 'Respiratory effort', 'O extraction ratio',
       'SNR', 'oximetry', 'latitude', 'longitude'],
      dtype='object')
```

[757]:
```python
station_df.columns
```

[757]:
```
Index(['QoS', 'code', 'latitude', 'revision', 'longitude', 'station'],
dtype='object')
```

[758]:
```python
patient_df.columns
```

[758]:
```
Index(['company', 'current_location', 'ssn', 'name', 'mail', 'user_id',
       'residence', 'username', 'birthdate', 'address', 'registration',
       'blood_group', 'station_ID'],
      dtype='object')
```

[759]:
```python
for column in observation_df.columns:
    if column in station_df.columns:
        print ('observation_df and station_df share column :' + str(column) )
    if column in patient_df.columns:
        print ('observation_df and patient_df share column :' + str(column) )

for column in patient_df.columns:
    if column in station_df.columns:
        print ('station_df and patient_df share column :' + str(column) )
```

```
observation_df and station_df share column :latitude
observation_df and station_df share column :longitude
```

we can see that observation and station dataframes might be joinable via coordinates but after manual revision we can see that patient.station_ID will probably map to station ids

before joining the datasets, lets perform some basic EDA

3 Fáza 1

3.1 1.1 Základný opis dát spolu s ich charakteristikami

3.1.1 A) Analyza struktur dat ako subory + zaznamy

station_df

[760]:
```python
station_df.head()
```

[760]:
```
           QoS code  latitude              revision  longitude      station
0         good   JP  36.00000            2020-11-25  139.55722      Okegawa
1    excellent   IN  11.93381  05/24/2021, 00:00:00   79.82979   Puducherry
2  maintenance   DE  52.21099            2022-05-10    7.02238       Gronau
3    excellent   CN  41.09822            2018-01-23  120.74792      Nanpiao
4         good   US  33.54428           08 Jun 2024  -84.23381  Stockbridge
```

[761]:
```
station_df.shape
```

[761]:
```
(703, 6)
```

[762]:
```
station_df.columns
```

[762]:
```
Index(['QoS', 'code', 'latitude', 'revision', 'longitude', 'station'],
dtype='object')
```

[763]:
```
station_df.dtypes
```

[763]:
```
QoS             object
code            object
latitude       float64
revision        object
longitude      float64
station         object
dtype: object
```

[764]:
```
#2 nas, not bad
station_df.isna().sum()
```

[764]:
```
QoS            0
code           2
latitude       0
revision       0
longitude      0
station        0
dtype: int64
```

[765]:
```
station_df[station_df['code'].isna()]
```

[765]:
```
             QoS code  latitude              revision  longitude    station
274  maintenance  NaN -21.98333  02/23/2016, 00:00:00   16.91667  Okahandja
318         good  NaN -21.98333           06 Dec 2021   16.91667  Okahandja
```

[766]:
```
#mby there is valid code for Okahandja?
station_df[station_df['station'] == 'Okahandja']
#there is not :(
```

[766]:
```
             QoS code  latitude              revision  longitude    station
274  maintenance  NaN -21.98333  02/23/2016, 00:00:00   16.91667  Okahandja
318         good  NaN -21.98333           06 Dec 2021   16.91667  Okahandja
```

[767]:
```
station_df.nunique()
```

[767]:
```
QoS             4
code           98
```

```
latitude     498
revision     683
longitude    497
station      498
dtype: int64
```

[768]:
```
#prob useless
station_df.describe()
```

[768]:
```
         latitude   longitude
count  703.000000  703.000000
mean    28.699220   16.946846
std     24.406067   70.122555
min    -44.396720 -156.474320
25%     14.354040  -14.410810
50%     36.650000   13.321270
75%     47.432685   71.552920
max     65.848110  171.253640
```

patient df

[769]:
```
patient_df.head()
```

[769]:
```
                        company  \
0
1  Gray, Cunningham and Morales
2                        Walter
3
4                 Munari s.r.l.

                                   current_location               ssn  \
0      (Decimal('32.168477'), Decimal('9.804478'))       302-73-9054
1     (Decimal('-80.289857'), Decimal('2.308813'))       499-92-6793
2   (Decimal('63.5169555'), Decimal('-48.876252'))       925-81-9055
3   (Decimal('-71.015803'), Decimal('140.978474'))       175-19-6965
4  (Decimal('-58.1525245'), Decimal('-120.099037'))  FRSMRL26C50L167Z

               name                  mail  user_id  residence  \
0                      takuma47@gmail.com     1770        NaN
1  Nicholas Campbell    curtis06@yahoo.com      946        NaN
2        Raissa Rose  junkgisbert@yahoo.de     2010        NaN
3                     morimomoko@gmail.com     1100        NaN
4  Eraldo Anguillara   bpergolesi@poste.it     1247        NaN

            username   birthdate  \
0          snakajima  1937-03-07
1         benjamin02  1993-05-15
2           jkoehler         NaN
```

```
3        yamaguchikana  2000-08-20
4  guglielmomicheletti         NaN

                                         address          registration  \
0                                    27  2 7             2020-08-15
1  0515 Angela Run\r\nPort Thomasberg, GU 35535            2018-11-30
2     Louise-Stey-Platz 79\r\n88420 Bremervörde  05/09/2025, 00:00:00
3                       26  5 4     985  10/21/2022, 00:00:00
4                                            NaN            2024-11-26

  blood_group  station_ID
0          B-         464
1          A-         109
2          O-         462
3          B-         191
4          B+         588
```

[770]:
```
patient_df.shape
```

[770]:
```
(2197, 13)
```

[771]:
```
patient_df.columns
```

[771]:
```
Index(['company', 'current_location', 'ssn', 'name', 'mail', 'user_id',
       'residence', 'username', 'birthdate', 'address', 'registration',
       'blood_group', 'station_ID'],
      dtype='object')
```

[772]:
```
patient_df.dtypes
```

[772]:
```
company              object
current_location     object
ssn                  object
name                 object
mail                 object
user_id               int64
residence           float64
username             object
birthdate            object
address              object
registration         object
blood_group          object
station_ID            int64
dtype: object
```

[773]:
```
patient_df.isna().sum()
#residence is full NaN so it will be dropped, birthdate and address probably␣
 ↪too,
#current location needs to be processed
```

```
[773]: company                0
       current_location     110
       ssn                    0
       name                   0
       mail                   0
       user_id                0
       residence           2197
       username               0
       birthdate            989
       address              330
       registration           0
       blood_group            0
       station_ID             0
       dtype: int64
```

```
[774]: patient_df.nunique()
       #many unique values
```

```
[774]: company             1989
       current_location    2087
       ssn                 2197
       name                2131
       mail                2192
       user_id             1407
       residence              0
       username            2175
       birthdate           1189
       address             1867
       registration        1987
       blood_group            8
       station_ID           677
       dtype: int64
```

```
[775]: patient_df.describe()
       #also useless
```

```
[775]:            user_id  residence   station_ID
       count  2197.000000        0.0  2197.000000
       mean   1105.308603        NaN   348.892126
       std     644.728055        NaN   205.367454
       min       0.000000        NaN     0.000000
       25%     547.000000        NaN   172.000000
       50%    1118.000000        NaN   340.000000
       75%    1668.000000        NaN   536.000000
       max    2196.000000        NaN   702.000000
```

observation df

```
[776]: observation_df.head()
```

```
[776]:         SpO         HR         PI         RR       EtCO        FiO  \
0  97.538229  87.194745  11.225419  14.812012  42.113735  33.852538
1  97.933271  80.787303  11.730935  14.964972  39.537692  65.326035
2  98.209983  79.733895  12.839449  14.840668  39.758706  53.925230
3  98.202790  86.156903  11.204152  14.523288  43.448577  35.227704
4  97.951933  78.966258  13.691758  14.992054  39.722280  35.005559

          PRV          BP  Skin Temperature  Motion/Activity index  …  \
0  144.504405  100.455727         35.961920              10.302567  …
1  110.615787  102.133386         36.274352               8.975704  …
2  107.208040  104.036654         35.583851               7.653790  …
3  143.282224  105.723603         36.463180               8.795732  …
4  118.524021   98.996494         35.080937               8.388887  …

         CO  Blood Flow Index  PPG waveform features  Signal Quality Index  \
0  4.022852         58.317397              49.143701             42.399816
1  4.002043         70.127865              15.557799             46.078137
2  4.001451         76.139163              53.879956             41.525607
3  4.015162         49.461570              58.701159             36.535021
4  4.001110         47.065823              52.338305             29.506008

   Respiratory effort  O extraction ratio        SNR  oximetry   latitude  \
0           46.497869            0.289012  39.334620       1.0  49.183239
1           53.351208            0.290879  26.006709       0.0  33.544280
2           52.124182            0.263171  31.890829       1.0 -27.505780
3           50.342830            0.256780  30.721375       1.0  37.656390
4           39.480811            0.276094  38.214856       0.0  51.202190

    longitude
0   15.454273
1  -84.233810
2  153.102360
3  126.835000
4    7.360270

[5 rows x 23 columns]
```

```
[777]: observation_df.shape
```

```
[777]: (12177, 23)
```

```
[778]: observation_df.columns
```

```
[778]: Index(['SpO ', 'HR', 'PI', 'RR', 'EtCO ', 'FiO ', 'PRV', 'BP',
              'Skin Temperature', 'Motion/Activity index', 'PVI', 'Hb level', 'SV',
              'CO', 'Blood Flow Index', 'PPG waveform features',
              'Signal Quality Index', 'Respiratory effort', 'O  extraction ratio',
              'SNR', 'oximetry', 'latitude', 'longitude'],
             dtype='object')
```

```
[779]: observation_df.dtypes
```

```
[779]: SpO                         float64
       HR                           float64
       PI                           float64
       RR                           float64
       EtCO                        float64
       FiO                         float64
       PRV                          float64
       BP                           float64
       Skin Temperature             float64
       Motion/Activity index        float64
       PVI                          float64
       Hb level                     float64
       SV                           float64
       CO                           float64
       Blood Flow Index             float64
       PPG waveform features        float64
       Signal Quality Index         float64
       Respiratory effort           float64
       O  extraction ratio         float64
       SNR                          float64
       oximetry                     float64
       latitude                     float64
       longitude                    float64
       dtype: object
```

```
[780]: observation_df.isna().sum()
       #great
```

```
[780]: SpO                         0
       HR                           0
       PI                           0
       RR                           0
       EtCO                        0
       FiO                         0
       PRV                          0
       BP                           0
       Skin Temperature             0
       Motion/Activity index        0
```

```
PVI                      0
Hb level                 0
SV                       0
CO                       0
Blood Flow Index         0
PPG waveform features    0
Signal Quality Index     0
Respiratory effort       0
O  extraction ratio     0
SNR                      0
oximetry                 0
latitude                 0
longitude                0
dtype: int64
```

[781]:
```
observation_df.nunique()
#makes sense, only oximetry, latitude and longitude are not completely unique
```

[781]:
```
SpO                     11997
HR                       11997
PI                       11997
RR                       11997
EtCO                    11997
FiO                     11997
PRV                      11997
BP                       11997
Skin Temperature         11997
Motion/Activity index    11997
PVI                      11997
Hb level                 11997
SV                       11997
CO                       11997
Blood Flow Index         11997
PPG waveform features    11997
Signal Quality Index     11997
Respiratory effort       11997
O  extraction ratio     11997
SNR                      11997
oximetry                     2
latitude                   498
longitude                  497
dtype: int64
```

[782]:
```
observation_df.describe()
```

[782]:
```
              SpO            HR            PI            RR          EtCO  \
count  12177.000000  12177.000000  12177.000000  12177.000000  12177.000000
```

```
mean     97.336001    83.397242    10.360642    16.158948    40.235152
std       0.657577     7.609815     2.417855     1.398210     1.715679
min      95.000000    60.000000     0.200000    12.000000    35.000000
25%      96.895657    77.573676     8.800161    15.044708    38.749846
50%      97.332851    84.323757    10.365288    15.979021    40.531056
75%      97.776356    89.763115    11.893853    17.393451    41.590048
max     100.000000   100.000000    20.000000    20.000000    45.000000

               FiO          PRV           BP  Skin Temperature  \
count 12177.000000 12177.000000 12177.000000      12177.000000
mean     58.821759   117.675964   104.591413         35.426048
std      12.119443    21.841513     4.088282          0.619283
min      21.000000    20.000000    90.000000         33.000000
25%      49.328258   103.101631   101.857377         35.007462
50%      59.402365   117.695370   104.604980         35.424762
75%      68.437184   132.088845   107.321633         35.845164
max     100.000000   200.000000   120.000000         38.000000

      Motion/Activity index  …           CO  Blood Flow Index  \
count          12177.000000  … 12177.000000      12177.000000
mean               9.436818  …     4.078126         52.640590
std                0.998907  …     0.222547         13.127091
min                5.652322  …     4.000000          0.000000
25%                8.766904  …     4.000762         43.996467
50%                9.432476  …     4.007395         52.709829
75%               10.105665  …     4.064212         61.440013
max               13.997052  …     8.000000        100.000000

      PPG waveform features  Signal Quality Index  Respiratory effort  \
count          12177.000000          12177.000000        12177.000000
mean              46.734247             47.572094           49.788653
std               13.374194             13.487056           13.006681
min                0.000000              0.000000            0.000000
25%               37.650597             38.396055           40.992562
50%               46.733166             47.810036           49.742898
75%               55.671672             56.736043           58.630016
max              100.000000            100.000000          100.000000

      O  extraction ratio          SNR     oximetry     latitude  \
count        12177.000000 12177.000000 12177.000000 12177.000000
mean             0.249557    29.994576     0.597602    28.701943
std              0.028947     5.765251     0.490401    24.402668
min              0.200000    20.000000     0.000000   -44.396720
25%              0.224466    24.978691     0.000000    14.082300
50%              0.249072    30.094799     1.000000    36.650000
75%              0.274733    34.961220     1.000000    47.484440
max              0.300000    40.000000     1.000000    65.848110
```

```
          longitude
count  12177.000000
mean      17.028640
std       70.059129
min     -156.474320
25%      -13.235600
50%       13.321270
75%       71.577370
max      171.253640

[8 rows x 23 columns]
```

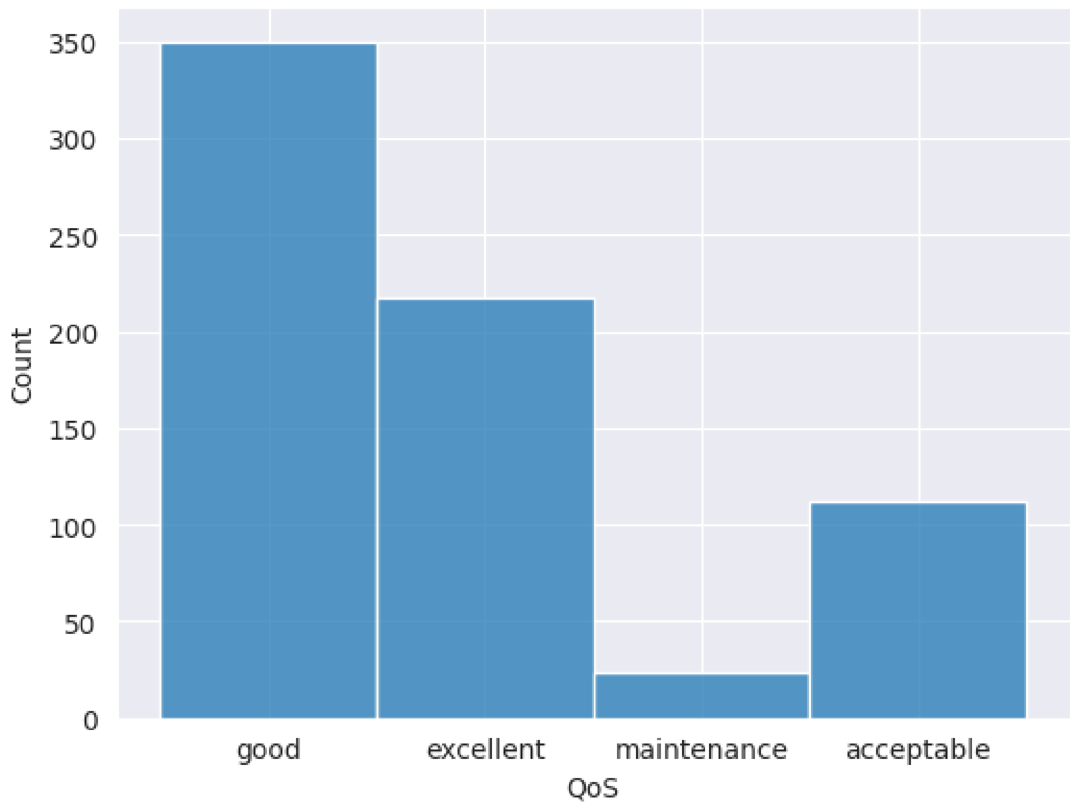
3.1.2 B) Analýza jednotlivých atribútov

[783]:
```
#Qos(station_df)
station_df['QoS'].unique().tolist()
```

[783]:
```
['good', 'excellent', 'maintenance', 'acceptable']
```

[784]:
```
sns.histplot(station_df['QoS'])
```

[784]:
```
<Axes: xlabel='QoS', ylabel='Count'>
```



[785]:
```
#for exact nums
station_df['QoS'].value_counts()
```

[785]:
```
QoS
good           350
excellent      217
acceptable     112
maintenance     24
Name: count, dtype: int64
```

[786]:
```
station_df['QoS'].isna().sum()
```

[786]:
```
np.int64(0)
```

[787]:
```
#latitude (from both station_df and observation_df)
print (station_df['latitude'].min(), observation_df['latitude'].min())
print (station_df['latitude'].max(), observation_df['latitude'].max())
#the min and the max are both realistic values, from -180 to 180

set(station_df['latitude']) == set(observation_df['latitude'])
#every station is included in observation by latitude
```

```
-44.39672 -44.39672
65.84811 65.84811
```

[787]:
```
True
```

[788]:
```
#longitude (from both station_df and observation_df)
print (station_df['longitude'].min(), observation_df['longitude'].min())
print (station_df['longitude'].max(), observation_df['longitude'].max())
#the min and the max are both realistic values, from -180 to 180

set(station_df['longitude']) == set(observation_df['longitude'])
#every station is included by longitude also

#this could be checked with patient -> current location but that needs␣
 ↪preprocessing in further steps
```

```
-156.47432 -156.47432
171.25364 171.25364
```

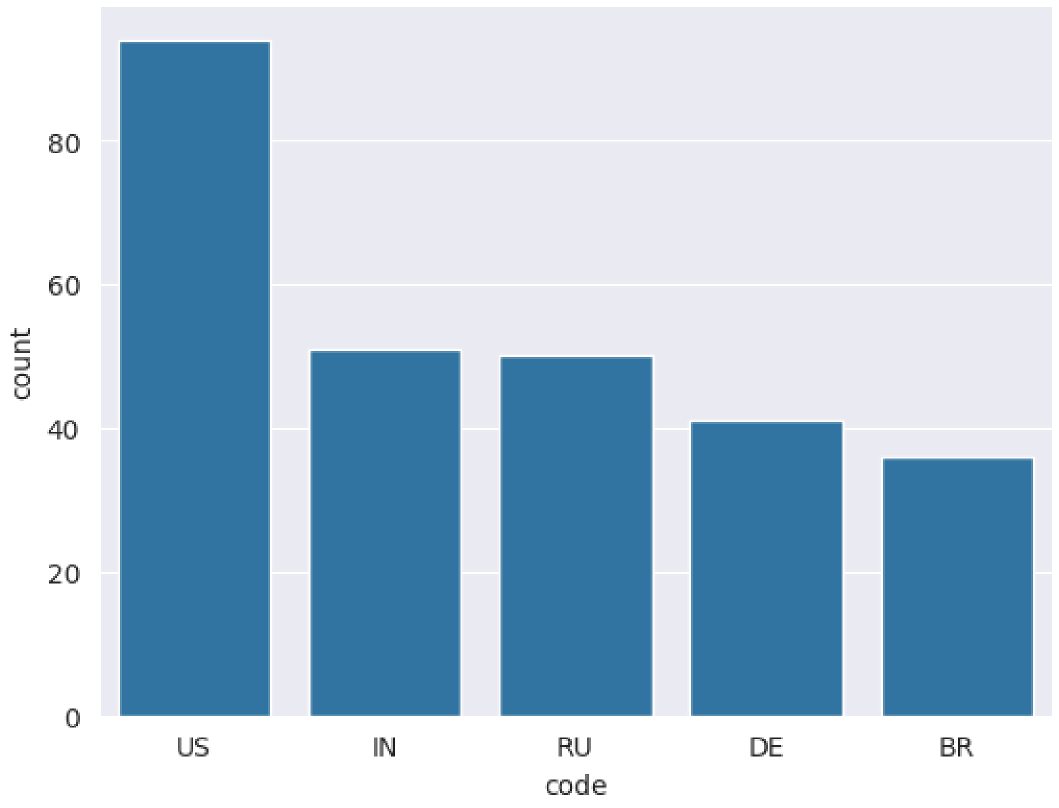
[788]:
```
True
```

[789]:
```
#Code (station_df)
station_df['code'].value_counts()
```

```
[789]: code
       US     94
       IN     51
       RU     50
       DE     41
       BR     36
              ..
       DK      1
       CU      1
       GH      1
       AF      1
       AT      1
       Name: count, Length: 98, dtype: int64
```

```
[790]: #top 5
       top5 = station_df['code'].value_counts().head(5).reset_index()
       top5.columns = ['code', 'count']

