UQAC
Université du Québec
à Chicoutimi

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LABORATOIRE D'INTELLIGENCE AMBIANTE
POUR LA RECONNAISSANCE D'ACTIVITÉS

MYORATIO APPLICATION
USER GUIDE

Version: 3.3.0

2023 September the 20th

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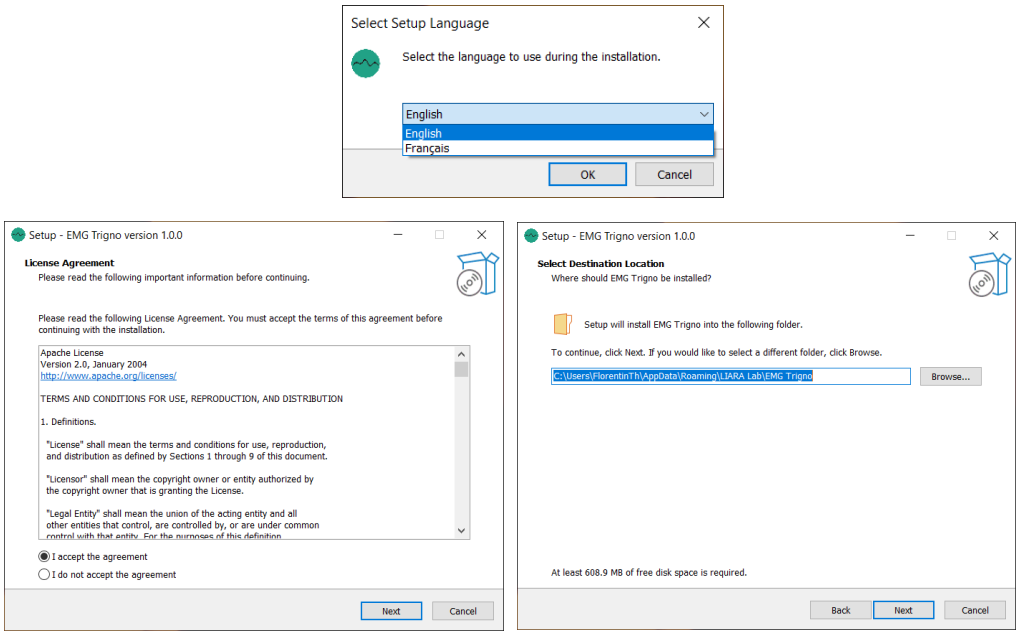
1. Installation

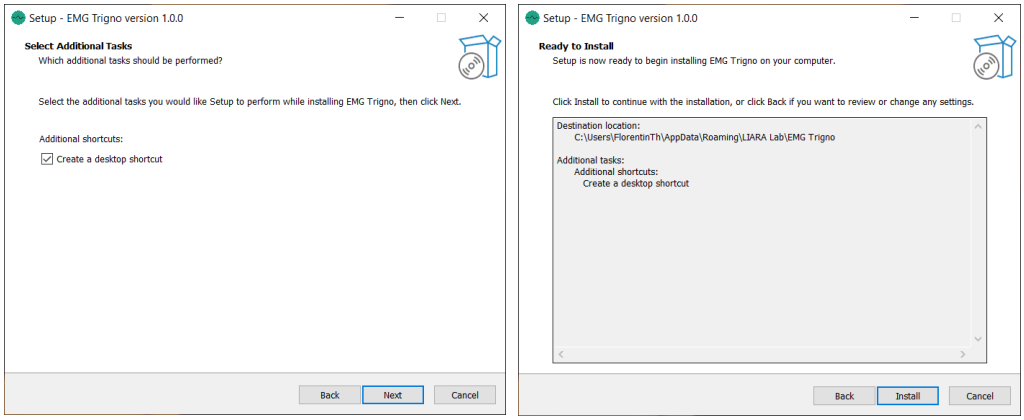
1.1 Windows

Start by launching the installer, then follow the following steps:

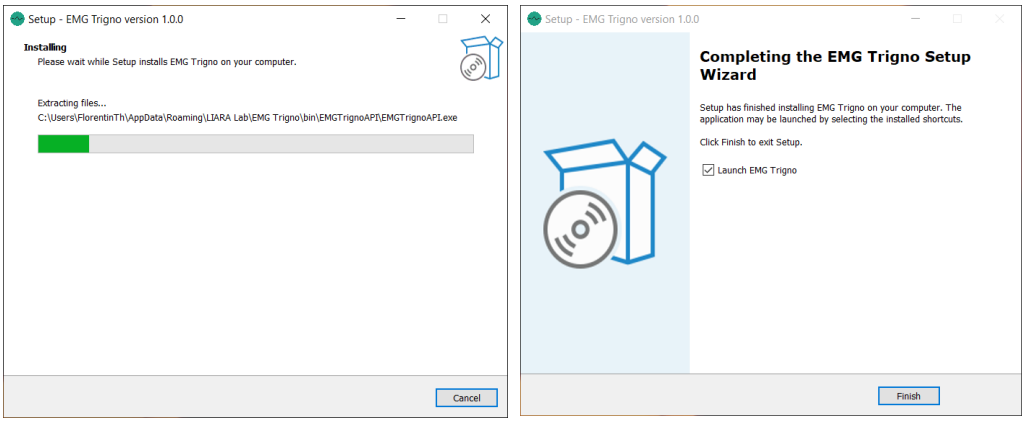


Update version 2.0.0 and above: read MyoRatio instead of EMG Trigno on the screenshots

Note: You can change the installation folder if you wish, but for now, I do not recommend it. In case I need to assist you with any issues, it should simplify my task.



Update version 2.0.0 and above: read MyoRatio instead of EMG Trigno on the screenshots



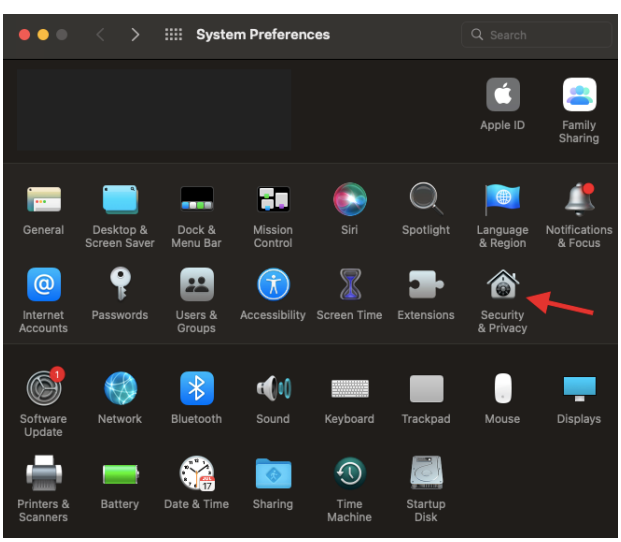
Update version 2.0.0 and above: read MyoRatio instead of EMG Trigno on the screenshots

