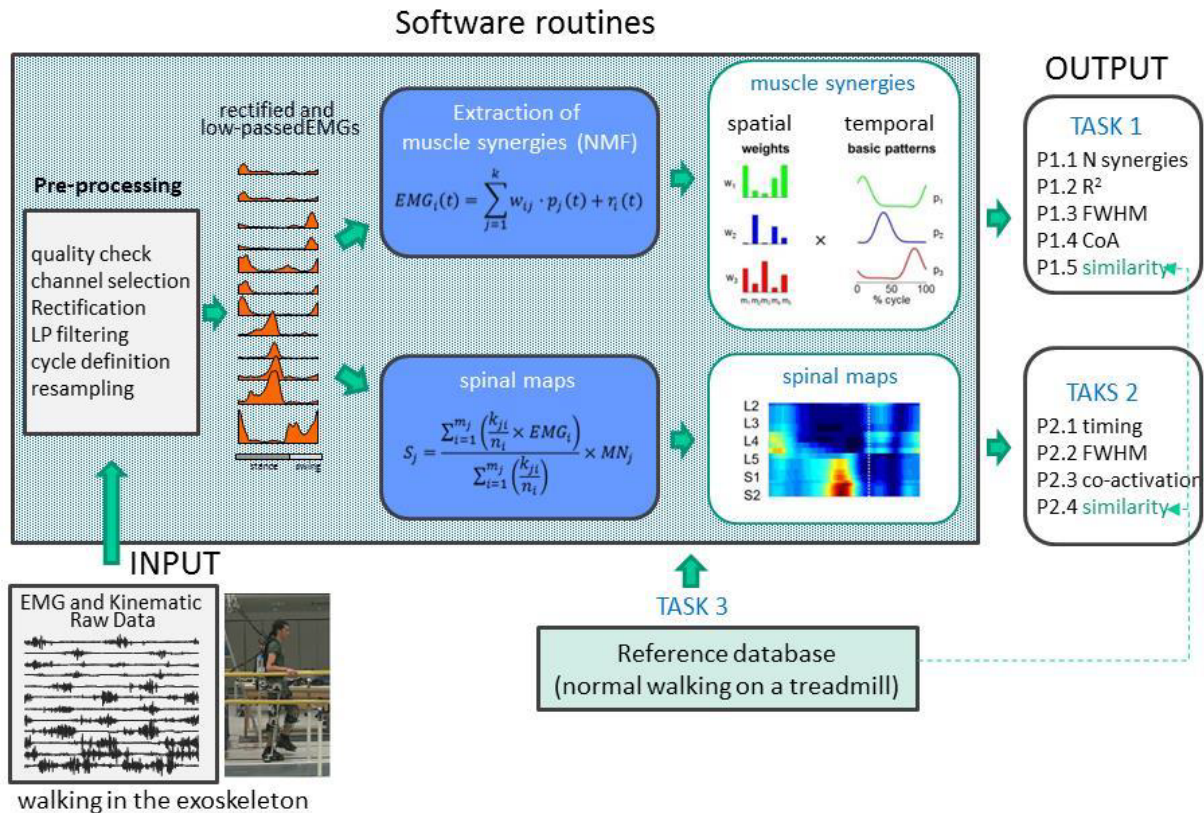# PEPATO Full Version User Guide

1. General information

PErformance indicators of spatiotemporal PATterns of the spinal muscle coordination Output during walking with an exoskeleton

The protocol consists in walking on a treadmill at a constant speed: 2, 4 and 6 km/h. At least 10 consecutive strides should be recorded for each speed condition. PEPATO software also allows to characterize only one or two speed conditions in case the participant cannot perform all speed conditions (e.g., some exoskeletons allow only slow walking).

Input and output data for the PEPATO software are compliant with the EUROBENCH Data Format.

1.1 Input

- EMGs of the lower limb. The current version of PEPATO processes 8 EMGs that are most accessible for recordings during walking in most exoskeletons: soleus (Sol), gastrocnemius medialis (GaMe), tibialis anterior (TiAn), rectus femoris (ReFe), vastus lateralis (VaLa), vastus medialis (VaMe), semitendinosus (SeTe), biceps femoris (long head, BiFe). Muscle order is not important. PEPATO also allows data reference updating to include more muscles, subjects and conditions. Raw EMG data are collected in .csv file.

- Gait events. Processed gait events should only specify the timing of touchdown events of the recorded strides and are saved in a .yaml file.

- File names format. EMG and Gait events files should be named the same:

*subject_**N**_run_**R**_speed**V**kmh_emg.csv*
*subject_**N**_run_**R**_speed**V**kmh_gaitEvents.yaml*

where: N – number of subject, R – number of experiment run (run number is the same for three different speeds), gait speed V should be from the list of [2, 4, 6] km per hour.

1.2 Output

There are two main groups of outcome indicators for evaluating muscle coordination during walking in the exoskeleton: muscle synergies [**TASK 1**] and spinal maps [**TASK 2**]. Both groups are generated using the above-mentioned input.

TASK 1 (muscle synergies) evaluates spatial (muscle weightings) and temporal (basic patterns) components of muscle modules (EMGs are normalized to its maximum value across speed conditions):

- **muscle_synergy_number** - the number of muscle synergies best describing the EMG data (for each speed)
- **emg_reconstruction_quality** - reconstruction quality (R^2) of EMG patterns from muscle synergies
- **pattern_fwhm** - FWHM (full width at half maximum), duration estimate of basic patterns
- **pattern_coa** - centre-of-activity (CoA) of basic patterns
- **patterns_similarity** - the degree of similarity of temporal components with the reference group (4 muscle module clusters for each speed) = the correlation between temporal components and reference temporal components of the module cluster centers.
- **synergies_similarity** - the degree of similarity of muscle synergies with the reference group (4 muscle module clusters for each speed) = the scalar product of muscle weightings to the reference muscle weightings of the module cluster centers.

