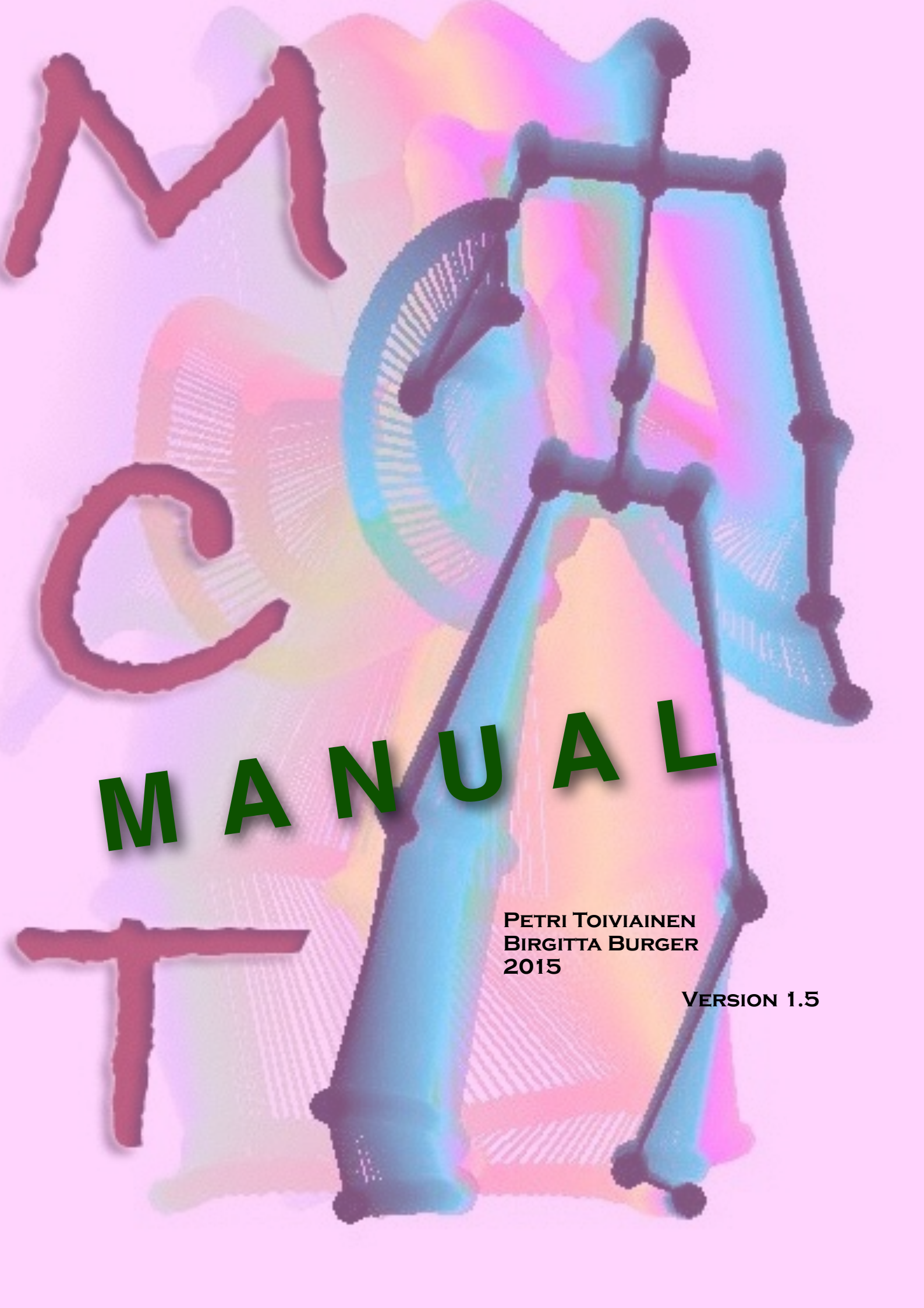


MANUAL

Petri Toiviainen
Birgitta Burger
2015

Version 1.5

MoCap Toolbox Manual

University of Jyväskylä, Finland

(vers. 07 Oct 2015)

Table of Contents

Foreword

This manual provides an introduction and a reference to the MoCap Toolbox, a Matlab® toolbox for the analysis and visualization of Motion Capture data. The toolbox is mainly aimed for the analysis of music-related movement, but might be useful in other areas of study as well. I wrote most of the toolbox and this manual during my sabbatical at the Center for Advanced Study in the Behavioral Sciences at Stanford University in 2007-8.

This manual requires that the user be familiar with the basic features of the Matlab software. Novices in this programming platform are advised to consult the cornucopia of Matlab tutorials available on the Internet. The reader should also be familiar with the basics of mechanics and calculus.

