Students:

Vincent Roduit
Caspar Henking
Fabio Palmisano
Bastien Marconato

PCA_for_EIT

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1 PCA for Source Separation of Ventilation and Cardiovascular Activity in Electrical Impedance Tomography (EIT)

1.1 Introduction

In this exercise we use PCA for processing image sequences of thoracic electrical impedance tomography (EIT) signals. EIT is a non-invasive, radiation-free imaging modality which uses small alternating currents to measure bioimpedance of the thorax [1]. These measurements are then converted into image sequences of thoracic impedance changes representing ventilation (i.e., air exchange in the lungs) and cardiovascular activity (e.g., heart movement or blood volume changes in heart and lungs).

In order to analyze these data it is important to properly separate ventilation and cardiovascular activity. Besides common techniques such as frequency filtering or ECG-triggered averaging, PCA can be used for separating these two sources of signals. The present example uses the method proposed by Deibele et al. [2] for which the block diagram is shown below:

1.2 References

[1] I. Frerichs et al., "Chest electrical impedance tomography examination, data analysis, terminology, clinical use and recommendations: consensus statement of the TRanslational EIT developmeNt stuDy group," Thorax, vol. 72, no. 1, pp. 83–93, Jan. 2017, doi: 10.1136/thoraxjnl-2016-208357.

[2] J. M. Deibele, H. Luepschen, and S. Leonhardt, "Dynamic separation of pulmonary and cardiac changes in electrical impedance tomography," Physiological Measurement, vol. 29, no. 6, pp. S1–S14, Jun. 2008, doi: 10.1088/0967-3334/29/6/S01.

[99]:
```
import numpy as np
from scipy.io import loadmat
from scipy.signal import filtfilt, butter
from scipy.linalg import eigh

import plotly.graph_objects as go
from plotly.offline import init_notebook_mode, iplot
from plotly.subplots import make_subplots
init_notebook_mode(connected=True)  # initiate notebook for offline plot

from ecgdetectors import Detectors
```

[100]:
```
# load data
data = loadmat('EIT_Data.mat')
t = data['tEit'].flatten()[data['IdxRange'].flatten().astype(bool)]
fs = 1/np.median(np.diff(t))
imgs_eit = data['Imgs']
b, a = butter(4, np.asarray([0.1, 12]), fs=fs, btype='bandpass')
imgs_eit = filtfilt(b, a, imgs_eit, axis=-1)
imgs_eit *= 1E3  # adapt scaling for plotting

# ECG data to be used for bonus question
ecg = {'time': data['Ecg'][0][0][2], 'value': data['Ecg'][0][0][1], 'fs':␣
 ↪data['Ecg'][0][0][3]}
ecg_range = (ecg['time'] > t[0]) & (ecg['time'] < t[-1])
ecg['time'] = ecg['time'][ecg_range]
ecg['value'] = ecg['value'][ecg_range]

# force all timings to start at zero
t -= t[0]
ecg['time'] -= ecg['time'][0]
```

[101]:
```
# plot input data
fig = make_subplots(rows=1, cols=2, column_widths=[1, 2])
fig.update_layout(width=950, height=400)

fig.add_trace(go.Heatmap(z=np.std(imgs_eit, axis=-1), zmin=0,
                         showscale=False, colorscale='magma'), row=1, col=1)
fig.update_yaxes(title='Right', showticklabels=False, autorange="reversed",␣
 ↪row=1, col=1)
fig.update_xaxes(title='Dorsal', showticklabels=False, row=1, col=1)
fig.update_layout(title='Overall EIT Activity')

fig.add_trace(go.Scatter(x=t, y=np.nansum(imgs_eit, axis=(0, 1)),
                         name='Overall Sum Signal', line_color='black'), row=1,␣
 ↪col=2)
fig.update_xaxes(title='Time (s)', row=1, col=2)
fig.update_yaxes(title='Impedance Change \Delta Z (A.U.)', row=1, col=2)
```

