About the project

The end goal of this project is to classify patients with high protein concentration in urine and the healthy group based on SERS (Surface Enchanced Raman Spectroscopy) spectral data and biomedical data.
This project is to be released as a research paper later in 2022 or 2023. Some information might not be fully shown here as a result.

The project is divided into several Jupyter notebooks with the following names: 1) Import raw urine spectra (part 1) 2) Spectra processing (part 2) 3) Classification of patients (part 3) 4) Biomedical data (part 4)

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Part of the upcoming abstract: Excessive protein excretion in human urine is an early and sensitive marker of diabetic nephropathy, primary and secondary renal disease. Kidney problems, particularly chronic kidney disease, remain among the few growing causes of mortality in the world. Therefore, it is important to develop efficient, expressive, and low-cost method for protein determination. Surface enhanced Raman spectroscopy (SERS) methods are potential candidates to achieve those criteria. In this paper, the SERS methods was developed to distinguish patients with proteinuria and the healthy group. Commercial gold nanoparticles with the diameter of 60 nm and 100 nm, and silver nanoparticles with the diameter of 100 nm were employed. Silver, gold, silicon and test slides covered with aluminium tape were utilized as substrates. Obtained spectra were analysed with several machine learning algorithms coupled with the PCA, ROC curve, and cross-validation methods.

Biomedical data (part 4)

About

The information below contains various summary data derived from biomedical 24h urine data that we used for SERS studies. Missing values, typos, conversions to the same units were addressed. Most of patients' data are available for Raman spectra acquisition, however, a few samples might not be available, and most importantly every sample contains information about protein concentration in mg/L.

Import data

Data was processed in Libre Office prior to putting here. The things that got addressed: white spaces, rows with None, translations, dates.

In [1]:
```python
import matplotlib.pyplot as plt
import pandas as pd

bio_data = pd.read_csv('urine biomedicals.csv')
bio_data
```

Out[1]:

	code	status	patient_ID	volume, L/day	sex	date of birth	date collection	Sodium, mmole/day	Protein, gramm/day	Po r
0	ASA 5791	diseased	139	4.84	F	04.01.1975	25.07.2022	445.2	3.51	
1	TM 5991	diseased	75	3.42	M	17.04.1995	15.11.2021	321.4	0.36	
2	AS 6891	diseased	44	3.40	M	17.05.1986	26.03.2021	479.4	0.78	
3	AD 4891	diseased	132	3.38	M	02.08.1984	18.07.2022	378.5	2.41	
4	TM 5991	diseased	20	3.28	M	17.04.1995	09.11.2020	387.0	0.62	
...	...	...	...	...	...	...	...	...	...	
113	SM 5891	healthy	92	0.54	F	07.11.1985	27.12.2021	185.0	0.11	
114	AN 8891	healthy	89	0.52	F	19.10.1988	27.12.2021	119.0	0.04	
115	DA7891	diseased	18	0.50	M	23.09.1987	01.10.2020	25.5	10.00	
116	KAA 7991	diseased	121	0.46	F	12.05.1997	01.06.2022	139.0	1.29	
117	ZAS 4891	healthy	93	0.38	M	10.08.1984	27.12.2021	270.0	0.05	

118 rows × 13 columns

In [2]:
```python
bio_data.isnull().sum()
```

Out[2]:
```
code                        0
status                      0
patient_ID                  0
volume, L/day               0
sex                         0
date of birth               0
date collection             0
Sodium, mmole/day           0
Protein, gramm/day          0
Potassium, mmole/L          0
Creatinine, mmole/day       2
Urea, mmole/L               0
Uric acid, mmole/L          1
dtype: int64
```

Convert all columns to the same measurements

In [3]:
```
bio_data['Protein, mg/L'] = bio_data['Protein, gramm/day']*1000 / bio_data['volume, L/
bio_data['Sodium, mmole/L'] = bio_data['Sodium, mmole/day'] / bio_data['volume, L/day'
bio_data['Creatinine, mmole/L'] = bio_data['Creatinine, mmole/day'] / bio_data['volume
```