       sns.barplot(x='code', y='count', data=top5)
```

```
[790]: <Axes: xlabel='code', ylabel='count'>
```

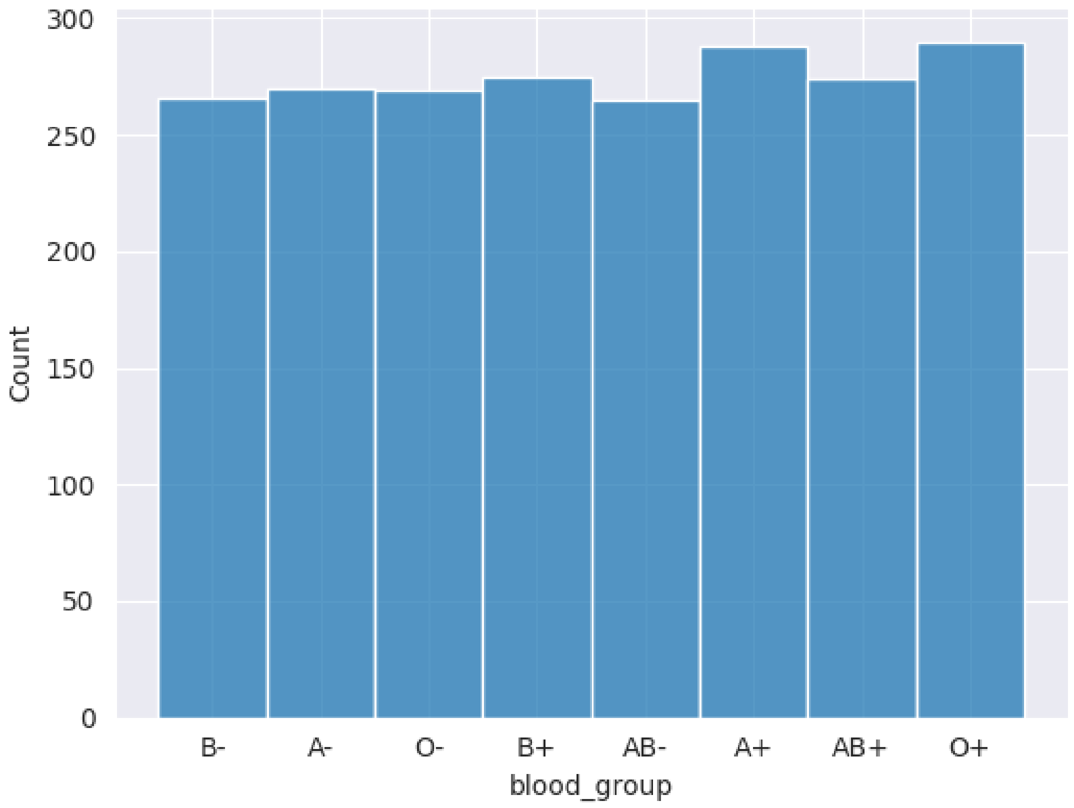


[791]:
```
#Blood group (patient_df)
patient_df['blood_group'].unique().tolist()
#All blood groups are represented
```

[791]:
```
['B-', 'A-', 'O-', 'B+', 'AB-', 'A+', 'AB+', 'O+']
```

[792]:
```
sns.histplot(patient_df['blood_group'])
#not that big of a range
```

[792]:
```
<Axes: xlabel='blood_group', ylabel='Count'>
```



[793]:
```
patient_df['blood_group'].value_counts()
```

[793]:
```
blood_group
O+     290
A+     288
B+     275
AB+    274
A-     270
O-     269
B-     266
```

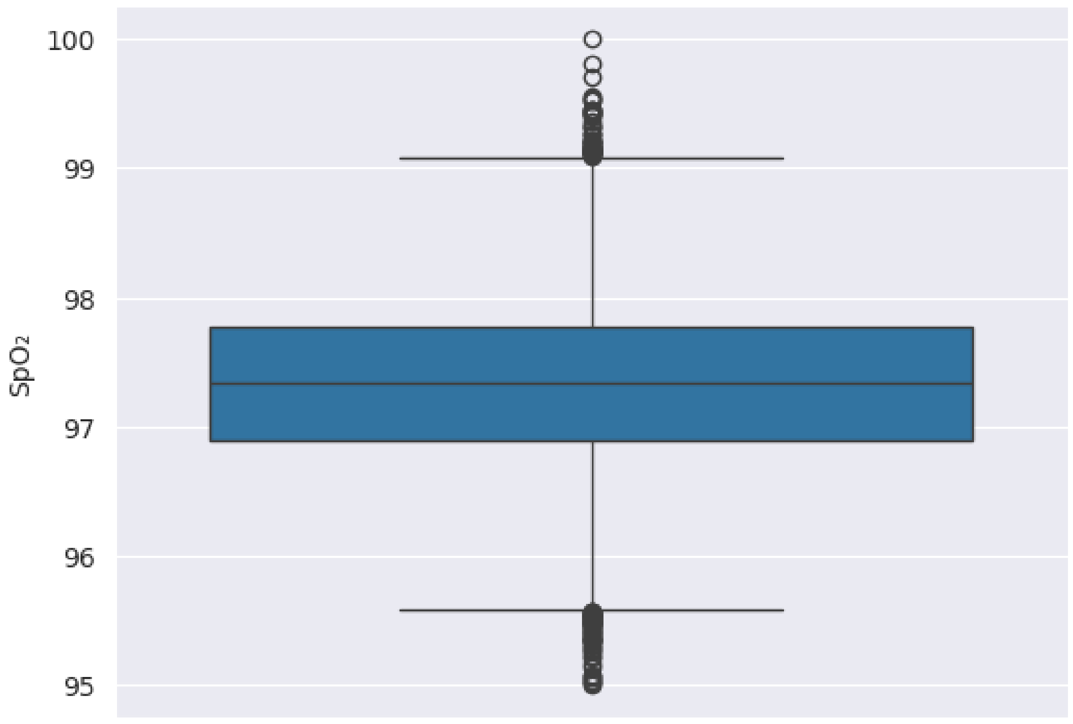
```
AB-    265
Name: count, dtype: int64
```

[794]:
```
patient_df['blood_group'].isna().sum()
#great
```

[794]:
```
np.int64(0)
```

[795]:
```
# SpO2
sns.boxplot(y = observation_df['SpO '])
```

[795]:
```
<Axes: ylabel='SpO '>
```

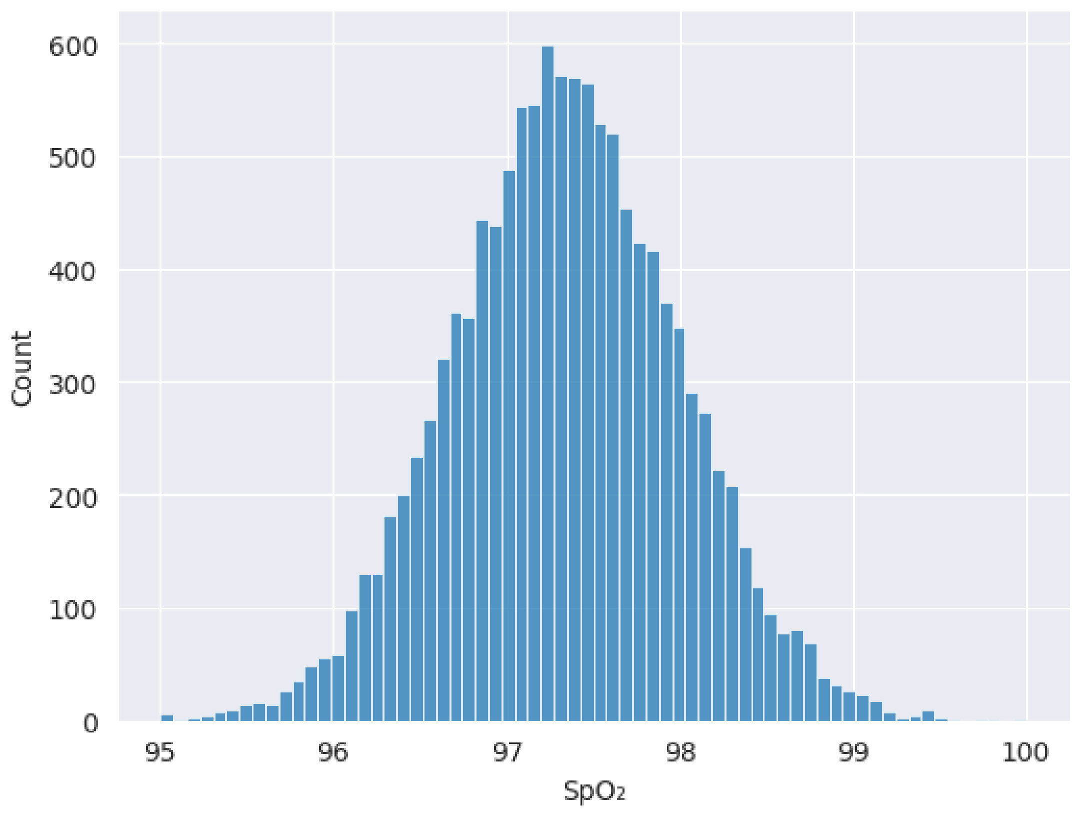


[796]:
```
#just to have the exact range
observation_df['SpO '].min(), observation_df['SpO '].max()
#realistic values
```

[796]:
```
(np.float64(95.0), np.float64(100.0))
```

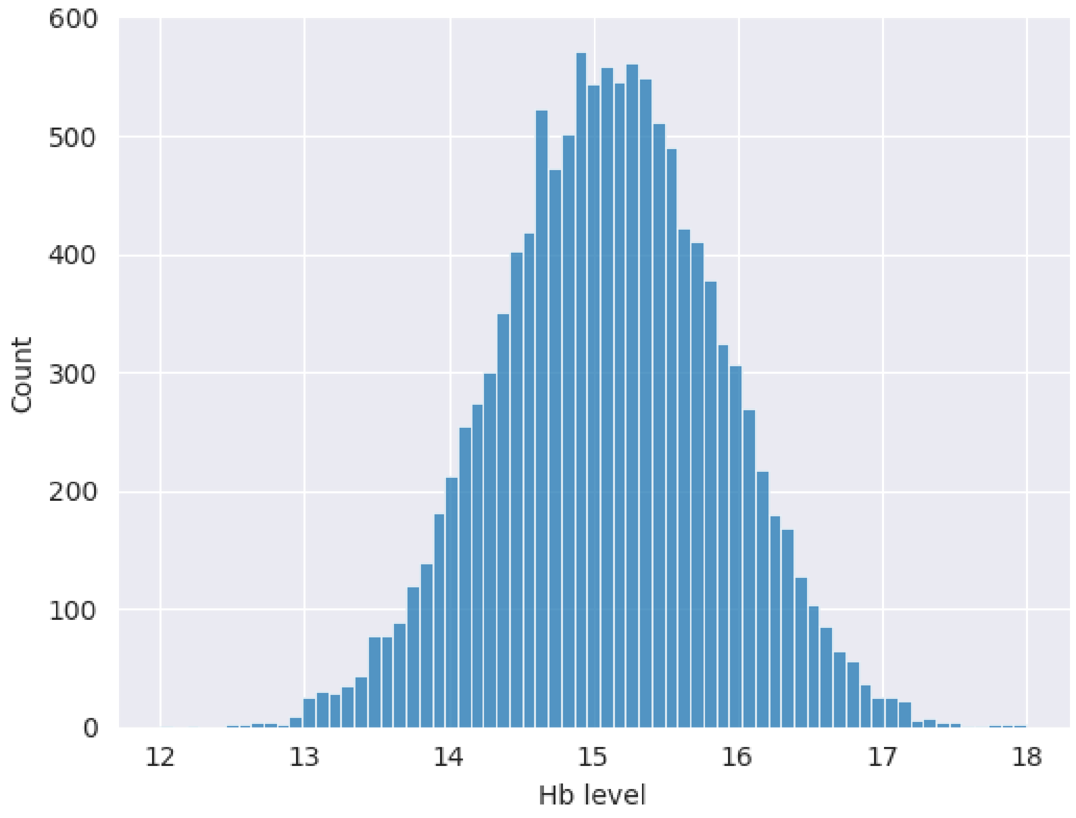
[797]:
```
sns.histplot(observation_df['SpO '])
#normal distribution
```

[797]:
```
<Axes: xlabel='SpO ', ylabel='Count'>
```



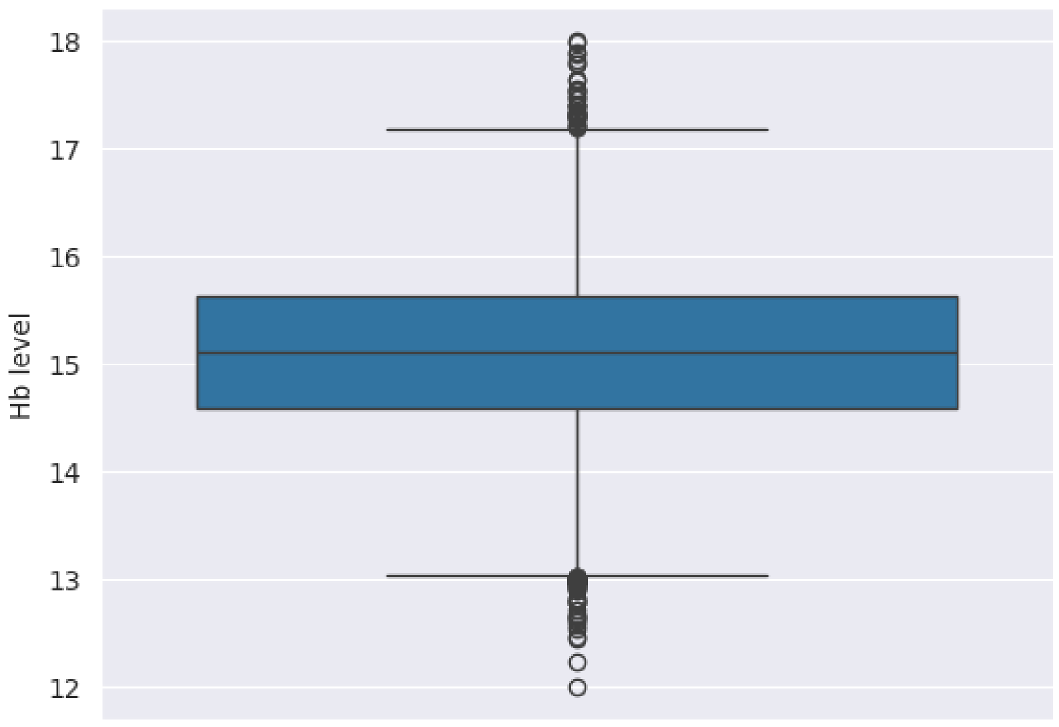
```
[798]: #Hemoglobin (Observation_df)
       sns.histplot(observation_df['Hb level'])
       #pretty normal, realistic values
```

```
[798]: <Axes: xlabel='Hb level', ylabel='Count'>
```

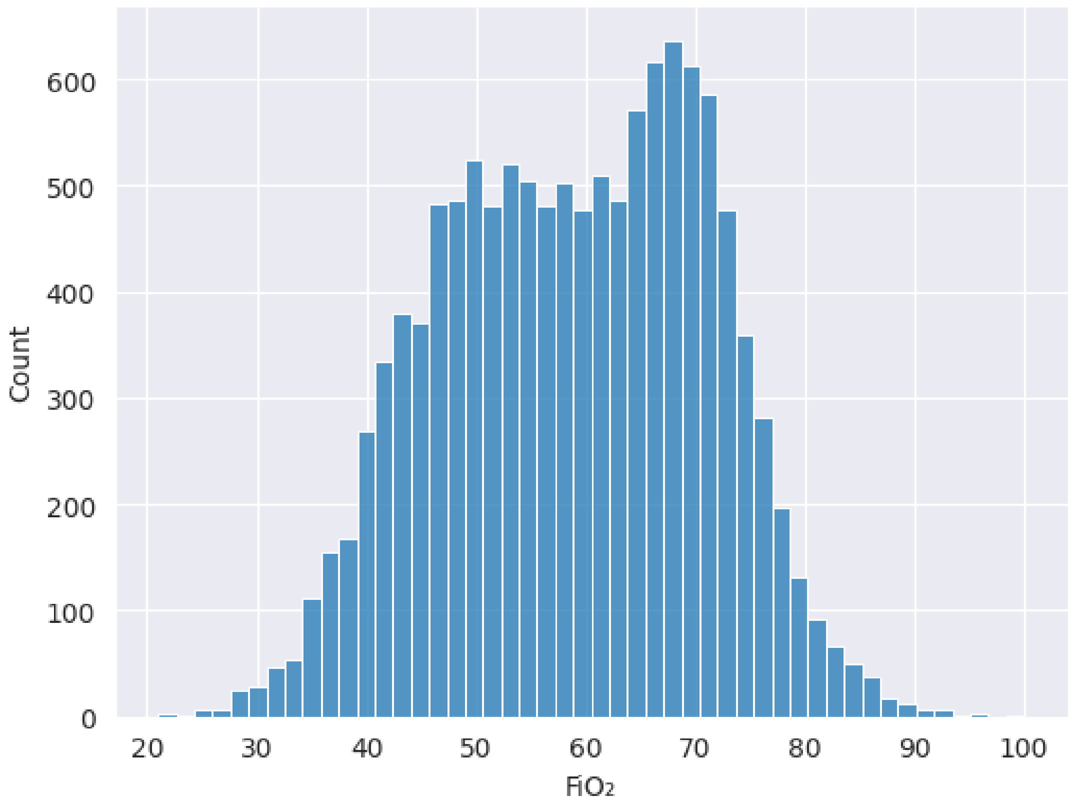


```
[799]: sns.boxplot(y = observation_df['Hb level'])
```

```
[799]: <Axes: ylabel='Hb level'>
```

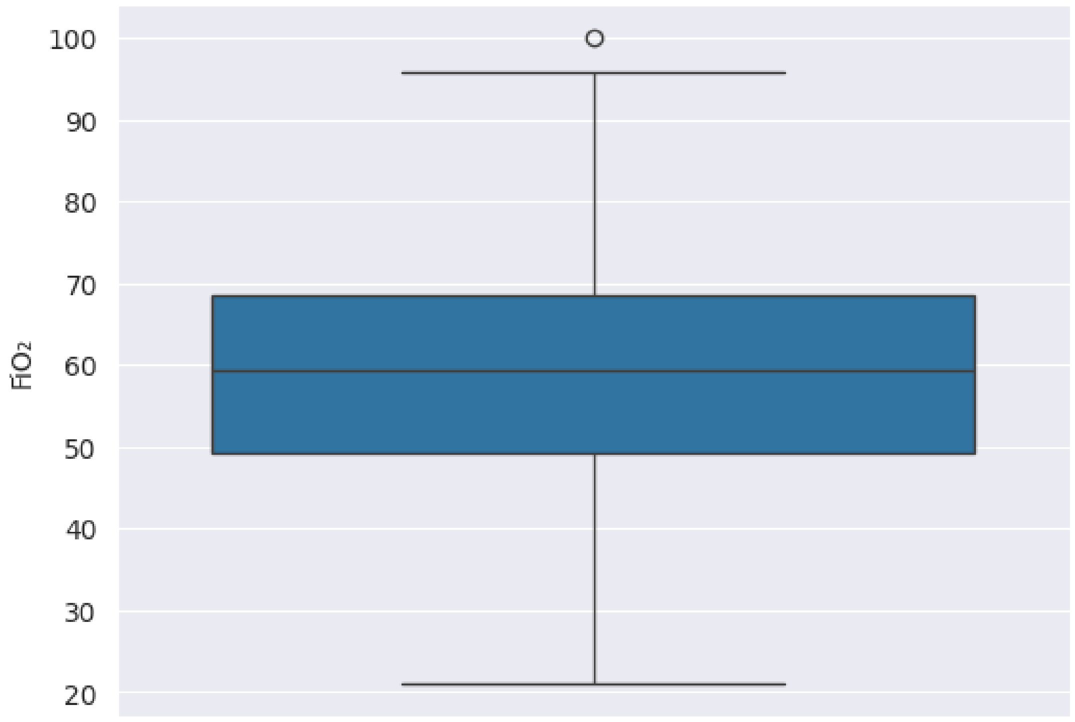


```
[800]: #exact range
       observation_df['Hb level'].min(), observation_df['Hb level'].max()

[800]: (np.float64(12.0), np.float64(18.0))

[801]: #Fio (Observation_df)
       sns.histplot(observation_df['FiO '])
       #not that normal, slight skew to the right at the peak
       #also values are not realistic for common people, probably on oxygen therapy or␣
        ↪something

[801]: <Axes: xlabel='FiO ', ylabel='Count'>
```



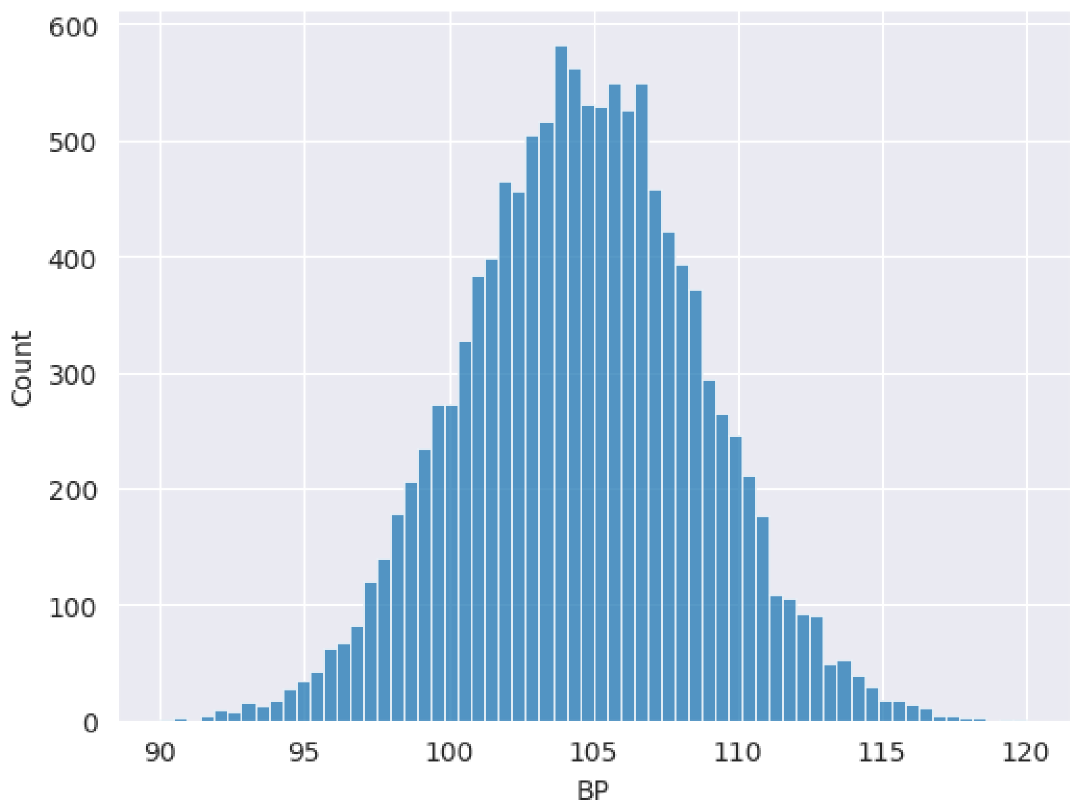
```
[802]: sns.boxplot(observation_df['FiO '])
```

```
[802]: <Axes: ylabel='FiO '>
```



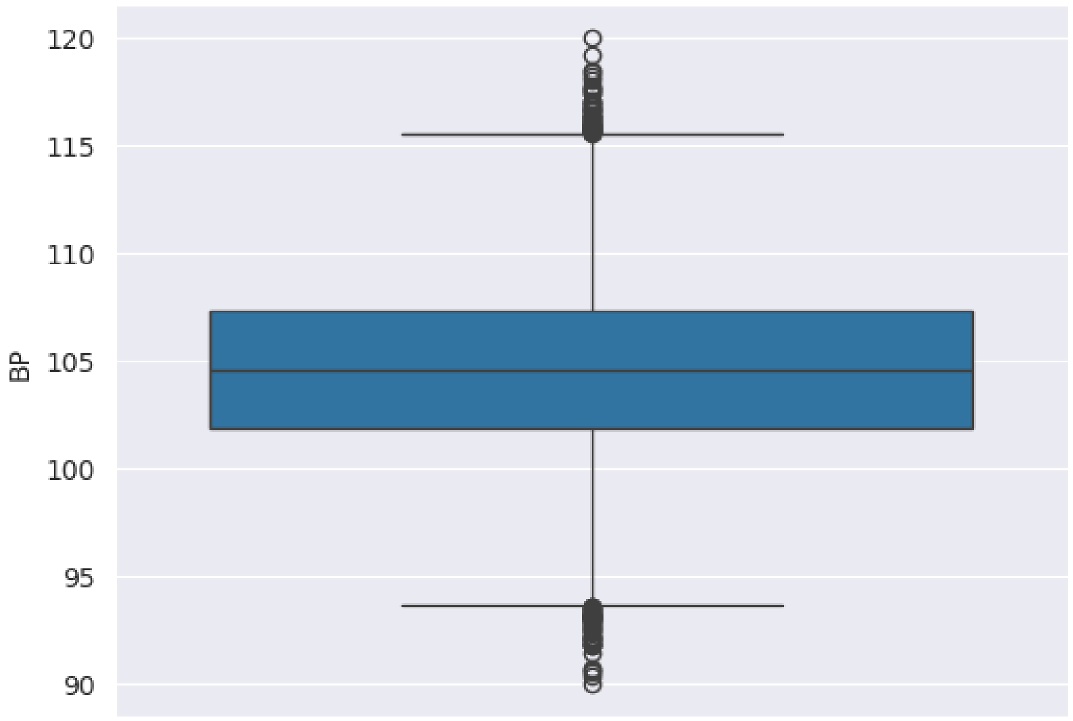
```
[803]: #blood pressure (observation_df)
       sns.histplot(observation_df['BP'])
       #normal distribution with usual values
```

```
[803]: <Axes: xlabel='BP', ylabel='Count'>
```



```
[804]: sns.boxplot(y = observation_df['BP'])
```

```
[804]: <Axes: ylabel='BP'>
```

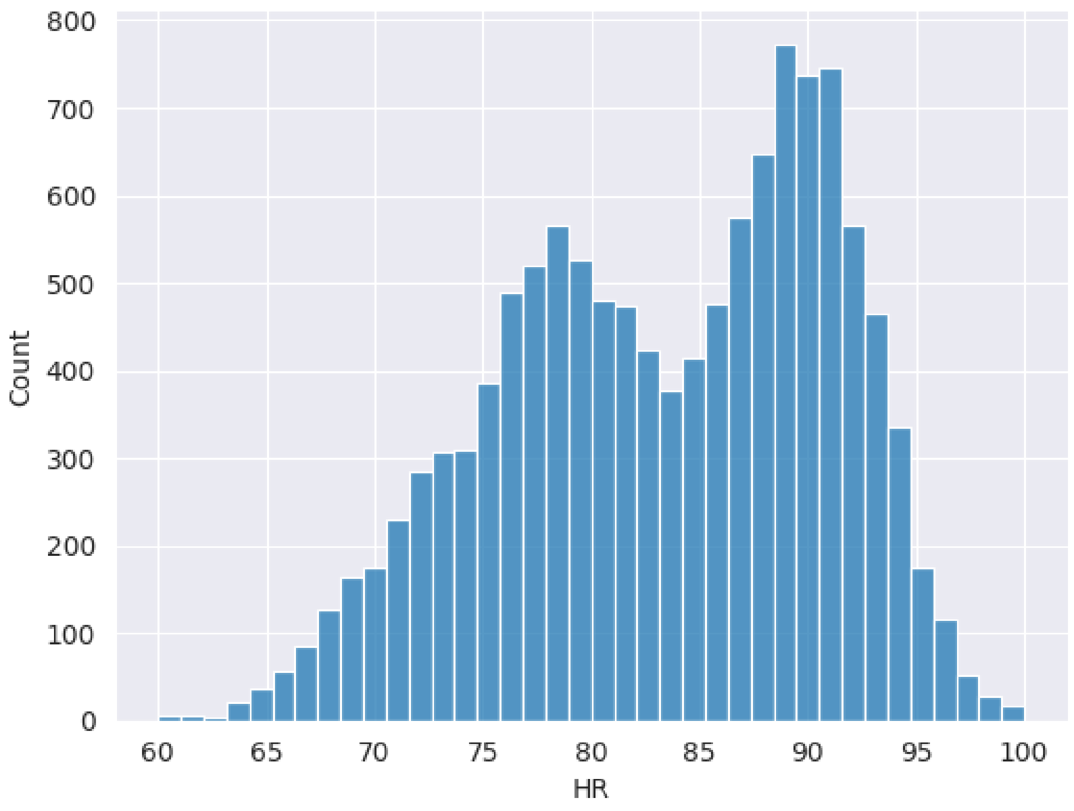


```
[805]: observation_df['BP'].min(), observation_df['BP'].max()
```

```
[805]: (np.float64(90.0), np.float64(120.0))
```

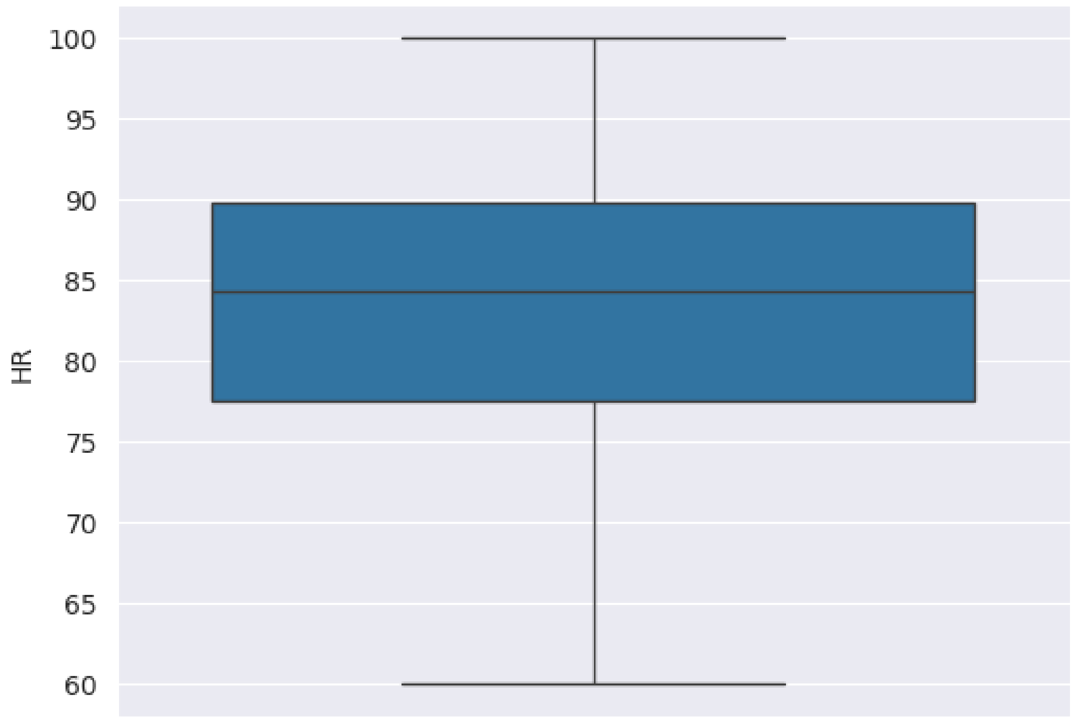
```
[806]: #Heart rate
       sns.histplot(observation_df['HR'])
       #pretty bimodal, but realistic values
```

```
[806]: <Axes: xlabel='HR', ylabel='Count'>
```



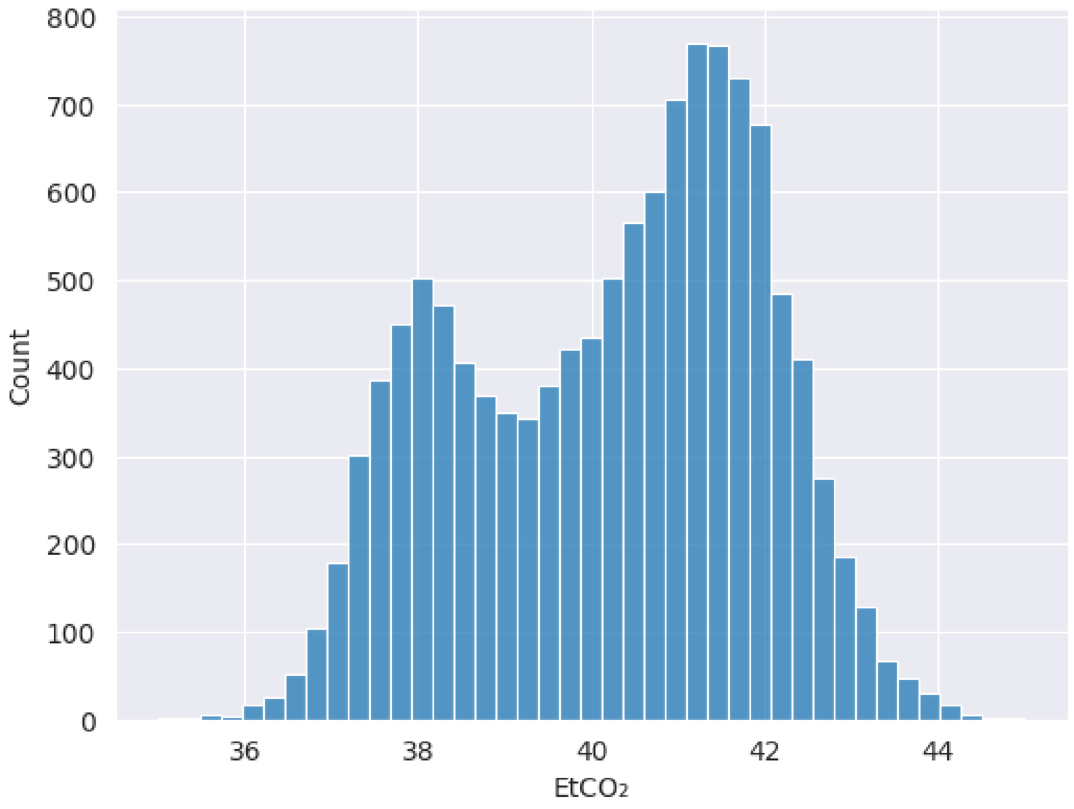
```
[807]: sns.boxplot(y = observation_df['HR'])
```