TASK 2 (spinal maps):

- **motor_pool_max_activation_timing** - timing of the main loci of MN activity: timing of maximum activation of sacral (S1+S2) and upper lumbar (L3+L4) motor pools (for each speed)
- **motor_pool_fwhm** - FWHM of activation of sacral and upper lumbar spinal motor pools
- **motor_pool_coactivation** - co-activation index of sacral and upper lumbar motor pools
- **motor_pool_similarity** - the degree of similarity (correlation) of activation of sacral and lumbar motor pools with respect to the reference group

1. Installation and Run

Requirements: MATLAB (version >= 2015b)

Download: https://github.com/dzhvansky/pepato

Run Application: in MATLAB Command Window from pepato home directory

PEPATO(8, 'left', 'cfg/initial_cfg.mat', 'db/db_healthy_adults_8m', ...
{'BiFe', 'SeTe', 'VaMe', 'VaLa', 'ReFe', 'TiAn', 'GaMe', 'Sol'});

Parameters to set:

- FontSize (**8** optimal for 15" screen diagonal)
- Side of the body (**'left'** / 'right') – depending on the data you have
- Path to configuration file (**'cfg/initial_cfg.mat'** as a default)
- Path to the reference database file (**'db/db_healthy_adults_8m'** or **'db/db_healthy_elderly_8m'** for healthy adults or elderly respectively for {'BiFe', 'SeTe', 'VaMe', 'VaLa', 'ReFe', 'TiAn', 'GaMe', 'Sol'} muscle list; you can create new database here using path which not exist)
- List of muscles to analyze (**{'BiFe', 'SeTe', 'VaMe', 'VaLa', 'ReFe', 'TiAn', 'GaMe', 'Sol'}** by default, there are reference databases for this set of muscles for adults and elderly subjects.)
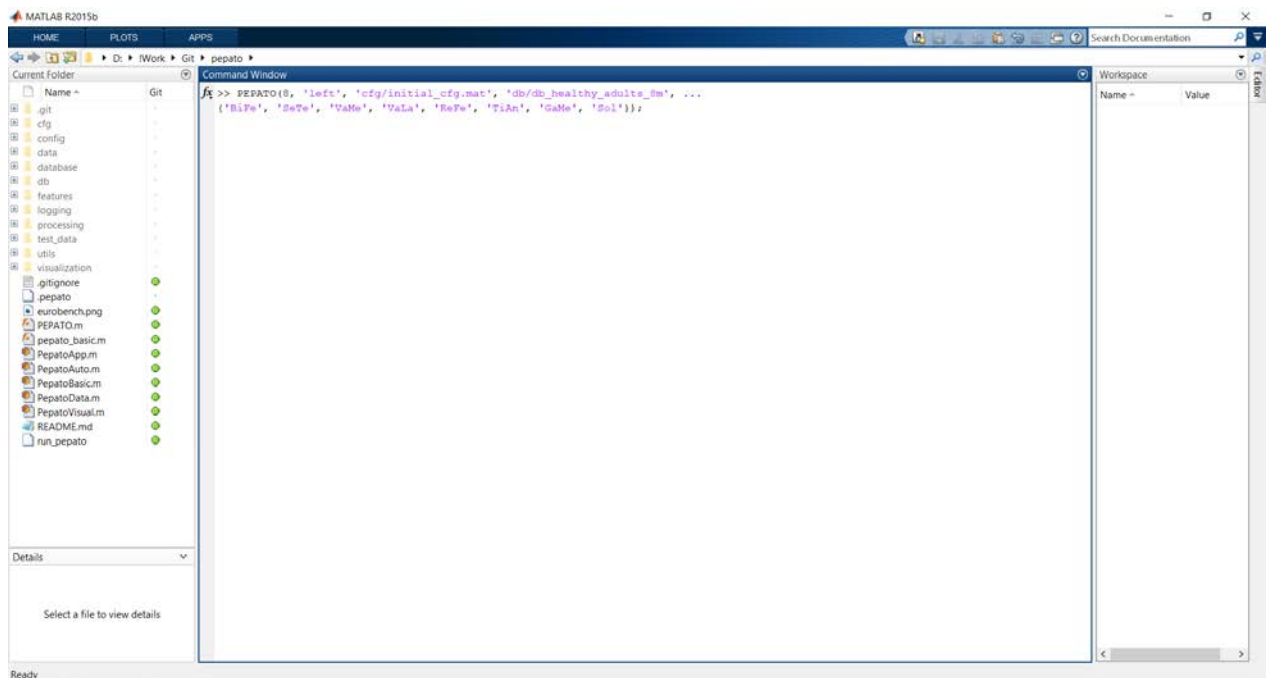
In case of the first run you will be prompted to save PEPATO folder paths:
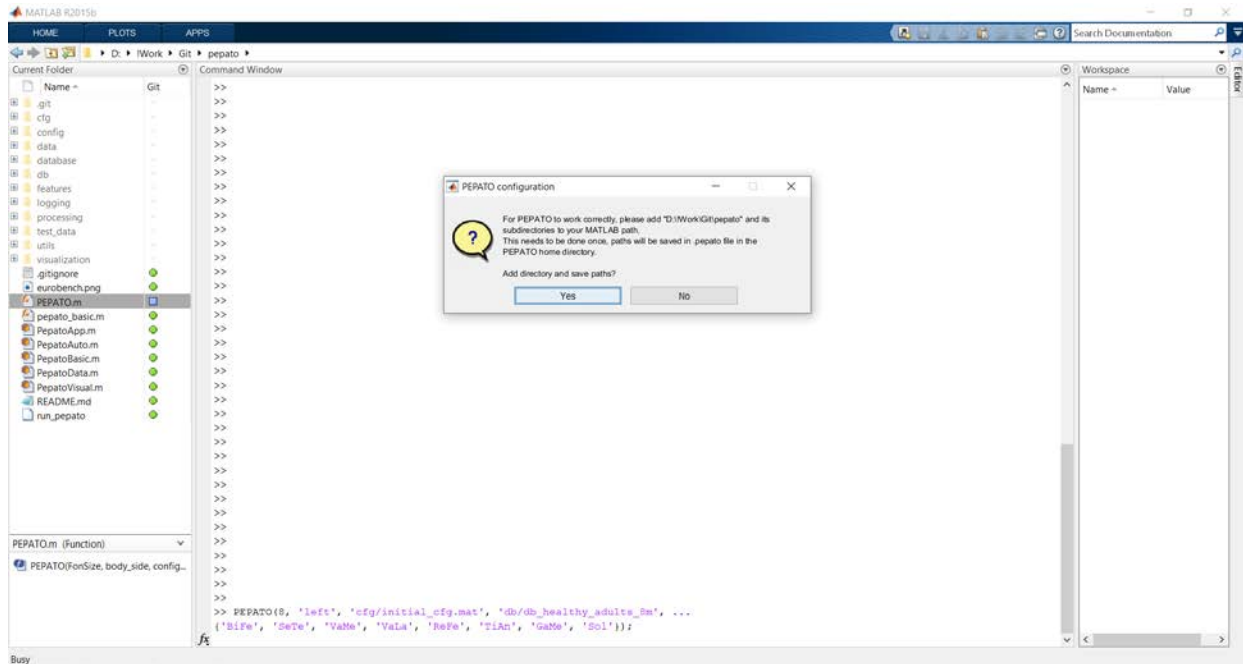
After adding the paths, the main application window will open in the new window
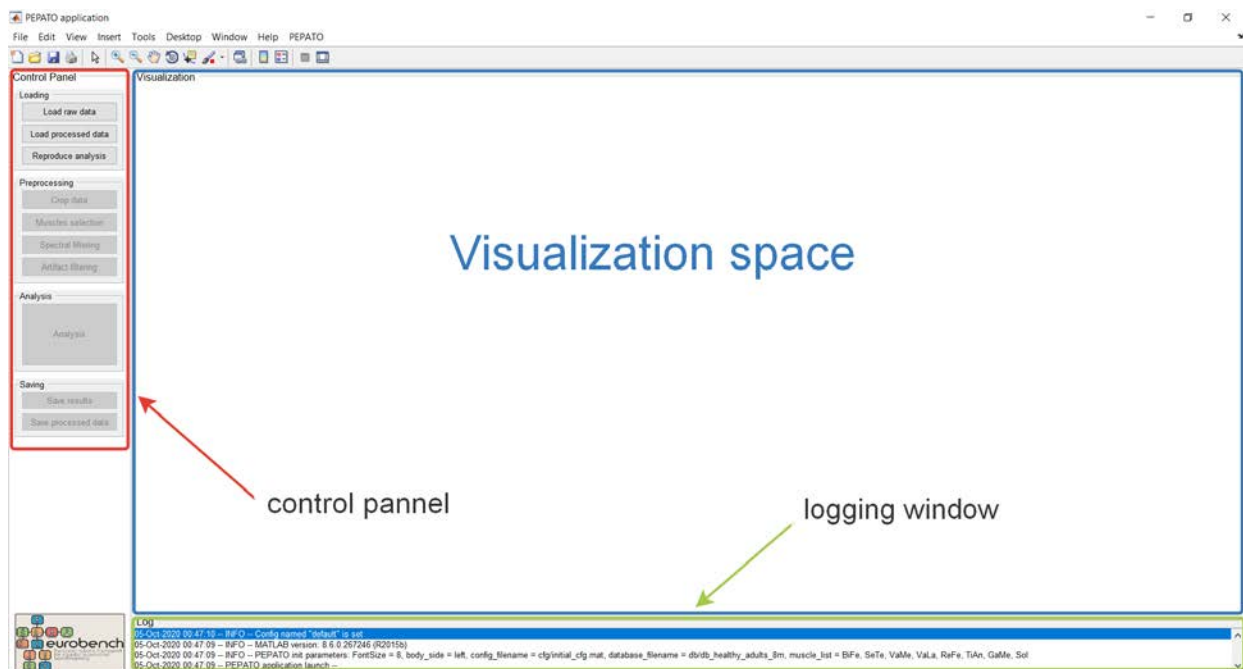
Here you can see the main panels: control panel, visualization space and logging window. If the application started correctly, you will see the launching log.