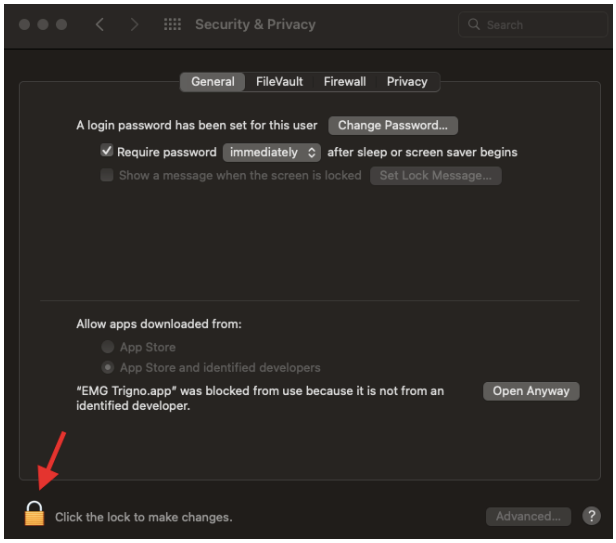
1.2 macOS

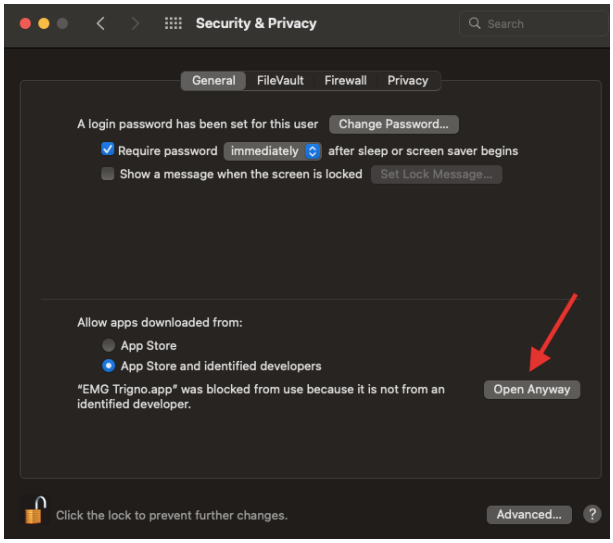
Begin by opening the `.dmg` file, then, like with any macOS application, drag and drop the MyoRatio application into the Applications folder. Wait for the copy to finish, then launch the application.

Update version 2.0.0 and above: read MyoRatio instead of EMG Trigno on the screenshots

CAUTION: on some versions of macOS, installed applications must be signed to run. MyoRatio is properly signed, but I am not a registered developer, so you may receive an error message when you first start the application. This is not a problem; simply close the error message (if it suggests moving the application to the trash, do not do that; instead, click on Cancel and the application should close). Then, select the Apple menu at the top left of your screen and choose `System Preferences`. Once the menu is open, follow the steps indicated by the red arrows in the screenshots below:



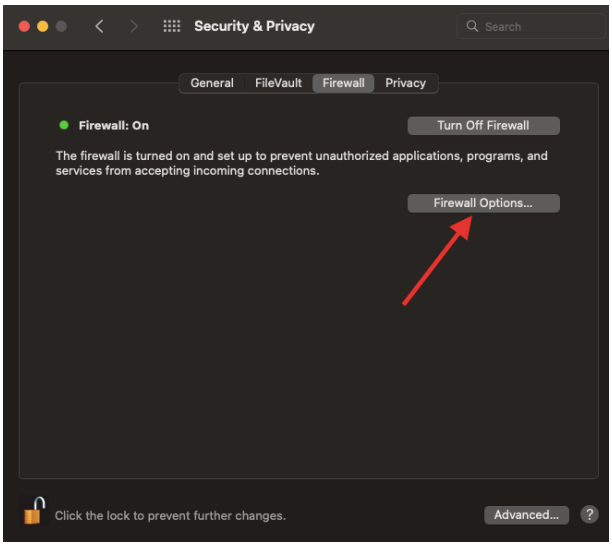


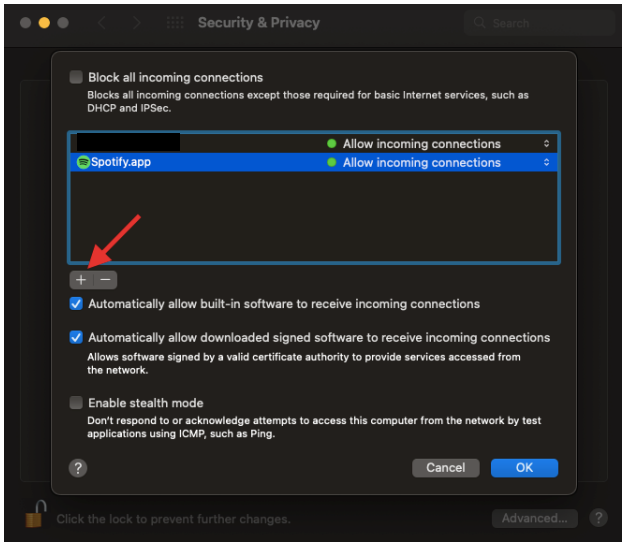


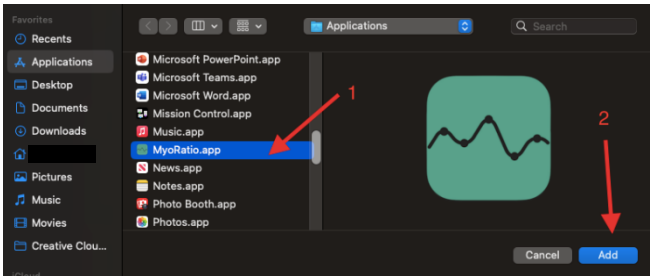
Update version 2.0.0 and above: read MyoRatio instead of EMG Trigno on the screenshots

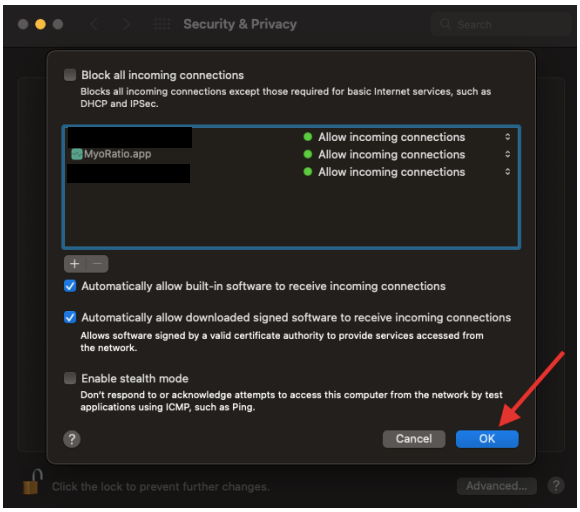
It's possible that the system may not display the final screen. If that's the case with your machine, don't worry; you can proceed to the next step.

Go to the `Firewall` tab and follow the procedure outlined by the red arrows in the following screenshots:



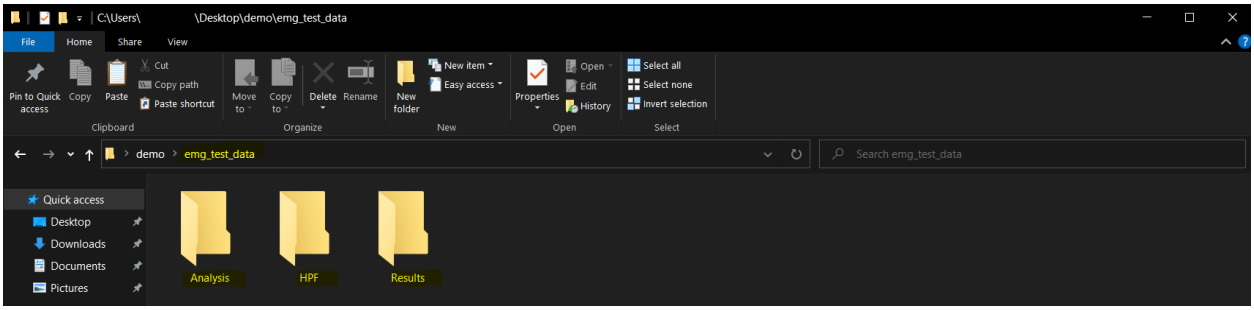




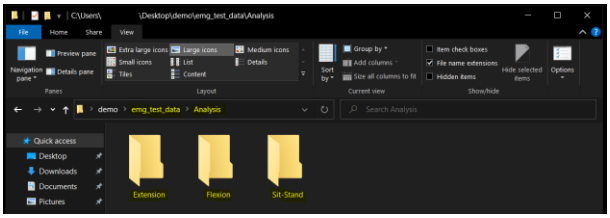


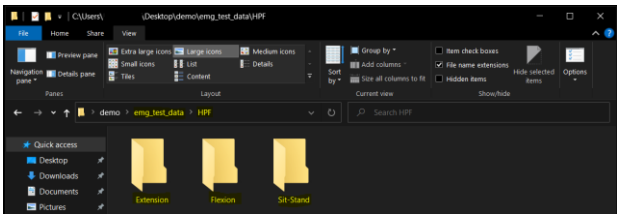
2. Data folder

To ensure the proper functioning of the application, the only prerequisite is to have a data folder organized according to a specific naming convention. Without this, the application will work, but you won't be able to perform various processes, and you will receive repeated error messages. Therefore, your root data folder (*e.g.*, **`emg_test_data`**) should at least contain the subfolder **`HPF`**. It is also possible for it to include the subfolders **`Analysis`** and **`Results`** as follows:



Ensuite, les deux dossiers **`HPF`** et **`Analysis`** (si ce dernier est présent) devraient contenir les trois sous-dossiers relatifs aux types d'analyses soit, **`Extension`**, **`Flexion`** et **`Sit-Stand`** :





It is important to note that the case for the names of all folders and files does not matter; they can be in uppercase, capitalized, or lowercase.

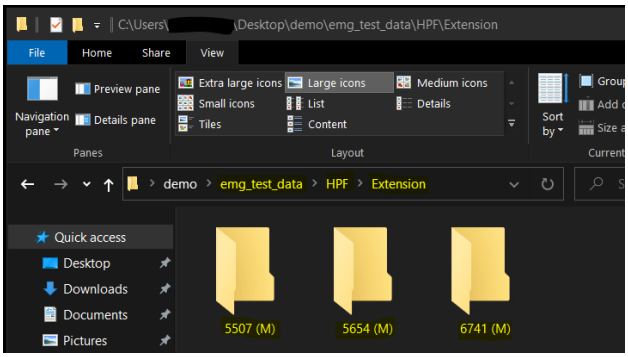
- The **`HPF`** folder is crucial for your data organization. This is where you will organize your raw data collected with the EMG and saved in *hpf* format. Therefore, each of the analysis subfolders within it should contain a folder for each participant in which the `.hpf` files will be placed. The subfolder for each participant must be formatted as follows:

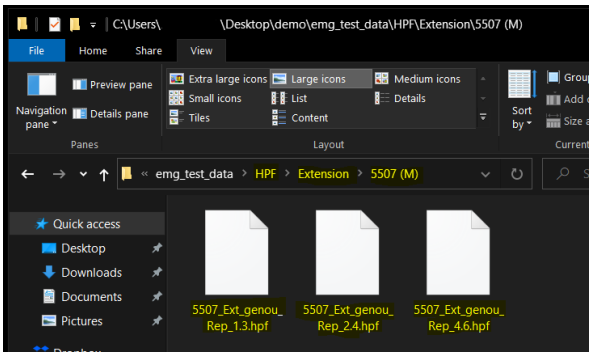
  `<participant_id>[space](<first_letter_type_of_participant>)`

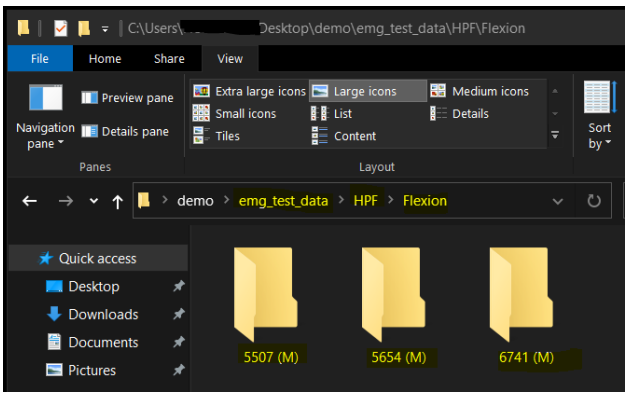
  As example, for a participant with the identifier *5565* and who was a *walker*, the name of their subfolder will be: `5565 (M)`

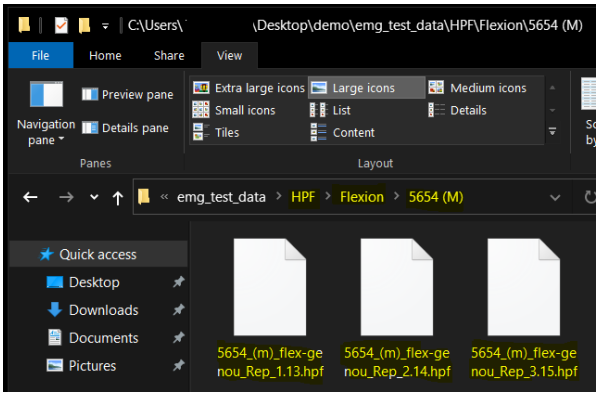
  Once again, the case does not matter. The names: `5565 (M)` and `5565 (m)` are considered identical by the application.

Here is an example of what the analysis folders should contain:









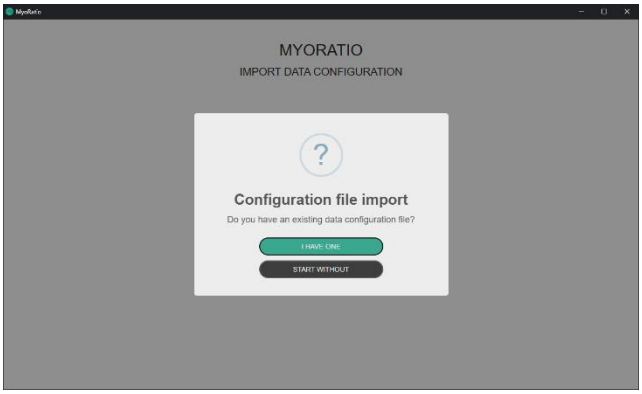
As for the names of `.hpf` files, there is no specific convention except that their names must be unique. In the example above, you can see that for one of the participants, the type is indicated, while for the other, it is not. However, I still recommend trying to maintain a certain naming convention as closely as possible, such as :

`<participant_id>_(<first_letter_type_of_participant>)_<analysis>_<iteration_number>`

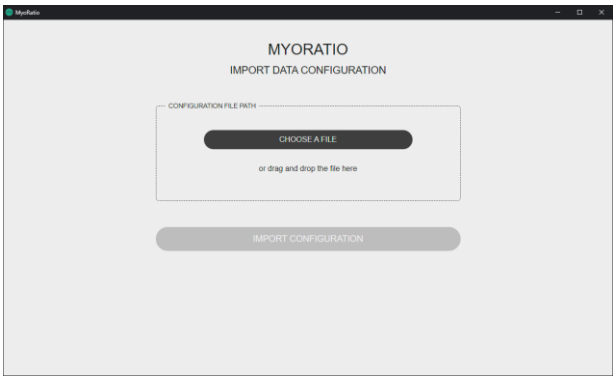
- The **`Analysis`** folder is where the application will generate certain files necessary for various processes. You should not need to perform any operations inside it, with one exception:
    - You have made a mistake in the organization of raw data within the **`HPF`** folder, and the metadata generated by the application for one or more specific participants needs to be reset. In this specific case, all you need to do is navigate to your root folder (**`emg_test_data`**), then into **`Analysis`**, and then into the analysis folder(s) corresponding to the issue. Delete the folder(s) of the participants that need to be reset completely. The application will automatically clean itself up. However, you will need to redo the data conversion process (see point 4.).