```
[807]: <Axes: ylabel='HR'>
```

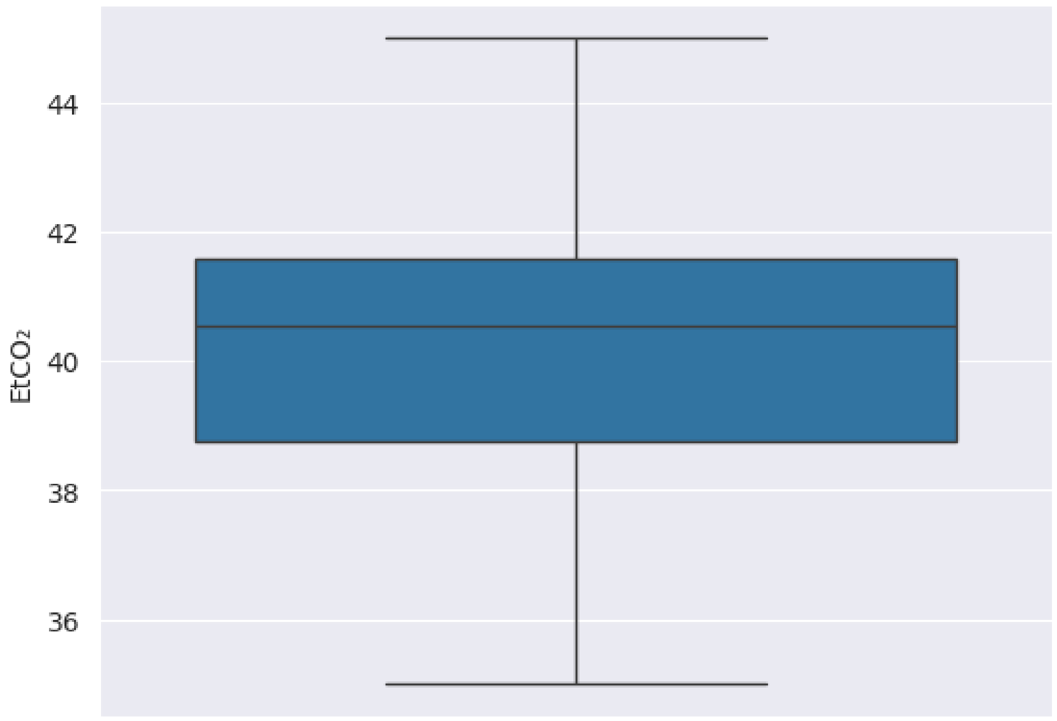


```
[808]: #ETCO2
       sns.histplot(observation_df['EtCO '])
       #also bimodal
```

```
[808]: <Axes: xlabel='EtCO ', ylabel='Count'>
```



```
[809]: sns.boxplot(observation_df['EtCO '])

[809]: <Axes: ylabel='EtCO '>
```



```
[810]: observation_df['EtCO '].min(), observation_df['EtCO '].max()
       #also usual values
```

```
[810]: (np.float64(35.0), np.float64(45.0))
```

```
[811]: #just checking if this is relevant
       patient_df['company'].nunique(), patient_df.shape
       #too many unique vals, irrelevant
```

```
[811]: (1989, (2197, 13))
```

3.1.3 C) Párová analýza dát: Identifikujte vzťahy a závislostí medzi dvojicami atribútov.

But first lets create a dataset with merged tables with only the attributes we consider as necessary

Creation of the joined df

```
[812]: #This is a list of attributes that will make up the new merged dataset

       #QoS might be of significance with Fio and other atts,
       #some codes may also have a touch (for example US station are healthier... idk)
       #latitude and longitude will be kept for potentional current location␣
        ↪(patient_df) relation
```

```
station_attributes = ['QoS', 'code', 'latitude', 'longitude', ]

#current location has been mentioned in station atts, may be dropped -> later␣
 ↪comment : it was dropped
#blood group may be relevant, may be not we will see
#user id just so we have some unique user identifier since we are dropping name␣
 ↪and everything
patient_attributes = ['user_id', 'blood_group', 'station_ID']

#everything apart from longitude and latitude since that is already kept from␣
 ↪station_attributes and we mentioned before that all stations are mentioned␣
 ↪in obs_df
observation_attributes = ['SpO ', 'HR', 'PI', 'RR', 'EtCO ', 'FiO ', 'PRV', 'BP',
       'Skin Temperature', 'Motion/Activity index', 'PVI', 'Hb level', 'SV',
       'CO', 'Blood Flow Index', 'PPG waveform features',
       'Signal Quality Index', 'Respiratory effort', 'O  extraction ratio',
       'SNR', 'oximetry']

#for check, lets count the atts
len(station_attributes) + len(patient_attributes) + len(observation_attributes)
```

[812]:
```
28
```

[813]:
```
station_df2 = station_df[station_attributes].copy()
patient_df2 = patient_df[patient_attributes].copy()
observation_df2 = observation_df[observation_attributes + ['latitude',␣
 ↪'longitude']].copy()
#this is needed to convert the ID into a normal attribute
station_df2 = station_df2.reset_index().rename(columns={'index': 'station_ID'})
```

[814]:
```
observation_df.shape
```

[814]:
```
(12177, 23)
```

[815]:
```
df_obs_stat = observation_df2.merge(
    station_df2,
    left_on=['latitude', 'longitude'],   # from merged patiens
    right_on=['latitude', 'longitude'],  # from observation_df
    how='inner'
)
```

[816]:
```
#the shape should be the same as observation_df.shape
df_obs_stat.shape
#it is not because in the following cell we can see that some stations have the␣
 ↪same coordinates
```

[816]:
```
(21385, 26)
```

```
[817]: station_df2[['latitude', 'longitude']].duplicated().sum()
```

```
[817]: np.int64(205)
```

```
[818]: df_obs_stat.head(5)
```

```
[818]:         SpO         HR         PI         RR       EtCO        FiO  \
       0  97.538229  87.194745  11.225419  14.812012  42.113735  33.852538
       1  97.933271  80.787303  11.730935  14.964972  39.537692  65.326035
       2  97.933271  80.787303  11.730935  14.964972  39.537692  65.326035
       3  98.209983  79.733895  12.839449  14.840668  39.758706  53.925230
       4  98.202790  86.156903  11.204152  14.523288  43.448577  35.227704

                 PRV          BP  Skin Temperature  Motion/Activity index  …  \
       0  144.504405  100.455727         35.961920              10.302567  …
       1  110.615787  102.133386         36.274352               8.975704  …
       2  110.615787  102.133386         36.274352               8.975704  …
       3  107.208040  104.036654         35.583851               7.653790  …
       4  143.282224  105.723603         36.463180               8.795732  …

          Signal Quality Index  Respiratory effort  O extraction ratio        SNR  \
       0             42.399816           46.497869            0.289012  39.334620
       1             46.078137           53.351208            0.290879  26.006709
       2             46.078137           53.351208            0.290879  26.006709
       3             41.525607           52.124182            0.263171  31.890829
       4             36.535021           50.342830            0.256780  30.721375

          oximetry   latitude   longitude  station_ID        QoS  code
       0       1.0  49.183239   15.454273         403       good    CZ
       1       0.0  33.544280  -84.233810           4       good    US
       2       0.0  33.544280  -84.233810         426  excellent    US
       3       1.0 -27.505780  153.102360         219  excellent    AU
       4       1.0  37.656390  126.835000         319  excellent    KR

       [5 rows x 26 columns]
```

```
[819]: #now we need to join the df_obs_stat with patient_df
       df = df_obs_stat.merge(
           patient_df2,
           left_on=['station_ID'],
           right_on=['station_ID'],
           how='inner'
       )
```

```
[820]: df.shape
       #now we have many more entries since there are many patients sharing the same␣
        ↪station as we can see in the next cell
```

```
[820]: (66973, 28)
```

```
[821]: patient_df2[['station_ID']].duplicated().sum()
```

```
[821]: np.int64(1520)
```

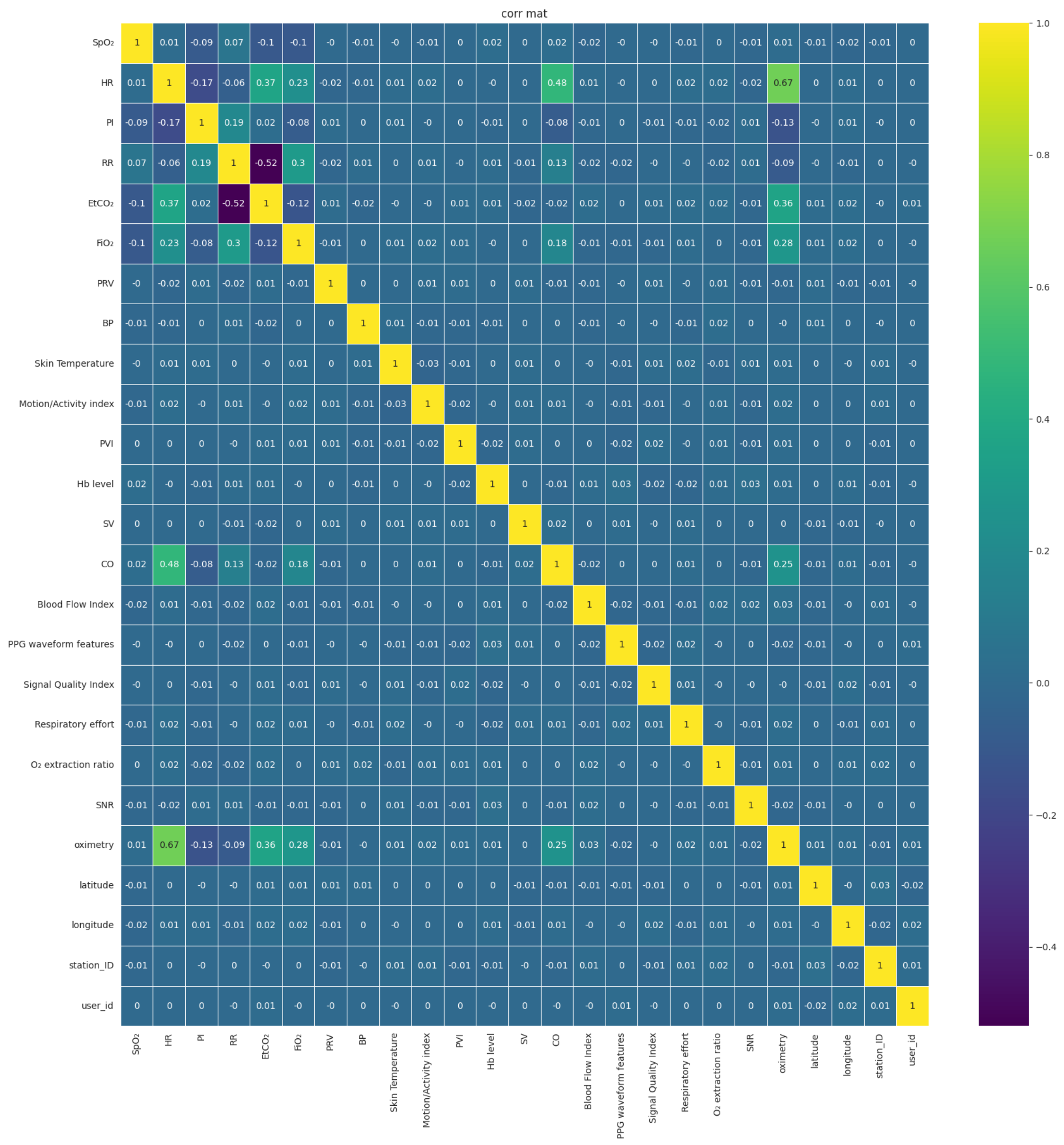
```
[822]: df.columns
```

```
[822]: Index(['SpO ', 'HR', 'PI', 'RR', 'EtCO ', 'FiO ', 'PRV', 'BP',
              'Skin Temperature', 'Motion/Activity index', 'PVI', 'Hb level', 'SV',
              'CO', 'Blood Flow Index', 'PPG waveform features',
              'Signal Quality Index', 'Respiratory effort', 'O  extraction ratio',
              'SNR', 'oximetry', 'latitude', 'longitude', 'station_ID', 'QoS', 'code',
              'user_id', 'blood_group'],
             dtype='object')
```

correlation matrix with heatmap

```
[823]: numeric_df = df.select_dtypes(include=['float64', 'int64'])

       corr_matrix = numeric_df.corr().round(2)
```

```
[824]: plt.figure(figsize=(20, 20))
       sns.heatmap(corr_matrix, cmap='viridis', annot=True,linewidths=0.5)
       plt.title("corr mat")
       plt.show()
```



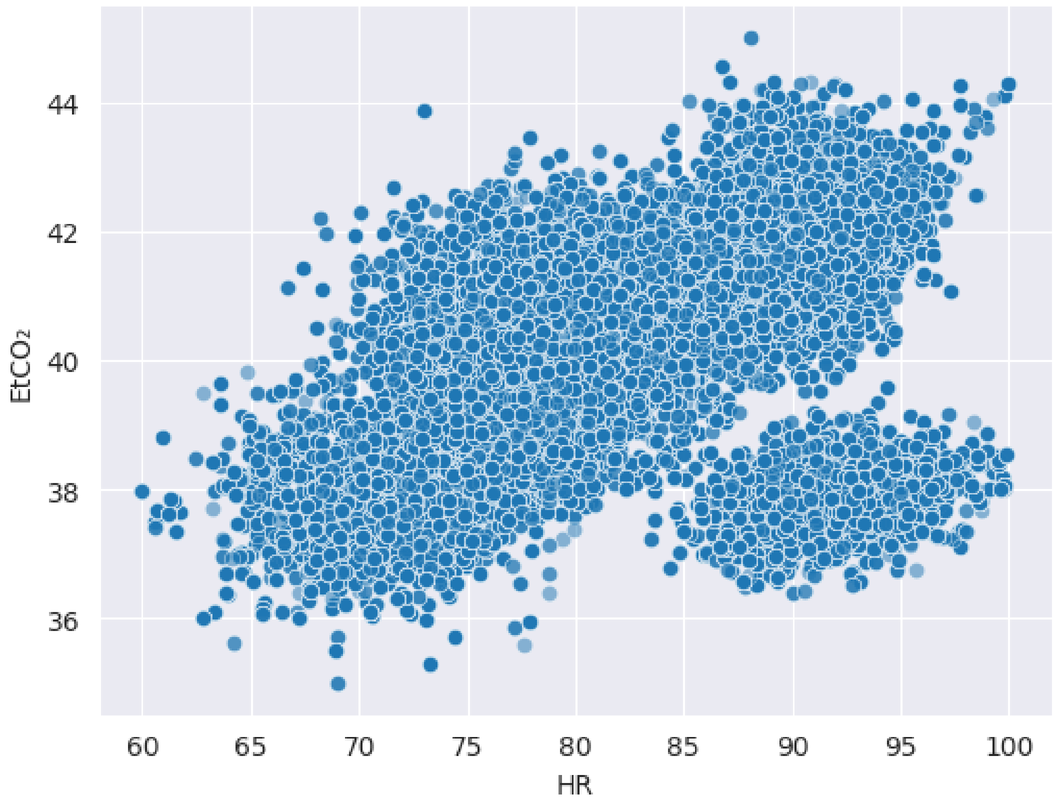
[825]:
```
#based on this heatmap lets write out all the correlations so we can take a␣
↪look at them later
#I only included minimum 0,2 corr

#GROUP 1 (WITHOUT OXIMETRY):              -- used in this step

#HR - EtCO2(weak), FiO2(weak), CO(mid)
#RR - Etco2(mid), FiO2(weak),

#Group 2(OXIMETRY):
```

```
#OX - HR(strong),EtCO2(weak) ,FiO2(weak), CO(weak)      -- used in 1D
```

solution for 1.1C) here are the comparisons between the attributes we got from the correlation heatmap

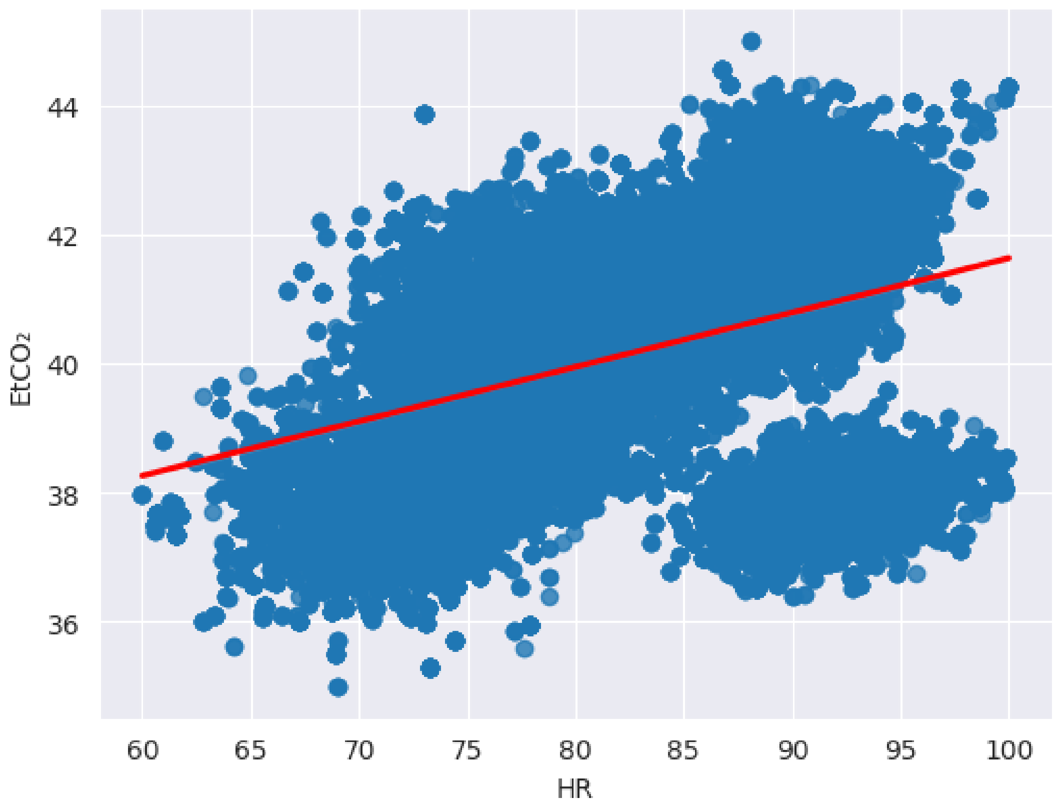
[826]:
```
#HR-EtCO2
sns.scatterplot(data=df, x='HR', y='EtCO ', alpha=0.5)
```

[826]:
```
<Axes: xlabel='HR', ylabel='EtCO '>
```



[827]:
```
sns.regplot(data=df, x='HR', y='EtCO ', line_kws={'color':'red'})
```

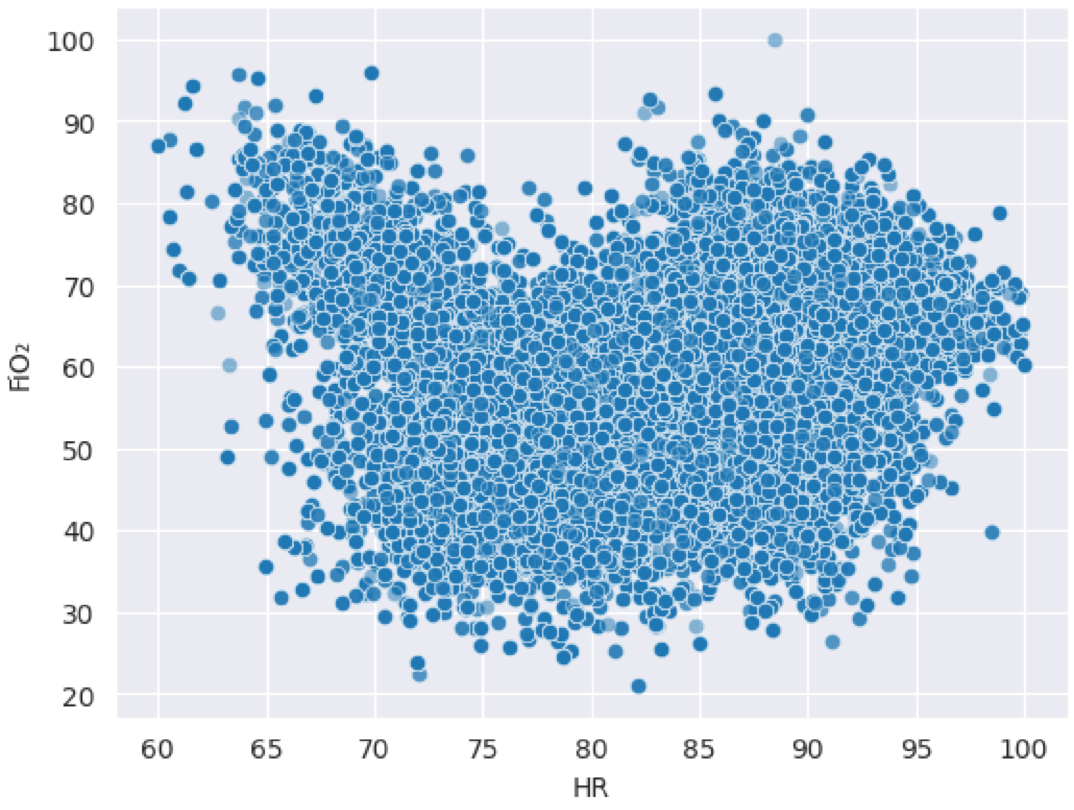
[827]:
```
<Axes: xlabel='HR', ylabel='EtCO '>
```



```
[828]: #this is not enough to determine that these two variables correlate, maybe␣
        ↪without the cluster around [92.5 , 38]
```

```
[829]: #HR-FiO2
       sns.scatterplot(data=df, x='HR', y='FiO ', alpha=0.5)
```

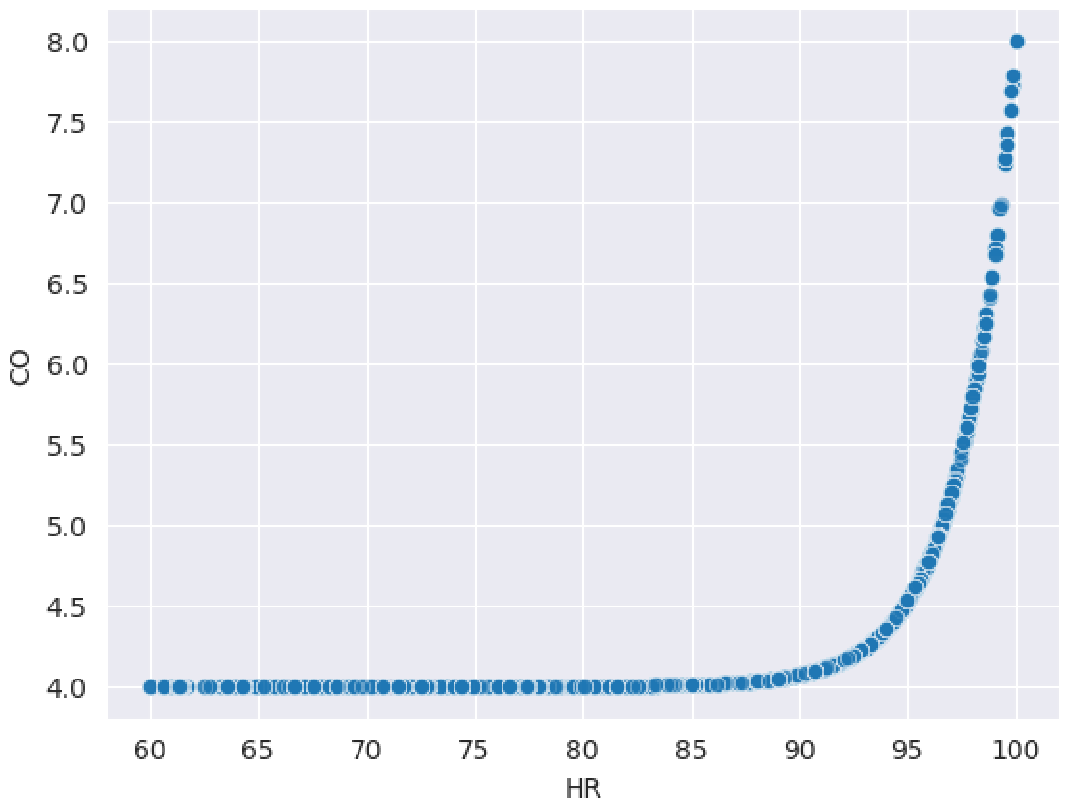
```
[829]: <Axes: xlabel='HR', ylabel='FiO '>
```



```
[830]: #way too spread out, insignificant
```

```
[831]: #HR-CO
       sns.scatterplot(data=df, x='HR', y='CO', alpha=0.5)
```

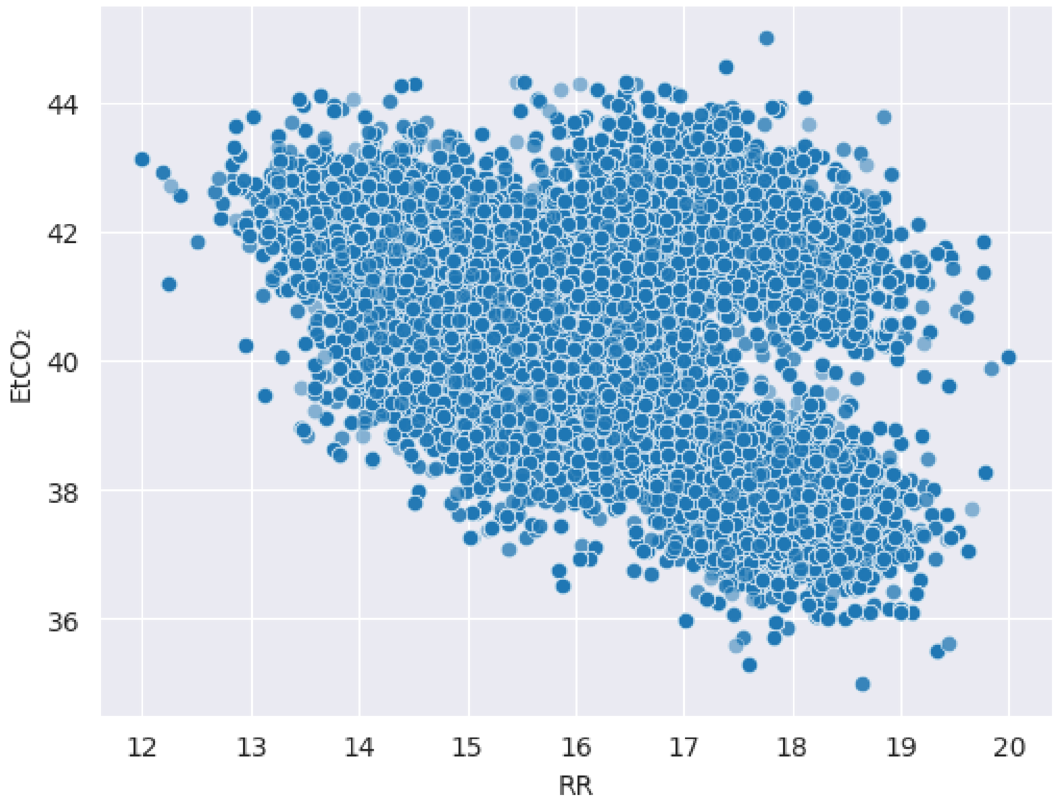
```
[831]: <Axes: xlabel='HR', ylabel='CO'>
```



```
[832]: #This is definitely a significant correlation, but not linear since CO values␣
        ↪are cut off at 4.0
```