I would like to thank the Academy of Finland and the Center for Advanced Study in the Behavioral Sciences at Stanford University for their support.

Stanford, June 1, 2008

Petri Toiviainen

Acknowledgments

Thanks to Dominique de Beul for the providing the bvh parser.

Thanks to JJ Loh for providing a faster version for reading in .c3d files.

Thanks to Kristian Nymoen for providing the function mcmocapgram and the real-time streaming.

Thanks to Roberto Rovegno for contributing to the mcwritetsv function.

Thanks to Erwin Schoonderwaldt for providing the function to read in .mat files (exported from QTM).

Thanks to Federico Visi for providing the mcpqom, mcplotpqom, and mcrepovizz functions and contributing to the mcsort function.

Thanks to Dominique de Beul, Michiel Demey, Frank Desmet, Tommi Himberg, Herbert Jäger, Alexander Refsum Jensenius, Luiz Naveda, Kristian Nymoen, and Erwin Schoonderwaldt for reporting bugs in the toolbox and suggesting improvements.

Release Notes

For new features and bug fixes done in previous versions, please refer to the releasenotes_v1.5.txt included in the toolbox release.

Version 1.5

New functions

mcaddframes: duplicates frames

mccomplexity: calculates the complexity of movement based on entropy of the first principal component

mcfluidity: calculates the fluidity/circularity of mocap data

mcrepovizz: exports MoCap structure as repoVizz files

mcreverse: reverses dimensions of motion-capture data

mcrotationrange: calculates the rotation range between two markers

mcsetlength: sets mocap data to the length given

mcsort: sorts mocap data according to marker names

Bug fixes

mcanimate, mcplotframe, mcinitanimpar: direct video file making; changing use of projection parameters; returning from function with setting video parameters, but without creating video

mcdemodata: updated animpar variables to fit new animation parameter structure

mcdemo6-mcdemo9: fit new animation parameter structure

mcgetmarkername: now for norm data as well

mchilbert: keep data structure same as input file, added flag for indicating phase wrap

mcinitstruct: fixed inconsistency in naming in the manual

mcmerge: fixing animation parameter structure merging

mcmocapgram: norm data included

mcplotframe: move axes definition outside the main plotting loop for efficiancy

mcread: added bvh support, added potential troubleshoot for c3d data

mcreadc3d: check for matching frame no and data size (Optitrack issue)

mcs2j: runtime efficiency

mctimeintegr: for norm data as well

readc3d: changed machinetype parameter - change back as indicated in script if you run into issues reading in c3d files

Introduction

The MoCap Toolbox is a Matlab® toolbox that contains functions for the analysis and visualization of motion capture data. It supports the generic .c3d file format, the .tsv data format produced by the Qualisys motion capture system, the .mat file format produced by the Qualisys motion capture system, and the .wii format produced by the WiiDataCapture software (available at www.jyu.fi/music/coe/materials/mocaptoolbox).

To use the toolbox, you need the Matlab software (www.mathworks.com). Before using it, the toolbox has to be added in the Matlab path variable. The toolbox should be compatible with most versions of Matlab and most platforms. The latest implementations and developments have been made on Matlab version 8.4 (R2014b) running on Macintosh OS X v10.10.

To use all the functions in the MoCap Toolbox, the following toolboxes must be included in Matlab's path:

- Signal Processing Toolbox
- FastICA Package, available at http://www.cis.hut.fi/projects/ica/fastica/ (for `mcicaproj`)
- Periodicity Toolbox, available at http://eceserv0.ece.wisc.edu/~sethares/downloadper.html (for `mcsethares`)
- For reading in .bvh files: http://staffwww.dcs.shef.ac.uk/people/N.Lawrence/mocap/ (mocap and ndlutil toolboxes – also the github versions work)

Register to the MoCap Toolbox mailing list: www.jyu.fi/music/coe/materials/mocaptoolbox
to stay informed about new releases, bug reports, and bug fixes. It also serves as a general discussion board for users, so feel free to post anything motion capture- and toolbox-related that might be of interest to other users and developers. The email address to send messages to the list is mocap-toolbox@freelists.org (requires registration to send).

The MoCap Toolbox comes with no warranty. It is free software, and you are welcome to redistribute it under certain conditions. See the file License.txt provided with the toolbox for details of GNU General Public License.

General

Functions

The MoCap Toolbox contains 64 functions for the analysis and visualization of motion capture data. The functions can be divided into nine categories:

- Data input and edit functions
- Coordinate transformation functions
- Coordinate system conversion functions
- Kinematic analysis functions
- Kinetic analysis functions
- Time-series analysis functions
- Visualization functions
- Projection functions
- Other functions

The following table provides an overview of the functions available in the MoCap Toolbox. Detailed descriptions of each function are provided in the Chapter *Function Reference*.

