%%%% READ me - Code extraction data (R-Platform) %%%%

Schematic map in Excel (Schematic_code_RP.xls)

HOW TO ORGANIZE DATA:

1. Create a folder for each day (ex: DAY01);
2. Inside each day create a folder for each animal (ex: R01);
3. In each folder of the animals put the corresponding tdms files and the tdms_index files created by the R-Platform during the recording.

HOW TO ANALYSE DATA:

1. Run **x01_Extract_RPlatform_data.m** (or **x01_Extract_RPlatform_data_vAdichtFiles.m**)
    a. Select the xxx.tdms file saved by the R-P during recording (ATTENTION, the respective xxx_info.tdms needs to be in the same folder of the selected file);
    b. Select the xxx.c3d file saved by VICON during recording (where are saved all data on EMG) or the xxx.adicht file if the EMG have been recorded with LABChart;
    c. Select one of the four video saved by SIMI during recording;
    d. Four subplots, where one frame coming from each camera is plotted, are showed; select the camera where the led and the meter is better visible;
    e. On the meter select two points that have a distance of 2 cm;
    f. Select an area around the LED from the field of view that is showed;
    g. Click on the LED; (now it will run for 15/20 minutes)
    h. Check in the plot if the switch of the LED is correctly identified: if yes, select ok, otherwise select delete and select manually the correct point;
    i. Visually check the synchronization of the files.
2. Run **x02_Join_and_Cleaning_Phase.m**
    a. Select the xxx.mat file create by x01 and saved in the folder of the xxx.tdms file;
    b. Select y/n according if you have other files to join or not, if you answer yes you have to select the other file/s (Files that need to be joined are the ones that are recorded in the same day and animals perform the same task; they are cut because some video are too long or the animal removed the paw during the recording)
    c. Force signal and number of cycle are plotted in the same graph, check if there are some not valid trials: in case write 1 in the first row and then write the number of trials that you want to remove in the following rows, otherwise write 0 in the first row and press OK.
3. Extraction of the trajectories from the SIMI cameras using DeepLabCut (neural network)
4. Run **x02bis_AddCoordinatesDLC.m**
    a. Select the xxx_x02.mat file create by x02;
    b. Select the .csv file created by DLC; (if you have previously joined more files, it will ask to upload one .csv file for the number of files that you have joined, ATTENTION to select them in the same order)
    c. Visually check the synchronization of the files.
5. Run **x03_Extraction_Parameters.m**
    a. Select the xxx_x02.mat file modified by x02bis;

    b. If 'Kinematic Data are not present in the selected struct' appeared, it means that x02bis is not been run; (x03 can be run also without x02bis because some results can be obtained also without the kinematic of the movement);
6. Run **x04_Activity_CorrelatedPeaks.m**
    a. Before running select if you want align data on the beginning of the movements or on the force peaks (in_case = 2 or in_case = 1 respectively);
    b. Select the xxx_AnalysisPeaks.mat file created by x03;
7. Extract single units activity from inscopix recordings with the Inscopix Software (ATTENTION, Files that are joined for the robot, have to be joined also in the Inscopix Software)
8. Run **x04bis_add_Inscopix.m** (ONLY for inscopix animals)
    a. Before running, select the folder where data are saved (matlab struct and csv file from inscopix), select the name of the animal, the name of the days and the type of task that you want to analyze;
9. Run **y01_PCA_Half_alongDays.m**
    a. Before running select the correct datapath (where are saved all the matlab struct)
10. Run **y02_PCA_activeVSpassive.m**
    a. Before running select the correct datapath (where are saved all the matlab struct)
11. Run **CellRegistration.m** (ONLY Inscopix animals)
    a. Before running, select the folder where are saved the .csv file created by the inscopix software, the rat, the days and the type of task that you want to analyze;
12. Run **CellReg.m** (Download from *https://github.com/zivlab/CellReg*) (ONLY Inscopix animals)
    a. Follow the instruction in CellReg-Master\DOC\User Manual.doc
13. Run **y02bis_Compare_ACTvsHALF_Inscopix.m** (ONLY Inscopix animals)
    a. Before running, select the animal that you want to analyze, the folder where are saved all matlab struct and where is saved the registration file, previously created
14. Run **y03_PCA_Active_alongDays.m**
    a. Before running select the correct datapath (where are saved all the matlab struct)
15. Run **y03bis_Comparison_Days_Inscopix.m** (ONLY Inscopix animals)
    a. Before running, select the animal that you want to analyze, the folder where are saved all matlab struct and where is saved the registration file, previously created
16. Run **y04_bis_Join_Inscopix_Results.m** (ONLY Inscopix animals)
    a. To plot the data of the inscopix animals together;
17. Run **y05_PCA_Half_BipvsQuad.m**
    a. PCA comparison of animals that perform the task in a different position
18. Run **y06_PCA_Half_1DOFvsMulti.m**
    a. PCA comparison between the task with 4 DOF and the same task when the freedom of the movement is limited to 1 direction
19. Run **y07_PCA_Half_consecutiveDAYS.m**
    a. PCA analysis single animals for multiple days

OUTPUTS:

1. **x01_Extract_RPlatform_data.m**
   Create a xxx.mat struct, where are stored multiple information: name of the file (Props), data saved in the xxx.tdms file by the robot (Recorded_Data), information about the type of the task and the paw (info), data from the Simi camera (SIMI) and data from Vicon system (VICON).