In [4]:
```
bio_data = bio_data.drop(['code', 'Protein, gramm/day', 'Sodium, mmole/day', 'Creatini
bio_data
```

Out[4]:

	status	patient_ID	volume, L/day	sex	date of birth	date collection	Potassium, mmole/L	Urea, mmole/L	Uric acid, mmole/L	
0	diseased	139	4.84	F	04.01.1975	25.07.2022	132.10	330.08	4.30	72
1	diseased	75	3.42	M	17.04.1995	15.11.2021	31.10	295.80	2.31	10
2	diseased	44	3.40	M	17.05.1986	26.03.2021	69.02	476.60	3.71	22
3	diseased	132	3.38	M	02.08.1984	18.07.2022	71.60	500.50	4.37	71
4	diseased	20	3.28	M	17.04.1995	09.11.2020	51.40	359.40	NaN	18
...	...	...	...	...	...	...	...	...	...	
113	healthy	92	0.54	F	07.11.1985	27.12.2021	61.50	149.90	2.11	20
114	healthy	89	0.52	F	19.10.1988	27.12.2021	71.70	133.30	2.01	7
115	diseased	18	0.50	M	23.09.1987	01.10.2020	31.50	345.50	2.65	2000
116	diseased	121	0.46	F	12.05.1997	01.06.2022	45.50	106.95	1.18	280
117	healthy	93	0.38	M	10.08.1984	27.12.2021	49.10	203.90	1.96	13

118 rows × 12 columns

In [5]:
```
%%capture
# supress all output including warnings

# create an empty list fill out later
list_date_birth = [None]*len(bio_data['date of birth'])
# create current timestamp to calculate age of each patient
now = pd.Timestamp('now')

# create a list containing ages for all patients
for i in range( len(bio_data['date of birth']) ):
    then = pd.Timestamp(bio_data['date of birth'][i])
    list_date_birth[i] = len(pd.date_range(then,now,freq='Y'))

# convert the list to pd.dataframe
bio_data['age'] = list_date_birth
```

In [6]:
```
bio_data = bio_data.drop(['date of birth', 'date collection'], axis=1)
bio_data
```

Out[6]:

	status	patient_ID	volume, L/day	sex	Potassium, mmole/L	Urea, mmole/L	Uric acid, mmole/L	Protein, mg/L	Sodium, mmole/L	C
0	diseased	139	4.84	F	132.10	330.08	4.30	725.206612	91.983471	
1	diseased	75	3.42	M	31.10	295.80	2.31	105.263158	93.976608	
2	diseased	44	3.40	M	69.02	476.60	3.71	229.411765	141.000000	
3	diseased	132	3.38	M	71.60	500.50	4.37	713.017751	111.982249	
4	diseased	20	3.28	M	51.40	359.40	NaN	189.024390	117.987805	
...	...	...	...	...	...	...	...	...	...	
113	healthy	92	0.54	F	61.50	149.90	2.11	203.703704	342.592593	
114	healthy	89	0.52	F	71.70	133.30	2.01	76.923077	228.846154	
115	diseased	18	0.50	M	31.50	345.50	2.65	20000.000000	51.000000	
116	diseased	121	0.46	F	45.50	106.95	1.18	2804.347826	302.173913	
117	healthy	93	0.38	M	49.10	203.90	1.96	131.578947	710.526316	