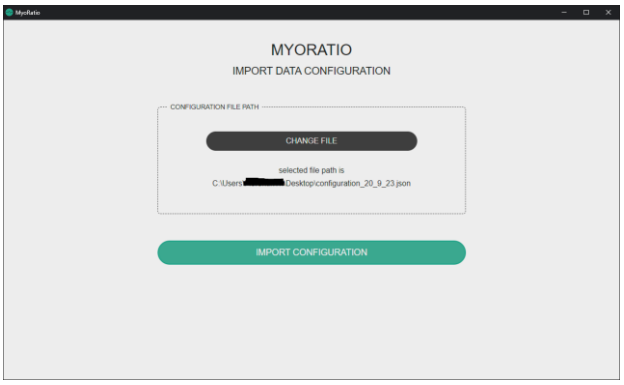
3. Application configuration

At the first launch of the application, after its installation, you will be asked whether you want to import a configuration file or if you want to manually configure the application yourself:

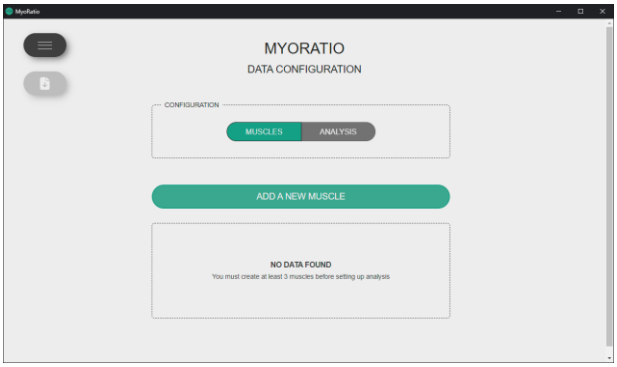


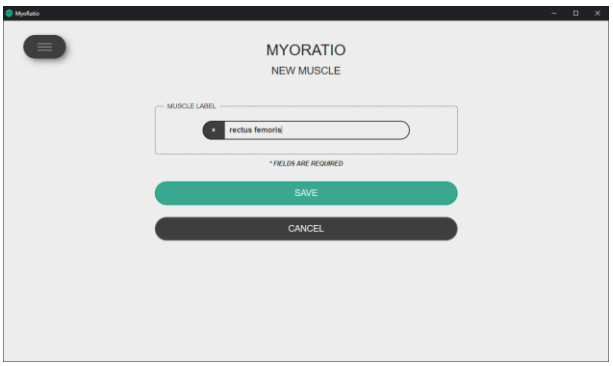
- To import an existing configuration file, you will need to select your configuration file or drag and drop it into the dashed area. Then, simply click the button to import it. The application will automatically configure itself based on the data in the file, and you will be redirected to the data processing page (“Data Processing” menu).

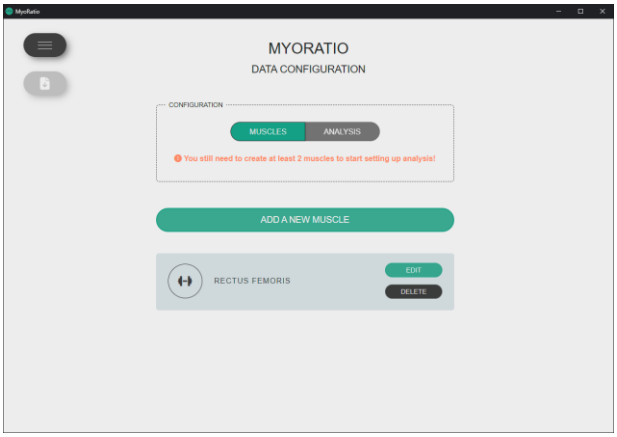


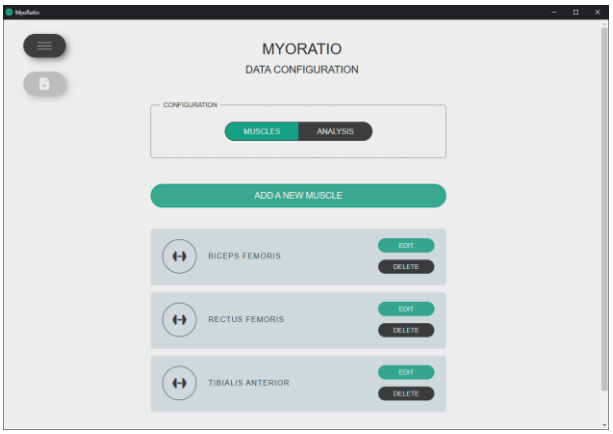


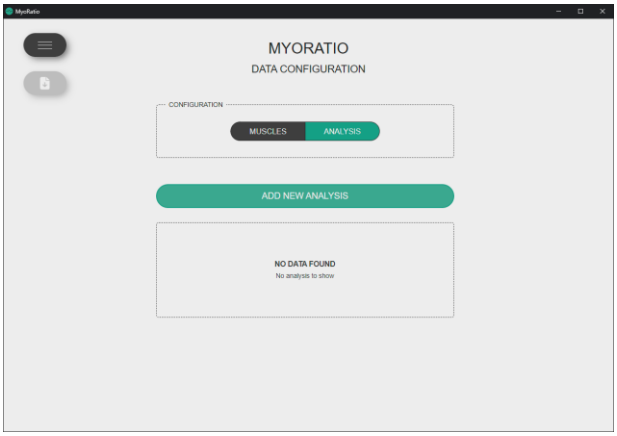
- If you wish to configure the application manually, you will need to start by adding at least three new muscles. Afterward, you can add at least one new analysis. Once the analysis is created, you will then have access to the data processing menu, which was disabled until now. Additionally, thanks to the export button on the main data configuration page (“Data Configuration” menu), you can save the configuration to avoid having to redo this task when changing to a new computer or if other individuals need to share the same configuration.

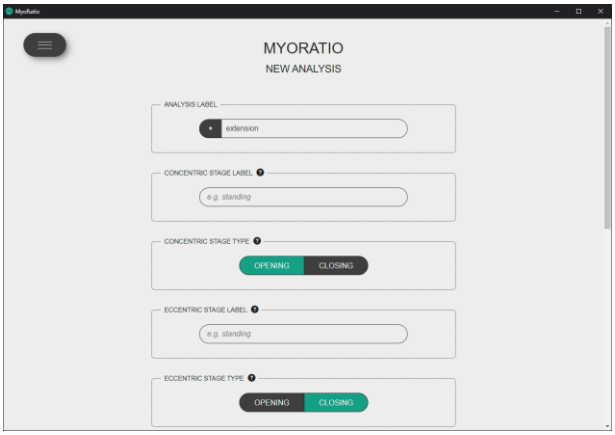

MYORATIO
DATA CONFIGURATION
CONFIGURATION
MUSCLES
ANALYSIS
ADD A NEW MUSCLE
NO DATA FOUND
You must create at least 3 muscles before setting up analysis

