

U.L.E.M.A. (Upper Limb Evaluation in Motion Analysis) 1.0.6

User Guide

1. Introduction

The aim of this document is to explain how to use the GUI (Graphical User Interface) to process upper limb 3D stereophotogrammetric data. ***Please do not refer to this document for any issue about code modification for developers.***

! Before starting the application – conventions:

1.1 - Folders/files structure:

The folder structure accepted by the application so far is a *tree*, i.e. a root folder containing subfolders that contain other subfolders and so on. The following is the tree structure related to a subject (patient):

subject name (folder)

|

|_ session 1 name (folder)

|

|_ session 2 name (folder)

|

|_ ...

|

|_ session N name (folder)

|

|_ C3D file 1 name (trials)

|

|_ C3D file 2 name (trials)

|

|_ ...

|

|_ C3D file M name (trials)

1.2 - C3D file names:

Calibration trials. The “KINEMATICS” processing section uses calibration trials (static trials) for anatomical landmark reconstruction. A calibration trial is a data acquisition during which the motion lab expert aims the pointer at a specific anatomical landmark. For a landmark called <AL>, the calibration trial must be named as followed:

`<prefix><AL>.c3d`

where `<prefix>` is a custom string that must be the same for **all** the calibration files.

Valid names are e.g.: `calIJ.c3d`, `calPX.c3d`, `calC7.c3d`, `calT8.c3d`, ...

Calibration trials must be located in the same session folder as the dynamic trials.

Dynamic trials. If you foresee to use the “BEST CYCLES SELECTION” processing section, the C3D file names should be composed as followed:

`<task name><number>.c3d`

where `<task name>` is the name of the task the subject is performing in the C3D file (e.g.: HTH, HTM, ...) and `<number>` is an ordinal number for the trial.

Valid names are e.g.: `HTH1.c3d`, `HTH2.c3d`, `Grasp01.c3d`, ...

Read “5. Processing sections; 5.4 - Best cycles selection” for more information.

1.3 - Joint angle names:

At the moment, parts of the application (such as the “Reference data creation” section) require the angle names to start with “R” or “L”, to be able to distinguish right from left upper limb. In case of body model file editing, the user should keep to this naming convention.

2. Starting the application

Start Matlab® and set the “Current Folder” to the application folder (“ULEMA_UpperLimbAnalyzer”).

Type:

```
>> mainGUI
```

in the command window.

The application will automatically take care of including the needed folders/files into the Matlab path.

NOTE

The wrapped libraries for writing data to C3D are currently only available for:

- Windows XP 32-bit
- Windows 7 64-bit

In case other operative systems are used, you will receive a warning about the fact that you cannot write to C3D and the section “Data export to C3D” will be disabled.

3. File loading

The application supports following type of files:

- C3D: contains raw data such as marker 3D coordinates, EMG signals, events...
- MAT: generated by the application during the processing (see "6. Before running the processing; 6.2 - Application MAT files generation" for more information)

NOTE

Only C3D files exported from Vicon Nexus/Workstation have been tested thus far. Although reading/writing data from/to C3D files coming from other sources should not pose problems, the full compatibility is currently not ensured.

3.1 - C3D (raw) files (no previous data loaded):

Click on "**File** → **Load**" and choose one of the following:

- "**C3D tree (single subject)**": you will be asked to select one root folder (subject folder), which contains other subfolders, i.e. the sessions for that subject. The session folders contain the C3D files.
- "**C3D tree (group of subjects)**": you will be asked to select one root folder (folder containing all the subjects subfolders). The subject subfolders each contain session subfolders (per subject). The session folders contain the C3D files.

After selecting the root folder, the loading process will start.

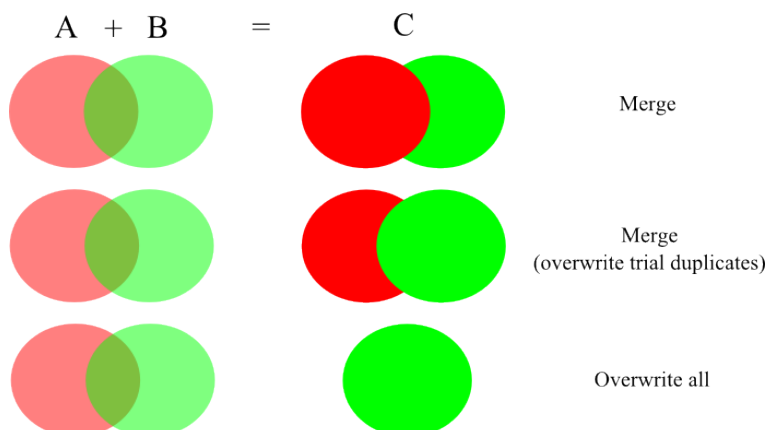
The subject, session and C3D file names should appear in the GUI, in the lists on the top.