```
[833]: #RR - Etco2
       sns.scatterplot(data=df, x='RR', y='EtCO ', alpha=0.5)
```

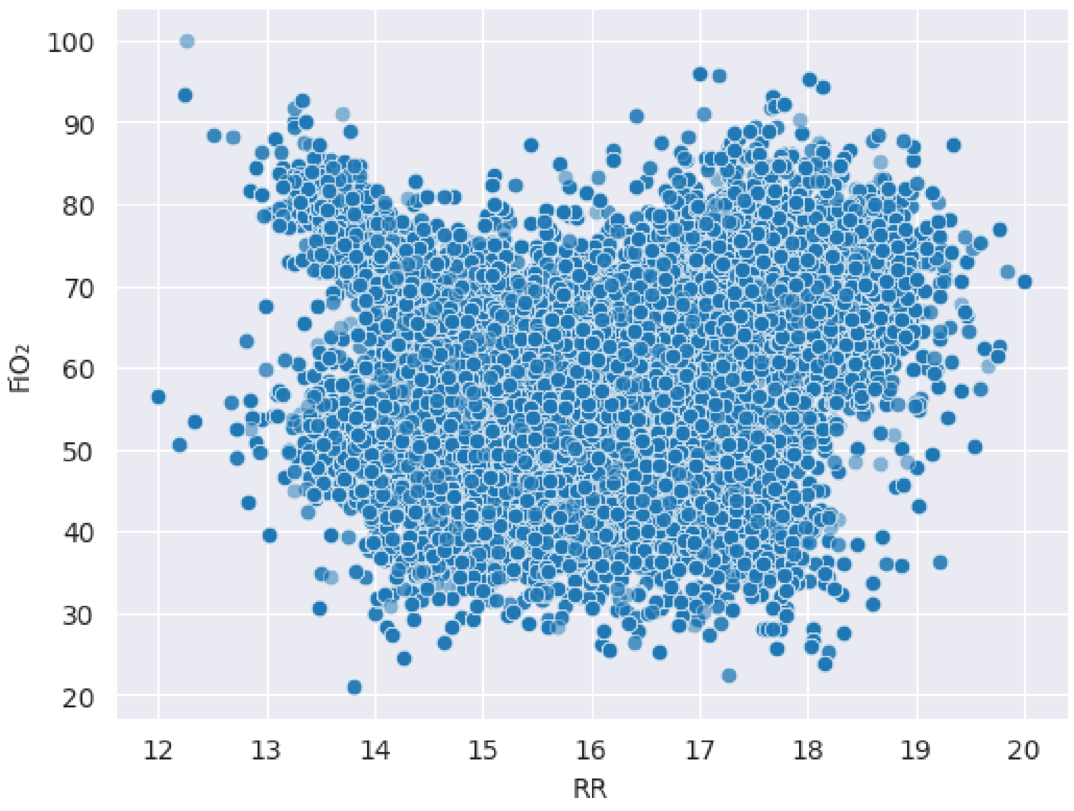
```
[833]: <Axes: xlabel='RR', ylabel='EtCO '>
```



```
[834]: #slight show of negative correlation, but ruined by the upper right cluster
```

```
[835]: #RR FiO2
        sns.scatterplot(data=df, x='RR', y='FiO ', alpha=0.5)
```

```
[835]: <Axes: xlabel='RR', ylabel='FiO '>
```



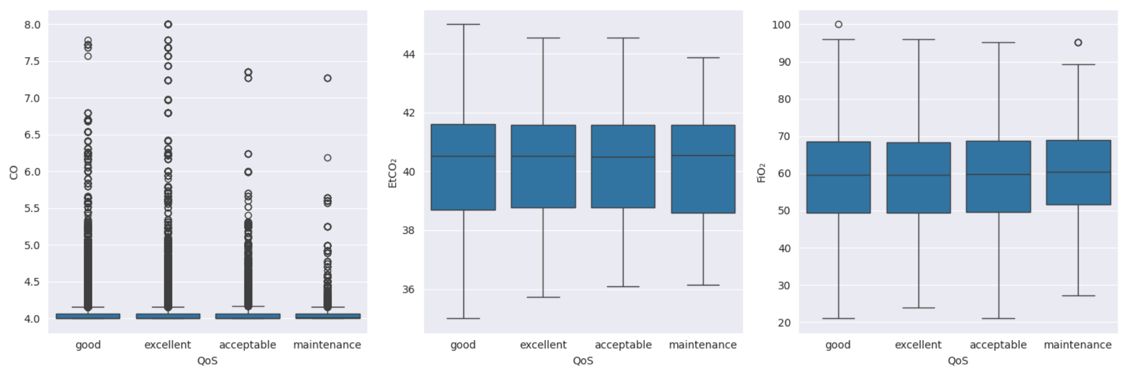
[836]:
```
#no correlation
```

these were only the numeric attributes we took from the heatmap, now lets take at look at non numeric correlations aswell

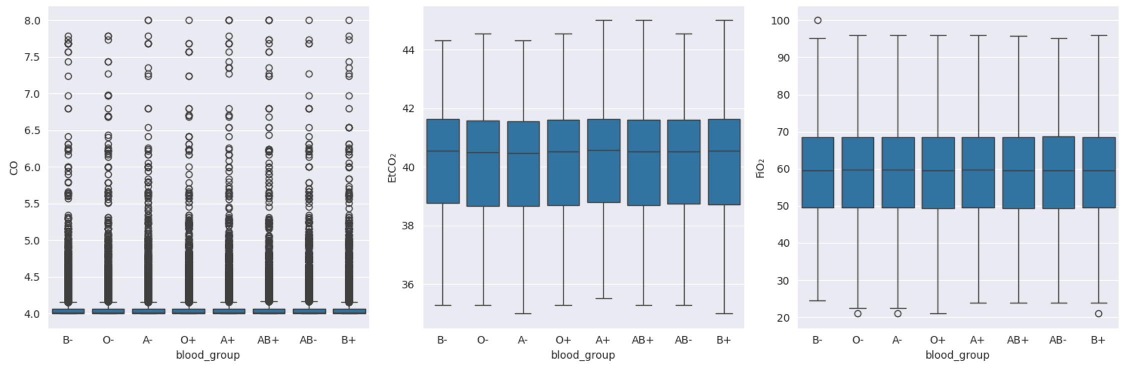
[837]:
```
non_numeric = df.select_dtypes(exclude=['float64', 'int64']).columns
print(non_numeric)
#these will be tested for correlation with CO,FIO2 and EtCO2 since these seem␣
↪to be the most important attributes
```

```
Index(['QoS', 'code', 'blood_group'], dtype='object')
```

[838]:
```
#QoS
fig, axes = plt.subplots(1, 3, figsize=(15, 5))

sns.boxplot(data=df, x='QoS', y='CO', ax=axes[0])
sns.boxplot(data=df, x='QoS', y='EtCO ', ax=axes[1])
sns.boxplot(data=df, x='QoS', y='FiO ', ax=axes[2])

plt.tight_layout()
plt.show()
#no real significance
```

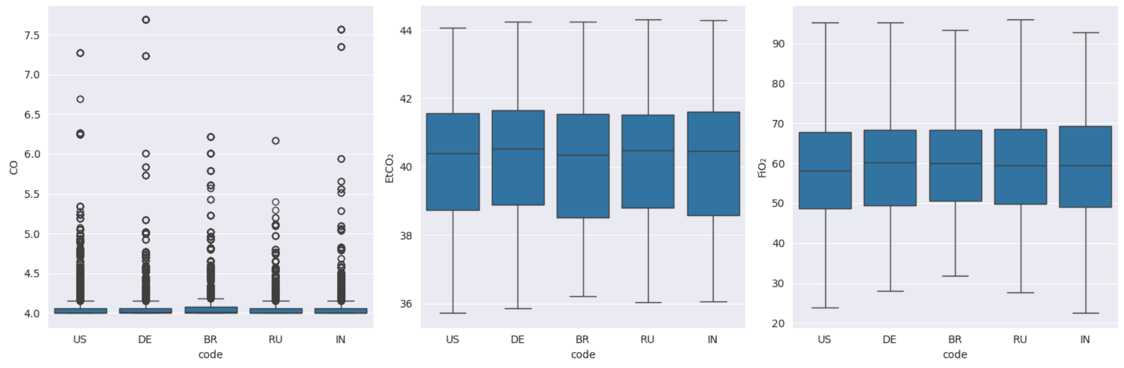


```
[839]: #QoS
       fig, axes = plt.subplots(1, 3, figsize=(15, 5))

       sns.boxplot(data=df, x='blood_group', y='CO', ax=axes[0])
       sns.boxplot(data=df, x='blood_group', y='EtCO ', ax=axes[1])
       sns.boxplot(data=df, x='blood_group', y='FiO ', ax=axes[2])

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



```
[840]: #code - top 5
       top_codes = df['code'].value_counts().head(5).index
       filtered_df = df[df['code'].isin(top_codes)]

       fig, axes = plt.subplots(1, 3, figsize=(15, 5))

       sns.boxplot(data=filtered_df, x='code', y='CO', ax=axes[0])
       sns.boxplot(data=filtered_df, x='code', y='EtCO ', ax=axes[1])
       sns.boxplot(data=filtered_df, x='code', y='FiO ', ax=axes[2])
```

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

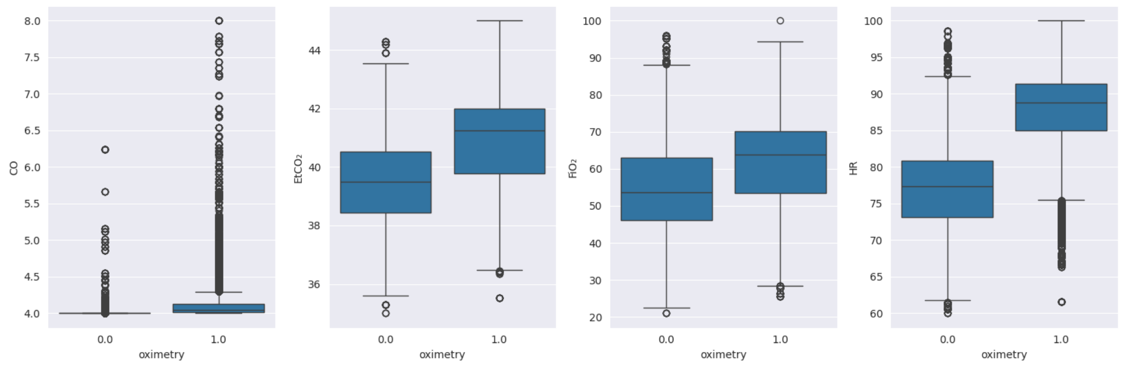


3.1.4 D)Párová analýza dát: Identifikujte závislosti medzi predikovanou premennou a ostatnými premennými (potenciálnymi prediktormi)

from the correlation heatmap we have these attributes that seem to have some correlation with the predicted attribute

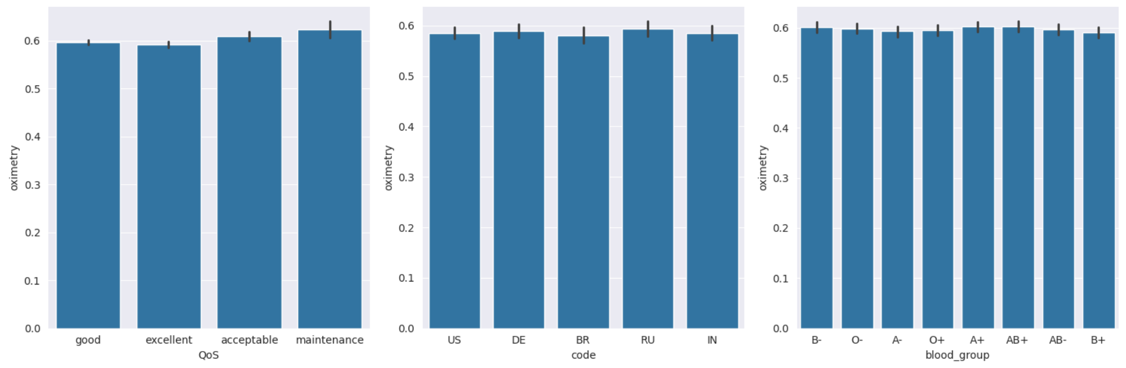
HR(strong),EtCO2(weak) ,FiO2(weak), CO(weak)

[841]:
```
fig, axes = plt.subplots(1, 4, figsize=(15, 5))

sns.boxplot(data=df, x='oximetry', y='CO', ax=axes[0])
sns.boxplot(data=df, x='oximetry', y='EtCO ', ax=axes[1])
sns.boxplot(data=df, x='oximetry', y='FiO ', ax=axes[2])
sns.boxplot(data=df, x='oximetry', y='HR', ax=axes[3])

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



[842]:
```
#CO is hard to determine, the IQRs are close but the outliers may mean a lot␣
↪(will probably see more after normalization), the EtCO2 and FiO2 seem to be␣
↪higher when oximetry is set to 1, HR seems to have a really significant␣
↪correlation with oximetry, as suggested by the correlation heatmap
```

[843]:
```
#correlation with non numerical values
fig, axes = plt.subplots(1, 3, figsize=(15, 5))

# QoS
sns.barplot(ax=axes[0], x=df['QoS'], y=df['oximetry'])
# code (top 5)
top5 = df['code'].value_counts().head(5).index
sns.barplot(ax=axes[1], x=df[df['code'].isin(top5)]['code'], y=df[df['code'].
↪isin(top5)]['oximetry'])
# blood_group
sns.barplot(ax=axes[2], x=df['blood_group'], y=df['oximetry'])

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



[844]:
```
#this graphs show the oximetry 1/0 ratio per each QoS, Code and blood group. So␣
↪rather than correlation, this shows that the data are evenly distributed
```

3.1.5 E) Findings, thought ect.

all of our thoughs and findings are thoroughly documented throughout the operations, but here is the summary:

Firstly we analysed each table and gave a quick look for every attribute, for dataset station, we used the coordinations to merge it with observation_df, we ended up not using the station name as it is insignificant as well as revision. The only missing values were 2 codes which will probably be filled later with a newly created code. The patient dataframe is full of insignificant attributes, we end up only using the blood group and station ID for merge with station df. From observation we keep every value, although some seem to be more signicicant than others, for example FiO2, CO,RR, EtCO2. We take some time to look at individual distributions of attributes in B), but we dont really find any abnormalities that would pose a threat to our models precition, most distributions are either normal or bimodal or uniform. In C) we needed to take a look at correlation between the attributes, so we needed to create a correlation heatmap which was created from a joint dataframe consisting of all three datasets, but only the attributes that we deemed as important. We discarded the useless features and we will not work with them from that point onward. However we find out minor correlation between HR and EtCO2 as well as a negative one between HR and FiO2 and a RR and EtCO2. HR and CO seem to have a strong positive correlation but since CO is capped at 4.0, it is not shown that nicely. In D) we see that the predicted value oximetry strongly correlates with HR, and FiO2 and EtCO2 also show medium signs of correlation. Correlation with CO is harder to determine without normalising the data first.

3.2 1.2 Identifikácia problémov, integrácia a čistenie dát

3.2.1 A) nevhodná štruktúra, nejednotne formaty ,duplikáty, chýbajúce hodnoty, vychýlene hodnoty, abnormalne hodnoty, nelogické vzťahy

[845]:
```
df.columns
```

[845]:
```
Index(['SpO ', 'HR', 'PI', 'RR', 'EtCO ', 'FiO ', 'PRV', 'BP',
       'Skin Temperature', 'Motion/Activity index', 'PVI', 'Hb level', 'SV',
       'CO', 'Blood Flow Index', 'PPG waveform features',
       'Signal Quality Index', 'Respiratory effort', 'O  extraction ratio',
       'SNR', 'oximetry', 'latitude', 'longitude', 'station_ID', 'QoS', 'code',
       'user_id', 'blood_group'],
      dtype='object')
```

[846]:
```
# I see many collumn name that are corectly name but it is so anoying to copy␣
↪the same ` ` symbol over and over again so that's why im gonna rename it just␣
↪for now

rename_map = {
    'SpO ': 'SpO2',
    'EtCO ': 'EtCO2',
    'FiO ': 'FiO2',
    'O  extraction ratio': 'O2 extraction ratio',
}
df = df.rename(columns={k:v for k,v in rename_map.items() if k in df.columns})
```

[847]:
```
for c in ['QoS','code','blood_group']:
    if c in df.columns:
        df[c] = df[c].astype('category')
```

[848]:
```
#checking if every value in oximetry col is type int so it does not make any␣
↪issues in the future but most of this is already done in previous cells in 1.
↪1

if 'oximetry' in df.columns:
    df['oximetry'] = df['oximetry'].astype(int)
```

```
[849]: df.dtypes.value_counts()
```

```
[849]: float64     22
       int64        3
       category     1
       category     1
       category     1
       Name: count, dtype: int64
```

```
[850]: df.duplicated().sum()
```

```
[850]: np.int64(0)
```

```
[851]: df.duplicated(subset=['HR','RR','BP']).sum()
```

```
[851]: np.int64(55244)
```

```
[852]: duplicates_output = df[df.duplicated(subset=[col for col in df.columns if col !
        ↪= 'user_id'], keep=False)]
       duplicates_output
```

```
[852]:            SpO2         HR         PI         RR      EtCO2       FiO2  \
       6      97.933271  80.787303  11.730935  14.964972  39.537692  65.326035
       7      97.933271  80.787303  11.730935  14.964972  39.537692  65.326035
       9      97.933271  80.787303  11.730935  14.964972  39.537692  65.326035
       30     96.851933  91.008225  11.323571  15.148349  42.056062  58.615353
       32     96.851933  91.008225  11.323571  15.148349  42.056062  58.615353
       …            …          …          …          …          …          …
       66965  96.698981  71.499309  13.427977  15.751513  41.201634  55.177636
       66966  96.698981  71.499309  13.427977  15.751513  41.201634  55.177636
       66967  96.698981  71.499309  13.427977  15.751513  41.201634  55.177636
       66968  96.698981  71.499309  13.427977  15.751513  41.201634  55.177636
       66970  96.698981  71.499309  13.427977  15.751513  41.201634  55.177636

                     PRV          BP  Skin Temperature  Motion/Activity index  …  \
       6      110.615787  102.133386         36.274352               8.975704  …
       7      110.615787  102.133386         36.274352               8.975704  …
       9      110.615787  102.133386         36.274352               8.975704  …
       30      77.660061  102.695264         35.163246              11.823341  …
       32      77.660061  102.695264         35.163246              11.823341  …
       …             …           …                …                    …  …
       66965  103.386006  102.693239         34.895596              11.429244  …
       66966  103.386006  102.693239         34.895596              11.429244  …
       66967  103.386006  102.693239         34.895596              11.429244  …
       66968  103.386006  102.693239         34.895596              11.429244  …
       66970  103.386006  102.693239         34.895596              11.429244  …

              O2 extraction ratio        SNR  oximetry  latitude  longitude  \
       6                   0.290879  26.006709         0  33.54428  -84.23381
       7                   0.290879  26.006709         0  33.54428  -84.23381
       9                   0.290879  26.006709         0  33.54428  -84.23381
       30                  0.285955  32.768112         1  10.29085  105.75635
       32                  0.285955  32.768112         1  10.29085  105.75635
       …                      …         …        …     …        …
       66965               0.283565  28.887543         1  51.04962   12.13690
       66966               0.283565  28.887543         1  51.04962   12.13690
       66967               0.283565  28.887543         1  51.04962   12.13690
       66968               0.283565  28.887543         1  51.04962   12.13690
       66970               0.283565  28.887543         1  51.04962   12.13690

              station_ID        QoS  code  user_id  blood_group
       6             426  excellent    US      398           O+
       7             426  excellent    US      988           O+
       9             426  excellent    US     2033           O+
       30            663  excellent    VN     1225           A-
       32            663  excellent    VN     1454           A-
       …           …          …    …       …          …
       66965         223  excellent    DE      575           B-
       66966         223  excellent    DE      468           O+
       66967         223  excellent    DE     1212           B-
       66968         223  excellent    DE      928           B-
       66970         223  excellent    DE       51           B-

       [21334 rows x 28 columns]
```

```
[853]: duplicates_output['user_id'].nunique(), len(duplicates_output)
```

```
[853]: (599, 21334)
```

```
[854]: duplicates_output['station_ID'].value_counts().head()
```

```
[854]: station_ID
       186    468
       8      414
       350    352
       208    318
       223    318
       Name: count, dtype: int64
```

After checking for duplicates, we found that some patients shared identical measurements. It is normal but not if we found out that 21 336 row that are similar. This was caused by merging patient_df and observation_df using station_ID.

```
[855]: na_count = df.isna().sum().sort_values(ascending=False)
       na_count
```

[855]:
```
code                        170
SpO2                          0
PI                            0
HR                            0
EtCO2                         0
FiO2                          0
PRV                           0
BP                            0
Skin Temperature              0
Motion/Activity index         0
PVI                           0
RR                            0
Hb level                      0
SV                            0
Blood Flow Index              0
CO                            0
Signal Quality Index          0
Respiratory effort            0
O2 extraction ratio           0
PPG waveform features         0
SNR                           0
oximetry                      0
longitude                     0
latitude                      0
station_ID                    0
QoS                           0
user_id                       0
blood_group                   0
dtype: int64
```

3.2.2 B) Kontrola správnosť v dátach

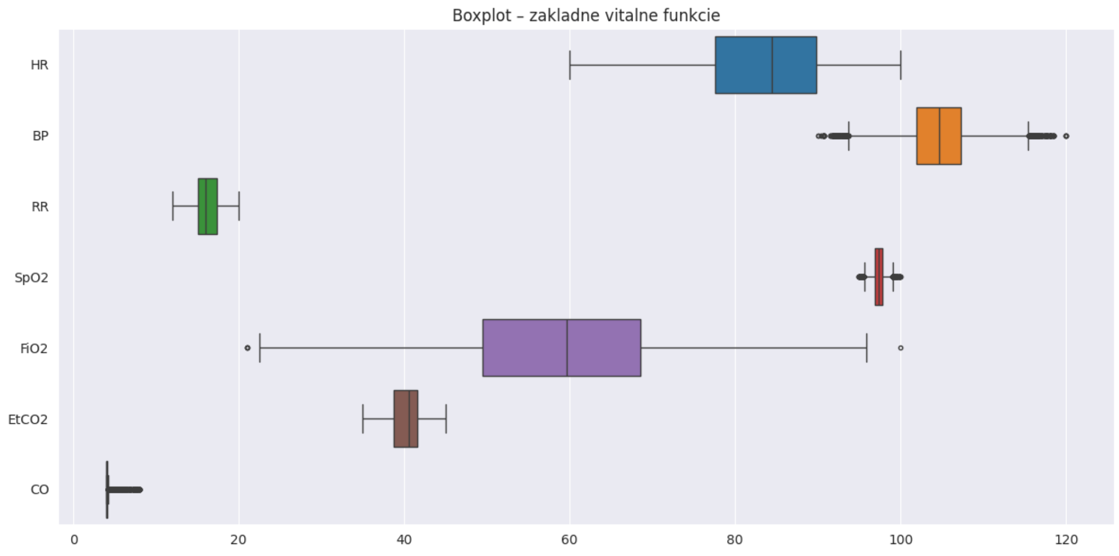
Most of the analyzing the atributes was done in part 1.1, individual findings were docummented along the way.

Some of the most important findings that were captured along the way about the abnormality of the data could be divided into 3 groups. 1) Value-range-wise, most of the attributes have real values, for example the latitude and longitude do range from -180 to 180, SPO2 and blood groups are also in check and so are many more atributes. The only attribute where this was not the case would be FIO2, where the patients must have been altered from normal people, for example on oxygen therapy. 2) Distribution-wise, no attributes are abnormaly different. Some distributions were normal, e.g. SPO2, Hb level. Some were uniform, for example blood group. Some were bimodal, for example HR or EtCO2 which does show quite a skew to abnormality. FIO2 is slightly abnormal, but in most values it would pass as a normal distribution. 3) Shape-wise, patients current location is mapped as an object, but we did not waste time with asserting this issue as we dropped the column alltogether. The station's revision attribute is also an anomaly, since the shape is inconsistent, sometimes having only the date, sometimes also the time... The residence attribute is empty, having no entries

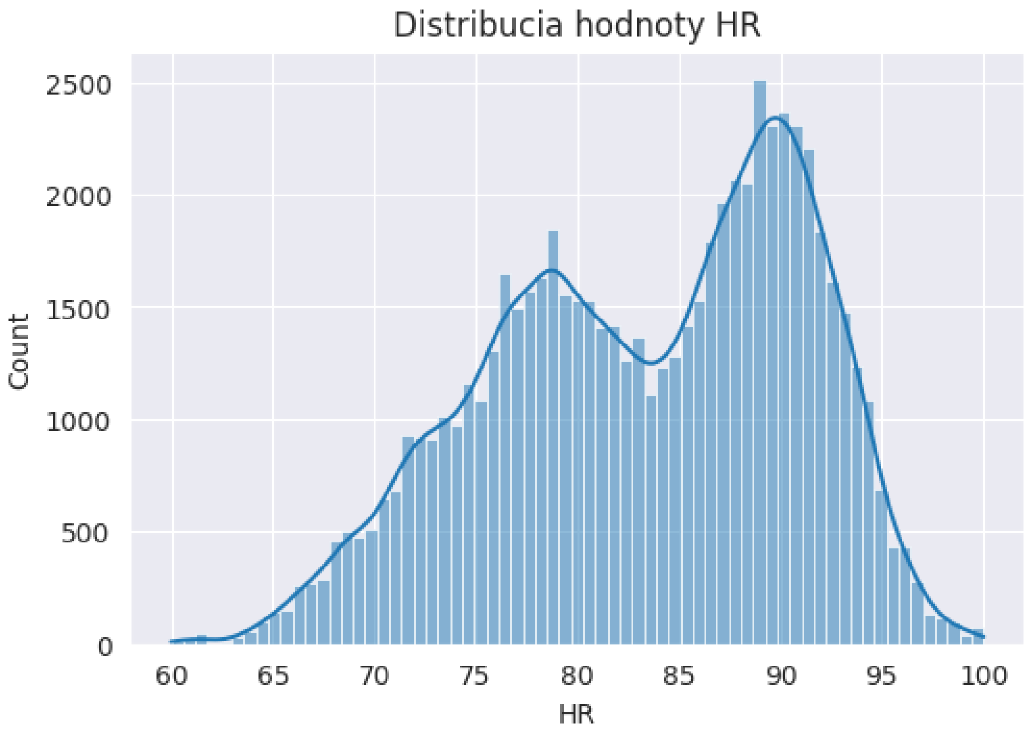
Illogical relationships would also be the division of the data into three tables. What struck me the most was the inability to find a patients observation, due to the fact that after merging patients and stations, we find out that multiple patient are linked to a singular station, and no further link to observation is provided apart than a 1:many relationship between a station and an observation with coordinates.