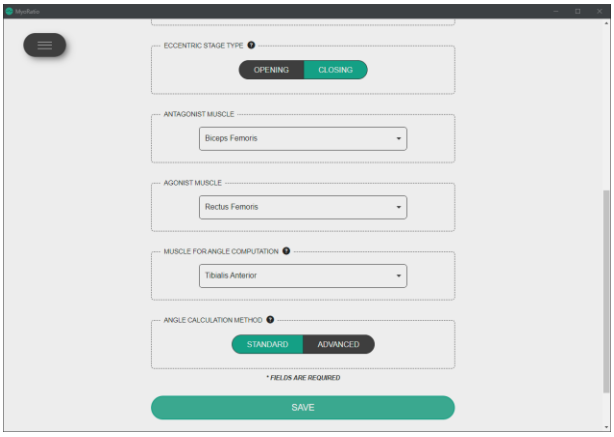

MYORATIO
NEW MUSCLE
MUSCLE LABEL
rectus femoris
* FIELDS ARE REQUIRED
SAVE
CANCEL

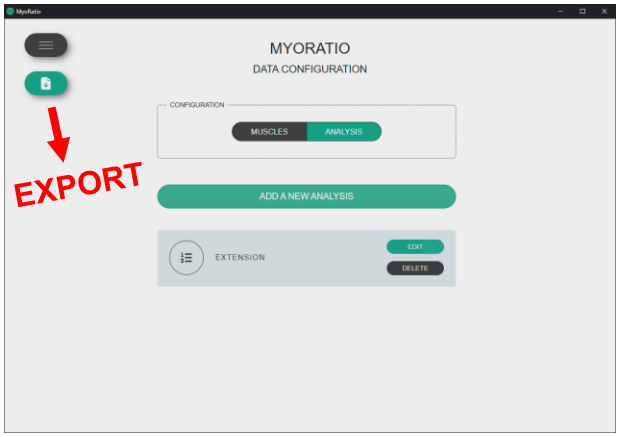

MYORATIO
DATA CONFIGURATION
CONFIGURATION
MUSCLES
ANALYSIS
You still need to create at least 2 muscles to start setting up analysis!
ADD A NEW MUSCLE
RECTUS FEMORIS
EDIT
DELETE


MYORATIO
DATA CONFIGURATION
CONFIGURATION
MUSCLES
ANALYSIS
ADD A NEW MUSCLE
BICEPS FEMORIS
RECTUS FEMORIS
TIBIALIS ANTERIOR
EDIT
DELETE


MYORATIO
DATA CONFIGURATION
CONFIGURATION
MUSCLES
ANALYSIS
ADD NEW ANALYSIS
NO DATA FOUND
No analysis to show


MYORATIO
NEW ANALYSIS
ANALYSIS LABEL
extension
CONCENTRIC STAGE LABEL
e.g. standing
CONCENTRIC STAGE TYPE
OPENING
CLOSING
ECCENTRIC STAGE LABEL
e.g. standing
ECCENTRIC STAGE TYPE
OPENING
CLOSING

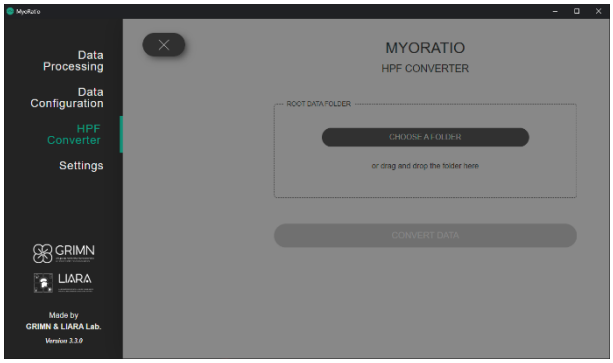

ECCENTRIC STAGE TYPE
OPENING
CLOSING
ANTAGONIST MUSCLE
Biceps Femoris
AGONIST MUSCLE
Rectus Femoris
MUSCLE FOR ANGLE COMPUTATION
Tibialis Anterior
ANGLE CALCULATION METHOD
STANDARD
ADVANCED
* FIELDS ARE REQUIRED
SAVE

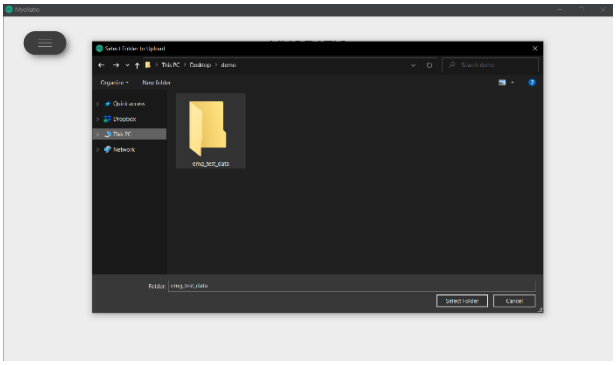

EXPORT
MYORATIO
DATA CONFIGURATION
CONFIGURATION
MUSCLES
ANALYSIS
ADD A NEW ANALYSIS
EXTENSION
EDIT
DELETE

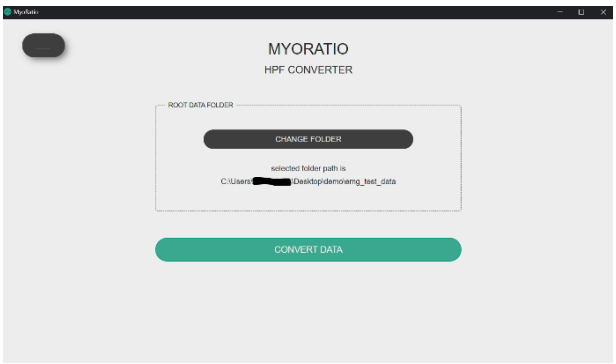
4. Conversion of HPF files

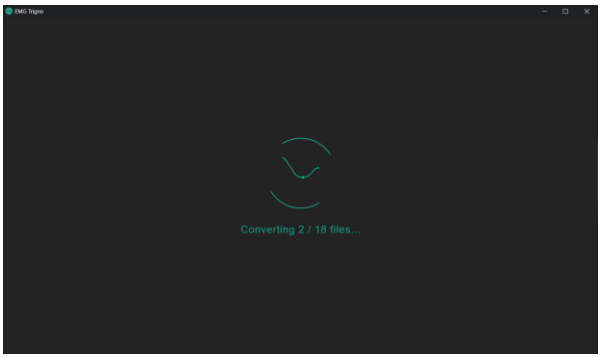
IMPORTANT: this functionality depends on a modified version of the program developed by the company that manufactures the EMG and only works on Windows. Therefore, even though the rest of the application remains functional on macOS, the data conversion process cannot be carried out on this platform. Make sure to complete this task beforehand on a Windows operating system computer and then copy the root data folder on your macOS computer to proceed with the following tasks.

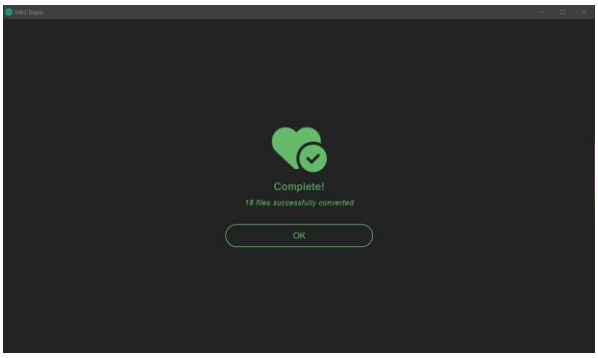
When you have finished organizing your raw data files within the HPF folder, the next step upon launching the application is to go to the “HPF Converter” menu. From there, you simply need to select your root data folder (**`emg_test_data`**) or drag and drop it into the dashed area, then click the convert button. The application will then recursively search for all `.hpf` files present in the folder and convert them so that the data can be used by the application, as these cannot be processed directly in hpf format. Depending on the number of files to be processed, the conversion may take more or less time. However, this step is incremental, meaning that if the files have already been converted, the process is not repeated. Only new files (including the resetting of previously processed participants) will be converted. The application informs you of the progress at each step and lets you know when everything is finished.





