Cours de traitement des signaux biomédicaux
3ème séance Matlab

Useful commands

resample	signal resampling
hilbert	analytical signal
polyfit	least-squares polynomial estimation
polyval	computation ppolynomial values

Additional command

num_ADN	numérisation d'une séquence d'ADN
envelopes	estimation of signal upper and lower envelopes

time-frequency toolbox commands

tfrstft	Short term Fourier transform, spectrogram
tfrwv	Wigner-Ville distribution
tfrspwv	smoothed pseudo Wigner-Ville distribution
tfrcw	Choi-Williams distribution
tfrzam	Zhao-Atlas-Marks distribution
tfrscalo	scalogram (Morlet wavelet)

Some remarks

- The time-frequency routines are in the toolbox développed by F. auger, P. flandrin, P. Gonçalvès, and O. Lemoine. This toolbox can be downloaded from the Web
- The cardiovascular signal sampling frequency is 4 Hz. Since the time-frequency routines are computationally intensive, sub-sample the signals at 1 Hz using resample (by all means interesting things take place only below 0.5 Hz). Do not forget to subtract the mean value.
- **Do not forget** to type a ″ ; ″ after the commands. Otherwise you see distribution values scrolling down for 10 minutes10 minutes, les valeurs de la distribution and Ctrl-C does not stop that.
- The menu that pops up with the figure figure allows you to display the signal and its power spectral density too (change the display layout). You can also change the threshold from 5 to 1, or use a logarithmic scale to get a better idea of the low-amplitude details.

Expériment 1 : Transcarnial Doppler (TCD) signals

Those signals are obtained from an ultrasound Doppler sensor placed at the level of the middle cerbral artery (sampling frequency 3000 Hz). They correspond to the migration of a solid (blood clot, blood plaque..., file **solides.mat**), gaseous (bubble, file **gazeux.mat**) corpuscle, or to an artifact (small shock, patient coughing…, file **artefacts.mat**). Visualize their time-frequency distribution estimate (preferably with tfrstft and tfrspwv, but give the other ones a shot) to highlight the différences between the three groups. **In the report, display only one time-frequency distribution for each signal class.** Interpret the time-frequency components with regard to the time evolution of the signals. Compare the advantadges of the various distributions for these signals. You can also verify tha the spectral density, estimated on the whole signal, averages the frequency events.

It is also worth to use tfrspwv once on the original signal (not the analytic one) to observe the spectral aliasing.

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Experiment 2

File **accel.dat** is a recording (sampling frequency 40 Hz) from an accelerometer on the wrist of a health worker. The goal is to detect the disinfection episodes (clinical soap on the hands and rubbing). It is known that in the recording disinfection takes place between time indices 900 and 1120. Use the envelope-based drift suppression technique with an appropriate window length, then display the time-frequency distribution (tfrstft or tfrspwv). What are the features that characterize disinfection ?

Experiment 3

File **emg2.dat** contains three sEMG signals (sampling frequency 1024 Hz). These signals were recorded on a thigh muscle during a 10-minute test (average to high intensity) on a, with a moderately trained subject. The columns correspond to the beginning, middle, and end of the test. Remove the mean values.

3.1 Visualize the time-frequency distributions of the three signals using tfrstft. What can be noticed in the bursts corresponding to muscular activity? What evolution can be seen along the three signals?

3.2 To quantify this evolution, we are going to estimate the mean frequency at each sampling instant in the bursts, and average these estimates on each signal.

- Apply envelopes to the signal (window size 45). Let us consider that burst samples are those for which the amplitude is larger than or equal to 10% of the maximum amplitude.
- If one uses :

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>> [W,T,F] = tfrstft(x) ;
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$|W|^2$ is the time-frequency distribution, and F the vector of normalized frequencies. Be careful : if N is the signal length, only the values between 1 and N/2, corresponding to normalized frequencies from 0 to 1/2 – 1/N , must be used. Compute the average mean frequency for the three signals. Conclusion ?

- Repeat this estimation on **emg1.dat**. Conclusion on this subject?

Experiment 4

File **sequence1.txt** contains 1000 elements of a real DNA sequence. It was determined that elements from 1 to 600 correspond to an exon, and elements from 601 to 1000 to an intron. The routine Num_ADN allows you to create numerical sequences (one signal per base) from this DNA sequence. Using a time-frequency analysis, determine which time-frequency event marks the intron and on which base it is most visible.