2. Data Loading

Here we have two main options: 1) raw data and 2) PEPATO preprocessed data. In both cases, you will manually choose files to upload (all data files for raw data and single file for preprocessed). If you have previously saved preprocessed data in *.mat* using PEPATO, you can load it so as not to repeat manual procedures. Otherwise, it is necessary to load raw EMG *.csv* and gait events *.yaml* files of one subject for different tasks.
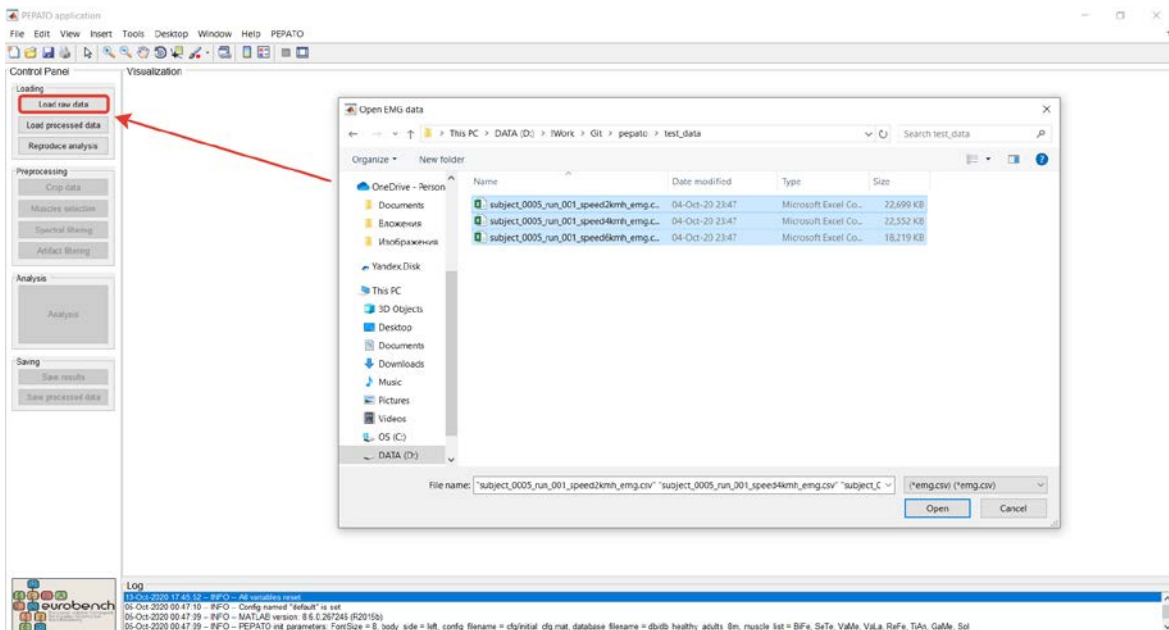
You should select only ***emg.csv*** files, ***gaitEvents.yaml*** files will be loaded automatically from the same folder.