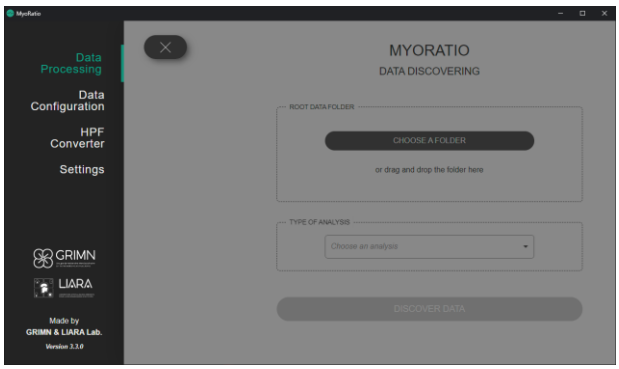


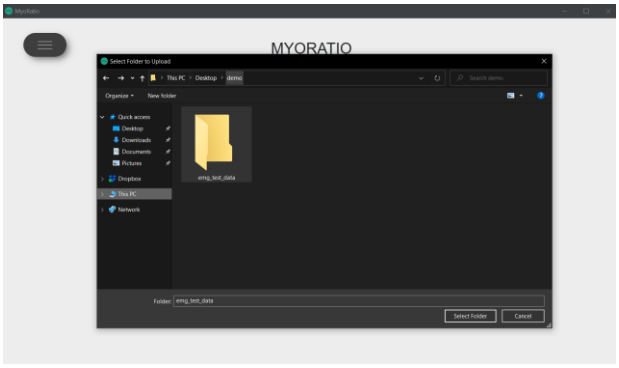




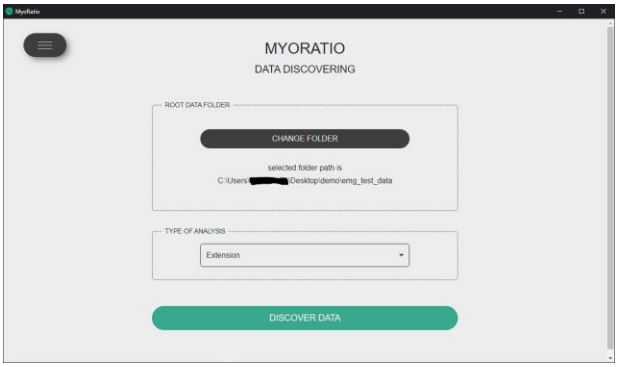
5. Data processing

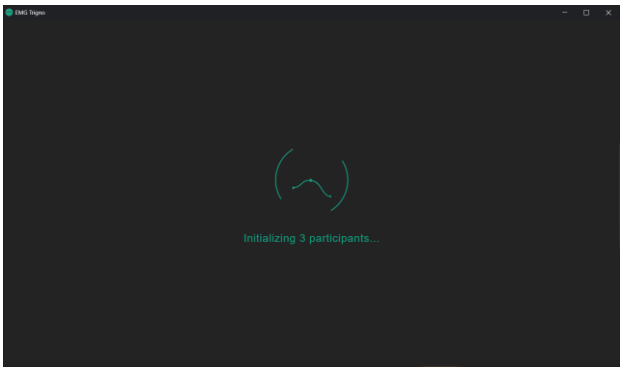
Once all the data has been converted into a usable format, you can then go to the “Data Processing” menu. This is the main menu, which starts by asking you to identify the root folder for your data (**`emg_test_data`**). As for the conversion, you can select it manually or drag and drop it. Next, you must choose the type of analysis you want to process and confirm your selection with the button. Then, the application will search for all participants that can be processed for this type of analysis. Once again, this step is incremental, which means the processing will take longer the first time but relatively quick in subsequent times.



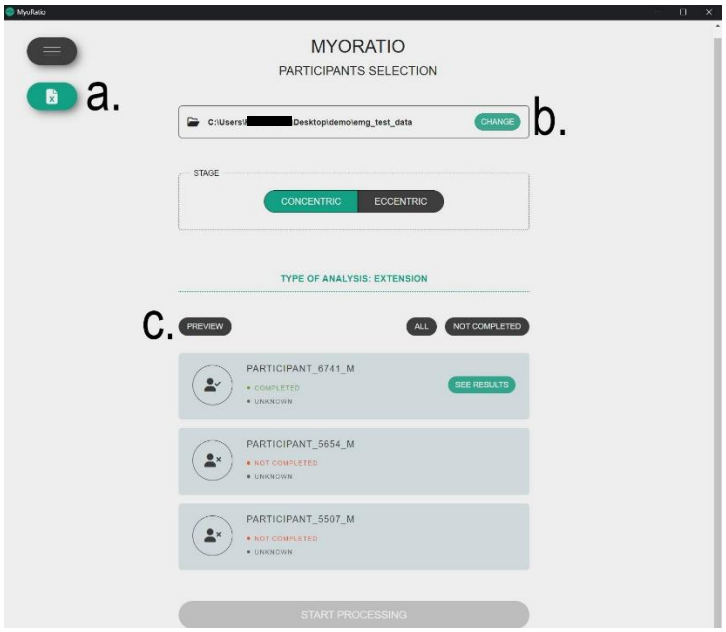


The application informs you of how many participants it has found for processing and presents them in the form of a list as illustrated in the screen below:





As soon as the loading is complete, you will find yourself in the following interface:



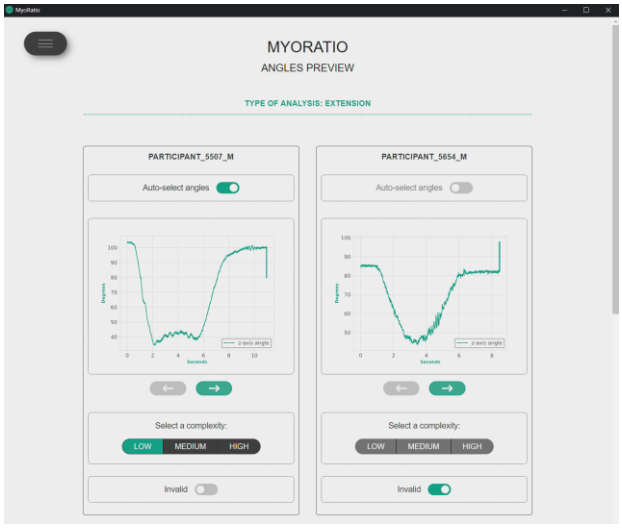
From this interface, several options are available to you:

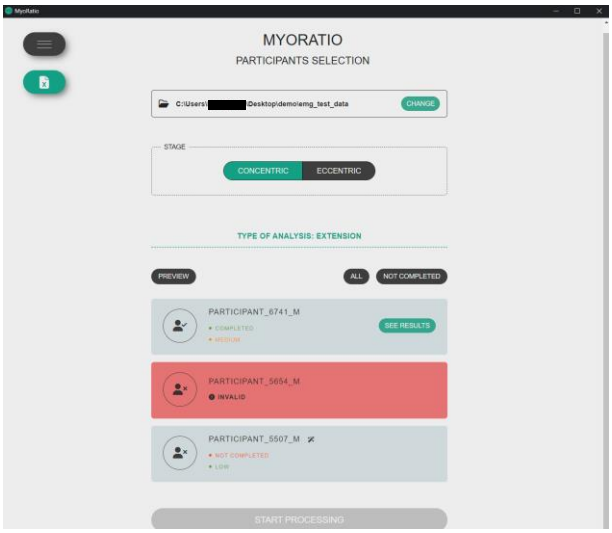
a. Represents the button to export analysis reports in Excel format (see point 5.).

b. Allows you to go back to the previous screen to change the type of analysis or the main data folder.