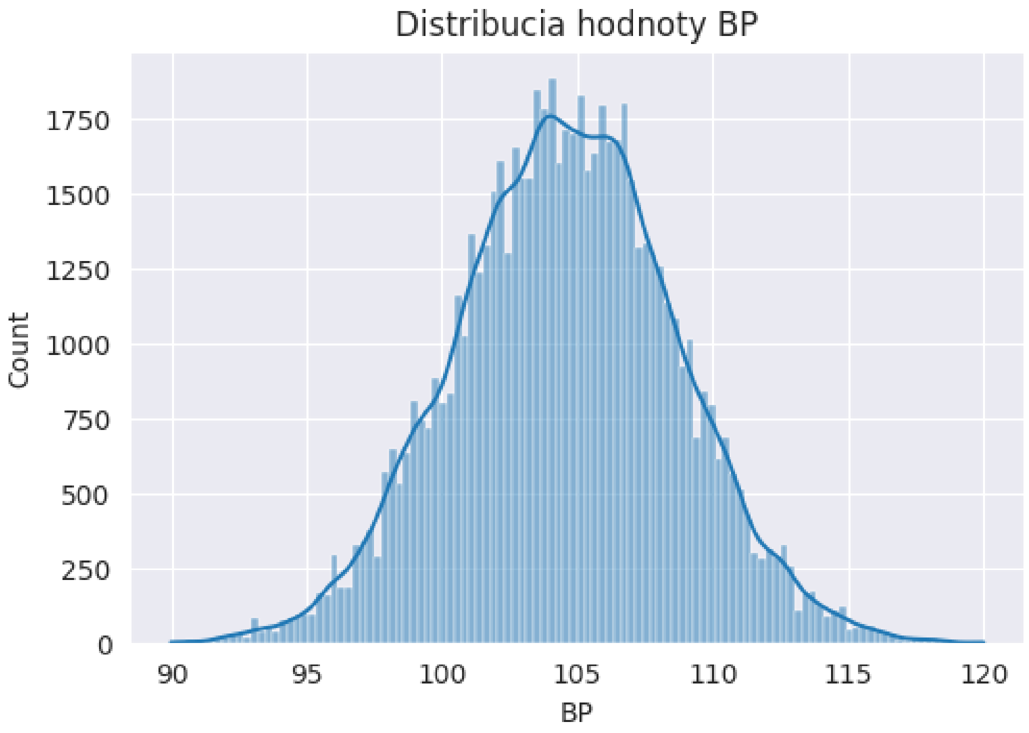
3.2.3 C) Outlier detection

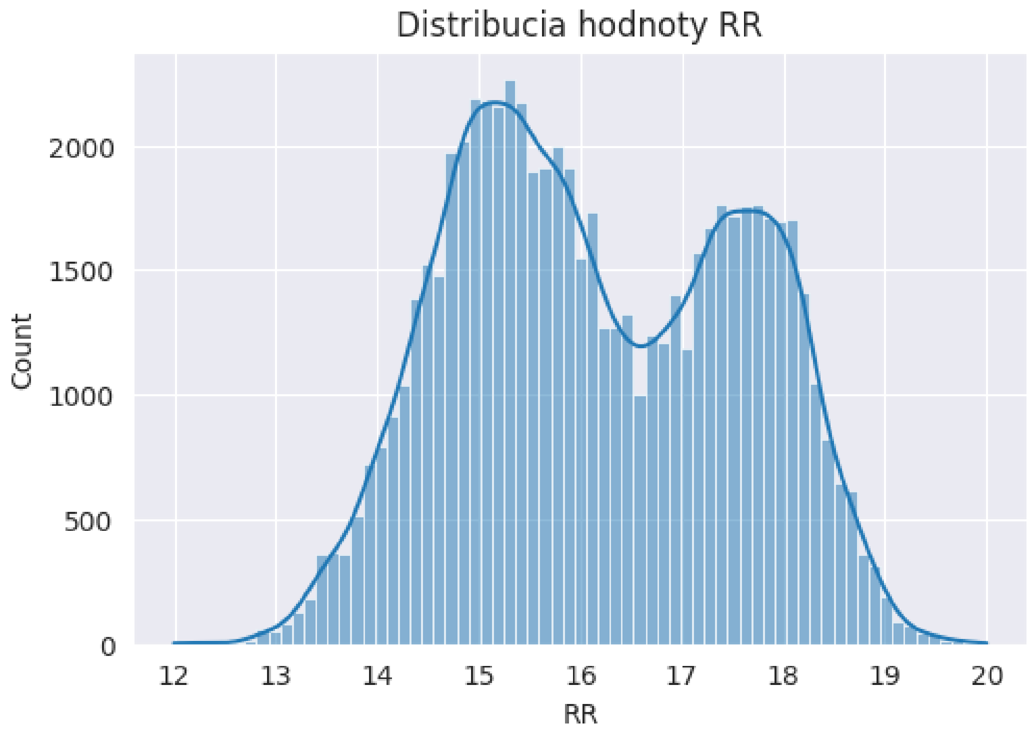
[856]:
```
cols1 = ['HR', 'BP', 'RR', 'SpO2', 'FiO2', 'EtCO2',"CO"]
plt.figure(figsize=(12, 6))
sns.boxplot(data=df[cols1], orient='h', fliersize=3)
plt.title('Boxplot - zakladne vitalne funkcie')
plt.tight_layout()
plt.show()
```

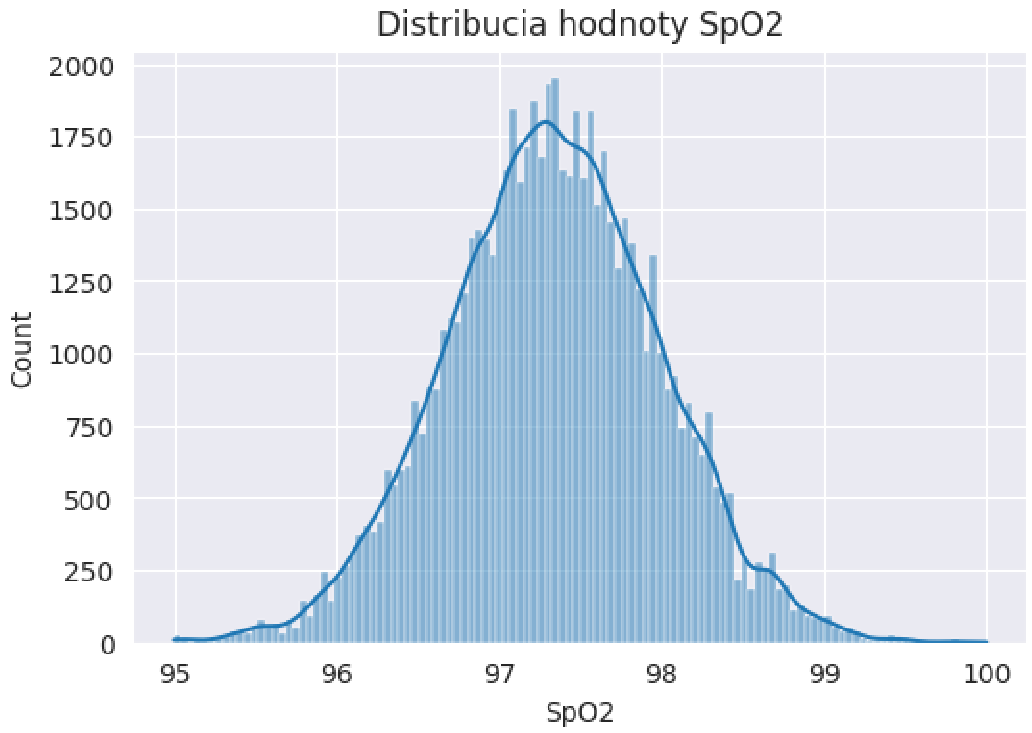


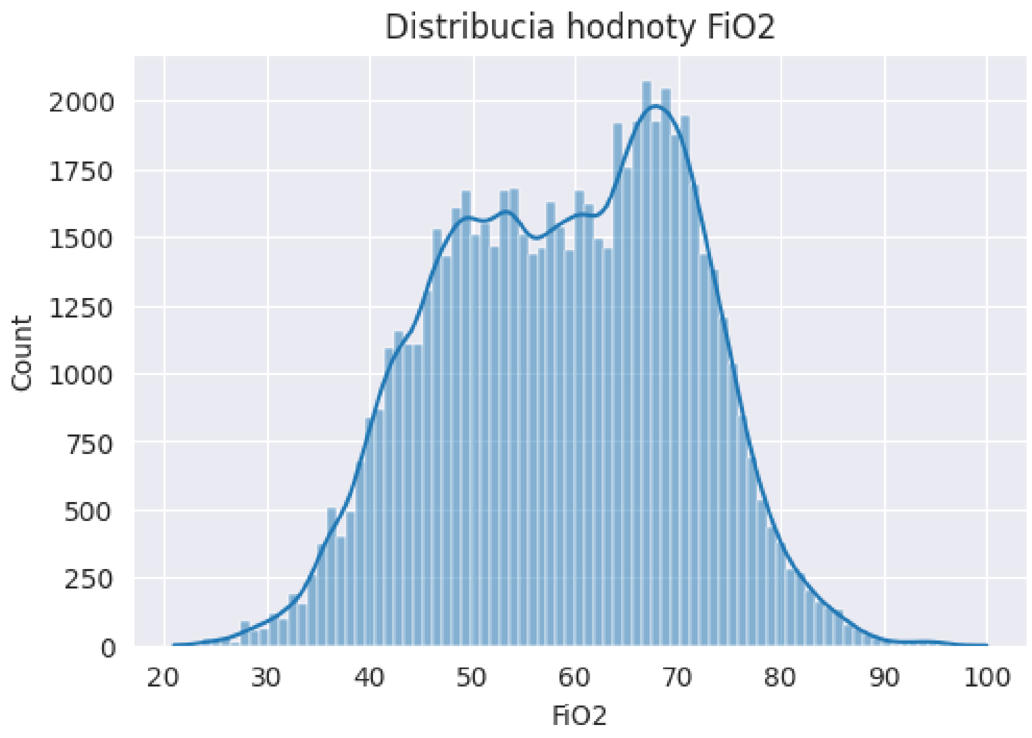
[857]:
```
for col in cols1:
    plt.figure(figsize=(6, 4))
    sns.histplot(df[col], kde=True)
    plt.title(f'Distribucia hodnoty {col}')
    plt.show()
```

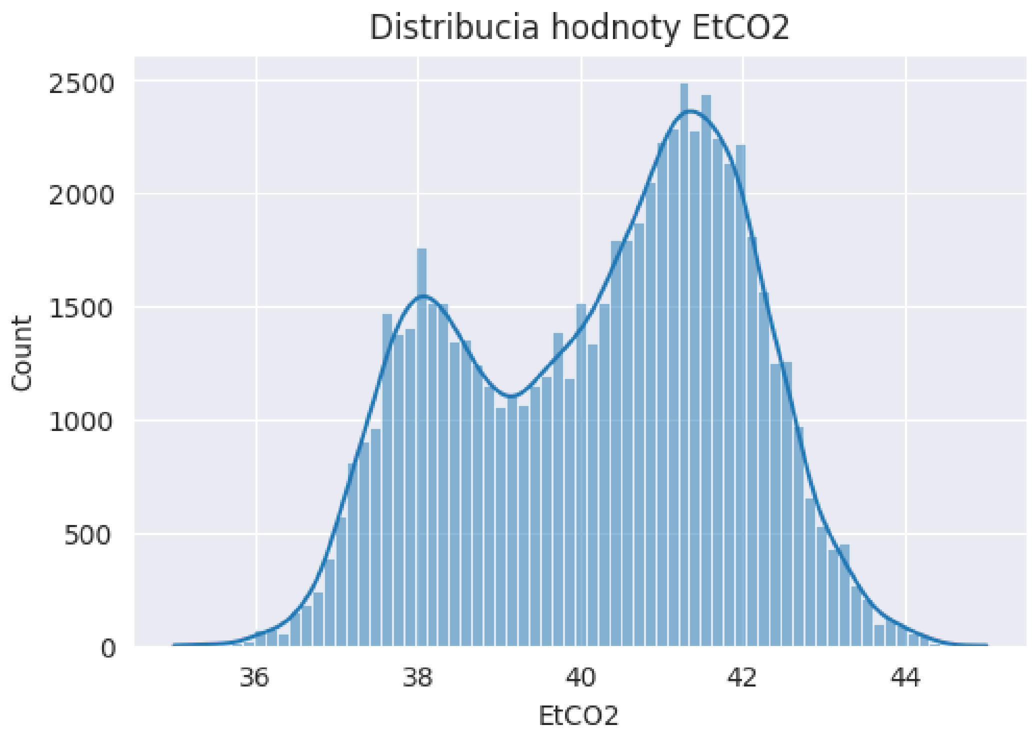

Distribucia hodnoty HR
Count
HR
0
500
1000
1500
2000
2500
60
65
70
75
80
85
90
95
100

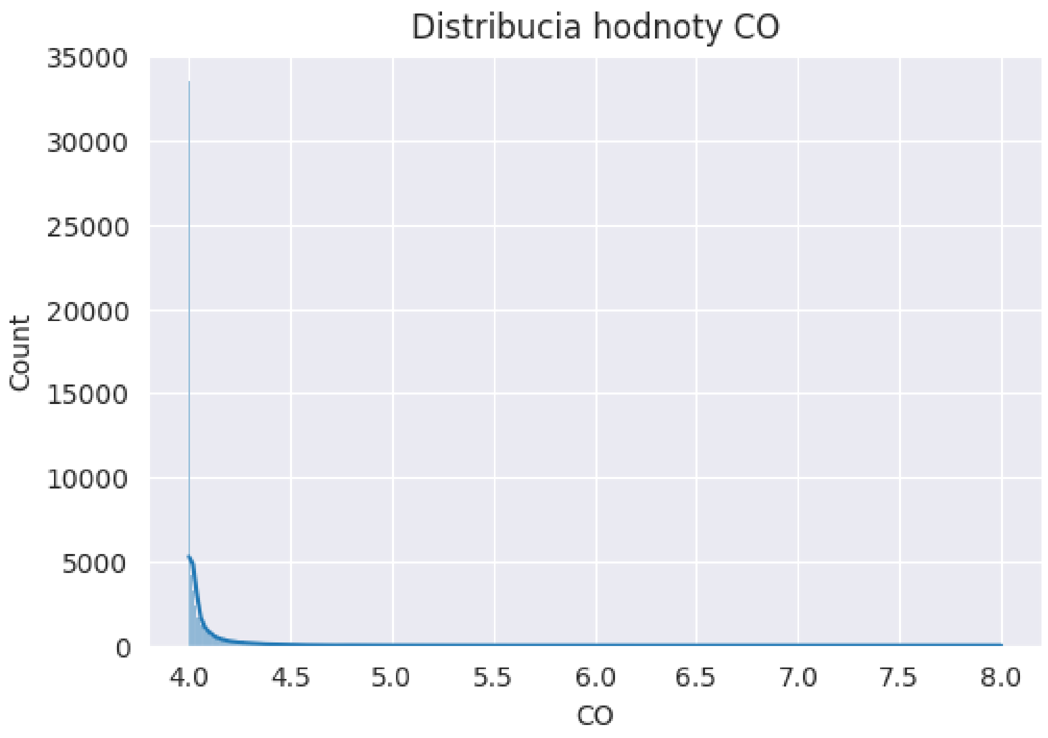

Distribucia hodnoty BP
Count
BP
0
250
500
750
1000
1250
1500
1750
90
95
100
105
110
115
120


Distribucia hodnoty RR
Count
0
500
1000
1500
2000
12
13
14
15
16
17
18
19
20
RR


Distribucia hodnoty SpO2
Count
0
250
500
750
1000
1250
1500
1750
2000
95
96
97
98
99
100
SpO2

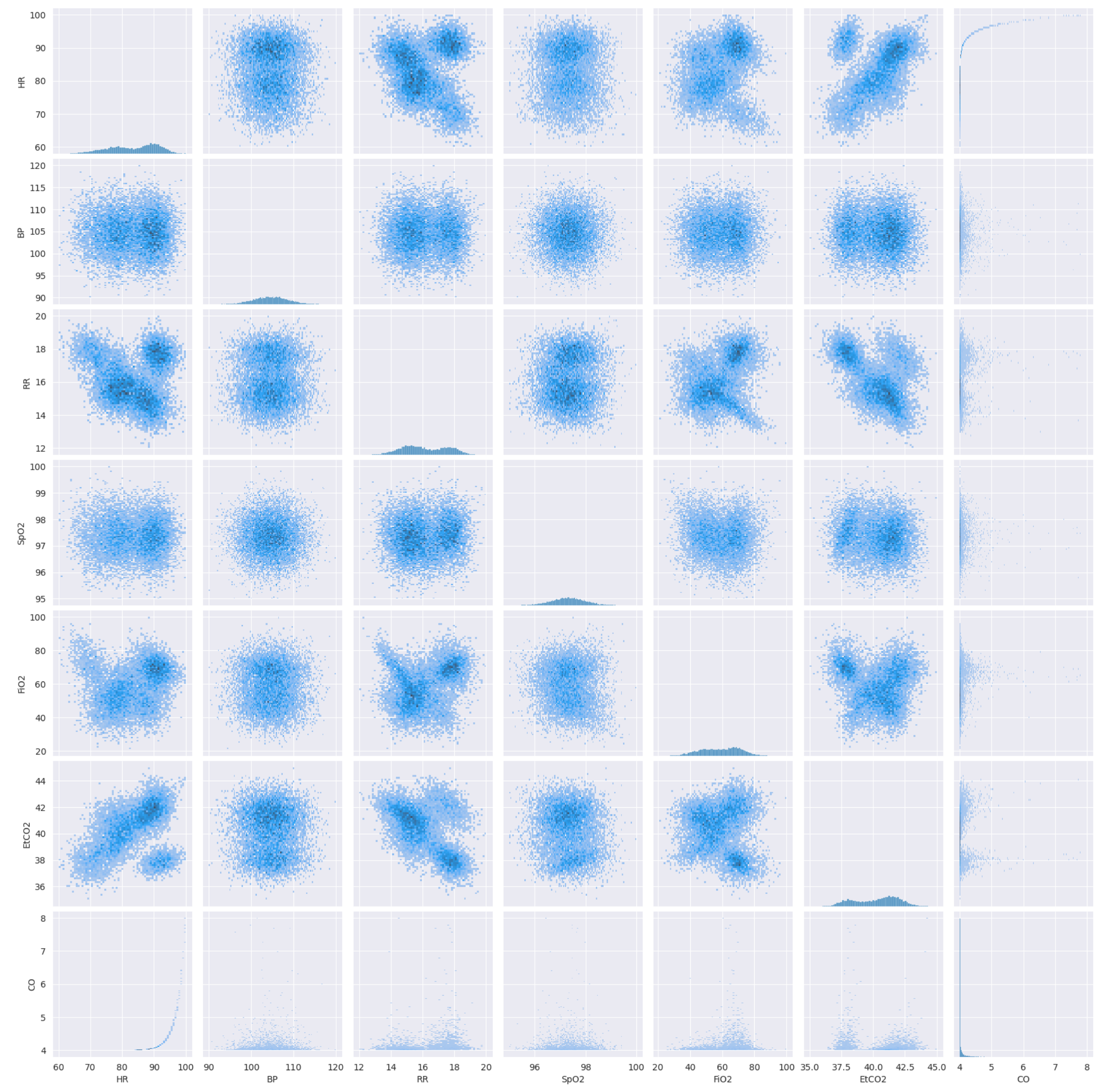

Distribucia hodnoty FiO2
Count
FiO2
0
250
500
750
1000
1250
1500
1750
2000
20
30
40
50
60
70
80
90
100


Distribucia hodnoty EtCO2
Count
EtCO2
0
500
1000
1500
2000
2500
36
38
40
42
44

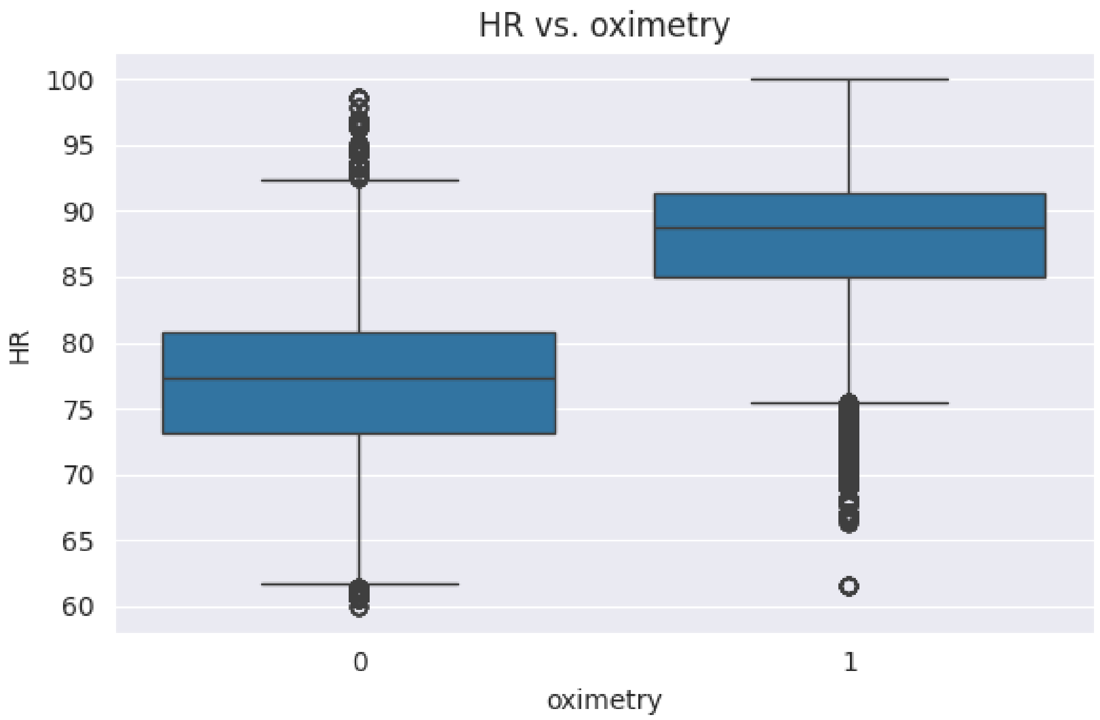


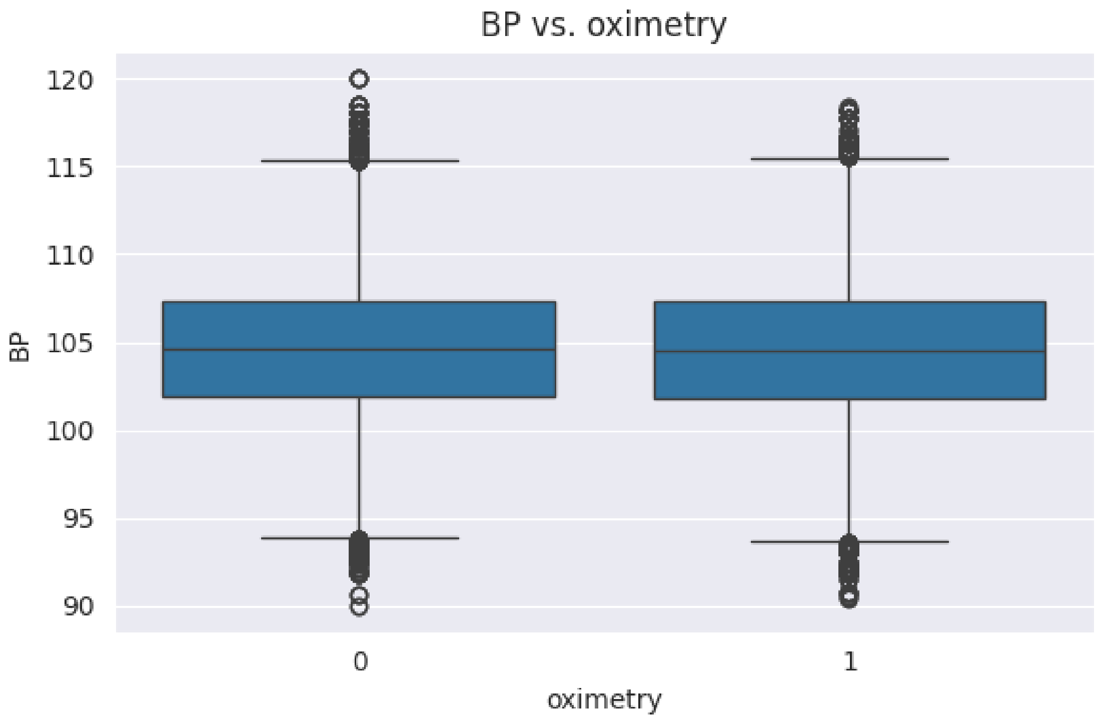
```
[858]: sns.pairplot(data=df[cols1], kind='hist')
```

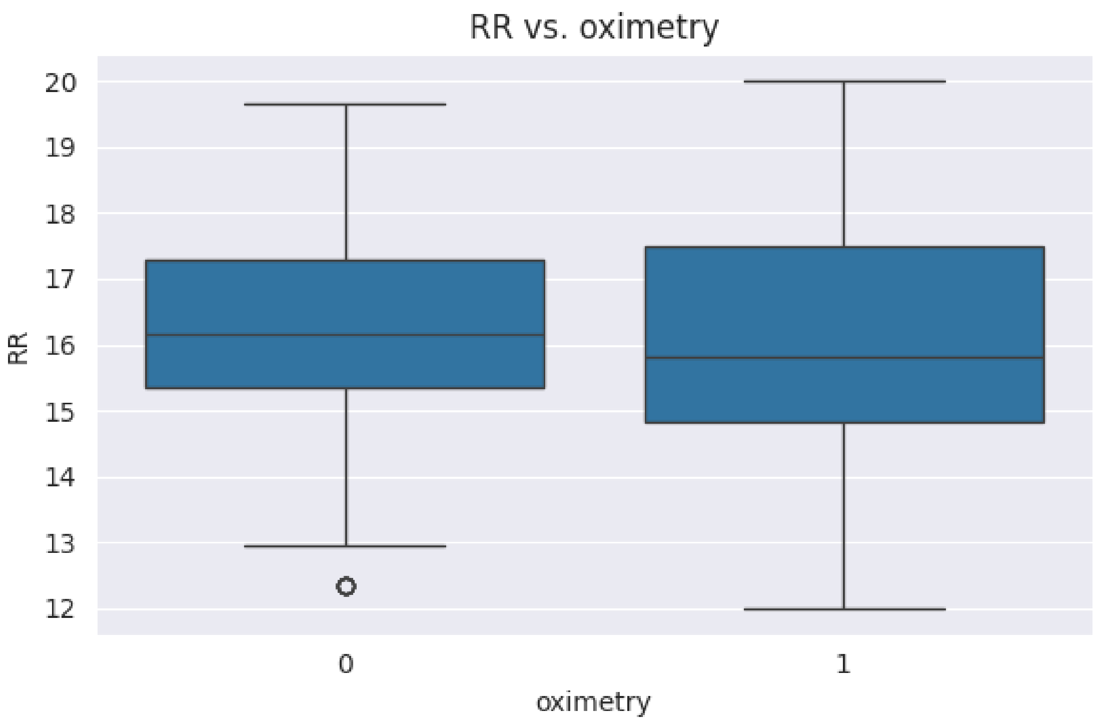
```
[858]: <seaborn.axisgrid.PairGrid at 0x2fb0f4f96e0>
```

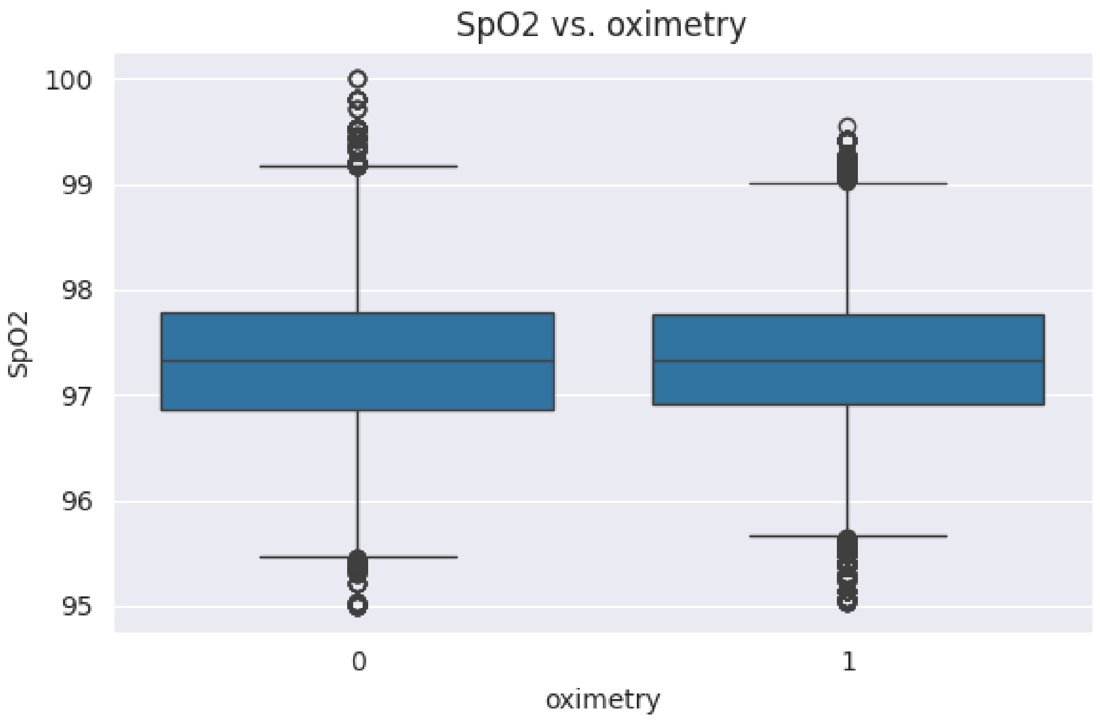


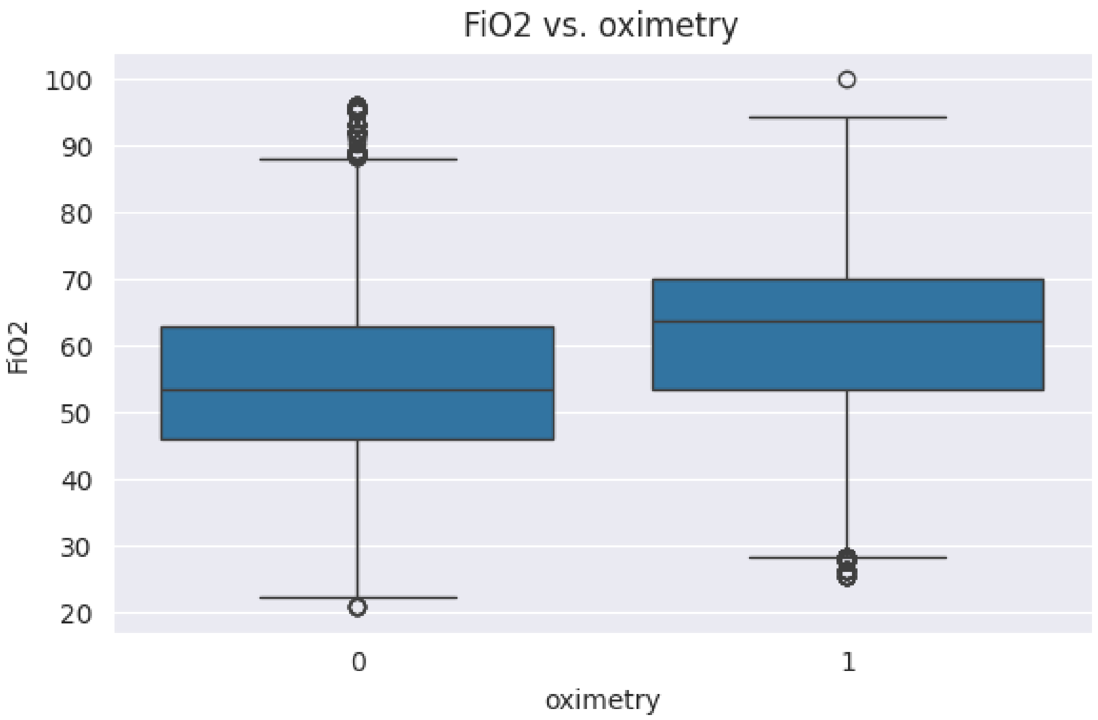
```
[859]: for col in cols1:
           plt.figure(figsize=(6,4))
           sns.boxplot(data=df, x='oximetry', y=col)
           plt.title(f'{col} vs. oximetry')
           plt.tight_layout()
           plt.show()
```

