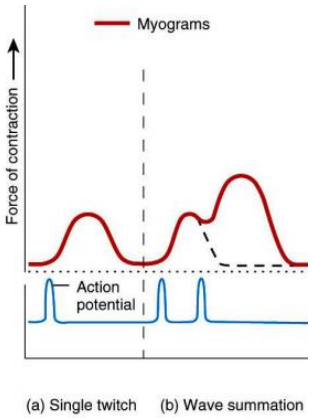
Electromyography

Introduction

The muscle contraction is stimulated by neuronal impulses incoming from the central nervous system (CNS) through the spinal cord, motor roots and nerves, that are composed of individual neural fibres. A motor fibre can innervate more muscle fibres that are together called a *motor unit*. Gradual activation of motor units for muscle contraction represents a *motor unit recruitment*. A muscle cell contraction cannot be continuously regulated therefore full contraction starts after action potential activation. Force of the muscle contraction is proportional to the amount of the activated motor units. The increasing frequency of incoming stimulations prevents the muscle cell returning to relaxation, that additionally strengthens the contractions. The permanent contraction of muscle cells is called tetanus. The nerve signal amplitude is very low (100 µV), but the summation of action potentials of non-synchronously activated muscle cells produces the strong signals (mV) called electroctomyogram (EMG).



Previous knowledge shows that the stronger muscle contraction recruits more motors units (higher amplitude of EMG) together with faster stimulations from CNS (shift of spectrum to higher frequencies).

The tired muscle cells lose the ability to generate the action potential after stimulation and cells stay relaxed.

Aims:

1. Analyse your or selected signal captured during volatile muscle contraction (weak, medium, maximal). The contraction should be longer as least as 1 s.
   Measure the delay between muscle activations (EMG) and contractions (force).
   - make the signal envelope of EMG (by the IIR integrator and FIR moving average MA-filter – choice the appropriate order)
   - use the autocorrelation to estimate the delay between muscle activation and force

   Parametrise the section of contractions (weak, medium, maximal) by:
   - energetic parameters (standard deviation, peak to peak, power)
   - frequency parameters (power spectral density PSD, median frequency, zero-crossing, 1st and 2nd spectral moments)

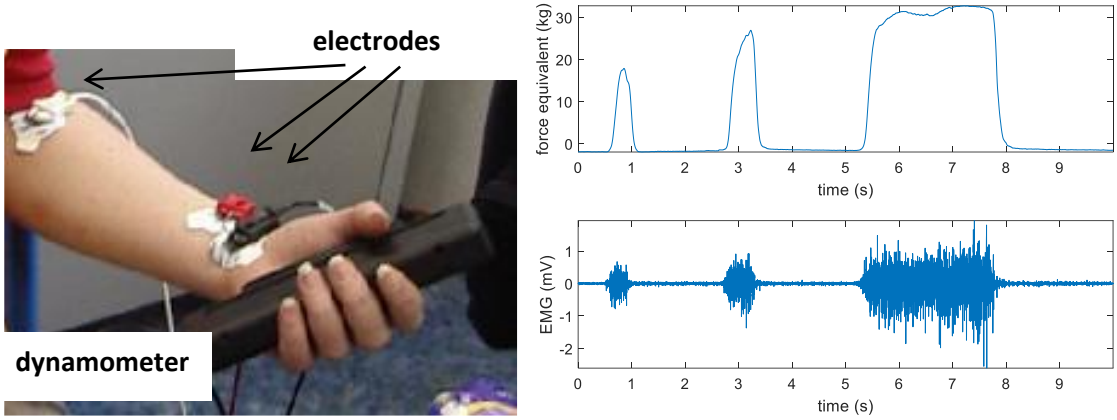
2. Use the similar parameters to evaluate muscle fatigue during prolonged muscle contraction.
   - Segment the EMG by appropriate windows with negative overlap. Parametrise each segment and figure the time dependency corresponding with fatigue.
   - Compare first 20 and last 20 segments using statistical test and identify parametrisation, that reliably describe the fatigue.