FIle tabs will open by the number of files, and seven sub-tabs will be available for each file tab. You can switch between tabs and sub-tabs for visual inspection of the data.

After loading the data, you can start preprocessing it.

3. Data Preprocessing

The program provides four stages of data preprocessing: 1) crop, 2) muscle selection, 3) spectral filtering and 4) artifact filtering – in standard order. The first two stages are used to isolate segments and muscles for further processing, you can skip them if needed. The pipeline only requires artifacts filtering, but spectrum filtering is highly recommended.

3.1 Crop Data

You can select any number of segments for each file, the data will be "glued" by gait cycle events.
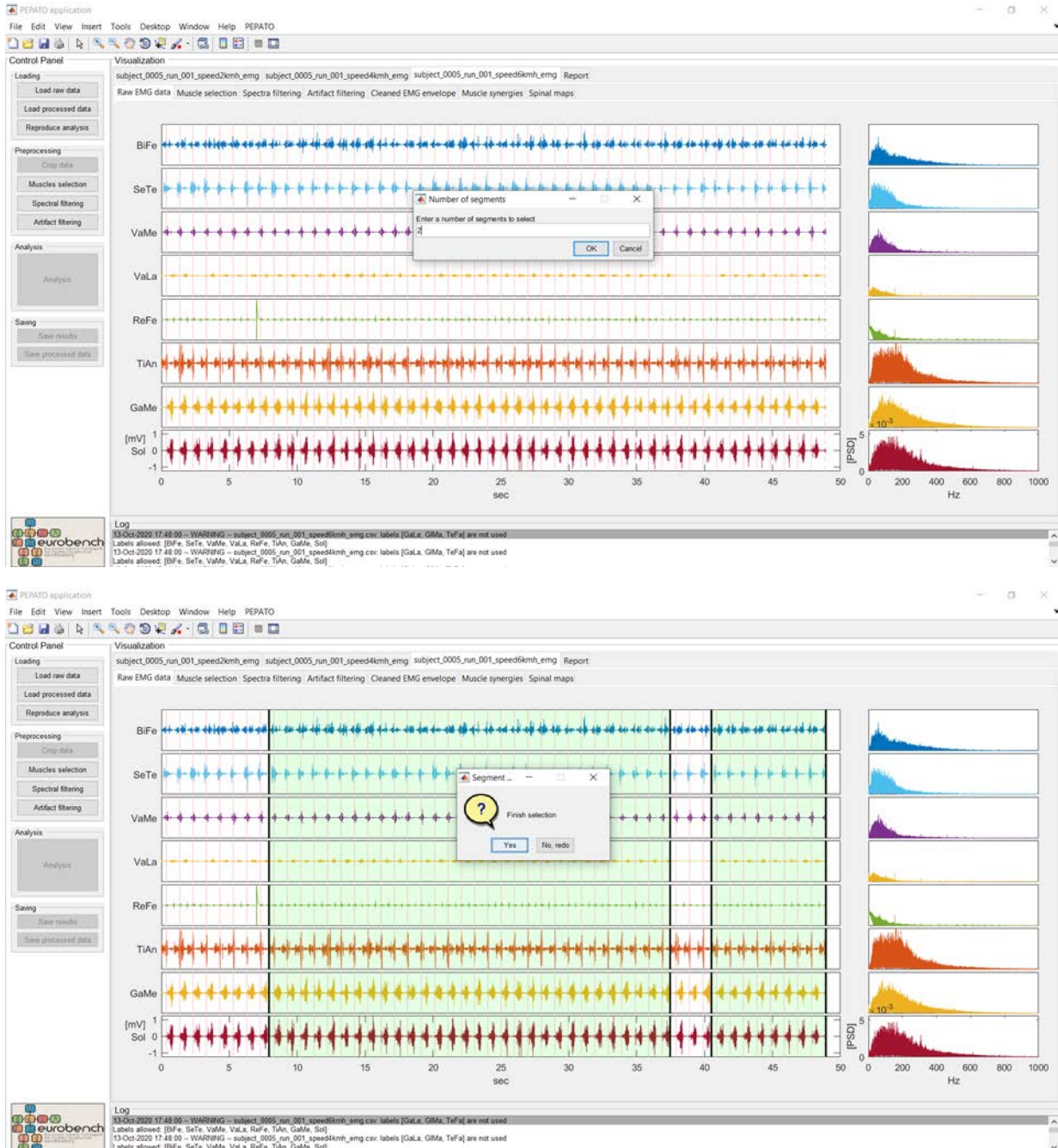
3.2 Select Muscles

You can select any number of muscles for each file, but if you want to compare the results with the reference database, you need to use the same muscle list for which the database was generated.

To drop the muscle, just push the muscle button.

After muscle dropping, you can restore the selection list or complete the stage.