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```

[102]:
```
def compute_principal_components(X):
    # perform PCA and compute principal components (pc) and eigenvalues of X
    A = np.dot(X.transpose(), X)  # covariance matrix
    [eigenvalues, eigenvectors] = eigh(A)
    pc = np.dot(X, eigenvectors)
    return pc, eigenvalues

def estimate_cardiac_frequency(s, fs):
    sign_cardiac = np.sign(s)
    # find where zero crossings occured
    index = np.where(np.diff(sign_cardiac) == 2)[0]
    # interpolate to a sub-sample resolution
    pos = index + s[index + 1] / (s[index + 1] - s[index])
    # interpolate RR interval values
    rr = np.diff(pos) / fs
    return 1/np.median(rr)

def lms(A, B):
    if B.ndim == 1:
        B = np.asmatrix(B).transpose()
    tmp = np.linalg.solve(np.dot(B.transpose(), B), B.transpose())
    return np.dot(np.dot(B, tmp), A)

# separate ventilation and cardiovascular activity using PCA
# according to the algorithm by Deibele et al., PhysMeas, 2008
# https://dx.doi.org/10.1088/0967-3334/29/6/S01
imgs_tmp = np.reshape(imgs_eit, [-1, imgs_eit.shape[-1]])
are_valid_pixels = np.all(~np.isnan(imgs_tmp), 1)
X = imgs_tmp[are_valid_pixels, :].transpose()

# first approximation (see block diagram)
X = X - np.repeat(np.reshape(np.mean(X, 0), [1, -1]), X.shape[0], 0)
PC1, lambda1 = compute_principal_components(X)
Bv = PC1[:, -1]
Xv_ = lms(X, Bv)
Xc_ = X - Xv_

# second approximation (see block diagram)
Xc_ = Xc_ - np.repeat(np.reshape(np.mean(Xc_, 0), [1, -1]), Xc_.shape[0], 0)
b, a = butter(6, np.asarray([0.92, 4.6]), fs=fs, btype='bandpass')
Xc_bp = filtfilt(b, a, Xc_, axis=0)
PC2, lambda2 = compute_principal_components(Xc_bp)
Bc_ = PC2[:, -2:]
fc = estimate_cardiac_frequency(Bc_[:, 0], fs)
```

```
# create cardiac template functions
Bc = np.hstack((Bc_, np.roll(Bc_, int(fs/fc/3), 0),
                np.roll(Bc_, -int(fs/fc/3), 0)))
Xc1 = lms(Xc_, Bc)
Xc2 = lms(Xv_, Bc)
Xc = (Xc1 + Xc2).transpose()
Xv = (Xv_ - Xc2).transpose()

# cardiovascular activity
imgs_card = np.full(imgs_tmp.shape, np.nan)
imgs_card[are_valid_pixels, :] = Xc
imgs_card = imgs_card.reshape(imgs_eit.shape)
# ventilation activity
imgs_vent = np.full(imgs_tmp.shape, np.nan)
imgs_vent[are_valid_pixels, :] = Xv
imgs_vent = imgs_vent.reshape(imgs_eit.shape)
```

[103]:
```
# plot ventilation acticity
fig = make_subplots(rows=1, cols=2, column_widths=[1, 2])
fig.update_layout(width=950, height=400)

fig.add_trace(go.Heatmap(z=np.std(imgs_vent, axis=-1), zmin=0,
                         showscale=False, colorscale='magma'), row=1, col=1)
fig.update_yaxes(title='Right', showticklabels=False, autorange="reversed",␣
 ↪row=1, col=1)
fig.update_xaxes(title='Dorsal', showticklabels=False, row=1, col=1)
fig.update_layout(title='Ventilation Activity')

fig.add_trace(go.Scatter(x=t, y=np.nanmean(imgs_vent, axis=(0, 1)),
                         name='Mean Signal', line_color='black'), row=1, col=2)
fig.update_xaxes(title='Time (s)', row=1, col=2)
fig.update_yaxes(title='Impedance Change \Delta Z (A.U.)', row=1, col=2)

# add example signals in ??? regions
regions = {'Region RL': ([10, 14], 'magenta'), 'Region LL': ([22, 14],␣
 ↪'orange')}
for reg, tmp in regions.items():
    fig.add_scatter(x=[tmp[0][0]], y=[tmp[0][1]], mode='markers',␣
 ↪marker_symbol='square-open',
                    marker_size=10, legendgroup=reg, marker_color=tmp[1],␣
 ↪name=reg, row=1, col=1)
    fig.add_trace(go.Scatter(x=t, y=imgs_vent[tmp[0][1], tmp[0][0], :],␣
 ↪legendgroup=reg,
                             showlegend=False, name=reg, line_color=tmp[1]),␣
 ↪row=1, col=2)

fig.show()
```