118 rows × 11 columns

Explore data

Descriptive statistics

In [7]:
```
bio_data.describe()
```

Out[7]:

	patient_ID	volume, L/day	Potassium, mmole/L	Urea, mmole/L	Uric acid, mmole/L	Protein, mg/L	Sodium, mmole/L	Creatini mmol
count	118.000000	118.000000	118.000000	118.000000	117.000000	118.000000	118.000000	116.000
mean	70.008475	1.684492	48.037203	286.543475	2.686410	1402.655321	121.618996	7.085
std	41.932077	0.766558	22.488046	131.015706	1.266605	2668.379547	80.275454	4.131
min	1.000000	0.380000	1.870000	54.300000	0.010000	40.000000	25.000000	0.713
25%	32.250000	1.180000	33.025000	212.425000	1.930000	97.348244	78.212778	4.601
50%	71.500000	1.540000	45.100000	276.100000	2.600000	368.029030	103.484127	6.353
75%	106.750000	2.100000	62.950000	354.800000	3.350000	1378.317503	145.250000	8.814
max	139.000000	4.840000	136.800000	959.400000	8.980000	20000.000000	710.526316	23.815

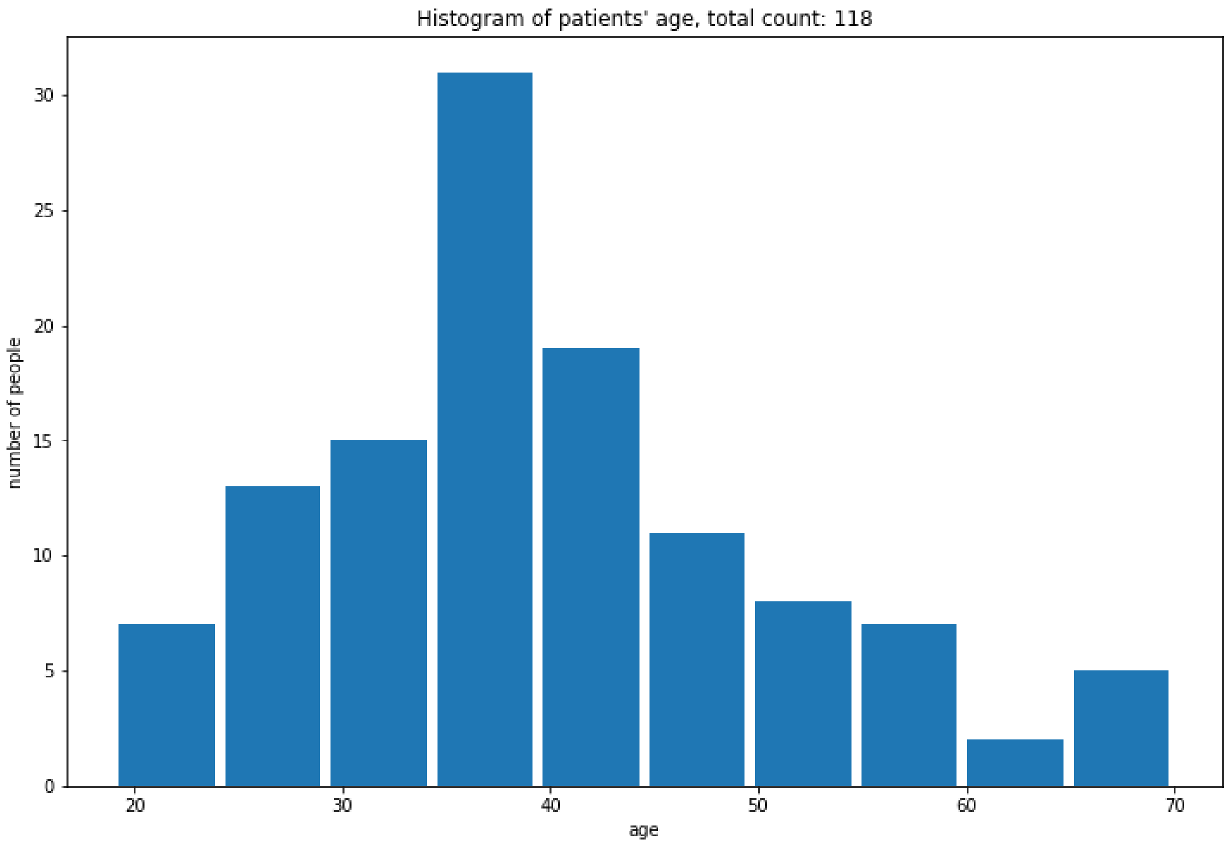
Age

The histogram below shows patients' age distribution. Total number of patients equals to 118. Most of them are available for Raman spectra acquisition, however, a few samples might not be available. Every sample contains information about protein concentration in mg/L.