Recorded_Data: t (recorded time), pos_DCX14_top, pos_DCX14_down, pos_Spindle_drive, pos_DCX08 (position in the time of the relatives actuators), Fx, Fy, Fz (force in the time in the three direction), Mx, My, Mz (moments in the time in the three direction), cicles (number of the cycle along recording), T_status (part of the trial: 0 = nothing, 1 = push phase, 2 = pull phase), Hall_start (output of hall sensor at home pos), Hall_end (output of hall sensor at the point of the extension), Wrong_trials (array of zero and one elements, cycles at which correspond one values have to be deleted), fS_robot (frequency rate of the robot).
SIMI: trig(time in seconds when the led switches on), fS_KIN (frequency rate of cameras), duration (duration of the video from trig to end), Px2cm (number of pixels that correspond to 2 cm).
VICON: EMG (synchronized emg signal), trig(frames when the trigger switches), fS_EMG (frequency rate Vicon), name (name of the VICON file).

2. **x02_Join_and_Cleaning_Phase.m**
   Create a xxx.mat struct, where are joined data from multiple files. All variables in the time are updated and the name and the duration of single files are saved. Props.SingleTime (length in seconds of every single file is saved), tTot (total length in seconds of the recording), good_trials (number of trials that have to be considered in the following analysis, with the start time and the end time of each trial).

3. Extraction of the trajectories from the SIMI cameras using DeepLabCut (neural network)
   .csv file, where for every selected bodypart is saved x and y coordinates and likelihood.
4. **x02bis_AddCoordinatesDLC.m**
   It adds the coordinates of the selected bodypart and it saves a figure with all synchronized data (xxx_SyncData.fig).
   SIMI: x (position of the paw in z direction), y (position of the paw in x direction)
5. **x03_Extraction_Parameters.m**
   It extracts all useful parameters from the raw data. It saves two figures of the probability density distribution in the push phase and in the pull phase.
   Recorded_Data: Analysis (for each force and moment signal it extracts positive and negative peaks and it saves for each peak many parameters described in Analysis.name_peaks_matrix).
   SIMI: pks (peaks of the speed calculated on the x position that correspond to a force peak, for each peak many parameters described in name_pks are saved), Analysis (parameters extracted by the trajectory in the x-y plane, for each parameter is saved the value for the whole trajectory, only for the push phase and only for the pull phase), trajectory (x-y trajectory of each good trial), start (time in seconds of the beginning of every pulling movement).
   VICON: EMGfilt(envelope of the emg signal), burst (burst for each recorded muscle with different parameters described in name_burst), Coactivation (probability density distribution evaluated on the whole movement or only in one phase).
6. **x04_Activity_CorrelatedPeaks.m**
   It analyses relations between the different type of data. It saves two figures (MaxEMG-vs… with the time of activation of the biceps and the triceps in relation of force peaks; xxx_BicForceRelation.fig with the regression between force in z direction and envelope of the biceps).
   Recorded_Data: Analysis.Area_cy (Integration of the force signal during pulling phase in intervals of 0.2 seconds).
   VICON: spect (spectrogram aligned on the force peaks in intervals of 1 seconds), EnvOnsetF.rel_max (for every force peak the distance between the maximum of the envelope of each muscle and the index of the fp is saved), EnvOnsetF.MeanEnvelope (mean of every emg

envelope for all force peaks), Analysis.Corr (correlation coefficient between the integration of the envelope of every emg and the Area_cy), Analysis.Area_cy (Integration of the emg envelope during pulling phase in intervals of 0.2 seconds).

7. Extract single units activity from inscopix recordings with the Inscopix Software
   Four .csv files for every day, animal, type are saved by extracting data from the Inscopix Software
8. **x04bis_add_Inscopix.m** (ONLY for inscopix animals)
   It add and synchronizes neural data.
   INSCOPIX: fS_ins (frequency rate of the Inscopix device), cells_name (name of the cells selected as good units in the software), cells_signal (fluorescence of the good units), cells_pos (x-y position of the center of the good neurons in the field of view), cells_size (diameter of good units), time, events (events selected by the inscopix software for every unit), cells_SNR (signal to noise ratio), Freq_rate (frequency rate of every units).
9. **y01_PCA_Half_alongDays.m**
   Principal component analysis of all parameters of all animals of all days during the Pull task to analyze the recovery of rats, plot and statistic of all parameters and plot of the two main parameters for the two selected PC.
10. **y02_PCA_activeVSpassive.m**
    Principal component analysis of all parameters of all animals in healthy condition to distinguish the Pull task from the Pass task, plot and statistic of all parameters and plot of the two main parameters for the two selected PC.
11. **CellRegistration.m** (ONLY Inscopix animals)
    It creates a map of the field of view with all the selected good units for each .csv group of files of the inscopix software. This map is necessary to make the registration of the units in different recordings.
12. **CellReg.m** (Folder: CellReg-master\GUI) (ONLY Inscopix animals)
    Read the instruction in CellReg-Master\DOC\User Manual.doc
13. **y02bis_Compare_ACTvsHALF_Inscopix.m** (ONLY Inscopix animals)
    Neural analysis in healthy animals to compare the Pull task with the Pass task. It plots and makes the statistic to discriminate different cell types in the two tasks. It creates a graph for every type of cells where all units are shown aligned on the force peaks. It plots a graph with all the synchronized signals. It study the raster plot of calcium events in rest and active intervals.
14. **y03_PCA_Active_alongDays.m**
    Principal component analysis of all parameters of all animals of all days during the Pass task to analyze the recovery of rats, plot and statistic of all parameters and plot of the two main parameters for the two selected PC.
15. **y03bis_Comparison_Days_Inscopix.m** (ONLY Inscopix animals)
    Neural analysis in during spontaneous recovery to analyze the reorganization of the units. It can be used to analyze the Pass task or the Pull task. It plots and makes the statistic to discriminate different cell types in different days. It creates a graph for every type of cells where all units are shown aligned on the force peaks. It plots a graph with all the synchronized signals. It study the raster plot of calcium events in rest and active intervals. It analyzes the movement of different units in different clusters after injury.