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[104]:
```
# plot cardiovascular acticity
fig = make_subplots(rows=1, cols=2, column_widths=[1, 2])
fig.update_layout(width=950, height=400)

fig.add_trace(go.Heatmap(z=np.std(imgs_card, axis=-1), zmin=0,
                         showscale=False, colorscale='magma'), row=1, col=1)
fig.update_yaxes(title='Right', showticklabels=False, autorange="reversed",␣
 ↪row=1, col=1)
fig.update_xaxes(title='Dorsal', showticklabels=False, row=1, col=1)
fig.update_layout(title='Cardiovascular Activity')

fig.add_trace(go.Scatter(x=t, y=np.nanmean(imgs_card, axis=(0, 1)),
                         name='Mean Signal', line_color='black'), row=1, col=2)
fig.update_xaxes(title='Time (s)', row=1, col=2)
fig.update_yaxes(title='Impedance Change \Delta Z (A.U.)', row=1, col=2)

# add three example signals in ??? regions
regions = {'Region A': ([18, 9], 'green'), 'Region B': ([10, 15], 'blue'),␣
 ↪'Region C': ([23, 15], 'red')}
for reg, tmp in regions.items():
    fig.add_scatter(x=[tmp[0][0]], y=[tmp[0][1]], mode='markers',␣
 ↪marker_symbol='square-open',
                    marker_size=10, legendgroup=reg, marker_color=tmp[1],␣
 ↪name=reg, row=1, col=1)
    fig.add_trace(go.Scatter(x=t, y=imgs_card[tmp[0][1], tmp[0][0], :],␣
 ↪legendgroup=reg,
                             showlegend=False, name=reg, line_color=tmp[1]),␣
 ↪row=1, col=2)
fig.show()
```

```
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```

2 Exercise Questions

Please provide your answers directly below each question.

2.1 Question 1

Determine the frequency of the ventilation activity (i.e., the respiratory rate), both expressed in `Hz` and `respirations/min`.

[105]:
```
vent_activity = np.nanmean(imgs_vent, axis=(0, 1))

from scipy.signal import find_peaks

vent_peaks, _ = find_peaks(vent_activity, distance=int(2*fs))

vent_peaks_t =  np.array(vent_peaks)/ fs
mean_resp_rate = np.mean(1 / np.diff(vent_peaks_t))

print('Mean ventilation frequency (respiratory rate): {:.2f} Hz'.
 ↪format(mean_resp_rate))
print('Mean ventilation frequency (respiratory rate): {:.2f} respirations/min'.
 ↪format(60*mean_resp_rate))
```

```
Mean ventilation frequency (respiratory rate): 0.33 Hz
Mean ventilation frequency (respiratory rate): 19.94 respirations/min
```

2.2 Question 2

Determine the frequency of the cardiovascular activity, both expressed in `Hz` and `beats/min`.

[106]:
```
card_activity = np.nanmean(imgs_card, axis=(0, 1))

card_peaks, _ = find_peaks(card_activity, distance=int(0.9*fs))
# The value of distance is set to 0.9*fs to avoid detecting multiple peaks
# in the same cardiac cycle, and we verify the correctness of the detected␣
 ↪peaks by visual inspection.
```

```
card_peaks_t =  np.array(card_peaks)/ fs
mean_card_freq = np.mean(1 / np.diff(card_peaks_t))

print('Mean cardiovascular frequency: {:.2f} Hz'.format(mean_card_freq))
print('Mean cardiovascular frequency: {:.2f} beats/min'.
  ↪format(60*mean_card_freq))
```