In [8]:
```
# count total number of patients
total_count = bio_data['age'].count()
total_count
```

Out[8]:
```
118
```

In [9]:
```
bio_data.hist(column='age', bins=10, rwidth=0.9, figsize=[12,8], grid=False, legend=Fa
plt.xlabel('age')
plt.ylabel('number of people')
plt.title(f"Histogram of patients' age, total count: {total_count}");
```

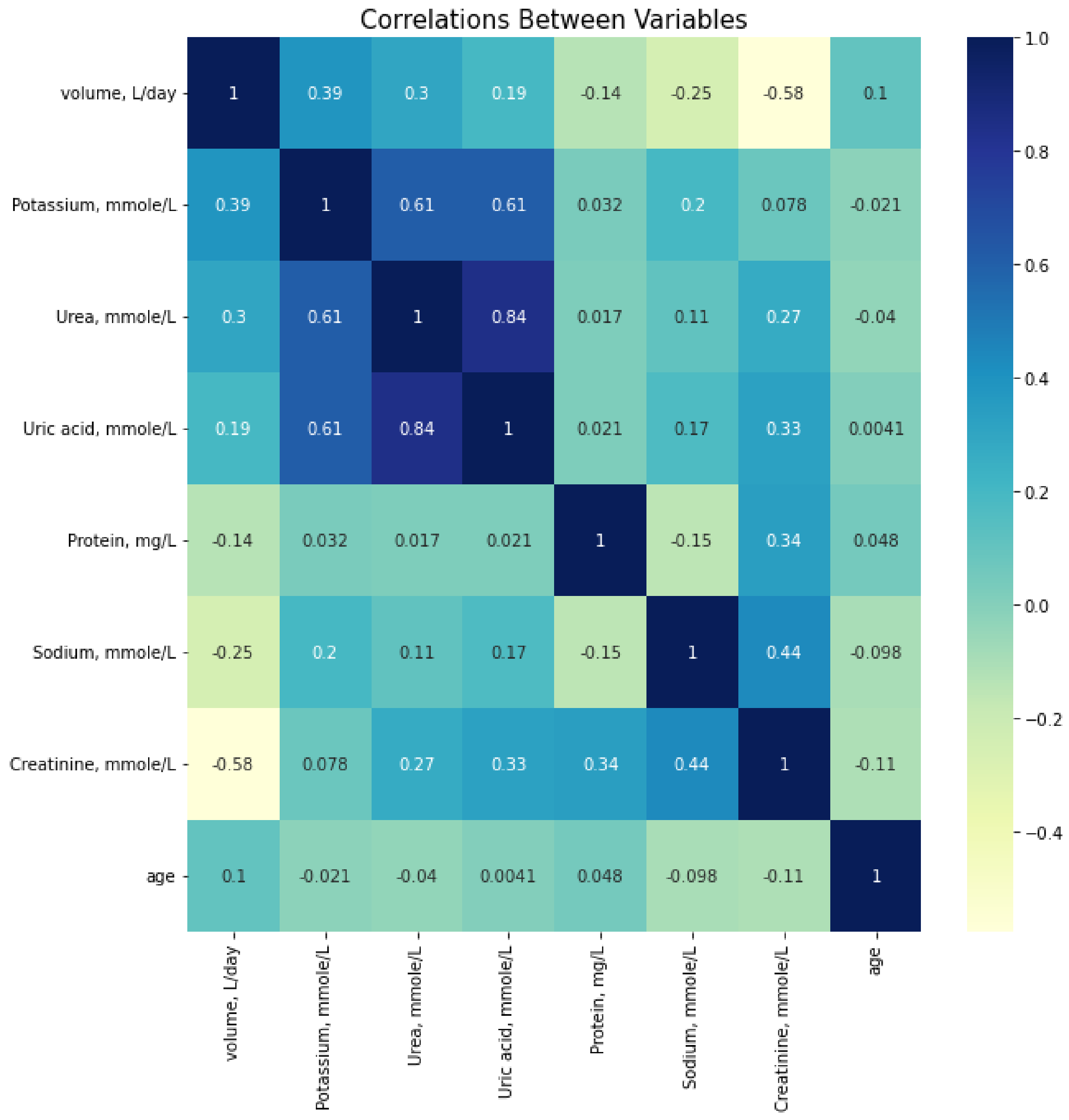


Correlation matrix

Uric acid and urea have high correlation (0.84). Potassium has correlation to urea and uric acid, in both cases 0.61. Volume is negatively correlated to creatinine -0.58. Protein has some correlation to creatinine 0.34, but no other meaningful correlations. Age is not correlated with anything.

In [10]:
```
# visualize correlations, also just for this plot drop 'patient_ID'
import seaborn as sns
plt.figure(figsize=(10,10))