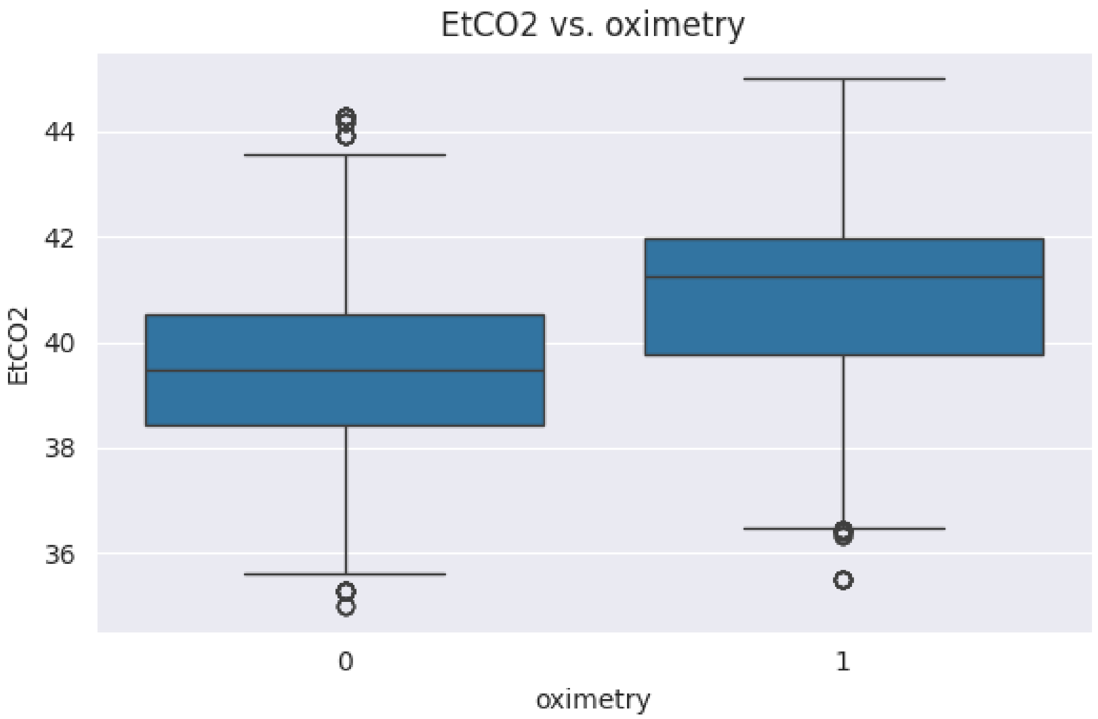

HR vs. oximetry
HR
100
95
90
85
80
75
70
65
60
0
1
oximetry

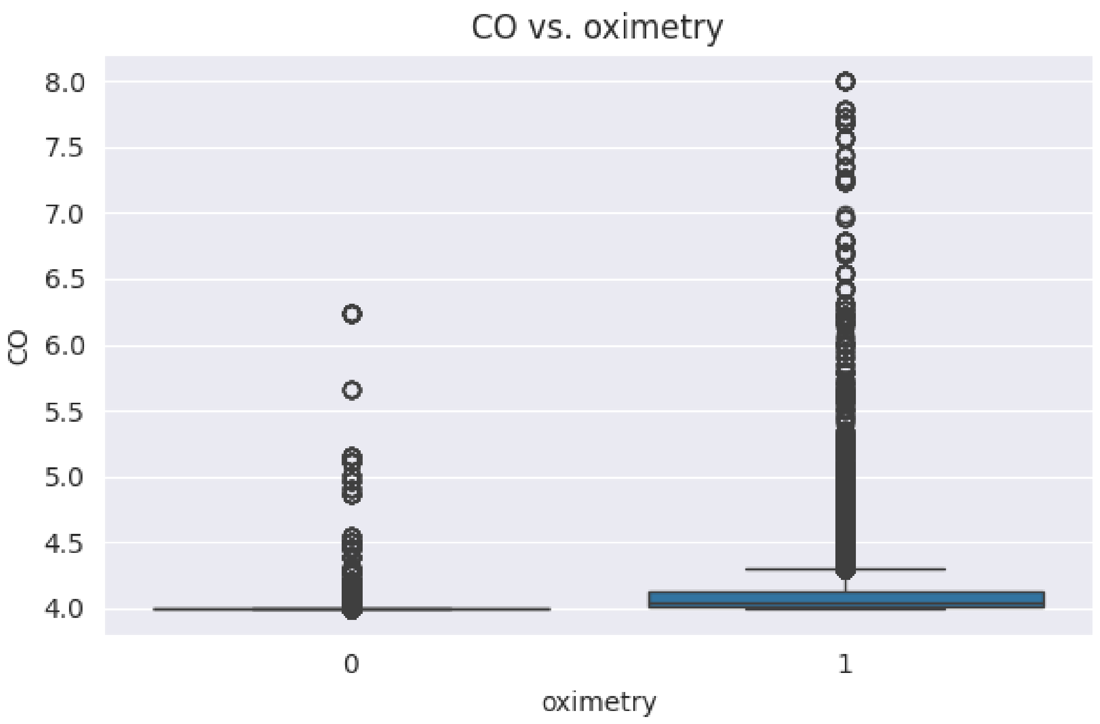

BP vs. oximetry
BP
120
115
110
105
100
95
90
0
1
oximetry


RR vs. oximetry
RR
20
19
18
17
16
15
14
13
12
0
1
oximetry


SpO2 vs. oximetry
SpO2
100
99
98
97
96
95
0
1
oximetry


FiO2 vs. oximetry
FiO2
100
90
80
70
60
50
40
30
20
0
1
oximetry


EtCO2 vs. oximetry
EtCO2
44
42
40
38
36
0
1
oximetry



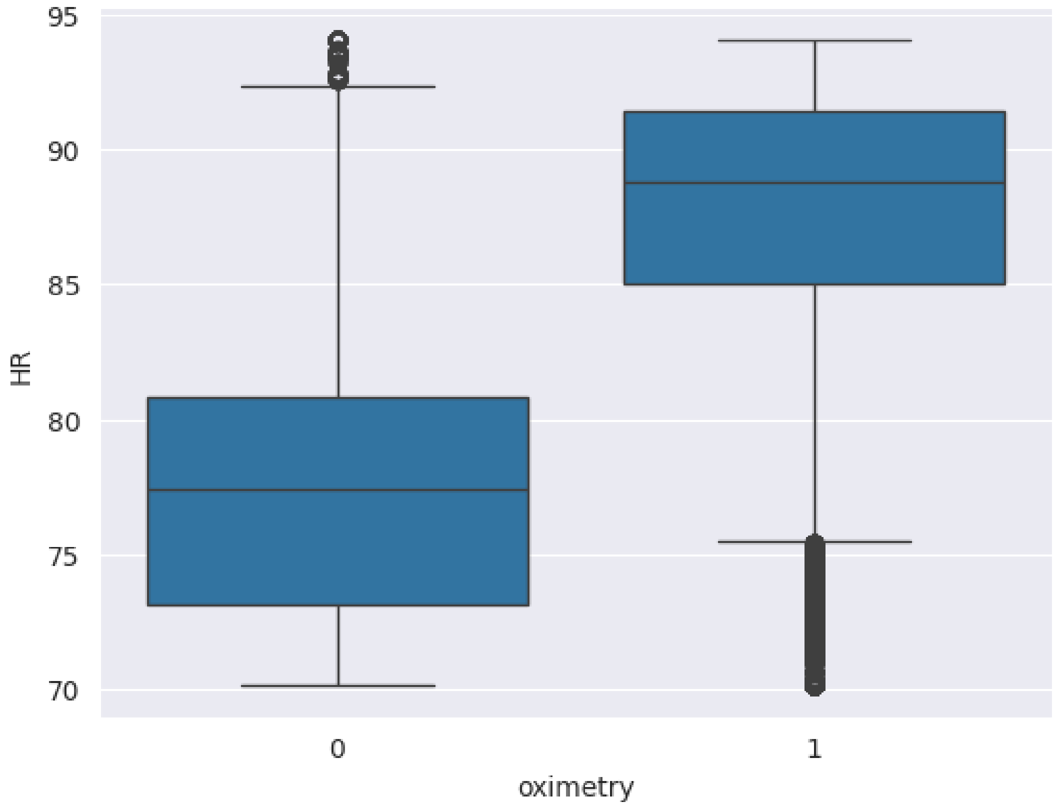
[860]:
```
# HR (Heart Rate) showed several extreme values .Very high for oximetry = 0 and␣
↪very low for oximetry = 1.
#These outliers can affect model accuracy, so in the next phase we will clean␣
↪them using the IQR method and winsorization (5th-95th percentile) to keep␣
↪only realistic heart rate values.

#The CO variable shows a highly right-skewed distribution with a long upper␣
↪tail, indicating a large number of potential outliers compared to other␣
↪attributes.
#These extreme values are likely to distort the model, so CO will require␣
↪normalization or outlier treatment (IQR filtering or winsorization).
```

[861]:
```
# Calculate 5th and 95th percentiles
low, high = df['HR'].quantile([0.05, 0.95])

# before winsorization
before = ((df['HR'] < low) | (df['HR'] > high)).sum()

# apply wins.
df_win = df.copy()
df_win['HR'] = df_win['HR'].clip(lower=low, upper=high)

# after winsorization
```

```
after = ((df_win['HR'] < low) | (df_win['HR'] > high)).sum()

print(f"Before winsorization: {before} outliers")
print(f"After winsorization: {after} outliers")

sns.boxplot(data = df_win, x='oximetry', y='HR')
```

```
Before winsorization: 6696 outliers
After winsorization: 0 outliers
```

[861]: `<Axes: xlabel='oximetry', ylabel='HR'>`



Now I can see that there is not such a values that are higher or lower to quntile range from 0.05 to 0.95 that's why we did not get any after winsortization value on the other hand we caught some outliers with the IQR method on df["CO"] atribute because he included many abnormal values

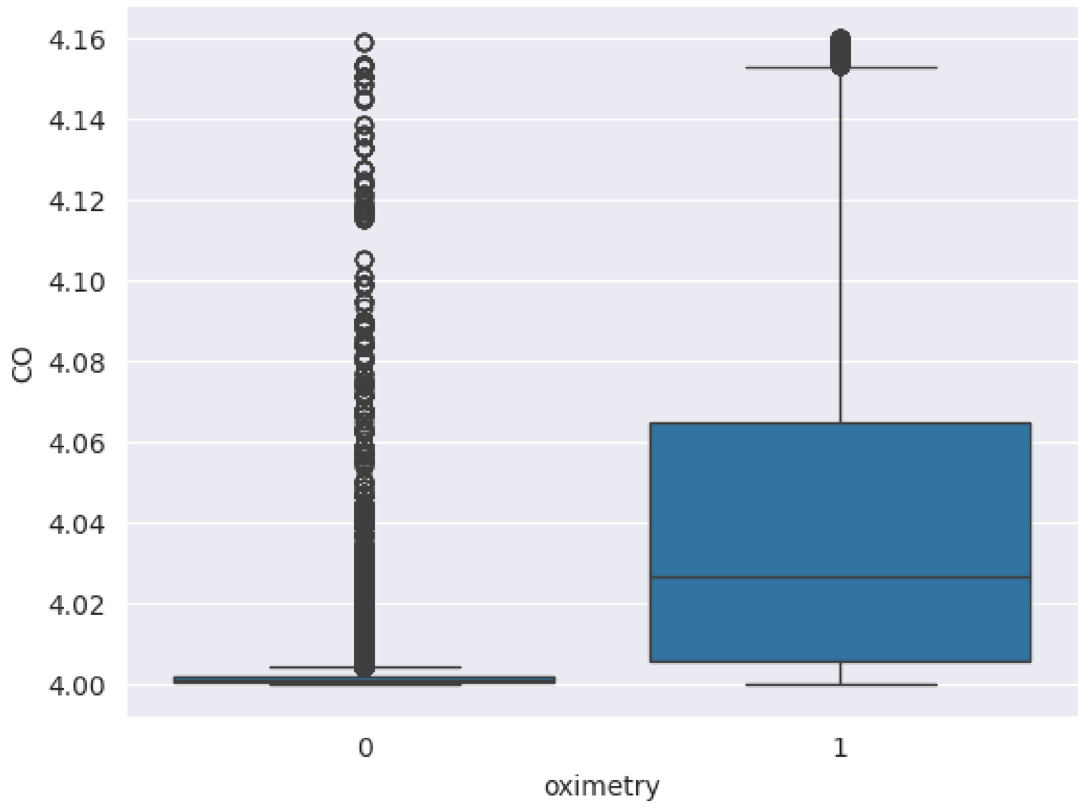
[862]:
```
# IQR bounders
Q1 = df['CO'].quantile(0.25)
Q3 = df['CO'].quantile(0.75)
IQR = Q3 - Q1

lower_bound = Q1 - 1.5 * IQR
```

```
upper_bound = Q3 + 1.5 * IQR

print(f"CO bounds (IQR): {lower_bound:.2f} - {upper_bound:.2f}")

# delete values out of range
df_iqr = df[(df['CO'] >= lower_bound) & (df['CO'] <= upper_bound)]

print(f"Removed {len(df) - len(df_iqr)} rows")
print(len(df_iqr))
```

```
CO bounds (IQR): 3.91 - 4.16
Removed 8460 rows
58513
```

[863]:
```
sns.boxplot(data=df_iqr, x='oximetry', y='CO')
```

[863]:
```
<Axes: xlabel='oximetry', ylabel='CO'>
```



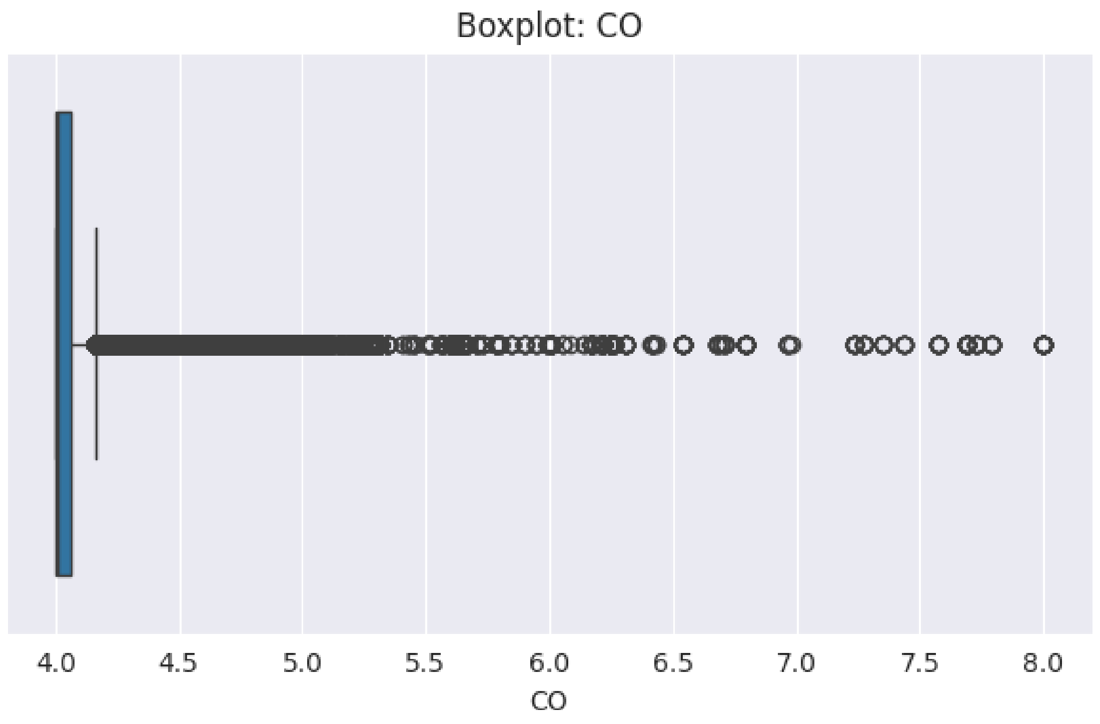
On the graph above we can see extreme difference on outlier values because the previous graph had values close to 9 and this has maximum values 4.16

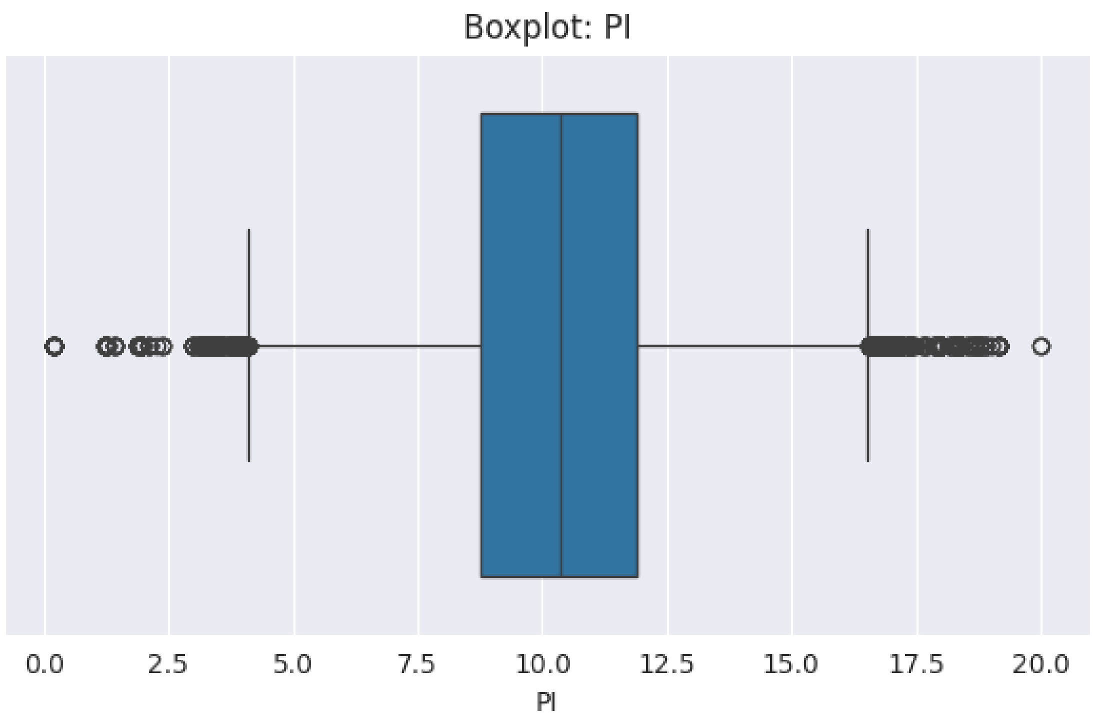
[864]:
```python
# all number collumns exept oximetry
num_cols = df.select_dtypes(include='number').columns.drop('oximetry',␣
 ↪errors='ignore')

#add collumns if in range of upper or lower bounder
iqr_summary = []
for col in num_cols:
    q1, q3 = df[col].quantile([0.25, 0.75])
    iqr = q3 - q1
    lower, upper = q1 - 1.5 * iqr, q3 + 1.5 * iqr
    outliers = ((df[col] < lower) | (df[col] > upper)).sum()
    iqr_summary.append([col, outliers, round(outliers / len(df) * 100, 2)])

# Display as a small DataFrame
iqr_df = pd.DataFrame(iqr_summary, columns=['Column', 'Outliers', 'Percent'])
iqr_df.sort_values('Percent', ascending=False, inplace=True)
iqr_df
```

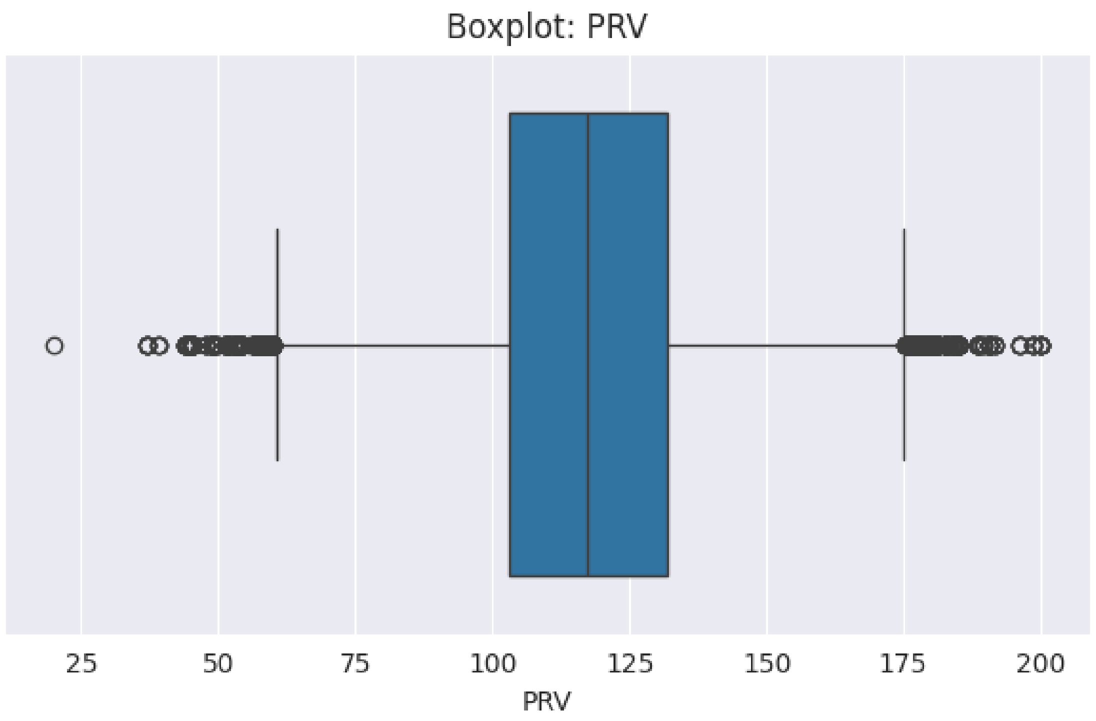
[864]:
```
                    Column  Outliers  Percent
13                      CO      8460    12.63
2                       PI       785     1.17
6                      PRV       633     0.95
20                latitude       627     0.94
14        Blood Flow Index       602     0.90
0                     SpO2       587     0.88
7                       BP       560     0.84
15   PPG waveform features       549     0.82
21               longitude       544     0.81
17      Respiratory effort       468     0.70
9    Motion/Activity index       472     0.70
12                      SV       439     0.66
8         Skin Temperature       432     0.65
11                Hb level       352     0.53
16    Signal Quality Index       351     0.52
10                     PVI       344     0.51
5                     FiO2         5     0.01
4                    EtCO2         0     0.00
1                       HR         0     0.00
3                       RR         0     0.00
19                     SNR         0     0.00
18     O2 extraction ratio         0     0.00
22              station_ID         0     0.00
23                 user_id         0     0.00
```

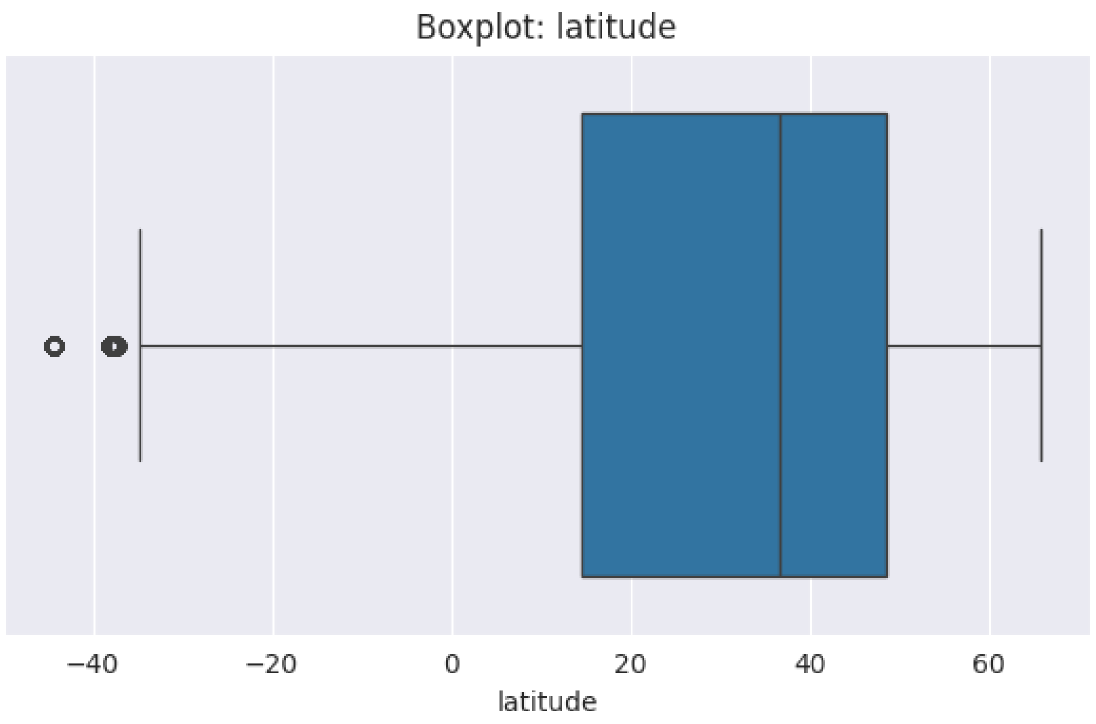
It's bad practice to analyze a atribute one by one so I created a list of numeric values that I can analyze at once. I calculated they're IQR based on dividing they're quantile (0.25 and 0.75) .If any value is less than lower value (<0.25) that it is added to list of outliers this process also include calculating if value is greater that upper bounder (>0.75).