3.2 - C3D (raw) files (other data previously loaded):

Proceed as in the previous section. At the end of the loading, a '**dialog window**' will popup with the **warning** that a data structure is already present. Options:

- "**Merge**": in case the existing Subjects – Sessions – Trials hierarchy (A) and the newly loaded (B) one share equal names, the application will add only the part of the hierarchy that is not already present.
- "**Merge (overwrite trial duplicates)**": in case the existing Subjects – Sessions – Trials hierarchy and the newly loaded one share equal names, the application will add the part of the hierarchy that is not already present and overwrite the shared part of the hierarchy with the new one.
- "**Overwrite all**": the existing hierarchy is completely removed and replaced by the new one.

Red ball is hierarchy A (the one currently loaded), and B (the green one) is the one to add. On the right part of the picture the result of every option is showed:



3.3 - MAT files (no previous data loaded):

Click on **“File → Load”** and choose one of the following:

- **“MAT file”**: load a single MAT file. You will be asked to select the specific MAT file to be loaded.
- **“All MAT files in a folder”**: load all MAT files that are located in a folder. You will be asked to select the folder containing all the MAT files. **NOTE** This can be convenient in case the user selected the option “Processing → Options → Split proc. data into .mat files for → Subjects” (see section “Before running the processing – Application MAT files generation” for more information).
- **“All MAT files in folder tree (depth: 2)”**: load all MAT files located in the subfolders of a root folder (Fig.1). You will be asked to select the root folder. **NOTE** This can be convenient in case the user selected the option “Processing → Options → Split proc. data into .mat files for → Sessions” (see section “Before running the processing – Application MAT files generation” for more information).
- **“All MAT files in folder tree (depth: 3)”**: load all MAT files located in a subfolder of the subfolders of a root folder (Fig.1). You will be asked to select the subfolder.

NOTE This can be convenient in case the user selected the option “Processing → Options → Split proc. data into .mat files for → Trials” (see “6. Before running the processing; 6.2 - Application MAT files generation” for more information).

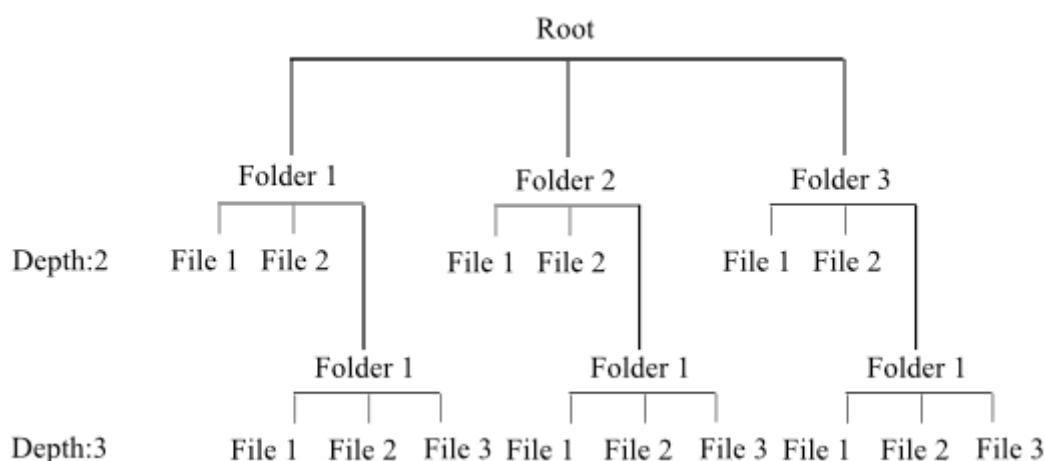


Figure 1

NOTE

- In case “Merge” or “Merge (overwrite trial duplicates)” is selected, a file called “Duplicates.txt” will be generated in the selected root folder, indicating the common part between the old and the new files structure hierarchy.
- The loading of files does NOT consist of loading all the data in memory for all the C3D files in the subfolders. This would require a massive amount of RAM in case a large number of files is present. The loading process will load the paths to the C3D files.

4. Protocol management

In the U.L.E.M.A.-GUI, a *protocol* refers to a set of options related to the following processing sections (see 5. Processing sections, 5.1 – 5.6):

- Raw data reading
- Kinematics
- Segmentation
- Best cycles selection
- MAP calculation

The protocols settings are stored in the file “ProtDB.mat”, which can be found in the folder “Prot” under the application’s main folder.