sns.heatmap(bio_data.drop('patient_ID', axis=1).corr(), cmap="YlGnBu", annot=True)
```

```
plt.title("Correlations Between Variables", size=15)
plt.show()
```



	volume, L/day	Potassium, mmole/L	Urea, mmole/L	Uric acid, mmole/L	Protein, mg/L	Sodium, mmole/L	Creatinine, mmole/L	age
volume, L/day	1	0.39	0.3	0.19	-0.14	-0.25	-0.58	0.1
Potassium, mmole/L	0.39	1	0.61	0.61	0.032	0.2	0.078	-0.021
Urea, mmole/L	0.3	0.61	1	0.84	0.017	0.11	0.27	-0.04
Uric acid, mmole/L	0.19	0.61	0.84	1	0.021	0.17	0.33	0.0041
Protein, mg/L	-0.14	0.032	0.017	0.021	1	-0.15	0.34	0.048
Sodium, mmole/L	-0.25	0.2	0.11	0.17	-0.15	1	0.44	-0.098
Creatinine, mmole/L	-0.58	0.078	0.27	0.33	0.34	0.44	1	-0.11
age	0.1	-0.021	-0.04	0.0041	0.048	-0.098	-0.11	1

Gender

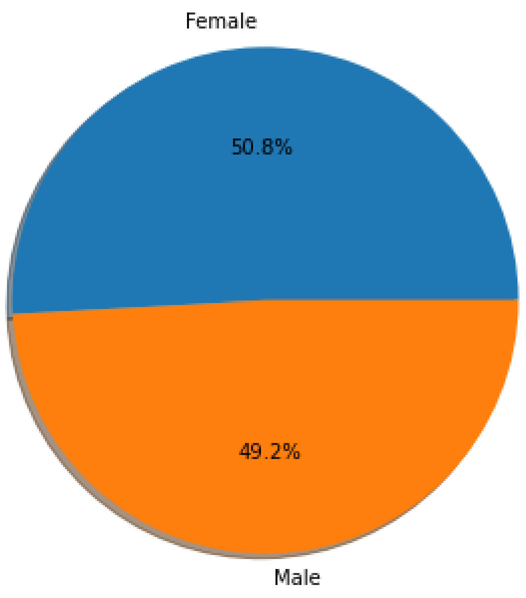
Our samples have roughly half women and men.