```
Mean cardiovascular frequency: 0.97 Hz
Mean cardiovascular frequency: 58.03 beats/min
```

2.3 Question 3

Determine the following three values:

- i) the maximal amplitude of ventilation activity;
- ii) the maximal amplitude of cardiovascular activity; and
- iii) the ratio between i) and ii), i.e., ventilation vs cardiovascular activity.

[107]:
```
vent_activity = np.std(imgs_vent, axis=-1)
card_activity = np.std(imgs_card, axis=-1)

max_amp_vent_activity = np.nanmax(vent_activity)
max_amp_card_activity = np.nanmax(card_activity)

ratio_ventilation_cardiovascular = max_amp_vent_activity / max_amp_card_activity
ratio_cardiovascular_ventilation = max_amp_card_activity / max_amp_vent_activity

print('i) Maximum amplitude of ventilation activity: {:.5f}'.
  ↪format(max_amp_vent_activity))
print('ii) Maximum amplitude of cardiovascular activity: {:.5f}'.
  ↪format(max_amp_card_activity))
print('iii) a) Ratio of ventilation to cardiovascular activity: {:.5f}'.
  ↪format(ratio_ventilation_cardiovascular))
print('iii) b) Ratio of cardiovascular to ventilation activity: {:.5f}'.
  ↪format(ratio_cardiovascular_ventilation))
```

```
i) Maximum amplitude of ventilation activity: 0.02816
ii) Maximum amplitude of cardiovascular activity: 0.00315
iii) a) Ratio of ventilation to cardiovascular activity: 8.93551
iii) b) Ratio of cardiovascular to ventilation activity: 0.11191
```

2.4 Question 4

Determine the eigenvalues of the first three principal components resulting from the first PCA (see variable `PC1`).

[108]:
```

```

```
# Determine the eigenvalues of the first three principal components resulting␣
 ↪from the first PCA (see variable `PC1`).
print('Eigenvalues of the first three principal components resulting from the␣
 ↪first PCA:')
print(lambda1[-1], lambda1[-2], lambda1[-3])
```

```
Eigenvalues of the first three principal components resulting from the first
PCA:
107.58688656183709 2.1114888816145285 0.8031524393717155
```

2.5 Question 5

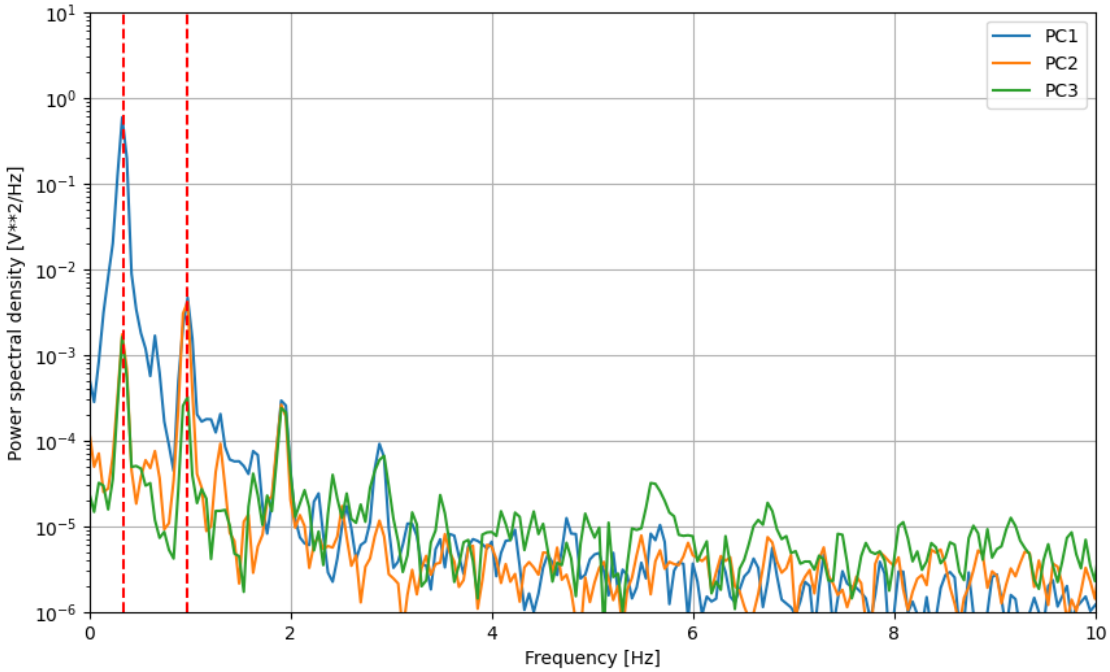
Similar to Question 4, determine the two most dominant frequencies for the first three principal components. Note that this would lead to a total of 6 values, 2 frequencies for each of the 3 PCA components. However, for some components only one dominant frequency might be present. For all 3 PCA components, which one is rather related to ventilation or cardiovascular activity?

[109]:
```
#Plot the power spectral density for the first three principal components␣
 ↪resulting from the first PCA (see variable `PC1`).
import matplotlib.pyplot as plt
from scipy.signal import welch