	Function	Synopsis
INPUT & EDIT	`mcread`	read MoCap data files
	`mcreademg`	read emg files in tsv format
	`mcmissing`	report missing frames and markers
	`mctrim`	extract a temporal segment from MoCap data
	`mccut`	cut two MoCap structures to the length of the shorter one
	`mcaddframes`	duplicate frames
	`mcsetlength`	set MoCap data to the length given
	`mcsmoothen`	smoothen MoCap data
	`mcmerge`	merge two MoCap data structures
	`mcsort`	sorts MoCap data according to marker names
	`mcgetmarker`	extract a subset of markers from MoCap data
	`mcsetmarker`	replace a subset of markers
	`mcconcatenate`	concatenate markers from different MoCap or norm data structure
	`mcgetmarkername`	get names of markers from MoCap data
	`mcfillgaps`	fill missing data
	`mcinitstruct`	initialize MoCap or norm data structure
	`mcreorderdims`	reorder the Euclidean dimensions in the MoCap data
	`mcreverse`	reverse dimensions of MoCap data
	`mcresample`	resample MoCap data
	`mcrepovizz`	export MoCap structure as repoVizz files
	`mcc3d2tsv`	convert a c3d file into a tsv file
	`mcwritetsv`	save MoCap structure as tsv file
COORDINATE TRANSFORMATION	`mccenter`	center MoCap data to have a mean of [0 0 0]
	`mctranslate`	translate MoCap data
	`mcrotate`	rotate MoCap data

	`mc2frontal`	rotate MoCap data to have a frontal view with respect to a pair of markers
	`mcvect2grid`	convert a MoCap structure vector to a MoCap structure with three orthogonal views
COORDINATE SYSTEM CONVERSION	`mcinitm2jpar`	initialize parameters for marker-to-joint mapping
	`mcm2j`	perform a marker-to-joint mapping
	`mcinitj2spar`	initialize parameters for joint-to-segment mapping
	`mcj2s`	perform a joint-to-segment mapping
	`mcs2j`	perform a segment-to-joint mapping
	`mcs2posture`	create a posture representation form segm data
KINEMATIC ANALYSIS	`mcnorm`	calculate the norms of Euclidean MoCap data
	`mctimeder`	estimate time derivatives of MoCap data
	`mctimeintegr`	estimate time integrals of MoCap data
	`mccumdist`	calculate the cumulative distance traveled by each marker
	`mcmarkerdist`	calculate the distance of a marker pair
	`mcboundrect`	calculate the bounding rectangle
	`mccomplexity`	calculate the complexity of movement
	`mcfluidity`	calculate the fluidity/circularity of MoCap data
	`mcrotationrange`	calculates rotation range between two markers
	`mcsegmangle`	calculate the angles between two markers
	`mcperiod`	estimate period of MoCap data
	`mcdecompose`	decompose kinematic variable into tangential and normal components
	`mcspectrum`	calculate amplitude spectrum of MoCap data
KINETIC ANALYSIS	`mcgetsegmpar`	return segment parameters of a body model
	`mckinenergy`	estimate instantaneous kinetic energy of the body

	`mcpotenergy`	estimate instantaneous potential energy of the body
TIME-SERIES ANALYSIS	`mcmean`	calculate mean of MoCap data
	`mcstd`	calculate std of MoCap data
	`mcvar`	calculate variance of MoCap data
	`mcskewness`	calculate skewness of MoCap data
	`mckurtosis`	calculate kurtosis of MoCap data
	`mcstatmoments`	calculate first four statistical moments
	`mcwindow`	perform windowed time-series analysis
VISUALIZATION	`mcplottimeseries`	plot time series data
	`mcplotphaseplane`	create phase plane plot
	`mcinitanimpar`	initialize animation parameters
	`mccreateconnmatrix`	create connection matrix for plotting and animations
	`mcplotframe`	plot frames from MoCap data
	`mcanimate`	make an animation
	`mcsimmat`	calculate similarity matrix
	`mcmocapgram`	plot mocapgram
PROJECTION	`mcpcaproj`	perform a PCA on MoCap data
	`mcicaproj`	perform an ICA on MoCap data
	`mcsethares`	perform either an m-best or a small-to-large Sethares transform
	`mceigenmovement`	generate eigenmovements from PCA
OTHER	`mcbandpass`	band pass filter MoCap data
	`mchilbert`	perform a Hilbert transform
	`mchilberthuang`	perform a Hilbert-Huang transform
	`mcfilteremg`	filter emg data