Dataset:

http://sami.fel.cvut.cz/bsg/cv04/Data_lab04.zip

Biological signal measurement:

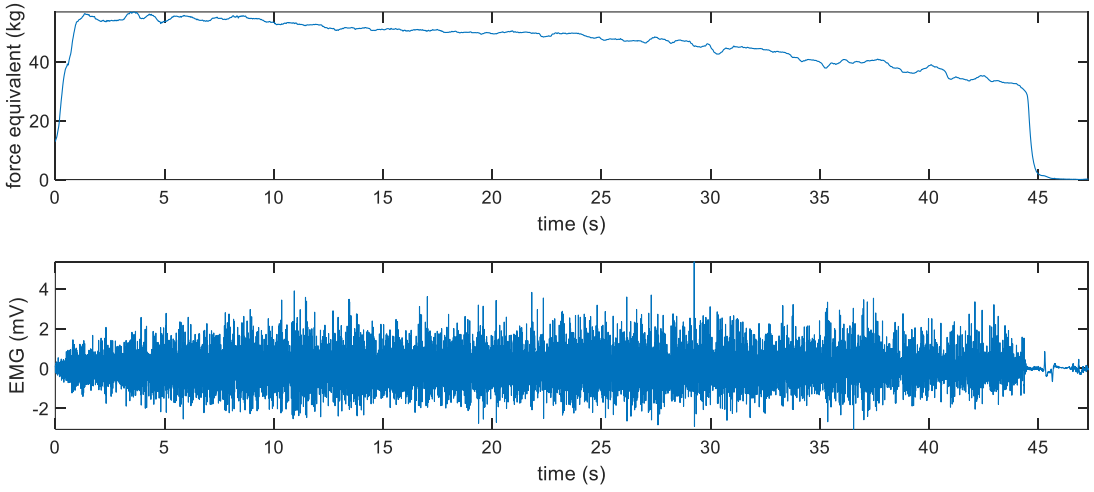
1. **Recording of skin surface EMG during volatile contraction.**
   Force is measured by dynamometer in hand, EMG by the skin electrodes. Grip the dynamometer in three trails for 1 s (weak, middle, maximal) during app. 10 s.



Data structure: e.g.: emg_3xR_03.txt

```
fs= 1000 Hz
1. column ... force equivalent [kg]
2. column ... EMG [mV]
```

2. **Recording of muscle fatigue.**
   Grip the dynamometer with maximal possible contraction and hold on as long as possible. Decrease force under app. 50% of initial value stops the experiment.



Data structure: e.g: vydrz01L.txt

```
fs= 1000 Hz
1. column ... force equivalent [kg]
2. column ... EMG [mV]
```

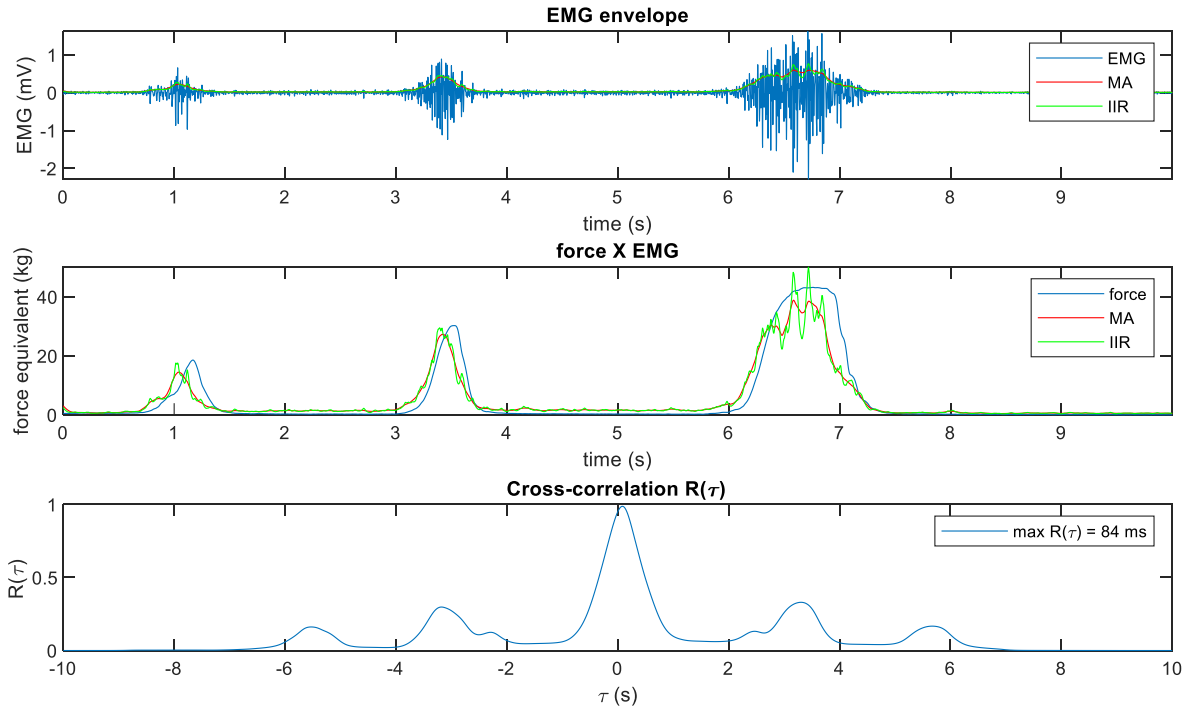
Useful functions:

`butter, filtfilt, fft, cumsum, xcorr, mod, ginput, polyfit, polyval`

Help:

Different intense contractions

```
data=load('emg_3xR_03.txt');
fs=1e3;
t=linspace(0,(size(data,1)-1)/fs,size(data,1)); % time axis
force=data(:,1); force=force-min(force); % removing of dynamometer offset
emg=data(:,2);

[bl,al]=butter(5,2*150/fs,'low'); % low pass filter 5. order <150 Hz
emg=filtfilt(bl,al,emg);


% moving average - MA filter
ma_time=0.1; % size of moving window e.g. 100 ms
N=ceil(ma_time*fs);
b=ones(N,1)/N; % [1/N ... 1/N]
ma_emg=filtfilt(b,1,abs(emg)); % MA envelope of rectified signal

% or IIR - integrator
b=1; a=[1 -0.95];
iir_emg=filtfilt(b,a,abs(emg)); % envelope of rectified signal, but without
corresponded energy -> normalization by the are under the curve
K=(sum(abs(emg))/sum(iir_emg)); % ratio of rectified EMG and envelope areas
iir_emg=K*iir_emg;

1)Show together: EMG, MA-EMG, K*IIR-EMG
2)Show together FORCE, MA-EMG, IIR-EMG (normalize it to force area)
3)Show autocorrelation of FORCE a envelope, identify the mutual lag
[R,lag]=xcorr(force,ma_emg,'coef');
[~,lag_max]=max(R); % position of maximum in autocorrelation
tau=lag(lag_max)/fs;
```

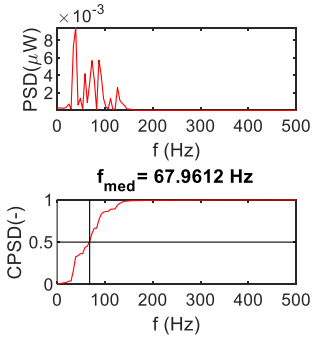


Parametrisation of individual contractions:

```
1)Use simple thresholding detector or manually select the sections of
contraction, try GINPUT.
[xt,~]=ginput(6); % 3x[start stop]
xn=ceil(xt*fs);
...
plot(t(xn(1):xn(2)),emg(xn(1):xn(2)),'r')
plot(t(xn(3):xn(4)),emg(xn(3):xn(4)),'g')
plot(t(xn(5):xn(6)),emg(xn(5):xn(6)),'c')

2) For each segment apply following energetic and frequency parameters
```

	energetic	**frequency**
time domain	standard deviation peak to peak (min-max) total energy total power	zero-crossing
Fourier spectrum	power spectral density (PSD)	median frequency 1st and 2nd spectral moments

```
segment=emg(xn(1):xn(2)); % e.g. first section (weak)

SD=std(segment); % standard deviation
PP=max(segment)-min(segment); % peak to peak
E=sum(segment.^2); % energy
PW=E/(length(segment)*fs); % power=energy per time

% (zero crossing - ZRC)
sg=sign(segment); % +1 above zero, -1 below zero, 0 is zero
sg(sg==0)=1; % rare zeros set to +1
ZRC=sum(diff(sg)~=0); % number of samples, where signum is changed, i.e.
                        zero-crossing
ZRCf=0.5*ZRC/(length(segment)/fs); % number of zrc per second divided
                        twice, because sin/cos period contains two zrc

% spectral parametrisation
S=(1/length(segment))*fft(segment); % (1/N)*FFT{x(n)}
S=2*S(1:ceil(end/2)); % one-side spectrum (2x energy)   notice: in column!
F=linspace(0,fs/2,length(S))'; % frequency axis 0:fs/2  notice: in column!

PSD=S.*conj(S); % power spectral density |S|^2

CPSD=cumsum(PSD)/max(cumsum(PSD)); % CPSD - cumulative
                                     distribution function
FMED=F(find(CPSD>=0.5,1)); % CPSD(f_MED)=50%
```