f, Pxx = welch(PC1[:, -1], fs=fs, nperseg=1024)
plt.figure(figsize=(10, 6))
plt.semilogy(f, Pxx, label='PC1')
f, Pxx = welch(PC1[:, -2], fs=fs, nperseg=1024)
plt.semilogy(f, Pxx, label='PC2')
f, Pxx = welch(PC1[:, -3], fs=fs, nperseg=1024)
plt.semilogy(f, Pxx, label='PC3')
plt.xlabel('Frequency [Hz]')
plt.ylabel('Power spectral density [V**2/Hz]')
plt.legend()
plt.xlim([0, 10])
plt.ylim([1E-6, 10])
plt.grid()
plt.vlines([mean_resp_rate, mean_card_freq], 1E-6, 10, colors='r',␣
 ↪linestyles='dashed')
plt.show()

# Print the values
print('The values of the first three principal components resulting from the␣
 ↪first PCA:')
print(PC1[:, -1])
print(PC1[:, -2])
print(PC1[:, -3])
print('Mean ventilation frequency (respiratory rate): {:.2f} Hz'.
 ↪format(mean_resp_rate))
```

```
print('Mean cardiovascular frequency: {:.2f} Hz'.format(mean_card_freq))
```




```
The values of the first three principal components resulting from the first PCA:
[-0.12186629 -0.11530548 -0.13045841 …  0.04332511  0.03668711
  0.03658657]
[ 0.01569289  0.08292314  0.08326825 … -0.12283211 -0.1106632
 -0.01996051]
[ 0.00341983  0.03634772  0.03486044 …  0.00031399 -0.001566
  0.00510862]
Mean ventilation frequency (respiratory rate): 0.33 Hz
Mean cardiovascular frequency: 0.97 Hz
```

From the plot above one can see the following frequency components: - PC1: first dominant frequency at around ~0.33 Hz (ventilation) and second component at ~0.97Hz (cardiovascular) - PC2: first dominant frequency at around ~0.97Hz (cardiovascular) Hz and second component at ~0.33Hz (ventilation) - PC3: first dominant frequency at around ~0.33 Hz (ventilation) and second component at ~0.97Hz (cardiovascular) with the corresponding harmonic at ~2Hz

2.6 Question 6

The three example signals (Regions A to C: **green, blue, red**) of cardiovascular activity show the impedance change over time. Can you guess the underlying anatomical structure for each of the three example signals (Regions A to C: **green, blue, red**).

Based on the *cardiovascular activity* plot, one can observe that the green region corresponds to the heart, while the blue and red regions to the lungs (resp. right and left).

2.7 Question 7 - *Bonus Question* (not graded)

Can you detect the QRS peaks (e.g., using `qrs = Detectors(fs).engzee_detector(ecg)`) on the ECG signal (see variable `ecg`) and plot them together with the cardiovascular EIT activity?

[110]:
```
qrs = Detectors(ecg['fs']).engzee_detector(ecg['value'])
time = ecg['time']
```

[111]:
```
# plot cardiovascular acticity
fig = make_subplots(rows=1, cols=2, column_widths=[1, 2])
fig.update_layout(width=950, height=400)

fig.add_trace(go.Heatmap(z=np.std(imgs_card, axis=-1), zmin=0,
                         showscale=False, colorscale='magma'), row=1, col=1)
fig.update_yaxes(title='Right', showticklabels=False, autorange="reversed",␣
 ↪row=1, col=1)
fig.update_xaxes(title='Dorsal', showticklabels=False, row=1, col=1)
fig.update_layout(title='Cardiovascular Activity')

fig.add_trace(go.Scatter(x=t, y=np.nanmean(imgs_card, axis=(0, 1)),
                         name='Mean Signal', line_color='black'), row=1, col=2)
fig.update_xaxes(title='Time (s)', row=1, col=2)
fig.update_yaxes(title='Impedance Change \Delta Z (A.U.)', row=1, col=2)