Data Structures

The MoCap Toolbox uses three kinds of data structures: the *MoCap data structure*, the *norm data structure* and the *segm data structure*. An instance of a *MoCap data structure* is created by the function `mcread`, when motion capture data is read from a file to the workspace. The *MoCap data structure* contains the recorded locations of the markers as well as some basic information, such as the name of the file from which the data were read, the number of frames in the data, the number of cameras used in the capture session, the number of markers in the data, the sampling frequency, or frame rate, of the data, the names of the markers. The `.data` field of the *MoCap data structure* is a matrix containing the locations of the markers. It has three columns for each marker, corresponding to the two horizontal dimensions (1st and 2nd column) and the vertical dimension (3rd column). For instance, column 1 contains the x coordinates of marker 1, column 2 contains the y coordinates of marker 1, column 3 contains the z (vertical) coordinates of marker 1, column 4 contains the x coordinates of marker 2 etc. Each row in the matrix corresponds to a frame. Additionally, the *MoCap data structure* contains a field that indicates the order of time differentiation of the data, with zero corresponding to location, one to velocity, two to acceleration etc. The value of this field is changed by the functions `mctimeder` and `mctimeintegr` that perform temporal derivation and integration, respectively. Finally, the *MoCap data structure* contains fields that can hold data captured from analog devices, such as EEG, GSR, etc.

An instance of a *MoCap data structure* is also created when the function `mcm2j` is called. This function performs a transformation from a marker representation to a joint. While these two representations use the same data structure, they are conceptually different in the sense that the marker representation is related to actual marker locations, whereas the joint representation is related to locations derived from marker locations. This representation is helpful when we wish to calculate the location of a body part where it is impossible to attach a marker. For instance the midpoint of a joint can be derived as the centroid of four markers located around the joint.

The *norm data structure*, created by the function `mcnorm`, is similar to the *MoCap data structure*, except that its `.data` field contains only one column per marker. This column holds the Euclidean norm of the vector data from which it was derived. If, for instance, the function `mcnorm` is applied to velocity data, the resulting *norm data structure* holds the magnitudes of velocities, or speeds, of each marker.

While the *MoCap* and *norm data structures* are related to points in space (markers or joints), the *segm data structure* contains data about segments of the body. The function `mcj2s`, which carries out a transformation from a joint representation to a segment representation, produces as output an instance of the *segm data structure*. The *segm data structure* contains most of the fields of the *MoCap data structure*. The `.data` field of the *MoCap data structure* is however replaced by a few other fields. The `.parent` field contains information about the kinematic chains of the body, in other words, how the joints are connected to each others to form segments, and how these segments are connected to each other. The location and orientation of the center of the body (the root) is contained in the fields `.roottrans` and `.rootrot`. The `.segm` field contains several subfields that store the orientation of the body segments in various forms. The `.eucl` subfield contains for each segment the euclidean vector pointing from proximal to distal joint of the segment. The `.r` subfield contains the length of each segment. The `.quat` subfield contains the rotation of each segment as a quaternion representation (to learn about the use of quaternions to represent 3D rotations, see for instance http://en.wikipedia.org/wiki/Quaternion). Finally, the `.angle` subfield holds the angle between each segment and its proximal segment.

A more detailed description of the data structures used in the MoCap Toolbox can be found in the Chapter *Data and Parameter Structure Reference*.

Parameter structures

To facilitate the converting between different representations (marker, joint, and segment) and the producing of certain visualizations, the MoCap Toolbox uses three different parameter structures: the *m2jpar*, *j2spar*, and *animpar structures*.

The *m2jpar structure* is used by the function `mcm2j` and contains information needed to carry out a transformation from a marker representation to a joint representation. Among other things, it contains a field that holds, for each joint, the numbers of the markers whose centroid defines the location of that joint.

The *j2spar structure* is used by the function `mcj2s` and contains information needed to carry out a transformation from a joint representation to a segment representation. Among other things, it contains the number of the joint that is the center (root) of the body. It also contains the numbers of three joints that define the frontal plane of the body. Finally, it contains a vector that indicates the

parent segment (the segment proximal in the kinematic chain) for each segment and a cell array with the segment names.

The *animpar structure* is used by the functions `mcplotframe` and `mcanimate`, and holds information needed to create frame plots and animations. These include, for both frame plots and animation, the limits of the plotted area, screen size, viewing angle, plotting colors, marker size, line widths, and connections between markers. Additionally, the structure holds the possibility to plot traces and the frames per second used when creating animations.