4.1 – Protocol modification

All available protocols are shown in the list “**Protocol list**” it is possible to see all the protocols available. Clicking on a specific protocol will show the settings/options belonging to that protocol in the GUI. The order of the protocols in the list can be changed using the up and down arrows.

Under the protocol list, following buttons are available:

- “**Create new protocol**”: a new protocol, with default settings, will be created.
- “**Copy protocol**”: the currently selected protocol will be copied (with its settings) and added to the list.
- “**Delete protocol**”: the currently selected protocol will be deleted from the list.
- “**Save protocol to file**”: changes to any of the settings of a protocol will be saved to the ProtDB.mat file.
- “**Don’t save protocol to file**”: changes to any of the settings of a protocol will be discarded.

Every protocol is identified by a name, i.e. “Protocol ID”. You can change this in the GUI and save it with the button “Save protocol to file”. The name will be updated in the list.

4.2 – Linking protocols to trials

Every trial loaded in the previous section, can be linked to an existing protocol. This protocol (and concurrent settings) will then be used to process the trial.

You can link a protocol to a trial by selecting one or more trials (in the same session) and then click on:

- “**Link/Unlink protocol to selected trial(s)**”: the behavior depends on the selected option
 - “For current session only”: the selected protocol will be added to/removed from the selected trial names for the currently selected session only.
 - “For all sessions (curr. sub.)”: the selected protocol will be added to/removed from the selected trial names, for every session of the currently selected subject.
 - “For all subjects”: the currently selected protocol will be added to/removed from the selected trial names, for every session of all the subjects in the list.

- **“Link/Unlink protocol to selected session”**: the currently selected protocol will be added to/removed from all the trials in the current session for the current subject
- **“Link/Unlink protocol to selected subject”**: the currently selected protocol will be added to/removed from all the trials for all the sessions for the current subject

5. Processing sections

5.1 - Kinematics

This section will read the necessary RAW data from the C3D files. In particular what will be read is:

- Marker data: the coordinates for all the markers contained in the file;
- Value of the frequency (Hz) used to acquire data marker;
- Data related to events: context, time, event type;

This allows the user to (re-)read raw data independently from the calculation performed.

5.2 - Kinematics

This section will compute JOINT ANGLES. Its core code is based on a modified version of the BodyMech engine (3.06.01, www.bodymech.nl). It is therefore strongly recommended to first read the BodyMech guide on how to create a body model.

Following options are the available:

- **“Body model”** body model M-file to use.

More body model files can be added in the application folder “BodyModels”. This folder is parsed every time the application is launched. In this phase, the software will automatically read the name of all the M files in this folder, so that the body models are available for this selection in the GUI.

- **“Static file”** calibration file (C3D) to define the reference frame for the technical clusters.

This C3D file must be located in the same session folder of the other trials that will be processed with the protocol. The application will automatically find the first frame in the file where all the needed markers are visible at the same time.

- **“Calibration files prefix”** a string identifying a prefix that every C3D calibration file must have.

See “1.2 - C3D file names” for more details.

- **“Kinematics function”** M-file defining the anatomical reference frame for each segment.

More kinematic files can be added in the application folder “AnatCalcs”. This folder is parsed every time the application is launched. In this phase, the software will automatically read the name of all the M files in this folder, so that the kinematics functions are available for selection in the GUI.

- **“Pointer”** M-file describing the geometry of the pointer (or stick) used to calibrate the anatomical landmarks.

More pointer files can be added in the application folder “Pointers”.

- **“Wanted joints”** list of joints present in the selected body model file. Selecting a different body model file will influence this list. The user can highlight the joints of interest, for which the angles will be calculated.
- **“Absolute angles”**: if “Reference position” is set, these angles refer to the motion of a segment from a reference position in a file (“Reference position” file) to a moving position of the same segment in the dynamic file. If “Laboratory reference frame” is set, the proximal reference frame of the joint is the laboratory reference frame (in the dynamic trial), while the distal reference frame is the reference frame of the segment in the dynamic trial.
The segments influenced by this option are indicated in section “Meaning of points/segments/joints/angles for the available body models”.
- **“Functional JC options”** every row of the table refers to a functional joint center. “Segment 1” is the proximal segment. “Segment 2” is the distal segment. Both segments are considered connected by a ball joint represented by the functional joint center. “Dynamic trial” is the name of the C3D file in which the calibration of the point is performed (e.g. shoulder circumduction task). “Assign to” indicates the name of the functional joint center to be created. **This name can be used in the kinematics file to define an anatomical reference frame (e.g. humerus).** “Method” refers to the algorithm to compute the functional joint center. Currently, the only available method is Gamage [1].