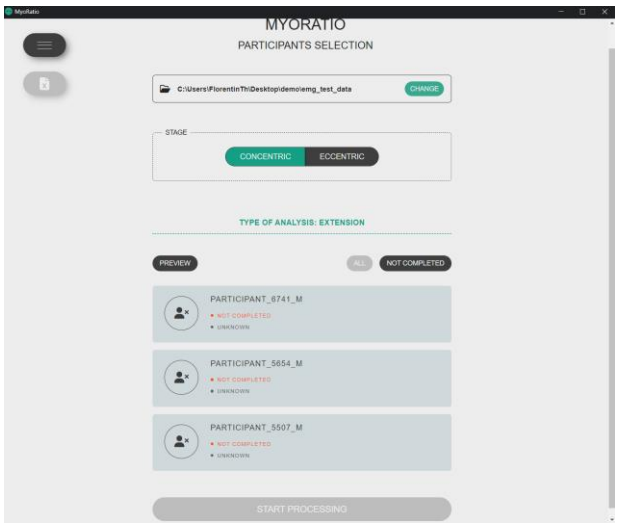
c. Represents the button that allows you to preview the angle charts for all participants found by the application at once.

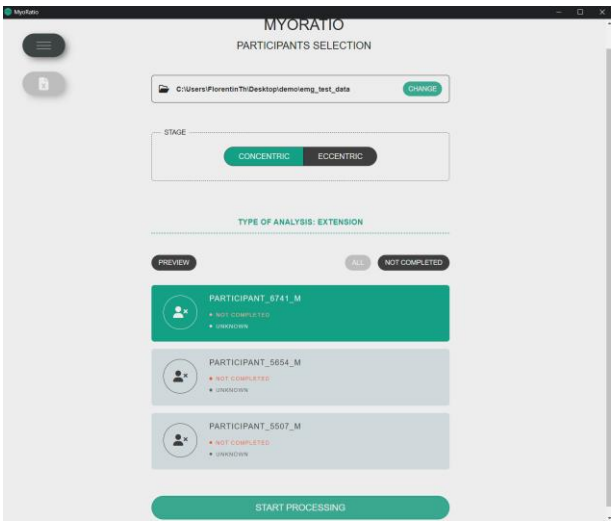
As regards the preview option (c.), this screen also allows you to annotate the complexity level of the analysis for each of the participants and thus activate or deactivate the auto-selection of points on the angle charts. Additionally, if the data for certain participants are not consistent, you also have the option, through this interface, to mark them as “invalid”. Therefore, all participants with this designation are clearly identified in the list and will not be selected for angle processing:



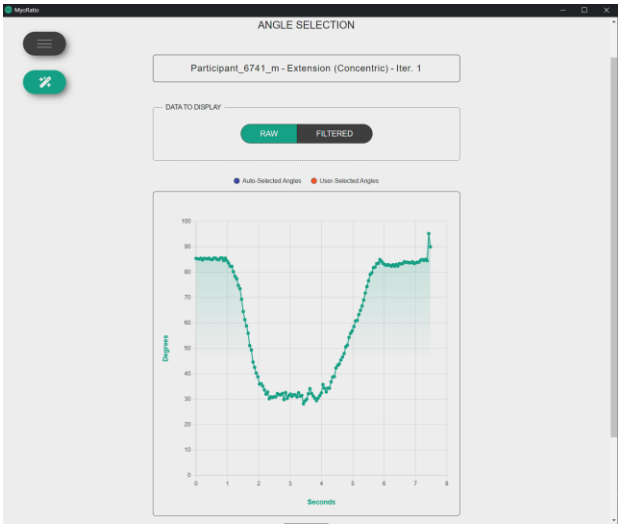


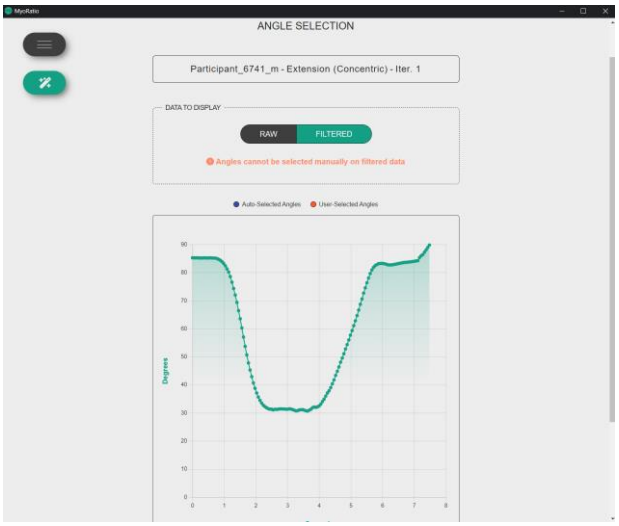
When you are on the list of participants, you can select the phase for which you want to perform the analysis. With each phase change, the list updates with the corresponding results when the point selection on the angle chart has been completed for each participant. To do this, you must select one or more participants by clicking on their card and then confirm your selection by clicking the “start” button:



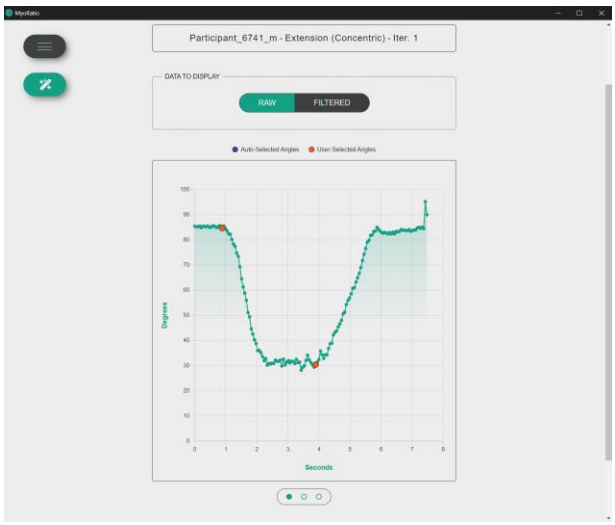


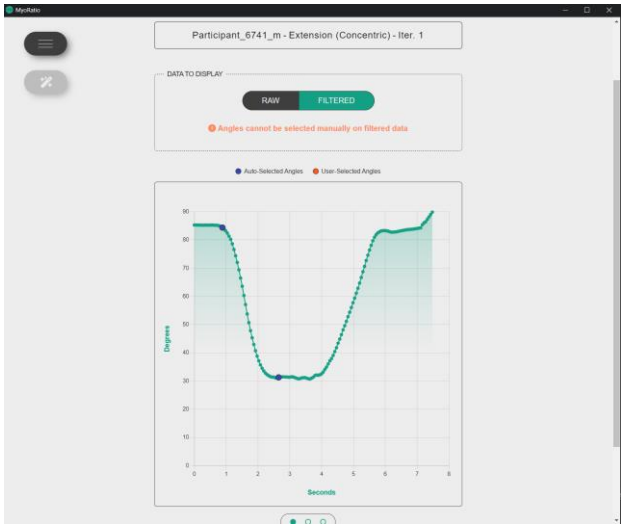
Interactive charts for each iteration of each selected participant will then be presented to you. If the complexity of the current participant is “low”, the button for automatic angle computation will be enabled. If so, when you select it, the angles will automatically appear on the interactive chart in purple. The algorithm that manages this functionality is not perfect, so you have the option to reposition these points manually. The color of the points will then change to red, indicating that you have manually selected your angles. When the automatic angle computation feature is not available (for participants with “medium” or “high” complexity), you must then choose the starting and ending points for the current phase, and these will appear directly in red. When you select a participant whose all iterations have been processed and it displays the status “completed”, you have the option to modify the points that were previously selected, whether they were determined automatically or manually.