A more detailed description of the parameter structures used in the MoCap Toolbox can be found in the Chapter *Data and Parameter Structure Reference*

Add-ons and extensions

Periodic quantity of motion

Functions that estimate and plot the periodic quantity of motion have been implemented by Federico Visi and Rodrigo Schramm. These functions can be downloaded from the mocap toolbox download page, section “Extensions”. To use the function, download the zip-folder and extract it either to the toolbox folder or to another folder that your Matlab distribution can access. A demo explaining the use of the functions is included in the package. For more information and support please contact Federico or Rodrigo and have a look at the following publication:

Visi, Federico, Schramm, Rodrigo and Miranda, Eduardo. Gesture in Performance with Traditional Musical Instruments and Electronics: Use of Embodied Music Cognition and Multimodal Motion Capture to Design Gestural Mapping Strategies. Proceedings of the International Workshop on Movement and Computing. MOCO '14, p. 100-105, ACM, Paris, 2014.

Realtime streaming of mocap data

A solution for realtime streaming of mocap data from the mocap toolbox has been implemented by Kristian Nymoen. It allows playback of synchronized sound and motion capture data, as well as looping, scrubbing, etc. You can visualise the data in 3D while interacting with the visualisation.

The visualisation and GUI is implemented in Max 6, and a standalone application for Mac is also included (meaning that it is not necessary to have Max installed). The files can be downloaded from http://www.fourms.uio.no/software/mcrtanimate/.

If somebody wants to have this running on Windows, it should work in theory, but you will have to have Max installed, and download the necessary dependencies (listed in the readme file).

The implementation requires the Instrument Control Toolbox for Matlab (http://www.mathworks.se/products/instrument/). A workaround without this Toolbox is under development and will be provided soon.

This is still a prototype implementation, so please provide feedback (suggestions, new features, ...) to Kristian.

Examples

This chapter contains a number of examples that are intended to serve as an introduction to the use of the MoCap Toolbox. The examples illustrate how MoCap data can be read into Matlab, edited, visualized, and transformed. They also explain how kinematic, kinetic, as well as time-series analysis can be performed and how animations can be created. Finally the chapter contains an example of the analysis and visualization of data captured using the Nintendo Wii remote controller.

The examples presented in this chapter can also be found in the function `mcdemo`. Just type `mcdemo` in the Matlab Command Window and follow the instructions.

Reading, Editing, and Visualizing MoCap Data (`mcdemo1`)

This example shows how you can read MoCap files into Matlab as well as how you can edit and visualize the data. Motion capture data can be imported into Matlab and stored as a *MoCap data structure* using the function `mcread`. Currently the function supports the generic *.c3d* format, the *.tsv* format produced by the Qualisys motion capture system, the *.mat* format produced by the Qualisys motion capture system, and the *.wii* file format. produced by the WiiDataCapture software (available at www.jyu.fi/music/coe/materials/mocaptoolbox)

The MoCap toolbox folder includes the .mat file `mcdemodata.mat` that contains motion capture data and associated parameter structures as Matlab variables. These data are used in the examples of this manual. The commands used in the demo files are marked in dark green.

```
load mcdemodata
whos
```

```
  Name          Size                Bytes  Class     Attributes
  dance1        1x1               1013572  struct
  dance2        1x1               1013572  struct
  j2spar        1x1                  2168  struct
  japar         1x1                  2530  struct
  m2jpar        1x1                  3464  struct
  mapar         1x1                  2914  struct
  walk1         1x1                241862  struct
  walk2         1x1                275474  struct
  wiidata       1x1                 45560  struct
```

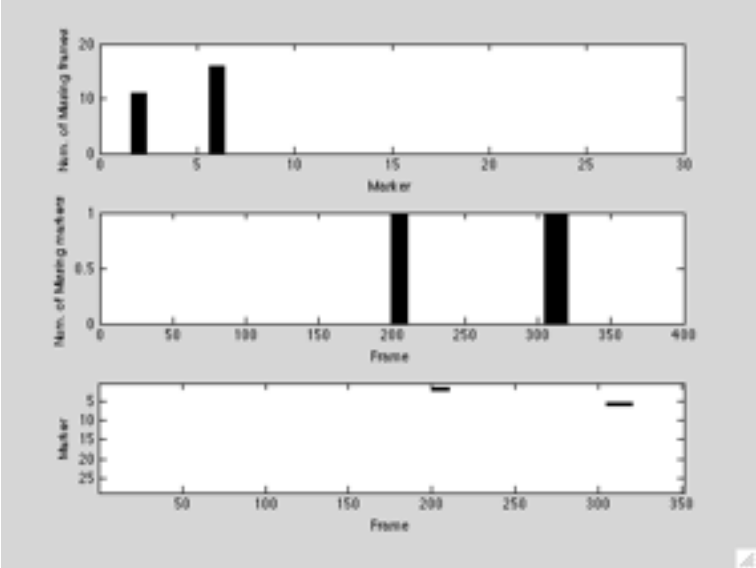
Variable `walk1` is a *MoCap data structure*:

```
walk1
```

```
walk1 =
            type: 'MoCap data'
        filename: '28-Karolien-Walking.tsv'
         nFrames: 351
        nCameras: 8
        nMarkers: 28
            freq: 60
         nAnalog: 0
         anaFreq: 0
    timederOrder: 0
      markerName: {28x1 cell}
            data: [351x84 double]
      analogdata: []
           other: [1x1 struct]
```