In [11]:
```
bio_data['sex'].unique()
```

Out[11]:
```
array(['F', 'M'], dtype=object)
```

In [12]:
```
no_f = bio_data['sex'].value_counts()['F']
no_m = bio_data['sex'].value_counts()['M']

plt.figure(figsize=[5,5])
plt.pie([no_f, no_m], labels=['Female', 'Male'], autopct='%1.1f%%', shadow=True)
plt.axis('equal');
```



Classification

In the 'status' column patients are divided into two groups 'diseased' and 'healthy'. These statuses were given by doctors. They considered not only the biomedical data of 24h urine but also patients' overall health condition. Thus, not all information related to the categorization is listed here. However, in the code below tries to use ML algorithms to make a prediction about the status of a patient. Despite limitations of data, it is possible to classify a patient with 90% accuracy as shown in the end. Classical machine learning algorithms were successful in determining a patient's status with only 24h urine data. Stratified cross validation method with 10 folds is used to avoid overfitting.

In [13]:
```
# check how many unique values for status
bio_data['status'].unique()
```

Out[13]:
```
array(['diseased', 'healthy'], dtype=object)
```

In [14]:
```
bio_data_classifier = bio_data
```

Prepare data for classification

Prepare target variable

In [15]:
```
# prepare target variable
y = [None] * len(bio_data_classifier['status'])
```

In [16]:
```
for i in range( len(bio_data_classifier['status']) ):
    if bio_data_classifier['status'][i] == 'diseased':
        y[i] = 1
    elif bio_data_classifier['status'][i] == 'healthy':
        y[i] = 0
```

Prepare independent vaiable

In [17]:
```
# prepare independent variables X
X = [None] * len(bio_data_classifier['status'])
X = bio_data_classifier[ ['Potassium, mmole/L',
                          'Urea, mmole/L',
                          'Uric acid, mmole/L',
                          'Protein, mg/L',
                          'Sodium, mmole/L',
                          'Creatinine, mmole/L'] ]

# modify X to fill nans with mean values
X['Uric acid, mmole/L'].fillna(X['Uric acid, mmole/L'].mean(), inplace=True)
X['Creatinine, mmole/L'].fillna(X['Creatinine, mmole/L'].mean(), inplace=True)
X.isnull().sum()
```

```
C:\Users\user\AppData\Local\Temp\ipykernel_8668\4086572763.py:11: SettingWithCopyWarn
ing:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/us
er_guide/indexing.html#returning-a-view-versus-a-copy
  X['Uric acid, mmole/L'].fillna(X['Uric acid, mmole/L'].mean(), inplace=True)
C:\Users\user\AppData\Local\Temp\ipykernel_8668\4086572763.py:12: SettingWithCopyWarn
ing:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/us
er_guide/indexing.html#returning-a-view-versus-a-copy
  X['Creatinine, mmole/L'].fillna(X['Creatinine, mmole/L'].mean(), inplace=True)
```

Out[17]:
```
Potassium, mmole/L     0
Urea, mmole/L          0
Uric acid, mmole/L     0
Protein, mg/L          0
Sodium, mmole/L        0
Creatinine, mmole/L    0
dtype: int64
```

Run estimator

In [18]:
```
from sklearn.model_selection import cross_val_score
from sklearn import svm
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.naive_bayes import GaussianNB

models = [KNeighborsClassifier(n_neighbors=13), LinearDiscriminantAnalysis(), Gaussiar
for model in models:
    scores = cross_val_score(model, X, y, cv=10)
    print(f'{model} mean score {round(scores.mean(),2)}, score std {round(scores.std()
```

```
KNeighborsClassifier(n_neighbors=13) mean score 0.89, score std 0.101
LinearDiscriminantAnalysis() mean score 0.77, score std 0.113
GaussianNB() mean score 0.79, score std 0.109
LogisticRegression(solver='liblinear') mean score 0.9, score std 0.115
```

Save to csv

```
In [19]: bio_data.to_csv('urine biomedicals processed.csv')
```

```
In [ ]:
```