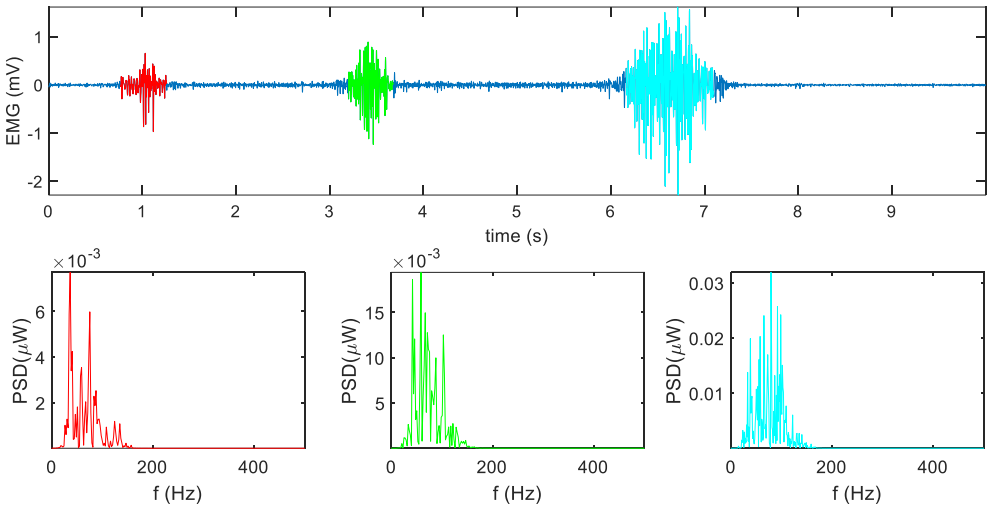


$$M_1 = \frac{\sum_{f=0}^{fs/2} f \times PSD(f)}{PSD}$$

```
MOM1=sum(F.*PSD)./sum(PSD);
```

$$M_2 = \sqrt{\frac{\sum_{f=0}^{fs/2} f^2 \times PSD(f)}{\sum PSD} - {M_1}^2}$$

```
MOM2=sqrt(sum((F.^2).*PSD)/sum(PSD)-MOM1.^2);
```



S.D.= 0.20 mV
P-P= 1.63 mV
PW= 0.00 μW
F_{ZRC}= 59.96 Hz
F_{MED}= 61.22 Hz
M_1= 65.80 Hz
M_2= 29.00 Hz

S.D.= 0.35 mV
P-P= 2.13 mV
PW= 0.00 μW
F_{ZRC}= 78.45 Hz
F_{MED}= 71.43 Hz
M_1= 74.12 Hz
M_2= 26.52 Hz

S.D.= 0.55 mV
P-P= 3.90 mV
PW= 0.00 μW
F_{ZRC}= 73.26 Hz
F_{MED}= 77.09 Hz
M_1= 76.44 Hz
M_2= 27.66 Hz

Evaluation of fatigue:

Segment the prolonged EMG by windows with overlap, parametrise segments and check the trends correspond to muscle fatigue.

```
win=ceil(1*fs); % window 1s
nov=ceil(0.5*win); % negative overlap 50%
index=1:win-nov:size(emg,1)-win; % indexes of segment starts

[xt,~]=ginput(2); % [start stop] select start and stop of contractions
xn=round(xt*fs);
index=index(index>xn(1) & index<xn(2)); % use only appropriate segments

T=t(index); % time marker of segment starts
for i=1:length(index)
    segment=emg(index(i):index(i)+win-1); % segment of EMG

    SD(i)=...
    PP(i)= ...
    ZRCf(i)=...
    FMED(i)=...
    MOM1(i)=...
    MOM2(i)=...
end
```

Linear fitting:

```
% polynomial coefficients
plin=polyfit(T',SD,1);

% linear approximation
lin=polyval(plin,T);
```

Statistical testing using Wilcoxon test:

```
p=ranksum(SD(1:20),SD(end-20+1:end));
...
```