5.3 - Segmentation

This section will segment (break apart) the trial into different cycles and optionally calculate spatiotemporal parameters.

The description of all available segmentation methods is contained in “EventsConfig.txt” located in the application folder “Seg”. This file contains a root section, [Segmentation] ... [/Segmentation], that can contain one or more [Method] ... [/Method] sections.

Every method section is composed out of following aspects (deleted are the aspects that do not affect the behavior of the application):

- **method**: an ordinal number defining the index of the method.
This is shown in the application in the “Method:” list
- **type**: the type of event detection. It can be “manual” (the user defines the events a priori), or “automatic”.
- **segName**: a description of the segmentation method.
This will be shown in the GUI when clicking on a method index.
- **evStart**: the event defining the start of the cycle. This can be: TO<n>, HS<n>, GE<n>.
<n> is a positive number.
- **evStartPlotName**: meaningful custom name for the start event.
- **evSync**: list of events (synchronization or sync events) between the first event and the last event.
See evStart for the accepted names.
- **evSyncPlotName**: list of meaningful custom names for the sync events.
- **evSyncTimePerc**: list of numbers indicating the percentage in the cycle at which the sync events should occur (0% = first event; 100% last events). This can be used for representation purpose; for instance, it can be useful for a plot in which all the cycles are printed and time-warped so that all the sync events occur at the percentages defined by evSyncTimePerc (e.g. TO → 60 %).
- **evStop**: the event defining the end of the cycle.

See evStart for the accepted names.

- **evStopName**: meaningful custom name for the final event.
- **evForOffset**: not used. Leave it ""
- **fieldsToShift**: not used. Leave it {}
- **fieldColToShift**: not used. Leave it []

See the file "EventsConfigExamples.txt" located in the "Seg" folder for more examples of segmentation methods.

In the GUI, further options are available:

- **"Contexts"**: this table associates the context of the event definitions (Vicon Nexus) to a particular moving side (left, right, general)
- **"Spatiotemporal parameters"**: the spatiotemporal parameters are linked to a point (technical marker or anatomical landmark) in a specific phase of the cycle. Every row of the table in the bottom part represents the calculation of the spatiotemporal parameters for one point in one phase. Check which spatiotemporal parameter is wanted (calculated per phase):
 - "Timing" duration of the phase (in seconds), duration in percentage of the total cycle duration, and time (in sec) at which maximum velocity is reached.
 - "Speed" maximum velocity (in mm/second).
 - "Traj. dev." the ratio between the total length of the followed path and the length of a straight line connecting first and last position. This number is always equal or greater than one.
 - "Jerk" the jerk curve, i.e. the third time-derivative of position, giving a measure of the "movement smoothness".
- **"Angles min, max, value at events"**: if checked, minimum, maximum and value at a specific event of the cycle will be calculated for all angles.

NOTE

- A current limitation of the GUI software is that only one segmentation method can be handled per protocol. In case various contexts are used, one context must be selected per protocol.
- For motion cycles in which a point starts in a certain position and must return approximately to that position at the end of the cycle (e.g. closed loop motion), the trajectory parameter (Traj. Dev.) calculated in the EntireCycle phase could very high, due to the discrepancy between travelled path and straight line between start and endpoint (virtually zero).

5.4 - Best cycles selection

This section will extract the best cycles relative to a task, context and phase, using the method described in [2]. Following options are available:

- **“Task table”** A computation of the best cycles for every row of this table.
For every row, the application will select all the trials (to process) whose prefix corresponds to the string in the “Task prefix” column (*see section “Before starting the application – C3D file names convention”*);

Data will be filtered by context, phase, and the desired angles (list appears on the right when clicking on the cell in column “Edit angles:”).

Finally, the algorithm described in [2] will be applied on the selected set of angles.

- **“Best cycles number”** The number indicates the number of best cycles to keep.

The algorithm described in [2] will be applied to select the desired number of cycles.

If the number of total existing cycles for a task-context-phase-angles combination (table row) is lower than this number, all the available cycles will be kept.

NOTE

- Every angle in the angles list associated to every row of the “task table” must first be processed in the “Kinematics” section. *See section “Meaning of points/segments/joints/angles for the available body models” to see the different angles associated to the joints.*
- There is currently no preliminary check on the validity of the values entered in every cell of the row of the task table. The user has to assure that a certain list of angles exists for the selected phase and context.
- The “Fast fill table...” sub-window, aimed at speeding up the process of filling the “task table” when processing a very large number of rows, currently presents a known bug. This will be solved as soon as possible.