3.3 Filter the spectrum

Standard EMG filtering (default, 30 Hz high-pass and 400 Hz low-pass – 4-th order Butterworth for both). Bandpass noise is also automatically searched, if you confirm the removal of a frequency band, it will be cut by the 6-th order Butterworth filter for all muscles.
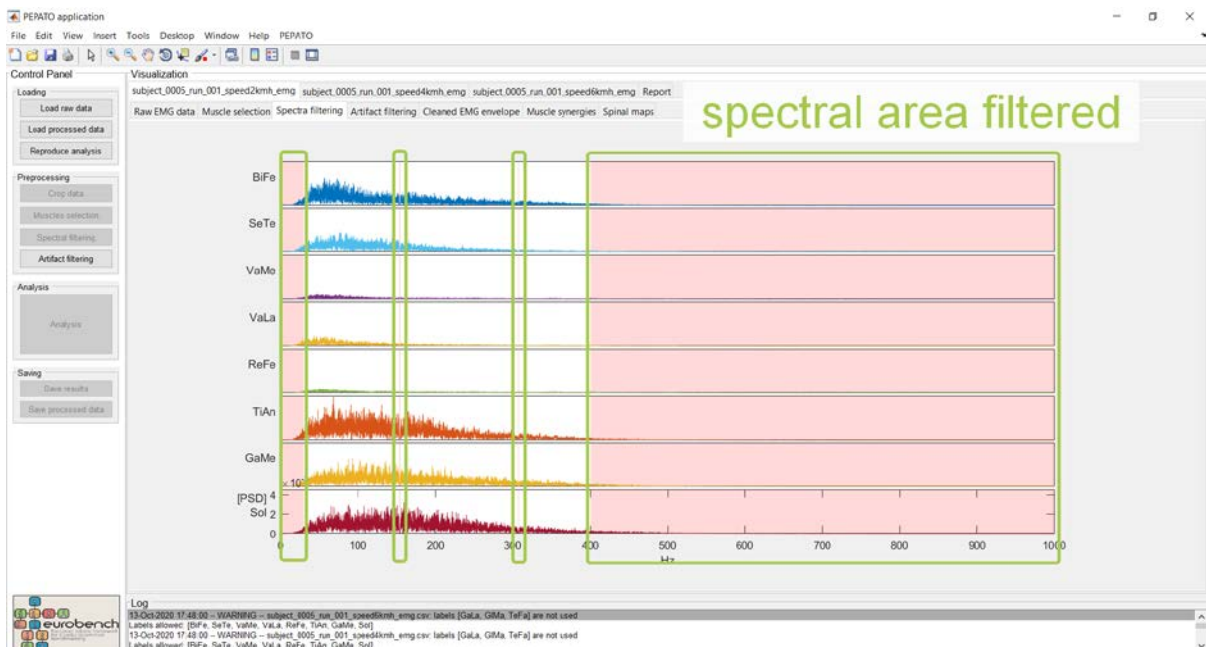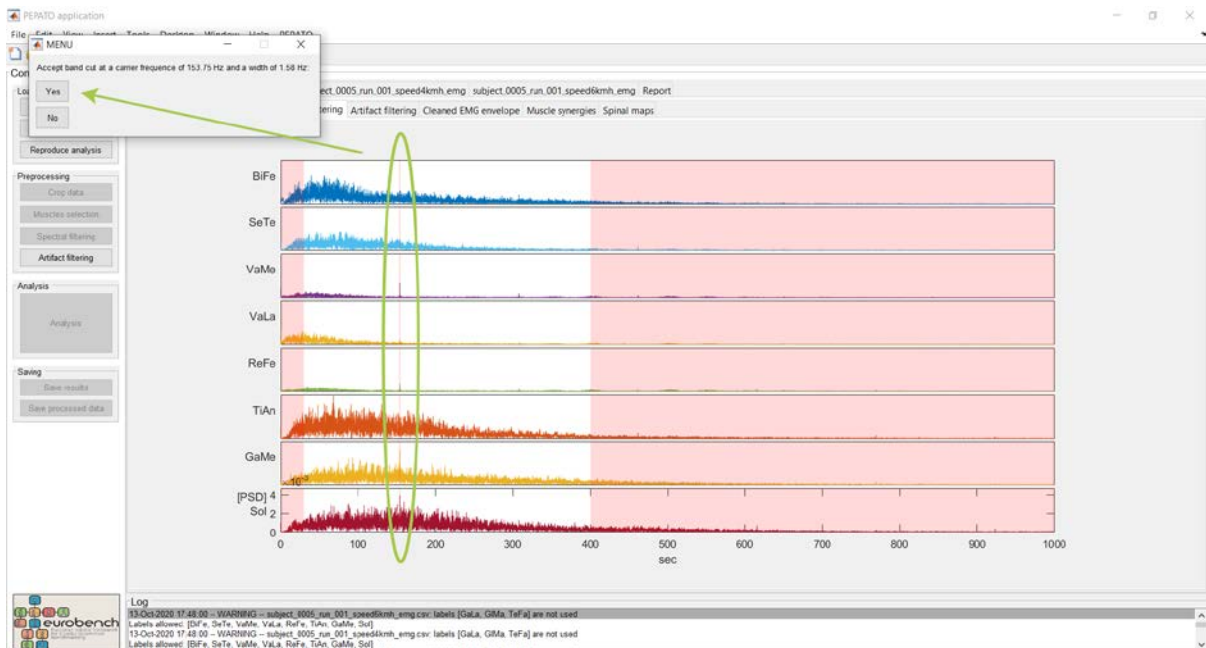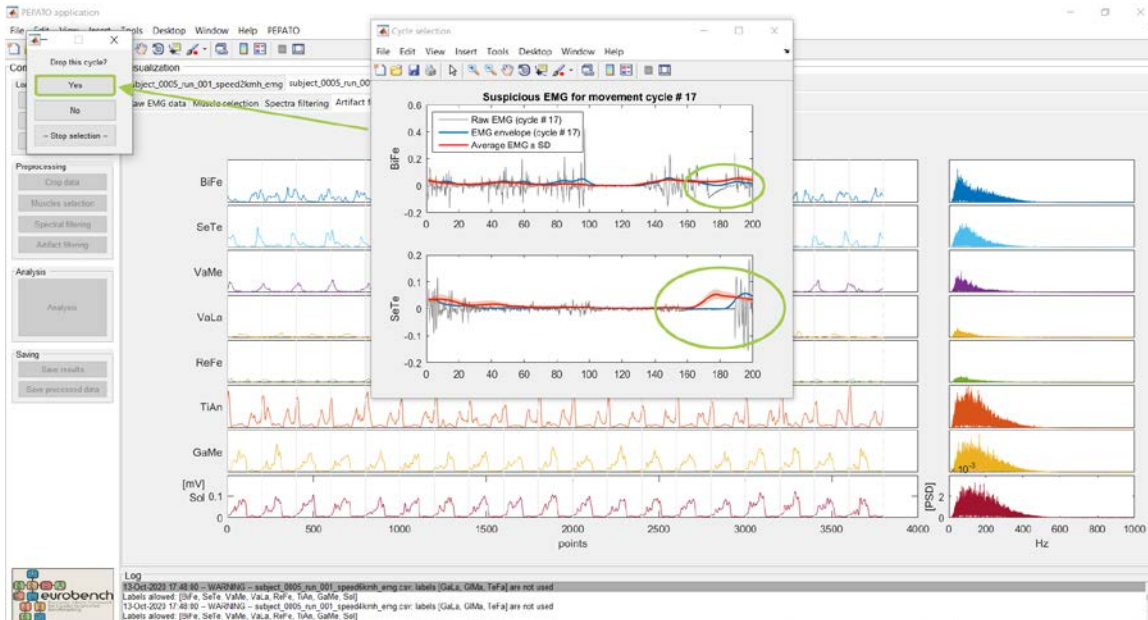
3.4 Filter artifacts