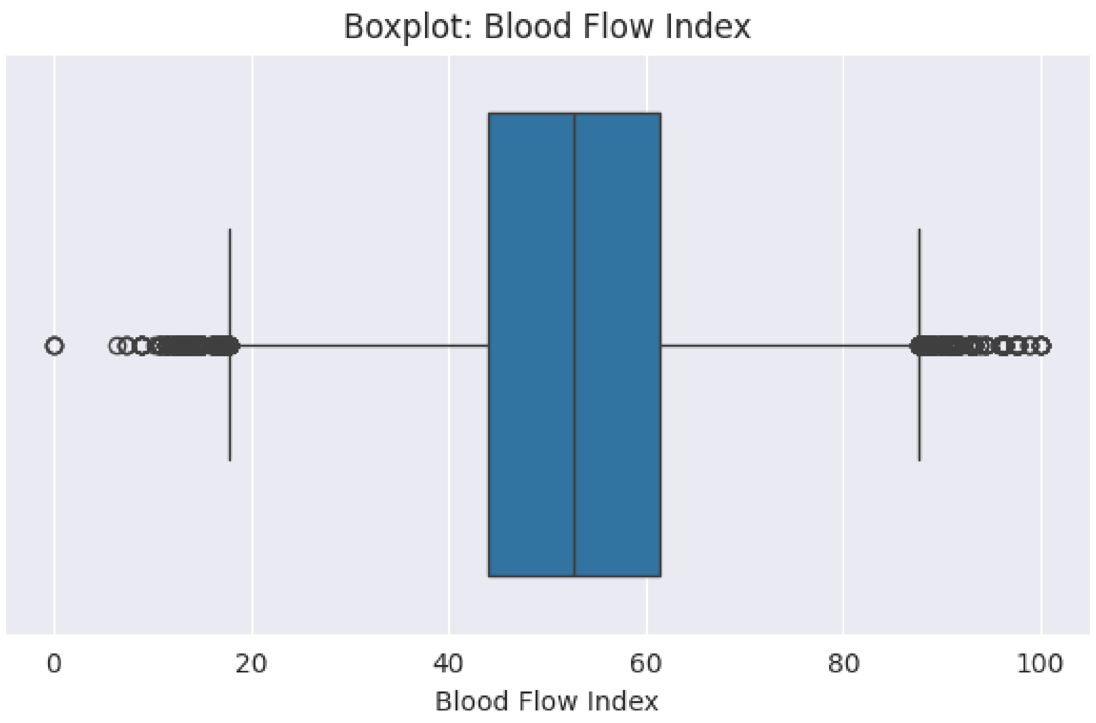
[865]:
```
suspects = iqr_df[ iqr_df['Outliers'] > 0 ]['Column'].head(6).tolist()

for col in suspects:
    plt.figure(figsize=(6,4))
    sns.boxplot(x=df[col])
    plt.title(f'Boxplot: {col}')
    plt.tight_layout()
    plt.show()
```

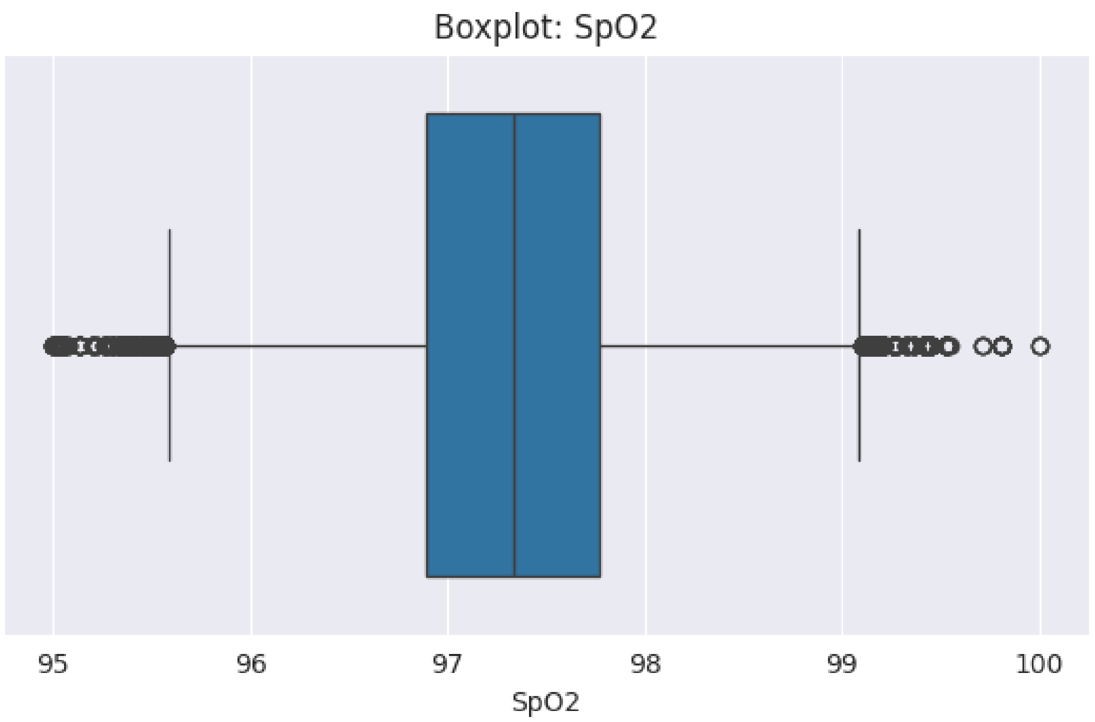



Boxplot: PI
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
PI


Boxplot: PRV
25
50
75
100
125
150
175
200
PRV


Boxplot: latitude
−40
−20
0
20
40
60
latitude


Boxplot: Blood Flow Index
0
20
40
60
80
100
Blood Flow Index



3.3 1.3 Formulácia a štatistické overenie hypotéz o dátach

3.3.1 Zle hypotezy

Hypotéza 1 – rozdiel v tepovej frekvencii podľa stavu saturácie

H (Null Hypothesis): The mean heart rate (HR) is the same for both groups — patients with oximetry = 0 and oximetry = 1.

H (Alternative Hypothesis): The mean heart rate (HR) differs between the groups — patients with oximetry = 0 and oximetry = 1.

[866]:
```
const_shapiro = 5000
# I will create 2 datasets hro0 (HE and oximtery = 0) and hro1 (HE column and␣
  ↪oximetry = 1)
hr0 = df[df['oximetry'] == 0]['HR']
hr1 = df[df['oximetry'] == 1]['HR']


sample_hr0 = hr0.sample(const_shapiro, random_state=42)
sample_hr1 = hr1.sample(const_shapiro, random_state=42)

print(shapiro(sample_hr0))
print(shapiro(sample_hr1))
```

```
ShapiroResult(statistic=np.float64(0.9964622127654921),
pvalue=np.float64(1.5086056537686 3e-09))
ShapiroResult(statistic=np.float64(0.9381229280127523),
pvalue=np.float64(1.7803348598149635e-41))
```

[867]:
```
#we can see that the pvalues from both samples are lower than 0.05 which␣
 ↪indicates to not normal distributed data
#based on that we need to perform Mann-whitney U test not basic T-test that␣
 ↪need normal distribution

stat, p = stats.mannwhitneyu(sample_hr0, sample_hr1)
print(f"Mann-Whitney U-test p-value: {p:.3e}")

# the value is super close to 0 that means that we denied H0 => there is a␣
 ↪statistically significant difference
# in heart rate (HR) between the groups (oximetry = 0 and oximetry = 1).
```

```
Mann-Whitney U-test p-value: 0.000e+00
```

Hypothesis 2 – Difference in EtCO based on oxygen saturation (oximetry)

H (Null Hypothesis): The mean EtCO level is the same for both groups — patients with oximetry = 0 and oximetry = 1.

H (Alternative Hypothesis): The mean EtCO level differs between the groups — patients with oximetry = 0 and oximetry = 1.

[868]:
```
df.columns
```

[868]:
```
Index(['SpO2', 'HR', 'PI', 'RR', 'EtCO2', 'FiO2', 'PRV', 'BP',
       'Skin Temperature', 'Motion/Activity index', 'PVI', 'Hb level', 'SV',
       'CO', 'Blood Flow Index', 'PPG waveform features',
       'Signal Quality Index', 'Respiratory effort', 'O2 extraction ratio',
       'SNR', 'oximetry', 'latitude', 'longitude', 'station_ID', 'QoS', 'code',
       'user_id', 'blood_group'],
      dtype='object')
```

[869]:
```
etco0 = df[df['oximetry'] == 0]['EtCO2']
etco1 = df[df['oximetry'] == 1]['EtCO2']

#sample for max 5000
sample_etco0 = etco0.sample(5000, random_state=42)
sample_etco1 = etco1.sample(5000, random_state=42)

# normality check
print(shapiro(sample_etco0))
print(shapiro(sample_etco1))
```

```
# if both p > 0.05 → data are normally distributed
# then perform Student's T-test
stat, p = stats.mannwhitneyu(etco0, etco1)
print(f"U-test p-value: {p:.3e}")
```

```
ShapiroResult(statistic=np.float64(0.9938690077488066),
pvalue=np.float64(8.316180710196192e-14))
ShapiroResult(statistic=np.float64(0.9191799162237433),
pvalue=np.float64(1.0762260080747649e-45))
U-test p-value: 0.000e+00
```

there is a statistically significant difference in mean EtCO between patients with oximetry = 0 and oximetry = 1.

3.3.2 A) Hypothesis 1 – Difference in SPO based on oxygen saturation (oximetry)

H (Null Hypothesis): The mean SPO level is the same for both groups — patients with oximetry = 0 and oximetry = 1.

H (Alternative Hypothesis): The mean SPO level differs between the groups — patients with oximetry = 0 and oximetry = 1.

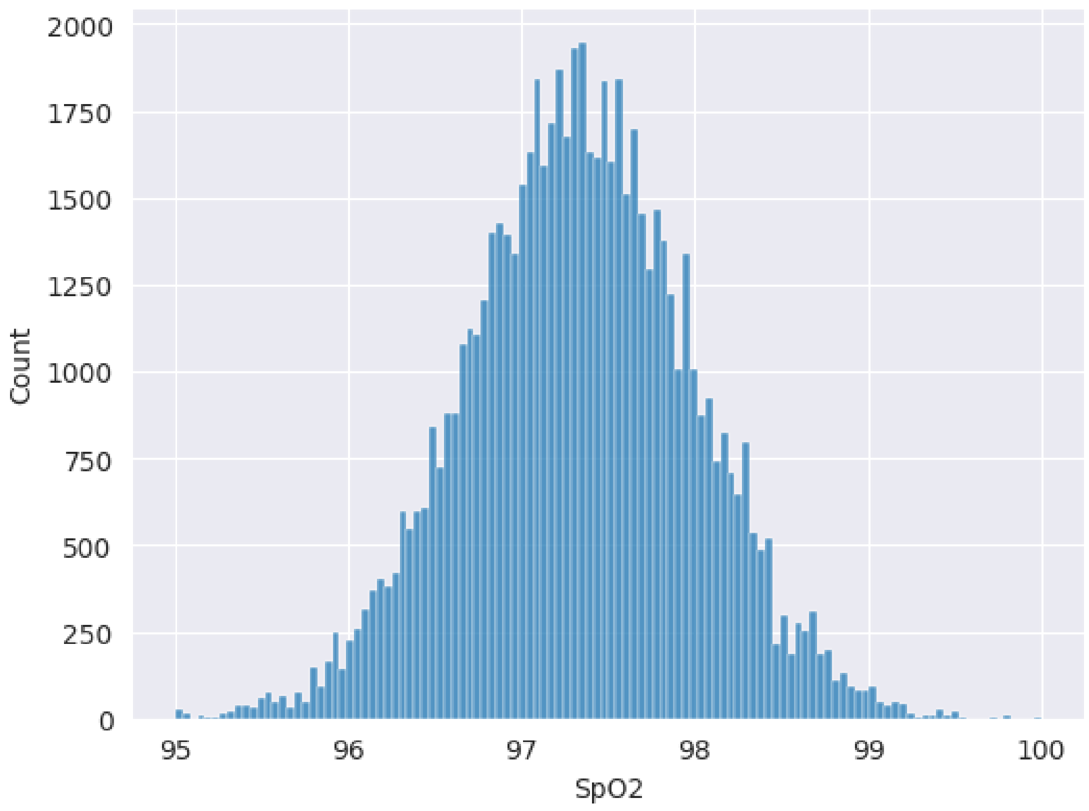
[870]:
```
#division of the data into oximetry == 1 and oximetry == 0 groups
g1 = df[df['oximetry'] == 1]['SpO2']
g0 = df[df['oximetry'] == 0]['SpO2']

#doing the shapiro test -> pvalue for both values
p1 = shapiro(g1).pvalue
p0 = shapiro(g0).pvalue
print('shapiro:', p1, p0)
# even if the p values do not indicate normal division of the data, we will␣
↪continue with levenne and ttest since from the histogram we can see that the␣
↪data is indeed rather normally distributed, this error is probably caused by␣
↪the table creation
```

```
shapiro: 9.472557968212563e-07 0.0018560650823116259
```

```
C:\Users\mudry\AppData\Local\Programs\Python\Python313\Lib\site-
packages\scipy\stats\_axis_nan_policy.py:579: UserWarning: scipy.stats.shapiro:
For N > 5000, computed p-value may not be accurate. Current N is 40029.
  res = hypotest_fun_out(*samples, **kwds)
C:\Users\mudry\AppData\Local\Programs\Python\Python313\Lib\site-
packages\scipy\stats\_axis_nan_policy.py:579: UserWarning: scipy.stats.shapiro:
For N > 5000, computed p-value may not be accurate. Current N is 26944.
  res = hypotest_fun_out(*samples, **kwds)
```

[871]:
```
sns.histplot(df['SpO2'])
```

[871]:
```
<Axes: xlabel='SpO2', ylabel='Count'>
```

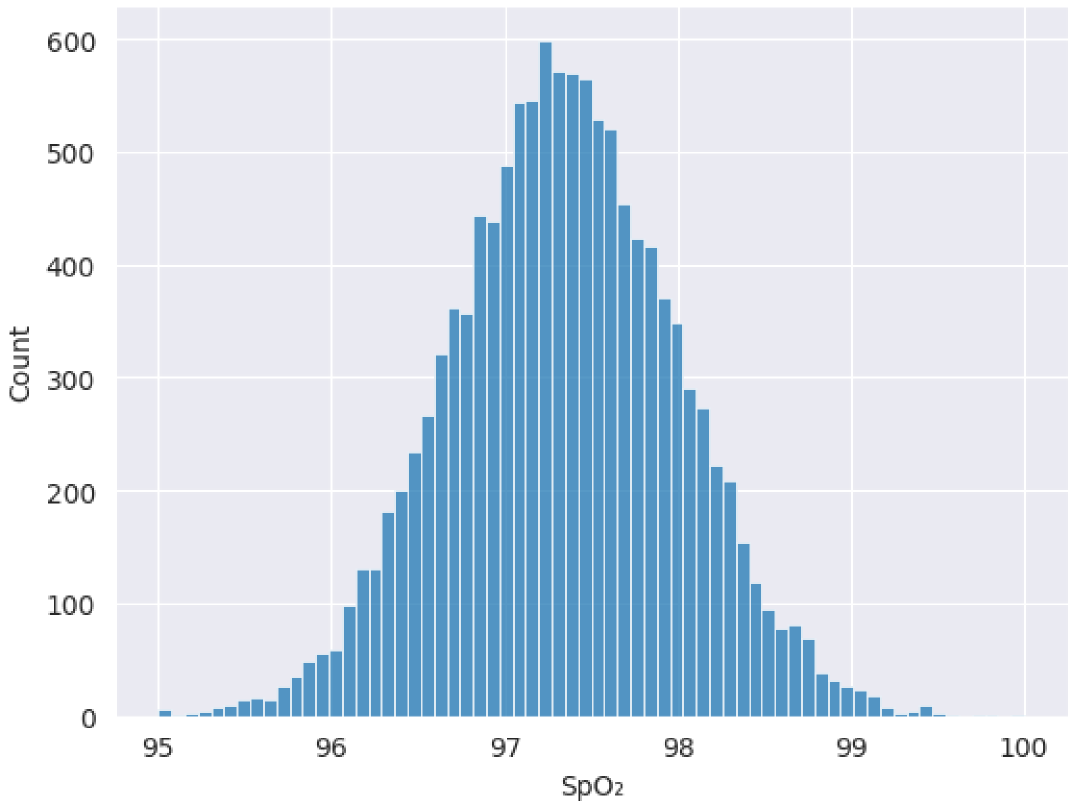


[872]:
```
#due to the findings in the previous cell, we found out the merging of the␣
↪tables reshaped the distribution of the data into not so normally␣
↪distributed, this however could be fixed by performing the tests on the␣
↪observation_df (non merged table).
g1 = observation_df[observation_df['oximetry'] == 1]['SpO ']
g0 = observation_df[observation_df['oximetry'] == 0]['SpO ']

#we need to set sample to max 5000 so the data are in range of the recommended␣
↪sample value
sample_g1 = g1.sample(3000, random_state=42)
sample_g0= g0.sample(3000, random_state=42)

#doing the shapiro test -> pvalue for both values
p1 = shapiro(sample_g1).pvalue
p0 = shapiro(sample_g0).pvalue
print('shapiro:', p1, p0)
#after performing the shapiro test we can see that the p values from both the␣
↪grous are larger than 0.05 which proves that the normal distribution is␣
↪present which leads us to perform the levene and t test
```

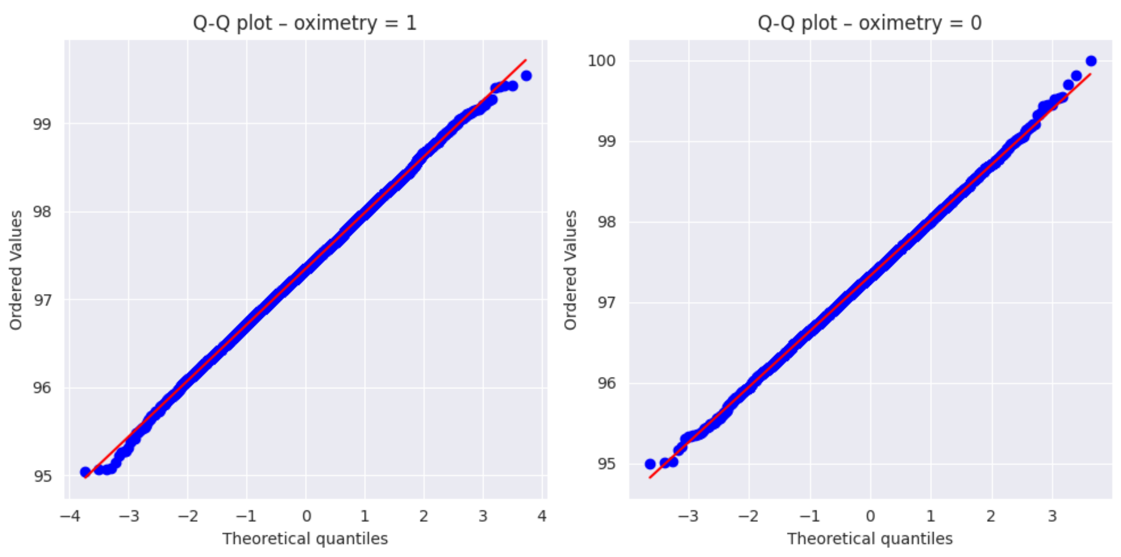
```
shapiro: 0.10880973933264598 0.6169824476877354
```

[873]:
```
sns.histplot(observation_df['SpO '])
```

[873]:
```
<Axes: xlabel='SpO ', ylabel='Count'>
```



[874]:
```
#lets verify the distributions of both the subsets via qqplot
fig, ax = plt.subplots(1, 2, figsize=(10, 5))

stats.probplot(g1, dist="norm", plot=ax[0])
ax[0].set_title("Q-Q plot - oximetry = 1")

stats.probplot(g0, dist="norm", plot=ax[1])
ax[1].set_title("Q-Q plot - oximetry = 0")

plt.tight_layout()
plt.show()
#they indeed are
```



[875]:
```
#levenne tests, this whole block is executed since the data are normally␣
↪distributed
p_lev = stats.levene(sample_g1,sample_g0).pvalue
print('levene:', p_lev)

if p_lev > 0.05:
    # since the variance is the same we can perfrom the usual t-test
    t, p = stats.ttest_ind(sample_g1, sample_g0)
    print('t-test', t, p)
else:
    # variances differ, use Welch's t-test - we know this wasnt in our class␣
↪notebooks, but we needed to find out if the two groups differ even though␣
↪they have different variance, so we found this method
    t, p = stats.ttest_ind(sample_g1, sample_g0, equal_var=False)
    print('Welch t-test (unequal variances):', t, p)
```

```
levene: 1.2531887614623825e-05
Welch t-test (unequal variances): 0.09803193034222664 0.9219102349142181
```

[876]:
```
# Both groups are normally distributed (Shapiro > 0.05), but their variances␣
↪differ (Levene < 0.05). The Mann-Whitney U test (p = 0.0984 > 0.05) shows no␣
↪statistically significant difference in SpO  levels between oximetry = 0 and␣
↪oximetry = 1.
```

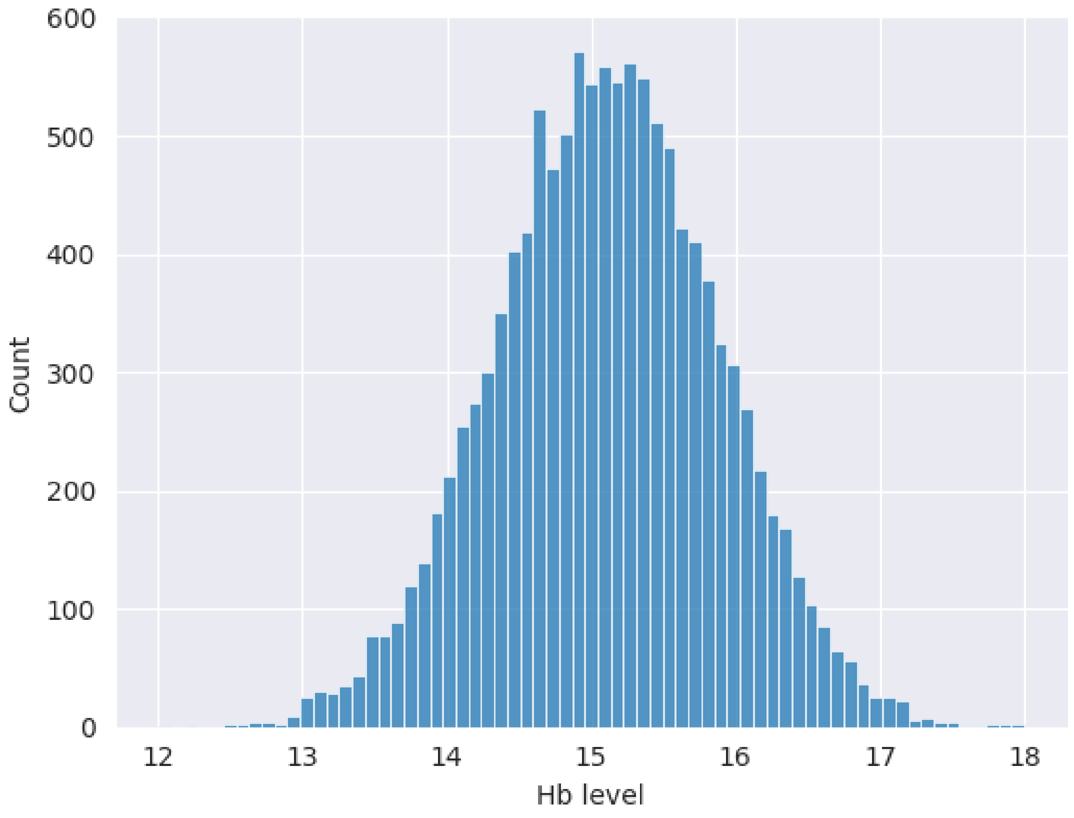
3.3.3 A) Hypothesis 2 - Comparison of Hemoglobin (Hb) Levels Between Oximetry Groups

H (Null Hypothesis): The mean hemoglobin (Hb) level is the same for both groups — patients with oximetry = 0 and oximetry = 1.

H (Alternative Hypothesis): The mean hemoglobin (Hb) level differs between the groups — patients with oximetry = 0 and oximetry = 1.

```
[877]: sns.histplot(observation_df['Hb level'])
```

```
[877]: <Axes: xlabel='Hb level', ylabel='Count'>
```

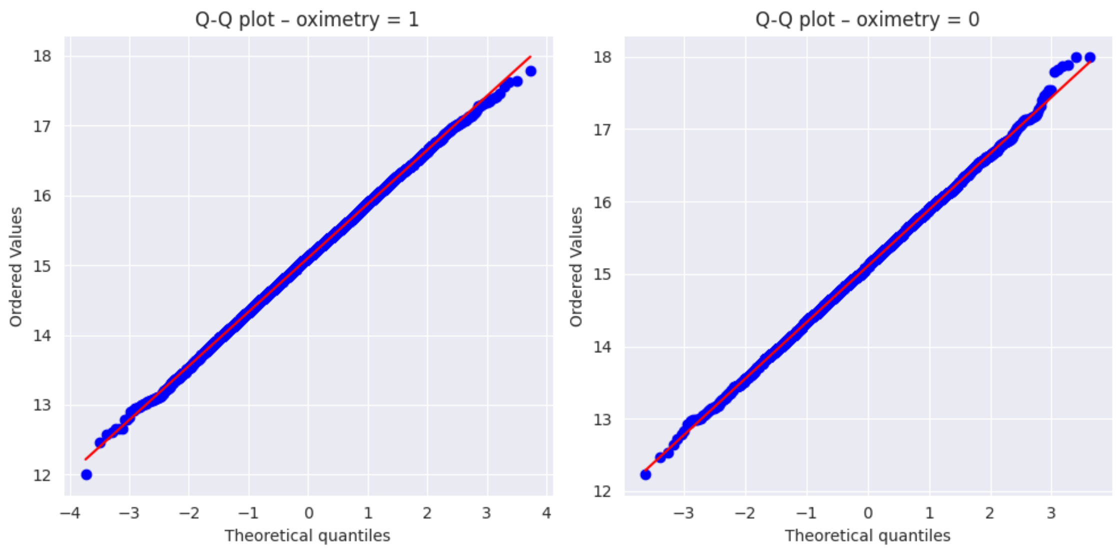


```
[878]: hb0 = observation_df[observation_df['oximetry'] == 0]['Hb level']
hb1 = observation_df[observation_df['oximetry'] == 1]['Hb level']

#we need to set sample to max 5000 so the data are in range of the recommended␣
 ↪sample value
sample_hb0= hb0.sample(2000, random_state=42)
sample_hb1 = hb1.sample(2000, random_state=42)

#doing the shapiro test -> pvalue for both values
p0 = shapiro(sample_hb0).pvalue
p1 = shapiro(sample_hb1).pvalue
print('shapiro:\np0:{} \np1:{}'.format(p0,p1))
```

```
shapiro:
p0:0.11878125043102106
```

```
p1:0.85391674151546
```

[879]:
```
#lets verify the distributions of both the subsets via qqplot
fig, ax = plt.subplots(1, 2, figsize=(10, 5))

stats.probplot(hb1, dist="norm", plot=ax[0])
ax[0].set_title("Q-Q plot - oximetry = 1")

stats.probplot(hb0, dist="norm", plot=ax[1])
ax[1].set_title("Q-Q plot - oximetry = 0")

plt.tight_layout()
plt.show()
#they indeed are
```



[880]:
```
#same as HO
p_lev = stats.levene(sample_hb1,sample_hb0).pvalue
print('levene:', p_lev)

if p_lev > 0.05:
    # this was explained in HO
    t, p = stats.ttest_ind(sample_hb1, sample_hb0)
    print('t-test ', t, p)
else:
    # this was explained in HO
    t, p = stats.ttest_ind(sample_hb1, sample_hb0, equal_var=False)
    print('Welch t-test (unequal variances):', t, p)
```

```
levene: 0.6624508281537517
```

```
t-test  -1.588383168023951 0.11227879476272101
```

[881]:
```
# Both groups are normally distributed (Shapiro > 0.05), with their variance␣
↪being very similar as well. Students t test shows that the difference of the␣
↪means was not statistically significant.
```

3.3.4 B) Overte či Vaše štatistické testy majú dostatok podpory z dát, teda či majú dostatočne silnú štatistickú silu.

[882]:
```
# SpO2 attribute
y0 = sample_g0.values
y1 = sample_g1.values

# base stats
m0, m1 = np.mean(y0), np.mean(y1)
s0, s1 = np.std(y0, ddof=1), np.std(y1, ddof=1)
n0, n1 = len(y0), len(y1)

# CI
se = np.sqrt(s0**2/n0 + s1**2/n1)
df_temp = (s0**2/n0 + s1**2/n1)**2 / ((s0**4)/((n0**2)*(n0-1)) + (s1**4)/
↪((n1**2)*(n1-1)))
ci = stats.t.interval(0.95, df_temp, loc=(m1 - m0), scale=se)
print(f"95% CI for delta means: {ci[0]:.3f} to {ci[1]:.3f}")
#very little difference -> strong statistical power
```

```
95% CI for delta means: -0.032 to 0.035
```

[883]:
```
#Cohen
sp = np.sqrt(((n0 - 1)*s0**2 + (n1 - 1)*s1**2) / (n0 + n1 - 2))
d = (m1 - m0) / sp
print(f"Cohen's d: {d:.3f}")
#almost 0 difference -> strong statistical power
```

```
Cohen's d: 0.003
```