5.5 - MAP

This section allows calculating the Arm Variable Scores (AVS), the Arm Profile Scores (APS) and the MAPs [2] for every task. Following options are available:

- **“Choose reference file...”**: choose a reference file previously created with this application (by using the “Create reference data”). After the selection, the name of the file will appear in the GUI and the name of the reference subject(s) will be available in the column “Ref. subject name” of the “Subject match table”.
- **“Subject match table”**: this table associates each subject, for which AVSs, APSs and MAPs have to be created, with a specific reference group inside the reference file. This could be useful, for instance, when there is the need to match subjects with age, height or sex matched reference data.
- **“Save match table...”**: this allows to save the content of the subject match table to a text file.
- **“Load match table...”**: this allows to load the content of the subject match table from text file.

NOTE

- The reference data created with the section “Reference data creation” has only one subject, which is data from a group of children or adults, named “Normal subject”. In the second column of the subject match table, only this subject is available.
- There is currently no preliminary check on the validity of the subject names entered in the first column of the subject match table. All the subjects used here must first have been processed.

5.6 - Data exportation to C3D

This section allows exporting data to C3D. Following options are available:

- **“Create new C3D”**: the application will pick the original C3D (using the recovery path), add data and save it (with the same name) to a new folder named “ProcC3D”. This folder is located within the folder of the original C3D file.
- **“Add data to C3D”**: the application will pick the original C3D (using the recovery path), add data and overwrite the original C3D.
This is a convenient option when using Vicon Nexus, i.e. replacing the C3D with a information-rich one will allow to continue to use the associated files such as VSK, MKR, AVI, ... without having to copy them to the “ProcC3D” folder. These files are used to:
 - show the subject model (the markers connected by colored lines)
 - create reports using Vicon Polygon (data is written back in such a way that it is visible in Polygon)

Data added to original C3D:

- technical markers originally available, eventually with gaps automatically filled
- reconstructed anatomical landmarks (virtual markers)
- calculated joint angles
- spatiotemporal parameters (if computed previously in the “Segmentation” section) for each context. cycle, marker, phase:
 - duration (s): coded as “duration”
 - duration of the phase in percentage of the cycle duration (%): coded as “percentageTiming”
 - time at which the total velocity of the point is reached (s): coded as “timeVmax”
 - maximum velocity of the marker (mm/s): coded as Vmax

Every parameter will appear in the C3D with the following name:

`<context>_<cycle>_<marker>_<phase>_<spatio-temporal parameter>`

NOTE

The minimum, maximum, initial and final values for each joint angle are not saved in the C3D, although these have been calculated (“Segmentation” section). This is due to the fact that the amount of data is more than the maximum numbers of parameters available for a C3D file.

5.7 - Export to CSV/PDF

This section exports the previously computed data to CSV and the MAPs (if available) to PDF. Following options are available:

- i. Click “**Choose save path...**” to select the root folder where the CSV/PDF files will be saved.
- ii. Check boxes
 - “**Save trials as CSV**”: a CSV per computed trial will be saved under the root selected in “Choose save path...”.

Specifically, the application will create (if not existing) a folder, under the root, with the name of the subject. Under this subject-folder, a subfolder representing the session will be created. Under the session-folder, the trial CSV is created.
 - “**Save moving side only**”: option for bilateral markers placement, has effect only when “Save trials as CSV” is checked (trials saved in same location as described above).

Specifically, in case of bilateral marker placement and unilateral task execution, the angles relative to both sides are saved for every cycle. However, one might only be interested in the angles for the unilaterally moving side. The angles from the non-moving side will be discarded from the CVS when this option is checked.
 - “**Save best cycles info/MAPs data as CSV/PDF**”: a CSV containing information about the best cycles extraction (if available) and the MAPs (if available) will be saved under the root selected in “Choose save path...”.

Specifically, the application will create (if not existing) a folder, under the root, with the name of the subject. Under this subject-folder, a CSV file (with the same name of the session) will be created.

If available, the MAPs data will be converted into a bar graph and saved as PDF, in the same folder of the session CSV: `<session>_<task>_<context>_<cycle>.pdf`

5.8 - Export to XML

This section exports the previously computed data to XML. This is necessary when using the **ReportGenerator toolbox**. Following options are available:

- i. click “**Choose save path...**” to select the root folder where the XML files will be saved.
- ii. “**Save best cycles to XML**”: for every processed subject and session, all available data will be screened and only best cycles data will be saved.

Specifically, the application will create (if not existing) a folder, under the root, with the name of the subject. Under this subject-folder, a subfolder representing the session will be created. Under this session-folder, the trial XML file is created.