Automatic search for artifacts by comparing the EMG envelope of the gait cycle with the average envelope. All cycles here are normalized to the same number of points (200 by default).

A separate figure shows muscles with a deviating envelope. You can drop the cycle (for or all muscles at once – due to further analysis) or leave it by visual criteria. All gait cycles will be searched twice as the average envelope can change significantly after discarding cycles with artifacts after the first search. You can also stop searching for artifacts at any time (not recommended).


After filtering artifacts, preprocessing is completed, and we can save the data for further analysis, so as not to repeat preprocessing that requires manual validation. The data is compressed to the EMG envelopes normalized by the movement cycles, so the data requires little disk space.

After this stage (or loading preprocessed data), you can start PEPATO data analysis
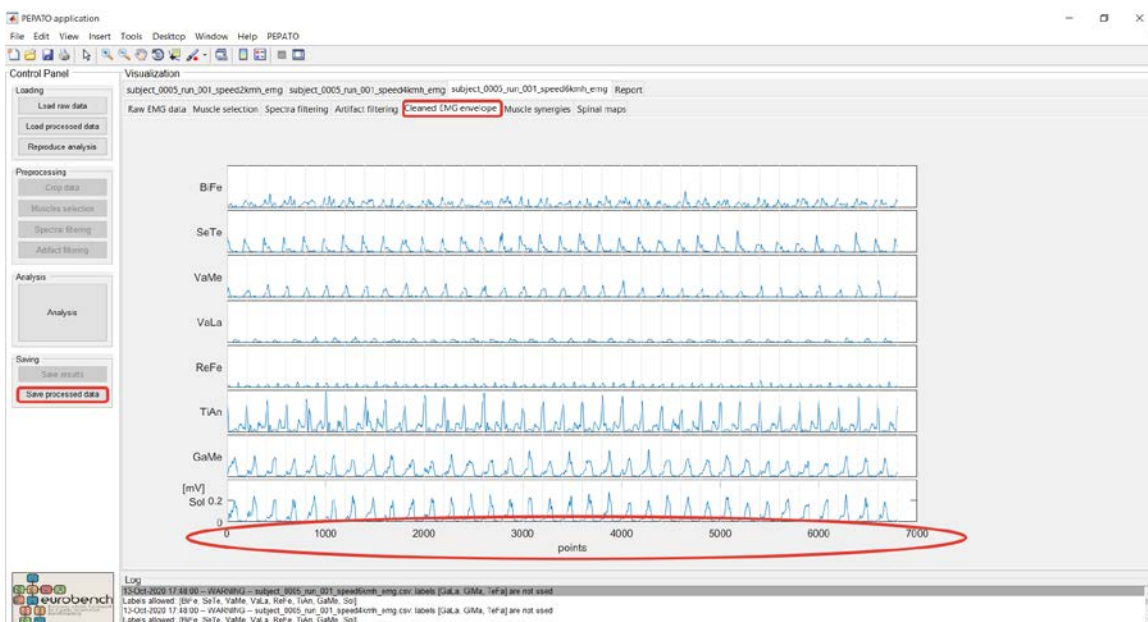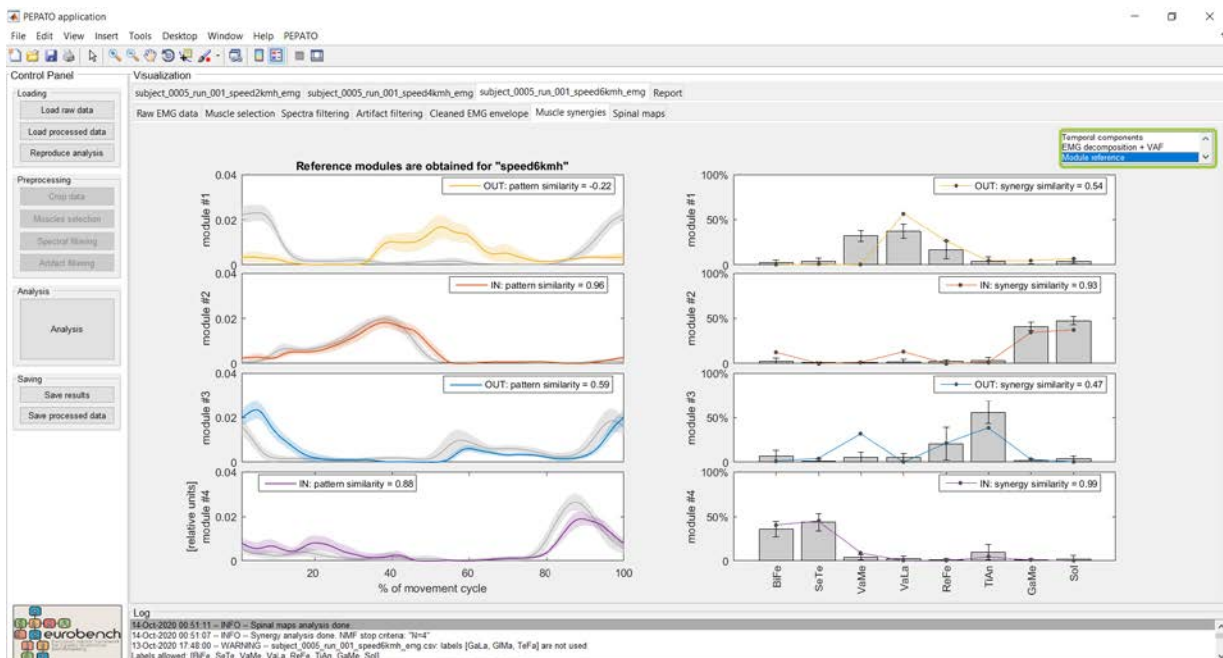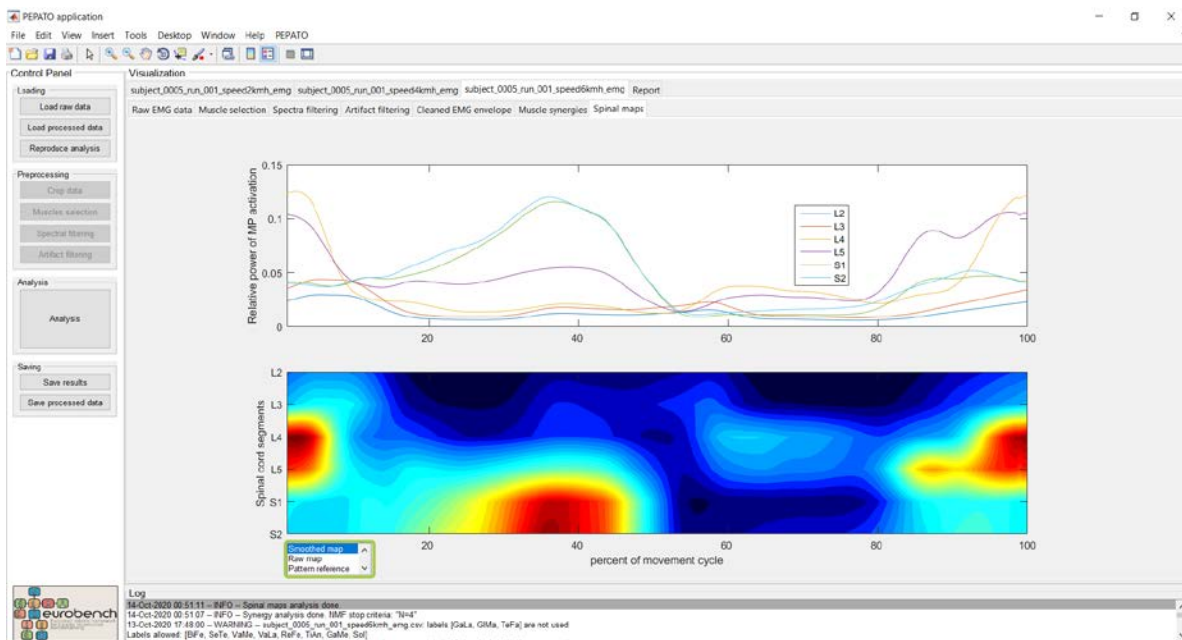
4. Data Analysis