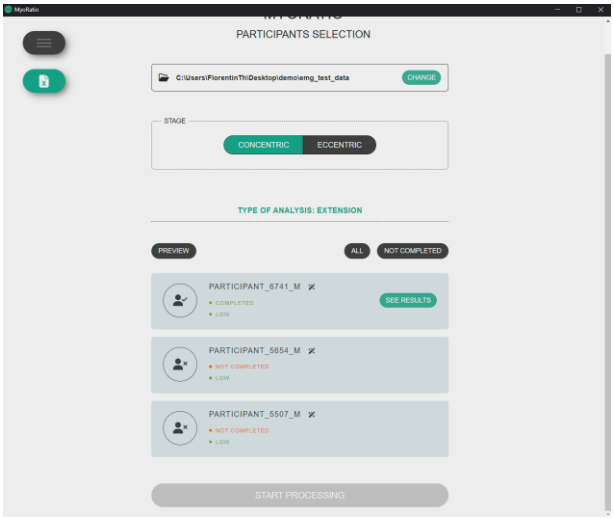


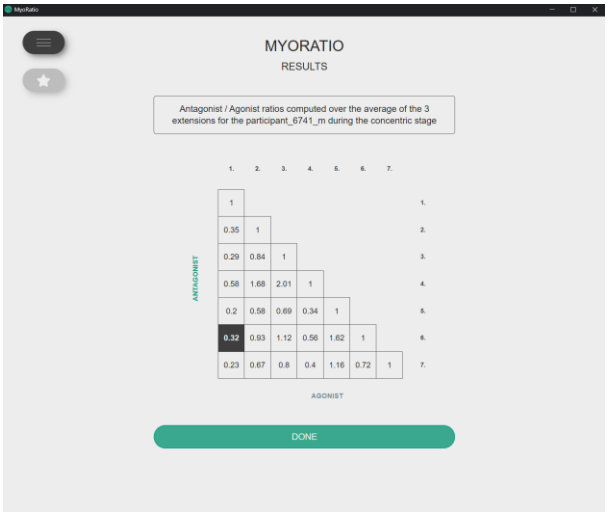
During the angle selection task, you have the option to view the angle curve on which filtering is applied to simplify your understanding of the data when the case is more complex. However, you cannot interact directly with this curve since it is not the data that will be processed in the subsequent computation tasks. This is done to avoid any inconsistencies in your manual selection of both the starting and ending points.





When the point selection task is completed for your selected participants, a “view results” button appears on their card. By selecting it, you will arrive at the screen that presents the diagonal matrix of antagonist-to-agonist ratios for each muscle combination.

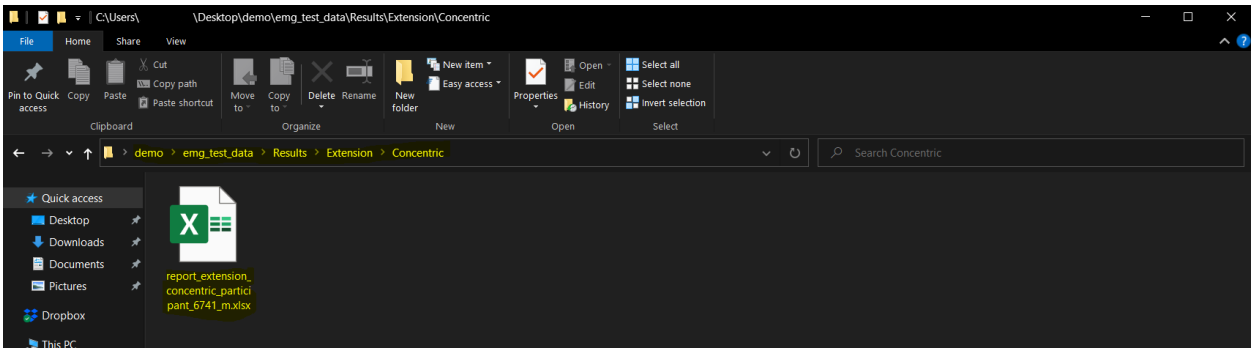




6. Excel reports

When the button to export Excel reports (a.) is selected, all the reports for the current analysis for completed participants are generated at the root of the data folder. For example, for the reports of the extension analysis on the concentric phase, the reports will be generated under:

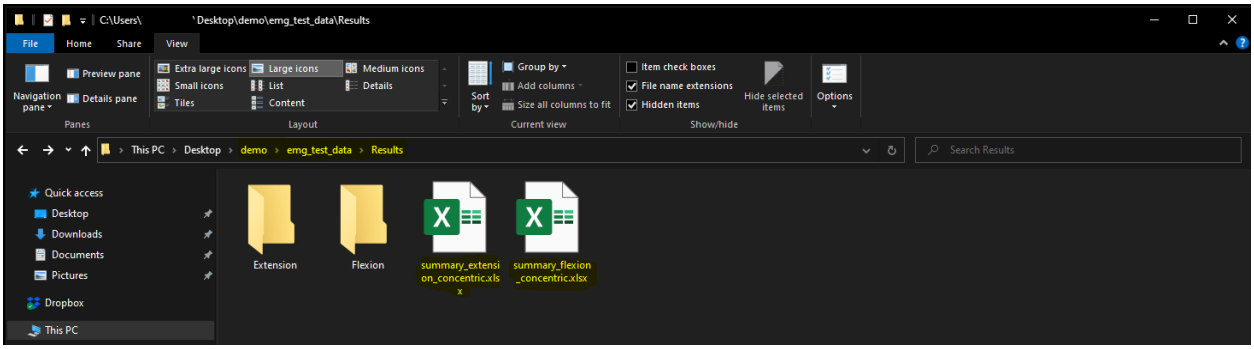
`<root_data>/results/extension/concentric/*.xslx`



7. Analyses summaries

After generating the reports, the application also automatically produces analysis summaries in Excel format. These files are generated at the root of the data folder in the **`Results`** subfolder. For example, the path to the summary for the extension analysis on the concentric phase will be:

`<root_data>/results/summary_extension_concentric.xslx`


C:\Users\ `Desktop\demo\emg_test_data\Results
File
Home
Share
View
Navigation pane
Preview pane
Details pane
Panes
Extra large icons
Large icons
Medium icons
Small icons
List
Details
Tiles
Content
Layout
Sort by
Group by
Add columns
Size all columns to fit
Current view
Item check boxes
File name extensions
Hidden items
Hide selected items
Show/hide
Options
This PC › Desktop › demo › emg_test_data › Results
Search Results
Quick access
Desktop
Downloads
Documents
Pictures
Dropbox
This PC
Extension
Flexion
summary_extension_concentric.xlsx
summary_flexion_concentric.xlsx