5.9 - Reference data creation

This section creates the reference data MAT file (from non-pathological population) that can be used in the “MAP” section. The generated MAT file will contain following data, for every task and phase previously computed in the “Best cycles selection” section:

- original angle curves for the cycles (individual curves)
- mean curve for every angle (group average)
- standard deviation curve for every angle (group SD)

Following options are available:

- **“Output type”**:
 - “Mix right and left side”: the application will use the angles from both sides to generate mean and standard deviation curves.
 - “Only right movement” or “Only left movement”: the application will consider only the data for that specific side, ignoring the data for the contralateral side, if existing.
 - “Bilateral”: the application will use data for the right side to produce mean and standard deviation data for the right side. This process will be repeated for the left side. In the final MAT file there will be 2 sets of mean and standard deviation curves.
- **“Choose reference data folder...”**: this allows the select the folder in which the MAT file must be generated.
- **“Reference data file name”**: this is the name of the MAT file to be generated.

NOTE

The generated MAT file also contains the raw curves that were used to generate the statistics (mean, SD,...). As such, it is theoretically possible to update the file by adding/removing new/bad raw curves and recalculating the statistics. This feature is however not yet available in the software.

5.10 - Export reference data to XML

This section converts the control data MAT file to XML format. This operation is necessary when using the **ReportGenerator toolbox**. Following options are available:

- i. Click **“Choose input file folder...”** to select the folder where the converted MAT file needs to be fetched.
- ii. **“MAT file name”**: the name of the MAT file to be converted.
- iii. Click **“Choose output file folder...”** to select the folder where the XML file will be saved.
- iv. **“XML file name”**: the name of the XML file to be generated.

- v. “**Keep only mean and std dev**”: if checked, only data regarding mean and standard deviation will be exported.

This is strongly suggested, since the conversion of all MAT files will otherwise easily result in a large XML file, with a very long conversion process.

6. Before running the processing

6.1 - Processing sections selection

In the menu “Processing → Sections” check all the sections you want to compute. This table shows the section inter-dependencies:

To run	Required section								
	RawR	Kin	Seg	Bcy	Map	C3D	RdMAT	CSV	XML
RawR									
Kin	•								
Seg	•	•							
Bcy	•	•	•						
Map	•	•	•	•			•		
C3D	•	•	(1)						
RdMAT	•	•	•	•					
CSV	•	•	•	(2)	(2)				
XML	•	•	•	•					
RdXML	•	•	•	•			•		

Legend: RawR: raw data reading; Kin: kinematics; Seg: segmentation; Bcy: best cycle selection; Map: AVS, APS, A-MAP; C3D: Export to C3D; RdMAT: Create reference data; CSV: Export to CSV/PDF; XML: Export to XML; RdXML: export reference data to XML;

(1) While exporting to C3D, if Segmentation data was previously computed, some spatiotemporal parameters data will also be written back to C3D.

(2) While exporting to CSV, if Best Cycle Selection and MAP data was previously computed, it will be exported.

6.2 - Application MAT files generation

During data processing, upon completion of one section, the application will write or update MAT files containing the computed data. These MAT files allow:

- the user to continue the processing later on without having to start “from scratch” using C3D files.
- the application to continue with the processing using the last created MAT files. For instance, if the user wants to read raw data and process kinematics consecutively, raw data reading code will read C3D files and produce the MAT files, while kinematics code will start from those MAT files and update them.

1. Click on **“Processing → Split proc. data into .mat files for”** and select one or more modalities for file saving:

- **“Subjects”**: one MAT file per processed subject
- **“Sessions”**: one MAT file per processed session
- **“Trials”**: one MAT file per processed trial

☐ The individual MAT files can be uploaded in the GUI instead of the original C3D files or the one main MAT file containing all data.

2. Click on **“Processing → Set proc. data path”** to select the folder where to save the individual MAT files. In this root folder, the files will be saved in different structures depending on the selected settings for “Split proc. Data into .mat files for”:

- **“Subjects”**: MAT files will be saved in the selected root folder
- **“Sessions”**: subject-folders will be created under the selected root folder where the session MAT files will be saved.
- **“Trials”**: subject-folders will be created under the selected root folder; within the subject-folder, the session-folders will be created where the trial MAT files will be saved.

NOTE

If the modality “Subjects” is used and many sessions and trials are selected, the final subject MAT files can become very large. Thus, it could be better to use the “Sessions” or even “Trials” modality, to have (more but) smaller files to deal with.

6.3 - Recovery path

The *Recovery path* is a path needed when data needs to be read from C3D files. The path must point to a root folder containing structures described in the section “1.1 - Folders/files structure”.