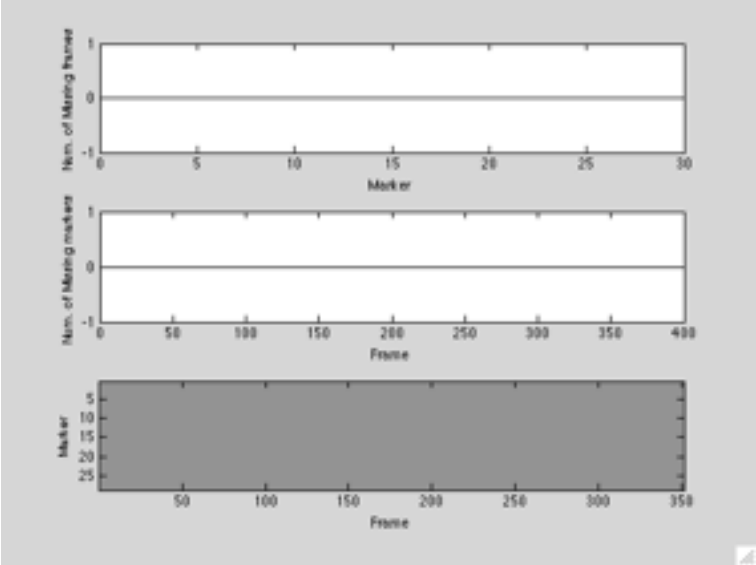
Let us look if there are any missing data in the variable `walk1`:

```
[mf, mm, mgrid] = mcmissing(walk1);
figure, set(gcf,'Position',[40 200 560 420])
subplot(3,1,1), bar(mf), xlabel('Marker'), ylabel('Num. of Missing frames')
subplot(3,1,2), bar(mm), xlabel('Frame'), ylabel('Num. of Missing markers')
subplot(3,1,3), imagesc(-mgrid'), colormap gray, xlabel('Frame'),
ylabel('Marker')
```



Markers 2 and 6 have missing frames. The missing data can be filled using the function `mcfill-gaps`:

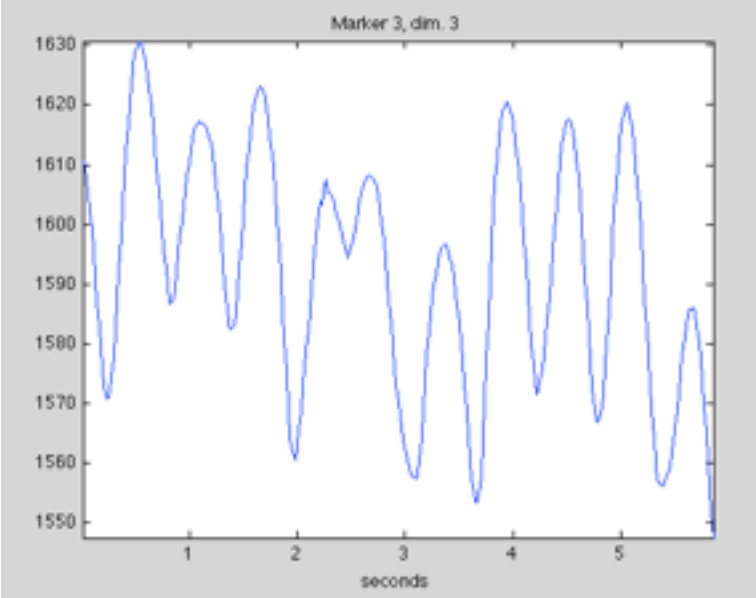
```
walk1 = mcfillgaps(walk1, 100);

[mf, mm, mgrid] = mcmissing(walk1);
subplot(3,1,1), bar(mf), xlabel('Marker'), ylabel('Num. of Missing frames')
subplot(3,1,2), bar(mm), xlabel('Frame'), ylabel('Num. of Missing markers')
subplot(3,1,3), imagesc(-mgrid'), colormap gray, xlabel('Frame'),...
 ylabel('Marker')
```