Muscle synergies and spinal maps analysis will be done automatically after pressing the button "Analysis". Analysis parameters are set in the config file and can be changed in the editor before loading the data files. For muscle module analysis details see paragraph 7.1.
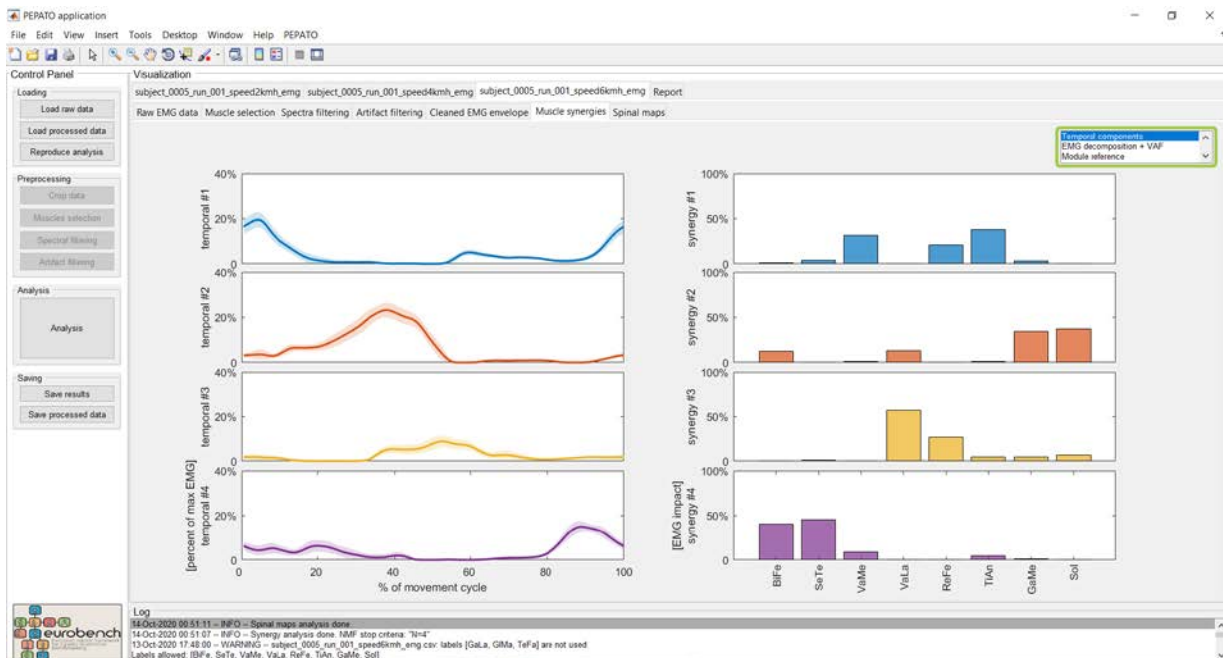
In Muscle synergies sub-tab you can switch between Temporal components, EMG decomposition and Module reference subplots. Module reference will only be available for a specific muscle list (see paragraph 1. Installation and Run).