The recovery path has to be specified in following cases (Settings background colored in orange in the GUI).

SECTION	SETTING	CASES (see “6.5 - Particular cases”)
Kinematics	Static file	<ul style="list-style-type: none">▪ case 2b and if the names of the static file in the old protocol and the one currently in the list do not match▪ always if FD is set
	Reference posture file	<ul style="list-style-type: none">▪ case 2b and if the names of the reference posture file in the old protocol and the one currently in the list do not match▪ always if FD is set
	Calibration prefix	<ul style="list-style-type: none">▪ case 2b and if the calibration prefixes in the old protocol and the one currently in the list do not match▪ always if FD is set
	DJC file name(s)	<ul style="list-style-type: none">▪ case 2b and if, for the protocol currently in the list, more DJC calibration files are needed or the names do not match between the old protocol and the one currently in the list▪ always if FD is set
	All available settings	<ul style="list-style-type: none">▪ always if it is the first time that kinematics is calculated (after raw data reading)
Export to C3D	All available settings	<ul style="list-style-type: none">▪ always

Legend: FD: “Force data reprocessing” option in “Processing → Options”; DJC: dynamic joint calibration

6.4 - Data re-processing

When a section has been computed and the data stored into the MAT file(s), the application automatically detects the stored data during the next computation. In case an already computed section is checked under “**Processing** → **Sections**”, the application will skip this section and will not perform processing again.

Checking the option “**Processing** → **Options** → **Force re-processing**” will trigger re-processing of the sections to recomputed.

6.5 - Particular cases

There is a set of particular situations that are worthwhile to be discussed:

* 1) A protocol is appended to some trials and later removed from the list of protocols or the name of that protocol has changed. When running the processing:

1.1) If the trial is loaded from a MAT file (where also the protocol of the latest processing was saved), the user is asked if:

a) *the user wants to use the protocol inside the MAT file*

b) *the user wants to stop the processing.*

1.2) If the trial is loaded from a C3D file, it is not possible to proceed and the process will stop.

* 2) The user loads data from MAT files(s), and for some trials the protocol appended in the previous computation has a different content from the one currently in the list of the application. When running the processing, the user is asked if:

a) the user wants to use the old protocol

b) the user wants to use the protocol content that is currently in the list

c) the user wants to stop the processing

6.6 – MAT files overwriting/merging

When data is loaded from MAT files, it is possible to choose if to merge the data to process to the loaded MAT files (“**Processing** → **Options** → **Proc. data saving** → **Safe merge**”), or to overwrite them (“**Processing** → **Options** → **Proc. data saving** → **Overwrite**”). Suppose that you have processed some files that are now in the form of MAT files. Suppose that you want to load them to perform some reprocessing. For instance, you realized that, for a subset of files, marker gap filling was not ok so you want to reprocess kinematics and segmentation. You can unlink the protocol from all the files apart from the ones to be reprocessed, set the “Data re-reprocessing” option (see 6.4) and set the safe merging of MAT files. In this case, the MAT files generated during the reprocessing will be the result of merging the new data to the “old” data (i.e. data related to the files which protocol was removed before processing). If you choose to overwrite the MAT files *and* the processed data path contains the loaded MAT files, then these files will be overwritten. In the described example, these files will be smaller in size, because they will only contains the data relative to the reprocessed files.

NOTE

The “Safe merge” modality will not work for the best cycles selection, but it will work like an “Overwrite” modality. If you reprocess only a subset of trials of a certain task (and “Best cycles selection” is part of that processing), then best cycles data relative to that task is replaced with the best cycles data relative to the newly processed trials.

7. Computation running

Click on “**Processing** → **Run**” to run the data processing.

See “7.1 - Typical errors during computation” in case of errors during computation.

7.1 - Typical errors during computation

See folder TypicalErrors for more details:

Message: *Input to SVD must not contain NaN or Inf*
Function name: RigidBodyTransformation_VECT_OPT

Cause: one or more markers still have gaps or are not present in the C3D file.

Figure: MarkerWithGaps.png

Other errors will be added if detected during the routinary use of the application.