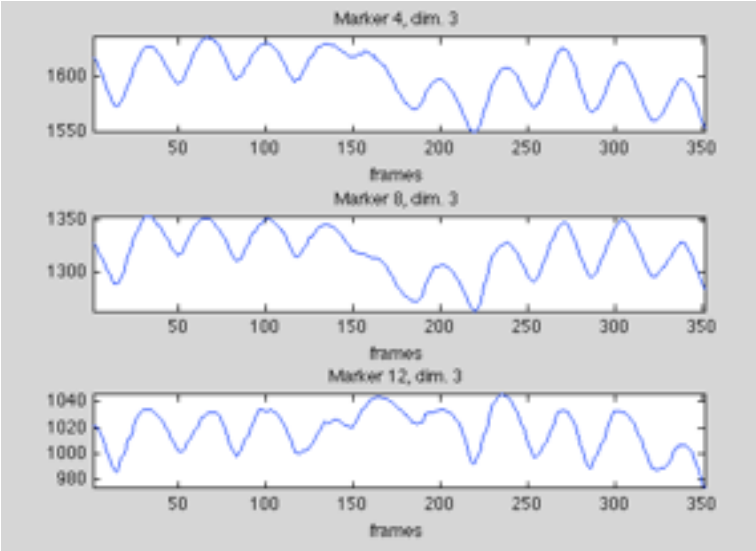
The variable `walk1` has no more missing frames.

Marker location data can be plotted as a function of time using the function `mcplottimeseries`:

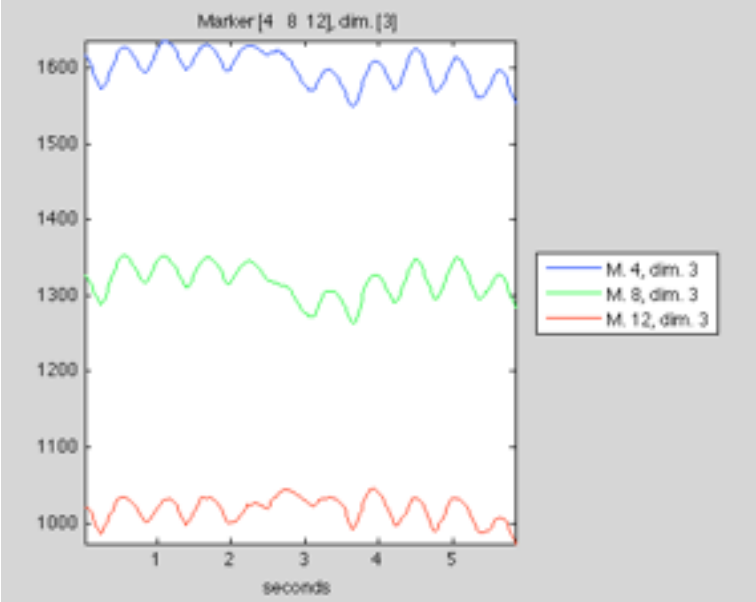
```
mcplottimeseries(walk1, 3, 'dim', 3) % marker 3, dimension 3
```



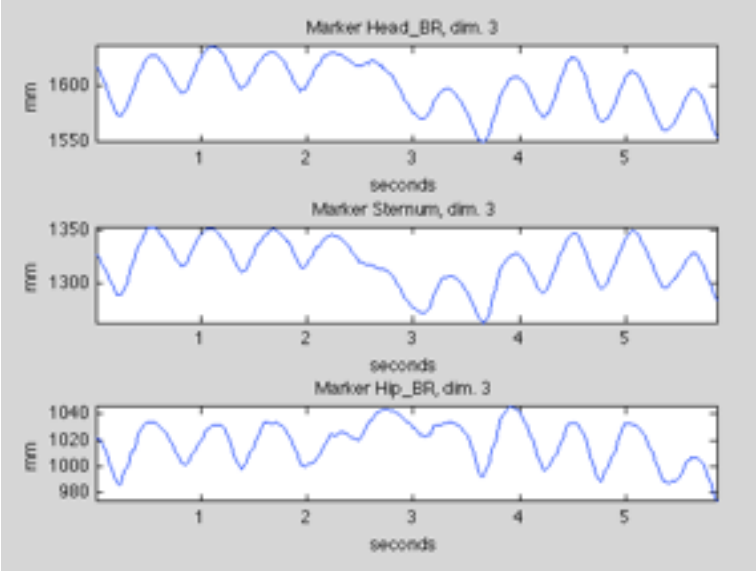
```
mcplottimeseries(walk1, [4 8 12], ‘dim’, 3, ‘timetype’, 'frame')
% markers 4,8, & 12, dimension 3, frames on x-axis
```