For spinal maps you can also switch between subplots. Pattern reference requires also specific muscle list.

All output indicators are stored in the report tab and can be saved in *.mat* format.

5. PEPATO configuration

By default, PEPATO will use the standard parameters for data preprocessing and analysis:

- N points – number of points for gait cycle normalization (200 by default)
- High pass frequency – for EMG filtering (30 Hz by default)
- Low pass frequency – for EMG filtering (400 Hz by default)
- Maximal number of synergies – for muscle synergies analysis (8 by default)
- NMF replicates – number of replicates for Non-negative Matrix Factorization algorithm (20 by default, the larger the number, the better the convergence and the longer the calculations)
- NMF stop criterion – criterion for determining the number of synergies ('N=4' by default – for fixed number of synergies equal to 4; other possible values: 'N=3', 'N=5', 'R2=0.90', 'R2=0.95' for to determine the number of synergies through the minimum value of R^2, and also 'BLF' for best linear fit method)

You can set other values for these parameters using Config editor (open: Ctrl+M in application or using PEPATO tab on the top ribbon). To change the parameters you will have to interrupt the current analysis.
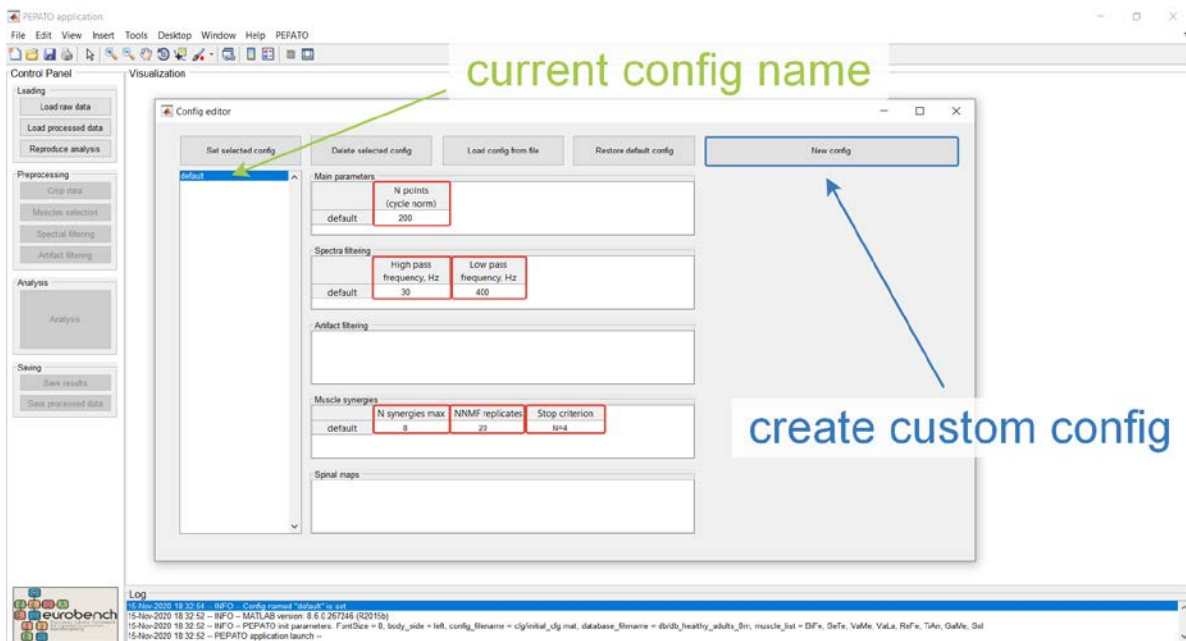
6. Database creation

The program has the option to create a database or add data to an existing database. This functionality is only available from the command line.

First, you need to process all files (cropping and filtering) using the PEPATO UI and save them in **.mat** format in a separate directory. The muscle list for all files must be the same. Then you need to run the script to generate the database from the MATLAB Command Window:

db_generator('path/to/folder/with/preprocessed/files', 'cfg/initial_cfg.mat', 'db/db_new', {'BiFe', 'SeTe', 'VaMe', 'VaLa', 'ReFe', 'TiAn', 'GaMe', 'Sol'}, {'BLF', 'N=4', 'R2=0.90'});

Parameters to set:
- Path to the folder with saved preprocessed **.mat** files
- Path to configuration file (**'cfg/initial_cfg.mat'** as a default)
- Path to existing or new database file (for existing database check the muscle list below is the same as in the database)
- List of muscles to analyze (**{'BiFe', 'SeTe', 'VaMe', 'VaLa', 'ReFe', 'TiAn', 'GaMe', 'Sol'}** by default)
- List of NMF stop criterion for muscle synergy analysis (see paragraph 5 for values available). You can choose only one criterion, but for more reliable clustering of muscle modules, it is recommended to use several different methods.

Finally, to create a reference for muscle modules and spinal maps, execute the following commands:

1. **module_clustering('db/db_new', 4, 0.8, 2, 'db/module_ordering_8m_4.mat');**
   Where **'db/db_new'** is the path to the database; **N_clusters = 4** is number of modules expected; **mean_threshold = 0.8, max_threshold = 2** in terms of standard scaled features distance between sample and the center of the cluster; and **'db/module_ordering_8m_4.mat'** – optional parameter, path to the required order of muscle modules (the default one was generated for 8 muscles mentioned above and 4 muscle modules expected).

2. **maps_patterns('db/db_new');**
   Where **'db/db_new'** is the path to the database.

7. Appendix

7.1 Schematic algorithm for muscle modules classification

extraction of muscle modules (NMF)