# add three example signals in ??? regions
regions = {'Region A': ([18, 9], 'green'), 'Region B': ([10, 15], 'blue'),␣
 ↪'Region C': ([23, 15], 'red')}
for reg, tmp in regions.items():
    fig.add_scatter(x=[tmp[0][0]], y=[tmp[0][1]], mode='markers',␣
 ↪marker_symbol='square-open',
                    marker_size=10, legendgroup=reg, marker_color=tmp[1],␣
 ↪name=reg, row=1, col=1)
    fig.add_trace(go.Scatter(x=t, y=imgs_card[tmp[0][1], tmp[0][0], :],␣
 ↪legendgroup=reg,
                             showlegend=False, name=reg, line_color=tmp[1]),␣
 ↪row=1, col=2)

# add ecg signal
fig.add_trace(go.Scatter(x=time, y=ecg['value'], name='ECG Signal',␣
 ↪line_color='orange'), row=1, col=2)
#add qrs peaks
fig.add_trace(go.Scatter(x=time[qrs], y=ecg['value'][qrs], mode='markers',␣
 ↪marker_symbol='triangle-up',
                         marker_size=10, marker_color='red', name='QRS Peaks'),␣
 ↪row=1, col=2)

fig.show()
```

```
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```

PCA_for_FetalECG

November 26, 2024

1 PCA for Source Separation of Abdominal ECG Signals

1.1 Introduction

In this exercise we use PCA for the separation of maternal and fetal electrocardiography (ECG) signals in abdominal ECG (aECG) data recorded on the belly of a pregnant woman. Due to the low signal strengh of fetal ECG (fECG) signals it is an "algorithmic challenge" to properly separate fECG from much stronger maternal ECG (mECG) signals [1].

The present example uses a simplified version of the method proposed by Varanini et al. [2].

1.2 References

[1] R. Kahankova et al., "A Review of Signal Processing Techniques for Non-Invasive Fetal Electrocardiography," IEEE Reviews in Biomedical Engineering, vol. 13, pp. 51–73, 2020, doi: 10.1109/RBME.2019.2938061.

[2] M. Varanini, G. Tartarisco, L. Billeci, A. Macerata, G. Pioggia, and R. Balocchi, "An efficient unsupervised fetal QRS complex detection from abdominal maternal ECG," Physiol. Meas., vol. 35, no. 8, pp. 1607–1619, Aug. 2014, doi: 10.1088/0967-3334/35/8/1607.

[3] Source of data: https://physionet.org/content/challenge-2013/1.0.0/

[1]:
```
import numpy as np
import pandas as pd
from scipy.signal import filtfilt, butter
from sklearn.decomposition import PCA

import plotly.graph_objects as go
from plotly.offline import init_notebook_mode, iplot
from plotly.subplots import make_subplots
init_notebook_mode(connected=True)  # initiate notebook for offline plot

from mqrs_utils import cancel_mqrs
from ecgdetectors import Detectors
```

[2]:
```
# load abdominal ECG (aECG) data
# transformed from initial source: https://physionet.org/content/challenge-2013/
  ↪1.0.0/set-a/a13.dat
filename = 'aecg_a13.hdf5'
```

```
aecg = pd.read_hdf(filename, key='signals').values
fs = 1000
t = np.arange(aecg.shape[0]) / fs
```

[3]:
```
# bandpass filter data
b, a = butter(4, np.asarray([3, 45]), fs=fs, btype='bandpass')
aecg = filtfilt(b, a, aecg, axis=0)

# plot
fig = go.Figure()
for i in range(aecg.shape[1]):
    fig.add_trace(go.Scatter(x=t, y=aecg[:, i], name='AECG{:d}'.format(i)))
fig.update_xaxes(title='Time (s)')
fig.update_yaxes(title='AECG Amplitude (A.U.)')
fig.update_layout(title='Bandpass-Filtered AECG Signals')
fig.show()
```