7.2 - Meaning of points/segments/joints/angles for the available body models

Available body models:

1. BodyModel_UL_6Segm_Right
2. BodyModel_UL_6Segm_Left
3. BodyModel_UL_12Segm_Bilat

Point (marker name)	Definition
RUA1,2,3,4 LUA1,2,3,4	Technical markers the for humerus
RLA1,2,3,4 LLA1,2,3,4	Technical markers for the forearm
RH1,2,3 LH1,2,3	Technical markers for the hand
RACR1,2,3 LACR1,2,3	Technical markers for the scapula
ST1,2,3	Technical markers for the trunk
CH1,2,3	Markers for the chair
P1,2,3,4	Pointer markers
REL, REM LEL, LEM	Lateral and medial epicondyle (palpated)
RUL, RRS LUL, LRS	Ulnar and radial styloid (palpated)
RMC3, RMCP2,3,5 LMC3, LMCP2,3,5	proc styl metacarpal 3, metacarpo-phalangeal 2, metacarpo-phalangeal 3, metacarpo-phalangeal 5 (palpated)
RAA, RAI, RTS, RPC, RAC LAA, LAI, LTS, LPC, LAC	Ang acromialis, ang inferior, trig spin scapula, proc coracoideus, art acromioclavicularis (palpated)
IJ, PX, C7, T8	Proc spin C7, proc spin T8, inc jungularis, proc xyphoideus (palpated)
RGH LGH	Glenohumeral joint rotation center (calculated)

For a list of relevant anatomical landmarks (static calibration files), the reader is referred to [3].

Joint	Rot seq.	Definition	Angles (*)
Right_H2Shoulder Left_H2Shoulder	YXY	Joint between sternum and humerus ([3], 2nd humerus definition)	RElevationplaneH2, RShoulderElevationH2, RShoulderRotationH2 LElevationplaneH2, LShoulderElevationH2, LShoulderRotationH2
Right_H1Shoulder Left_H1Shoulder	YXY	Joint between sternum and humerus ([3], 1st humerus definition)	RElevationplaneH2, RShoulderElevationH2, RShoulderRotationH2 LElevationplaneH2, LShoulderElevationH2, LShoulderRotationH2
Right_Elbow Left_Elbow	ZXY	Joint between humerus ([3], 1st humerus definition) and forearm	RElbowFIExt, <i>No angle</i> , RElbowProSupination LElbowFIExt, <i>No angle</i> , LElbowProSupination
Right_Wrist Left_Wrist	ZXY	Joint between forearm and hand	RWristFIExt, RWristDeviation, <i>No angle</i> LWristFIExt, RWristDeviation, <i>No angle</i>
Right_Scapula Left_Scapula	YZZ	Joint between trunk and scapula	RScapProRetraction, RScapRotation, RScapTilting LScapProRetraction, LScapRotation, LScapTilting
Right_Trunk Left_Trunk	YZZ	Case 1 (**): Joint between trunk and global reference frame Case 2 (**): Joint between trunk in a reference position and trunk	RTrunkFIExt, RTrunkLateralFI, RtrunkAxialRotation LTrunkFIExt, LTrunkLateralFI, LTrunkAxialRotation
Right_H2Sh1 Left_H2Sh1	ZXY	Joint between sternum and humerus ([3], 2nd humerus definition)	RH2SAG_Flexion, RH2SAG_Abduction, RH2SAG_Rotation LH2SAG_Flexion, LH2SAG_Abduction, LH2SAG_Rotation
Right_H2Sh2 Left_H2Sh2	XZY	Joint between sternum and humerus ([3], 2nd humerus definition)	RH2FRONT_Abduction, RH2FRONT_Flexion, RH2FRONT_Rotation LH2FRONT_Abduction, LH2FRONT_Flexion, LH2FRONT_Rotation
Right_H1Sh1 Left_H1Sh1	ZXY	Joint between sternum and humerus ([3], 1st humerus definition)	RH1SAG_Flexion, RH1SAG_Abduction, RH1SAG_Rotation LH1SAG_Flexion, LH1SAG_Abduction, LH1SAG_Rotation
Right_H1Sh2 Left_H1Sh2	XZY	Joint between sternum and humerus ([3], 1st humerus definition)	RH1FRONT_Abduction, RH1FRONT_Flexion, RH1FRONT_Rotation LH1FRONT_Abduction, LH1FRONT_Flexion, LH1FRONT_Rotation

(*) The angles are listed in the same order of the axis sequence in “Rot seq.” column.

(**) If in “Kinematics” the “Absolute angles” option is set to “Reference position”, then Case 1 is realized; Case 2 otherwise.

For a definition of the anatomical reference frames, the reader is referred to [3].

7.3 - Meaning for the cycle phases (shared by different sections)

There are 10 default phases that can be used in the application.

“Phase i” is the phase between the i event and i+1 event.

Phase 1 is the phase between the first event and the second event;

Phase 2 between second and third event, and so on.

“EntireCycle” is the phase between the first event and the last event, so the full movement cycle.

8. References

- [1] Gamage SS, Lasenby J. New least squares solutions for estimating the average centre of rotation and the axis of rotation. *J Biomech.* 2002 Jan;35(1):87-93.
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