CI ranging from -0.032 to 0.035 and cohens'd being 0.003 shows us that there is strong statistical power and that the tests have enough support from the data to be legitimate

[884]:
```
# HB level attribute
y0 = sample_hb0.values
y1 = sample_hb1.values

# base stats
m0, m1 = np.mean(y0), np.mean(y1)
s0, s1 = np.std(y0, ddof=1), np.std(y1, ddof=1)
n0, n1 = len(y0), len(y1)

# CI
```

```
se = np.sqrt(s0**2/n0 + s1**2/n1)
df_temp = (s0**2/n0 + s1**2/n1)**2 / ((s0**4)/((n0**2)*(n0-1)) + (s1**4)/
 ↪((n1**2)*(n1-1)))
ci = stats.t.interval(0.95, df_temp, loc=(m1 - m0), scale=se)
print(f"95% CI for delta means: {ci[0]:.3f} to {ci[1]:.3f}")
#same result as with SPO2
```

```
95% CI for delta means: -0.087 to 0.009
```

[885]:
```
#Cohen
sp = np.sqrt(((n0 - 1)*s0**2 + (n1 - 1)*s1**2) / (n0 + n1 - 2))
d = (m1 - m0) / sp
print(f"Cohen's d: {d:.3f}")
#almost 0 difference -> strong statistical power
```

```
Cohen's d: -0.050
```

CI ranging from -0.087 to 0.009 and cohens'd being -0.050 shows us that there is strong statistical power and that the tests have enough support from the data to be legitimate

4 Fáza 2

4.1 2.1 Realizácia predspracovania dát

4.1.1 A)

Before doing the magic with spliting data we need to set them up by filtering only atributes we need and are usefull in future analysis

[886]:
```
df_2 = df.copy()

# we want to work with the data that has some connectivity to "health"␣
 ↪specification not anything like position ...
drop_cols = [c for c in ['user_id','station_ID','latitude','longitude'] if c in␣
 ↪df_2.columns]
df_2 = df_2.drop(columns=drop_cols)

df_2 = df_2.drop_duplicates()
```

[887]:
```
target = "oximetry"

#split featires and target
X = df_2.drop(columns=[target])
y = df_2[target]
```

[888]:
```
X_train, X_test, y_train, y_test = train_test_split(
    X, y,
    test_size=0.2,
    random_state=42,
    stratify=y
)

print("Train dataframe:", X_train.shape)
print("Test dataframe:", X_test.shape)
print("Oximetry=1/total for train:", y_train.mean().round(3))
print("Oximetry=1/total for test:", y_test.mean().round(3))
#we can see the division of the original df into train and test subdatasets, we␣
↪can also see the stratification focused on the oximetry attribute worked
```

```
Train dataframe: (41501, 23)
Test dataframe: (10376, 23)
Oximetry=1/total for train: 0.597
Oximetry=1/total for test: 0.597
```

4.1.2 B)

[889]:
```
X_test.head()
```

[889]:
```
            SpO2         HR          PI         RR      EtCO2       FiO2  \
49445  96.601411  80.344377   8.884552  15.344047  38.825321  55.089020
30741  97.993688  83.684406  11.323195  15.208839  41.193087  63.886566
52230  96.805991  89.893353   7.491702  14.655980  42.801724  62.273550
50948  97.293984  77.630562  11.833415  16.148954  42.182432  65.501698
58059  97.263038  84.972915  10.198301  14.049168  39.057607  59.162991

              PRV          BP  Skin Temperature  Motion/Activity index  …  \
49445   84.643454  105.944792         34.263087              10.094809  …
30741  111.221376  106.803949         34.890998               9.349818  …
52230  108.099974  101.153579         36.156039              10.064168  …
50948  130.012206  100.104509         35.036113               8.346491  …
58059  129.506948   99.689616         36.135584               9.809290  …

             CO  Blood Flow Index  PPG waveform features  \
49445  4.001692         67.333233              38.870747
30741  4.005741         42.993997              33.119117
52230  4.067662         50.017832              37.370695
50948  4.000921         49.619197              60.764507
58059  4.009634         60.365075              58.944290

       Signal Quality Index  Respiratory effort  O2 extraction ratio  \
49445             76.138614           40.726619             0.268550
30741             24.206459           33.059317             0.256908
52230             59.558249           44.561747             0.210238
50948             42.742079           46.305055             0.219876
58059             55.162309           69.790015             0.245487
```

```
             SNR          QoS  code  blood_group
49445  25.952849         good    AM          AB+
30741  31.628228    excellent    PH           O-
52230  28.975340    excellent    AU           O+
50948  29.580558  maintenance    FR           O+
58059  22.505126    excellent    IN           A+

[5 rows x 23 columns]
```

[890]:
```
X_train.columns
```

[890]:
```
Index(['SpO2', 'HR', 'PI', 'RR', 'EtCO2', 'FiO2', 'PRV', 'BP',
       'Skin Temperature', 'Motion/Activity index', 'PVI', 'Hb level', 'SV',
       'CO', 'Blood Flow Index', 'PPG waveform features',
       'Signal Quality Index', 'Respiratory effort', 'O2 extraction ratio',
       'SNR', 'QoS', 'code', 'blood_group'],
      dtype='object')
```

[891]:
```
print(X_train.dtypes)
#every attribute is either category or float64, however this was not the case␣
↪when we started working with the dataset, QoS, code and blood group were␣
↪changed into category datatype in 1.2 A), 3rd cell -> we now have to turn␣
↪category attributes into numberic attributes
```

```
SpO2                      float64
HR                        float64
PI                        float64
RR                        float64
EtCO2                     float64
FiO2                      float64
PRV                       float64
BP                        float64
Skin Temperature          float64
Motion/Activity index     float64
PVI                       float64
Hb level                  float64
SV                        float64
CO                        float64
Blood Flow Index          float64
PPG waveform features     float64
Signal Quality Index      float64
Respiratory effort        float64
O2 extraction ratio       float64
SNR                       float64
QoS                      category
code                     category
blood_group              category
```

```
dtype: object
```

[892]:
```
X_train['QoS'].unique()
```

[892]:
```
['good', 'excellent', 'acceptable', 'maintenance']
Categories (4, object): ['acceptable', 'excellent', 'good', 'maintenance']
```

[893]:
```
#It makes sense to use ordinal encoding on QoS, since we can set which is the␣
↪best(excellent) and which is the worst(maintenece)
qos_order = CategoricalDtype(
    categories=["maintenance", "acceptable", "good", "excellent"],
    ordered=True
)

X_train["QoS"] = X_train["QoS"].astype(qos_order)

X_train["QoS_ord"] = X_train["QoS"].cat.codes
X_train = X_train.drop(columns=["QoS"])
```

[894]:
```
X_train['blood_group'].unique()
```

[894]:
```
['A-', 'B+', 'AB+', 'A+', 'AB-', 'O+', 'O-', 'B-']
Categories (8, object): ['A+', 'A-', 'AB+', 'AB-', 'B+', 'B-', 'O+', 'O-']
```

[895]:
```
X_train = pd.get_dummies(X_train, columns=["blood_group"], prefix="bg")
```

[896]:
```
X_train['code'].unique()
```

[896]:
```
['KR', 'CN', 'BJ', 'AR', 'US', …, 'EC', 'HK', 'CH', 'MK', 'CF']
Length: 97
Categories (96, object): ['AF', 'AM', 'AO', 'AR', …, 'VE', 'VN', 'VU', 'ZA']
```

[897]:
```
#we also remember that the code attribute is the only attribute that has a␣
↪missing value which belonged to Okinawa station, we will simply drop these␣
↪rows
#I did think about imputing the station with a new code for Japan, but its␣
↪really only 100 rows and we cant use an imputing strategy that could be␣
↪later replicated as this is Okinawa only...
X_train = X_train.dropna()
```

[898]:
```
#after further analysis we decided to drop code column alltogether, as the only␣
↪viable encoding option was frequency encoding but that would eventually make␣
↪no sense...
#We know we should not change te test dataset in this part but this is not␣
↪really a preprocessing method
X_train = X_train.drop(columns=["code"])
X_test = X_test.drop(columns=["code"])
```

```
[899]: print(X_test.dtypes)
       #We can see that there are no more non numeric attributes!
```

```
SpO2                         float64
HR                           float64
PI                           float64
RR                           float64
EtCO2                        float64
FiO2                         float64
PRV                          float64
BP                           float64
Skin Temperature             float64
Motion/Activity index        float64
PVI                          float64
Hb level                     float64
SV                           float64
CO                           float64
Blood Flow Index             float64
PPG waveform features        float64
Signal Quality Index         float64
Respiratory effort           float64
O2 extraction ratio          float64
SNR                          float64
QoS                         category
blood_group                 category
dtype: object
```

4.1.3 C)

```
[900]: X_train.dtypes.head(30)
```

```
[900]: SpO2                         float64
       HR                           float64
       PI                           float64
       RR                           float64
       EtCO2                        float64
       FiO2                         float64
       PRV                          float64
       BP                           float64
       Skin Temperature             float64
       Motion/Activity index        float64
       PVI                          float64
       Hb level                     float64
       SV                           float64
       CO                           float64
       Blood Flow Index             float64
       PPG waveform features        float64
```

```
Signal Quality Index     float64
Respiratory effort       float64
O2 extraction ratio      float64
SNR                      float64
QoS_ord                     int8
bg_A+                       bool
bg_A-                       bool
bg_AB+                      bool
bg_AB-                      bool
bg_B+                       bool
bg_B-                       bool
bg_O+                       bool
bg_O-                       bool
dtype: object
```

[901]:
```
num_cols = X_train.select_dtypes(include=["float64", "int64","int8"]).columns.
 ↪tolist()
num_cols
```

[901]:
```
['SpO2',
 'HR',
 'PI',
 'RR',
 'EtCO2',
 'FiO2',
 'PRV',
 'BP',
 'Skin Temperature',
 'Motion/Activity index',
 'PVI',
 'Hb level',
 'SV',
 'CO',
 'Blood Flow Index',
 'PPG waveform features',
 'Signal Quality Index',
 'Respiratory effort',
 'O2 extraction ratio',
 'SNR',
 'QoS_ord']
```

[902]:
```
# Scaniling #1 - Standart Scaler

std_scaler = StandardScaler()

X_train_std = pd.DataFrame(
    std_scaler.fit_transform(X_train[num_cols]),
    columns=num_cols,
    index=X_train.index
)
# values check
check_means = X_train_std[num_cols].mean().round(3)
check_stds  = X_train_std[num_cols].std(ddof=0).round(3)

print("Means (should be ~0):")
print(check_means.head(10))
print("\nStds (should be ~1):")
print(check_stds.head(10))
```

```
Means (should be ~0):
SpO2                     0.0
HR                      -0.0
PI                      -0.0
RR                       0.0
EtCO2                   -0.0
FiO2                    -0.0
PRV                     -0.0
BP                      -0.0
Skin Temperature        -0.0
Motion/Activity index    0.0
dtype: float64

Stds (should be ~1):
SpO2                     1.0
HR                       1.0
PI                       1.0
RR                       1.0
EtCO2                    1.0
FiO2                     1.0
PRV                      1.0
BP                       1.0
Skin Temperature         1.0
Motion/Activity index    1.0
dtype: float64
```

[903]:
```
#Scaling #2 - RobustScaler (outlierproof; median=0, IQR=1)

rob_scaler = RobustScaler(with_centering=True,with_scaling=True)

X_train_robust = pd.DataFrame(
    rob_scaler.fit_transform(X_train[num_cols]),
    columns=num_cols,
    index=X_train.index
)
```

```
#check if the values are fine
medians = X_train_robust[num_cols].median().round(3)
q75 = X_train_robust[num_cols].quantile(0.75)
q25 = X_train_robust[num_cols].quantile(0.25)
iqr = (q75 - q25).round(3)

print("Medians (should be ~0):")
print(medians.head(10))
print("\nIQR (should be ~1):")
print(iqr.head(10))
```

```
Medians (should be ~0):
SpO2                      0.0
HR                        0.0
PI                        0.0
RR                        0.0
EtCO2                     0.0
FiO2                      0.0
PRV                       0.0
BP                        0.0
Skin Temperature         -0.0
Motion/Activity index     0.0
dtype: float64

IQR (should be ~1):
SpO2                      1.0
HR                        1.0
PI                        1.0
RR                        1.0
EtCO2                     1.0
FiO2                      1.0
PRV                       1.0
BP                        1.0
Skin Temperature          1.0
Motion/Activity index     1.0
dtype: float64
```

[904]:
```
# Transformer #1 PowerTransformer
power_tx = PowerTransformer(method="yeo-johnson", standardize=True)

X_train_power = X_train.copy()
X_train_power[num_cols] = power_tx.fit_transform(X_train[num_cols])

# quick checks
means = X_train_power[num_cols].mean().round(3).head(10)
stds  = X_train_power[num_cols].std(ddof=0).round(3).head(10)
```

```python
print("PowerTransformer -> means ~0:\n", means)
print("\nPowerTransformer -> stds ~1:\n", stds)
```

```
PowerTransformer -> means ~0:
 SpO2                     0.0
HR                      -0.0
PI                      -0.0
RR                      -0.0
EtCO2                   -0.0
FiO2                    -0.0
PRV                      0.0
BP                      -0.0
Skin Temperature         0.0
Motion/Activity index   -0.0
dtype: float64

PowerTransformer -> stds ~1:
 SpO2                     1.0
HR                       1.0
PI                       1.0
RR                       1.0
EtCO2                    1.0
FiO2                     1.0
PRV                      1.0
BP                       1.0
Skin Temperature         1.0
Motion/Activity index    1.0
dtype: float64
```

[905]:
```python
nq = min(1000, len(X_train))  # practical cap
quant_tx = QuantileTransformer(
    n_quantiles=nq,
    output_distribution="normal",
    random_state=42
)

X_train_quant = X_train.copy()
X_train_quant[num_cols] = quant_tx.fit_transform(X_train[num_cols])

# quick checks
means_q = X_train_quant[num_cols].mean().round(3).head(10)
stds_q  = X_train_quant[num_cols].std(ddof=0).round(3).head(10)

print("QuantileTransformer -> means ~0:\n", means_q)
print("\nQuantileTransformer -> stds ~1:\n", stds_q)
```

```
QuantileTransformer -> means ~0:
 SpO2                       0.021
HR                         -0.002
PI                         -0.001
RR                         -0.007
EtCO2                       0.007
FiO2                       -0.002
PRV                         0.009
BP                         -0.005
Skin Temperature           -0.006
Motion/Activity index      -0.005
dtype: float64

QuantileTransformer -> stds ~1:
 SpO2                       0.998
HR                          1.003
PI                          1.003
RR                          0.999
EtCO2                       0.998
FiO2                        0.997
PRV                         1.002
BP                          0.998
Skin Temperature            1.015
Motion/Activity index       1.000
dtype: float64
```

[906]:
```
# we already did more techniques such as Outlier ( winsortizatoin , IQR ) , encoding
```

4.1.4 D)

As part of data preprocessing (section 2.1(C)), four commonly used transformation methods were applied to numerical attributes — two **scaling** and two **distribution transformation** techniques.

Scaling techniques

1. **StandardScaler**
   - Chosen as the baseline normalization method.
   - Scales each feature to have mean 0 and standard deviation 1.
   - Improves model convergence and training stability for algorithms sensitive to feature magnitude (e.g., Logistic Regression, SVM).
2. **RobustScaler**
   - Used as a more resilient alternative to handle outliers.
   - Scales data using the median and interquartile range (IQR), reducing the influence of extreme values (e.g., in the `CO` feature).

Transformation techniques

3. **PowerTransformer (Yeo–Johnson)**
   - Applied to stabilize variance and reduce skewness in feature distributions.

- Helps make distributions more symmetric and supports linear model assumptions.

4. **QuantileTransformer (normal)**
   - Maps the feature quantiles to a normal distribution, effectively reducing the impact of outliers and non-Gaussian shapes.
   - Useful for attributes with irregular or multimodal distributions.

Summary These four techniques cover the most relevant preprocessing needs for numerical data: - **StandardScaler** – baseline normalization, - **RobustScaler** – robust to outliers, - **PowerTransformer** – reduces skewness and stabilizes variance, - **QuantileTransformer** – enforces normal-like distribution.

This combination allows comparison of preprocessing effects in later phases (2.3 and 3), ensuring a replicable, consistent, and model-friendly data preparation workflow.

4.2 2.2 Výber atribútov pre strojové učenie

4.2.1 A)

[907]:
```
X = X_train.copy()
y = y_train.copy()

# 1) align indices first (very important if X was dropna'd earlier)
common_idx = X.index.intersection(y.index)
X = X.loc[common_idx]
y = y.loc[common_idx]

# 2) drop rows with any NaN in X (apply the SAME mask to both X and y)
mask = ~X.isna().any(axis=1)
X = X.loc[mask]
y = y.loc[mask]

print("Shapes after align -> X:", X.shape, "| y:", y.shape)
```

```
Shapes after align -> X: (41392, 29) | y: (41392,)
```

[908]:
```
scaler_minmax = MinMaxScaler()
X_chi = pd.DataFrame(
    scaler_minmax.fit_transform(X),
    columns=X.columns,
    index=X.index
)
chi_scores, p_values = chi2(X_chi, y)
chi_results = pd.Series(chi_scores, index=X.columns).
  ↪sort_values(ascending=False)

print("Top 10 features by Chi-Square:\n")
print(chi_results.head(10))
```

```
Top 10 features by Chi-Square:
```

```
HR                        1164.230502
CO                         435.709035
EtCO2                      305.397141
FiO2                       154.531106
PI                          21.104691
RR                          17.934760
O2 extraction ratio          1.538853
bg_B-                        1.303170
QoS_ord                      1.243664
bg_O+                        1.183909
dtype: float64
```

[909]:
```
X_chi[X_chi.columns]
```

[909]:
```
           SpO2        HR        PI        RR     EtCO2      FiO2       PRV  \
6475   0.525146  0.787473  0.513921  0.715944  0.326645  0.566474  0.530721
12274  0.506686  0.857688  0.723126  0.796223  0.532064  0.647200  0.518096
47746  0.386994  0.478045  0.546312  0.553884  0.475704  0.347002  0.626112
56807  0.445673  0.256708  0.625327  0.712715  0.307308  0.588409  0.687110
46687  0.474444  0.713392  0.461103  0.341468  0.683023  0.541257  0.390535
…           …         …         …         …         …         …         …
32793  0.460962  0.548346  0.474521  0.466746  0.580586  0.381199  0.677896
52966  0.264648  0.781487  0.534218  0.640457  0.617411  0.557990  0.635862
26667  0.477546  0.363955  0.680007  0.510529  0.509821  0.361080  0.791034
6446   0.466543  0.523679  0.486441  0.692979  0.301562  0.321686  0.402102
42302  0.403658  0.599102  0.467683  0.409394  0.466401  0.428401  0.404867

             BP  Skin Temperature  Motion/Activity index  …       SNR  \
6475   0.328978          0.259424               0.548962  …  0.581740
12274  0.263212          0.671844               0.273192  …  0.324382
47746  0.387173          0.243384               0.378412  …  0.681468
56807  0.580476          0.379736               0.410406  …  0.342466
46687  0.556896          0.454367               0.623607  …  0.524398
…           …                …                    …  …       …
32793  0.406224          0.354757               0.692835  …  0.704693
52966  0.688202          0.509013               0.420458  …  0.889518
26667  0.544325          0.440188               0.309792  …  0.316030
6446   0.436908          0.409603               0.415853  …  0.394871
42302  0.459714          0.463596               0.241395  …  0.700864

        QoS_ord  bg_A+  bg_A-  bg_AB+  bg_AB-  bg_B+  bg_B-  bg_O+  bg_O-
6475   0.666667    0.0    1.0     0.0     0.0    0.0    0.0    0.0    0.0
12274  1.000000    0.0    0.0     0.0     0.0    1.0    0.0    0.0    0.0
47746  1.000000    0.0    0.0     1.0     0.0    0.0    0.0    0.0    0.0
56807  0.666667    1.0    0.0     0.0     0.0    0.0    0.0    0.0    0.0
46687  0.666667    0.0    0.0     0.0     0.0    1.0    0.0    0.0    0.0
```

```
…         …      …      …      …      …     …     …     …     …
32793  1.000000    0.0    0.0     0.0     0.0    0.0    0.0    0.0    1.0
52966  0.666667    0.0    1.0     0.0     0.0    0.0    0.0    0.0    0.0
26667  0.333333    0.0    0.0     0.0     0.0    0.0    1.0    0.0    0.0
6446   0.666667    0.0    0.0     0.0     0.0    1.0    0.0    0.0    0.0
42302  0.666667    0.0    0.0     0.0     0.0    0.0    0.0    1.0    0.0

[41392 rows x 29 columns]
```

[910]:
```
X_mi = X.copy()
mi_scores = mutual_info_classif(X, y, random_state=42)
mi_results = pd.Series(mi_scores, index=X.columns).sort_values(ascending=False)

print("Top 10 features by Mutual Information:\n")
print(mi_results.head(10))
```

```
Top 10 features by Mutual Information:

HR                       0.559387
CO                       0.554434
EtCO2                    0.511240
RR                       0.489521
FiO2                     0.484673
PPG waveform features    0.482610
Blood Flow Index         0.482178
PVI                      0.479729
SV                       0.478260
PI                       0.477896
dtype: float64
```

[ ]:
```
rf = RandomForestClassifier(n_estimators=200, random_state=42)
rf.fit(X, y)

rf_importances = pd.Series(rf.feature_importances_, index=X.columns).
  ↪sort_values(ascending=False)

print("Top 10 features by Random Forest Importance:\n")
print(rf_importances.head(10))
```

[748]:
```
#compare 3 methods
feature_scores = pd.concat([
    mi_results.rename("Mutual Information"),
    chi_results.rename("Chi2"),
    rf_importances.rename("Random Forest")
], axis=1)

# normalize to 0-1 scale for easier comparison
```

```
feature_scores = feature_scores.apply(lambda x: (x - x.min()) / (x.max() - x.
↪min()))

# compute average score
feature_scores["Average"] = feature_scores.mean(axis=1)
feature_scores.sort_values("Average", ascending=False).head(10)
```

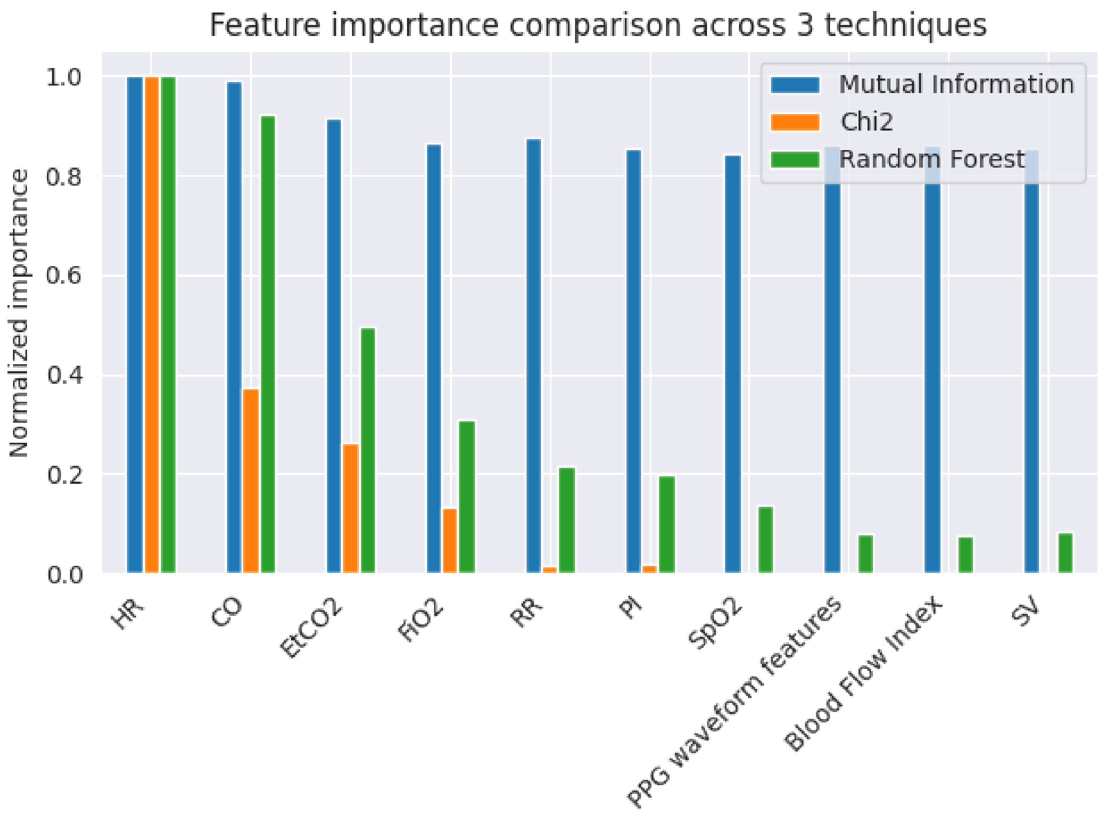
[748]:

```
                      Mutual Information      Chi2  Random Forest   Average
HR                              1.000000  1.000000       1.000000  1.000000
CO                              0.991147  0.374244       0.921206  0.762199
EtCO2                           0.913930  0.262314       0.494068  0.556771
FiO2                            0.866436  0.132730       0.308987  0.436051
RR                              0.875103  0.015402       0.215498  0.368668
PI                              0.854322  0.018125       0.197009  0.356485
SpO2                            0.843700  0.000513       0.137522  0.327245
PPG waveform features           0.862748  0.000470       0.077891  0.313703
Blood Flow Index                0.861977  0.000793       0.076666  0.313145
SV                              0.854972  0.000000       0.081849  0.312274
```

[749]:

```
#visualization
top10 = feature_scores.sort_values("Average", ascending=False).head(10)

plt.figure(figsize=(10,6))
top10[["Mutual Information", "Chi2", "Random Forest"]].plot(kind="bar")
plt.title("Feature importance comparison across 3 techniques")
plt.ylabel("Normalized importance")
plt.xticks(rotation=45, ha="right")
plt.tight_layout()
plt.show()
```

```
<Figure size 1000x600 with 0 Axes>
```



4.2.2 4.2.1 A) Findings & decisions (feature selection)

Setup. Informativeness of features for the target `oximetry` was evaluated by three independent methods: (1) Mutual Information (MI), (2) Chi-Square (^{2}; after MinMax scaling to ensure non-negativity), and (3) model-based Random Forest importance. Scores were normalized to 0,1 and averaged for comparison.

Consistent signals across methods. - **HR** and **CO** ranked **#1–#2** in both MI and Random Forest and stayed on top in the averaged ranking → strongest, method-agnostic predictors. - **EtCO2** and **FiO2** showed **high to medium** importance in MI and RF (respiratory physiology) → robust, clinically plausible predictors. - **RR** and **PI** were **medium**; **SpO2** medium-to-lower (still relevant). - Other waveform/flow indices (PPG waveform features, Blood Flow Index, SV) were **lower**, yet non-zero, suggesting auxiliary value.

Why ^{2} looks conservative. - ^{2} assumes independence on **binned/positive** data; with continuous variables (scaled to 0–1) it is less sensitive to nuanced, non-linear relations. - MI and RF capture **non-linear/monotone** effects better, therefore we weigh them more when resolving ties.

Decision – feature shortlist for ML (to carry forward). - **Core set (high confidence):** `HR`, `CO`, `EtCO2`, `FiO2`. - **Support set (keep / test with regularization):** `RR`, `PI`, `SpO2`. - **Optional (use if helpful in CV, otherwise drop to reduce complexity):** `PPG waveform features`, `Blood Flow Index`, `SV`.

Rationale. - Chosen features are consistently ranked by **2 methods** and align with earlier EDA (HR oximetry, respiratory parameters oxygenation). - Keeping a compact core reduces multicollinearity and speeds training; the support/optional groups allow controlled expansion if cross-validated performance improves.

Next steps (planned in 2.2/2.3). - Compare *Core* vs. *Core+Support* (and optionally +PCA) in stratified CV with the final preprocessing choice (scaling/transformers). - Use model regularization (e.g., L1/L2) or tree-based models to manage redundancy.

4.2.3 C)

4.3 2.3 Replikovateľnosť predspracovania

4.3.1 A)

4.3.2 B)