[4]:
```
# apply first PCA for enhancing maternal ECG component
pca1 = PCA()
pc1 = pca1.fit_transform(aecg)

# maternal ECG as the first principal component, note that this
# remains a guess and would need to be automated in the final solution
maternal_ecg = pc1[:, 0]

# detect maternal QRS peaks
mqrs_peaks = Detectors(fs).engzee_detector(maternal_ecg)

# plot
fig = go.Figure()
for i in range(pc1.shape[1]):
    fig.add_trace(go.Scatter(x=t, y=pc1[:, i], name='PC1[:,{:d}]'.format(i)))
    if i == 0:
        fig.add_trace(go.Scatter(x=t[mqrs_peaks], y=pc1[mqrs_peaks, i],␣
 ↪name='mQRS-Peaks',
                                 mode='markers', marker_color='red',␣
 ↪marker_symbol='circle-open'))
fig.update_xaxes(title='Time (s)')
fig.update_yaxes(title='PC1 (A.U.)')
fig.update_layout(title='Principal Components of First PCA Used to Enhance mECG␣
 ↪Signal')
fig.show()
```

[5]:
```
# remove maternal QRS complexes from signal to obtain a best possible fetal ECG␣
 ↪signal
x_residual, mecg_estimations = cancel_mqrs(fs, pc1, np.asarray(mqrs_peaks))
```

```
# plot
fig = make_subplots(rows=3, cols=1, shared_xaxes=True)
fig.add_trace(go.Scatter(x=t, y=pc1[:,0], name='Maternal ECG'), row=1, col=1)
fig.add_trace(go.Scatter(x=t[mqrs_peaks], y=pc1[mqrs_peaks, 0],␣
 ↪name='mQRS-Peaks', marker_color='red',
                         legendgroup='mQRS', mode='markers',␣
 ↪marker_symbol='circle-open'), row=1, col=1)
fig.add_trace(go.Scatter(x=t, y=mecg_estimations[:, 0], name='Interpolated mQRS␣
 ↪Signal'), row=2, col=1)
fig.add_trace(go.Scatter(x=t[mqrs_peaks], y=mecg_estimations[mqrs_peaks, 0],␣
 ↪name='mQRS-Peaks', marker_color='red',
                         legendgroup='mQRS', showlegend=False, mode='markers',␣
 ↪marker_symbol='circle-open'), row=2, col=1)
fig.add_trace(go.Scatter(x=t, y=x_residual[:, 0], name='mQRS-free Signal'),␣
 ↪row=3, col=1)
fig.add_trace(go.Scatter(x=t[mqrs_peaks], y=x_residual[mqrs_peaks, 0],␣
 ↪name='mQRS-Peaks', marker_color='red',
                         legendgroup='mQRS', showlegend=False, mode='markers',␣
 ↪marker_symbol='circle-open'), row=3, col=1)
fig.update_xaxes(title='Time (s)', row=3, col=1)
fig.update_layout(title='Maternal QRS Cancellation')
fig.show()
```

[6]:
```
# apply second PCA for enhancing fetal ECG component in residual signal
pca2 = PCA()
pc2 = pca2.fit_transform(x_residual)

# fetal ECG as the first principal component, note that this
# remains a guess and would need to be automated in the final solution
fetal_ecg = pc2[:, 0]
# detect fetal QRS peaks
fqrs_peaks = Detectors(fs).engzee_detector(fetal_ecg)

# plot
fig = go.Figure()
for i in range(pc2.shape[1]):
    fig.add_trace(go.Scatter(x=t, y=pc2[:, i], name='PC2[:,{:d}]'.format(i)))
    if i == 0:
        fig.add_trace(go.Scatter(x=t[fqrs_peaks], y=pc2[fqrs_peaks, i],␣
 ↪name='fQRS-Peaks',
                                 mode='markers', marker_color='black',␣
 ↪marker_symbol='triangle-down-open'))
fig.update_xaxes(title='Time (s)')
fig.update_yaxes(title='PC2 (A.U.)')
fig.update_layout(title='Principal Components of Second PCA Used to Enhance␣
 ↪fECG Signal')
```

```
fig.show()
```

[7]:
```
# plot for summarizing all
fig = make_subplots(rows=2, cols=1, shared_xaxes=True)
# maternal ECG with mQRS
fig.add_trace(go.Scatter(x=t, y=maternal_ecg, name='Maternal ECG'), row=1,␣
 ↪col=1)
fig.add_trace(go.Scatter(x=t[mqrs_peaks], y=maternal_ecg[mqrs_peaks],␣
 ↪name='mQRS-Peaks',
                         marker_color='red', mode='markers',␣
 ↪marker_symbol='circle-open'), row=1, col=1)
# fetal ECG with fQRS
fig.add_trace(go.Scatter(x=t, y=fetal_ecg, name='Fetal ECG'), row=2, col=1)
fig.add_trace(go.Scatter(x=t[fqrs_peaks], y=fetal_ecg[fqrs_peaks],␣
 ↪name='fQRS-Peaks',
                         marker_color='black', mode='markers',␣
 ↪marker_symbol='triangle-down-open'), row=2, col=1)
fig.update_xaxes(title='Time (s)', row=2, col=1)
fig.update_layout(title='Maternal vs. Fetal ECG')
fig.show()
```

2 Exercise Questions

Please provide your answers directly below each question.

2.1 Question 1

Determine the maternal heart rate, both expressed in `Hz` and `beats/min`.

[8]:
```
mqrs_peaks_t =  np.array(mqrs_peaks)/ fs
mean_hrb = np.mean(1 / np.diff(mqrs_peaks_t))

print('Mean Heart Rate of Maternal ECG: {:.2f} Hz'.format(mean_hrb))
print('Mean Heart Rate of Maternal ECG: {:.2f} bpm'.format(60*mean_hrb))
```

```
Mean Heart Rate of Maternal ECG: 1.37 Hz
Mean Heart Rate of Maternal ECG: 82.08 bpm
```

2.2 Question 2

Determine the fetal heart rate, both expressed in `Hz` and `beats/min`.

[9]:
```
fqrs_peaks_t =  np.array(fqrs_peaks)/ fs
mean_hrb = np.mean(1 / np.diff(fqrs_peaks_t))

print('Mean Heart Rate of Fetal ECG: {:.3f} Hz'.format(mean_hrb))
print('Mean Heart Rate of Fetal ECG: {:.3f} bpm'.format(60*mean_hrb))
```

```
Mean Heart Rate of Fetal ECG: 1.914 Hz
Mean Heart Rate of Fetal ECG: 114.860 bpm
```

2.3 Question 3

Determine the follwing three values:

- i) the average amplitude of the maternal QRS peaks (`mQRS`);
- ii) the average amplitude of the fetal QRS peaks (`fQRS`);
- iii) the ratio between the average amplitudes of i) `mQRS` and ii) `fQRS` peaks.

[10]:
```
avg_mqrs = np.mean(maternal_ecg[mqrs_peaks])
avg_fqrs = np.mean(fetal_ecg[fqrs_peaks])
ratio_fm = avg_fqrs / avg_mqrs
ratio_mf = avg_mqrs / avg_fqrs
print('Average amplitude of the maternal QRS complexes: {:.3f}'.
  ↪format(avg_mqrs))
print('Average amplitude of the fetal QRS complexes: {:.3f}'.format(avg_fqrs))
print('Ratio of fetal to maternal QRS complex amplitudes: {:.3f}'.
  ↪format(ratio_fm))
print('Ratio of maternal to fetal QRS complex amplitudes: {:.3f}'.
  ↪format(ratio_mf))
```

```
Average amplitude of the maternal QRS complexes: 103.253
Average amplitude of the fetal QRS complexes: 20.496
Ratio of fetal to maternal QRS complex amplitudes: 0.199
Ratio of maternal to fetal QRS complex amplitudes: 5.038
```

2.4 Question 4

How many of the principal components of the first PCA clearly show a maternal ECG signal? Which ones?

From the *Principal Components of First PCA Used to Enhance mECG Signal* plot, we can see that the two first components of the PCA (PC1[0:] and PC1[1:]) contains the ECG of the mother. The other two are not significant for the ECG.

2.5 Question 5

How many of the principal components of the second PCA clearly show a fetal ECG signal? Which ones?

For the fetal, only the first PCA component is relevant. It can be seen in the *Principal Components of Second PCA Used to Enhance fECG Signal* plot. The other three remaining components contain noises.

2.6 Question 6

Not all of the fetal QRS peaks seem to be detected properly. Do you have an explanation why this happens and under which circumstances? Is it a problem of the fQRS detector, the mQRS cancellation or of another block of the algorithm?

It can be seen that the fQRS peak detector fails to find all the relevant peaks. It often happens when the peak is close to a mQRS peak. It can be due to the fact that applying mQRS cancellation will also remove parts of the fetal ECG signal.