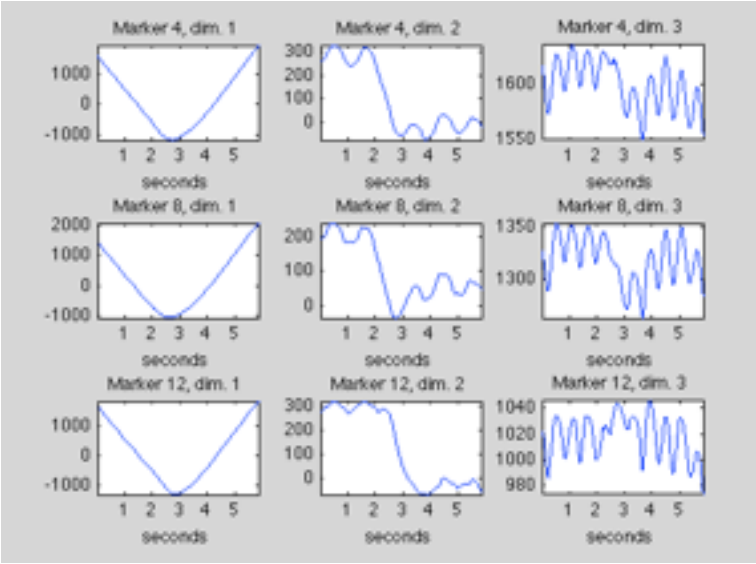

```
mcplottimeseries(walk1, [4 8 12], ‘dim’, 3, ‘plotopt’, ‘comb’)
% markers 4, 8, & 12, dimension 3, combined into one plot
```




```
mcplottimeseries(walk1, [4 8 12], 'dim', 3, 'label', 'mm', 'names', 1)
% markers 4, 8, & 12, dimensions 1:3, label on y-axis set, marker names in-
stead of numbers
```




```
mcplottimeseries(walk1, {'Head_BR', 'Sternum', 'Hip_BR'}, ‘dim’, 1:3)
% using marker names instead of numbers in function call, dimensions 1:3
```



Marker locations in single frames can be plotted using the function `mcplotframe`. This function plots the (x,z) projection of the markers:

```
mcplotframe(walk1, 160);
```

Because the parameter structure was not given in the previous call, the function used the default settings for the animation parameters:

```
mcinitanimpar
ans =
            type: 'animpar'
         scrsize: [800 600]
          limits: []
              az: 0
              el: 0
           msize: 12
          colors: 'kwwww'
    markercolors: []
      conncolors: []
     tracecolors: []
    numbercolors: []
          cwidth: 1
          twidth: 1
            conn: []
           conn2: []
             trm: []
             trl: 0
        showmnum: 0
         numbers: []
```

```
            showfnum: 0
             animate: 0
                 fps: 30
              output: 'tmp'
         videoformat: 'avi'
        createframes: 0
           getparams: 0
         perspective: 0
                pers: [1x1 struct]
```

To obtain a visualisation that is easier to understand, the markers should be connected. The variable `mapar` contains, among other things, the connection matrix:

```
mapar
mapar =
                type: 'animpar'
             scrsize: [400 300]
              limits: []
                  az: 0
                  el: 0
               msize: 6
              colors: 'kwwww'
        markercolors: []
          conncolors: []
         tracecolors: []
        numbercolors: []
              cwidth: 1
              twidth: 1
                conn: [43x2 double]
               conn2: []
                 trm: []
                 trl: 0
             showmnum: 0
              numbers: []
             showfnum: 0
```

```
            animate: 0
                fps: 30
             output: 'tmp'
        videoformat: 'avi'
       createframes: 0
          getparams: 0
        perspective: 0
               pers: [1x1 struct]
```

The connection matrix is in the field `.conn`:

```
mapar.conn'
ans =
  Columns 1 through 10
     1     2     3     3     5     9    10    11    11     8
     2     4     4     1     6    10    12    12     9     9
  Columns 11 through 20
     8     8     8     5     5     6     6     7     7     7
    10     5     6     9    11    10    12    11    12     5
  Columns 21 through 30
     7     5    13    13    16    15     6    14    14    17
     6    13    15    16    19    19    14    17    18    20
  Columns 31 through 40
    18     9    11    10    12    21    23    25    26    22
    20    21    21    22    22    23    25    26    23    24
  Columns 41 through 43
    24    27    28
    27    28    24
```

It also has a smaller screen size than the default:

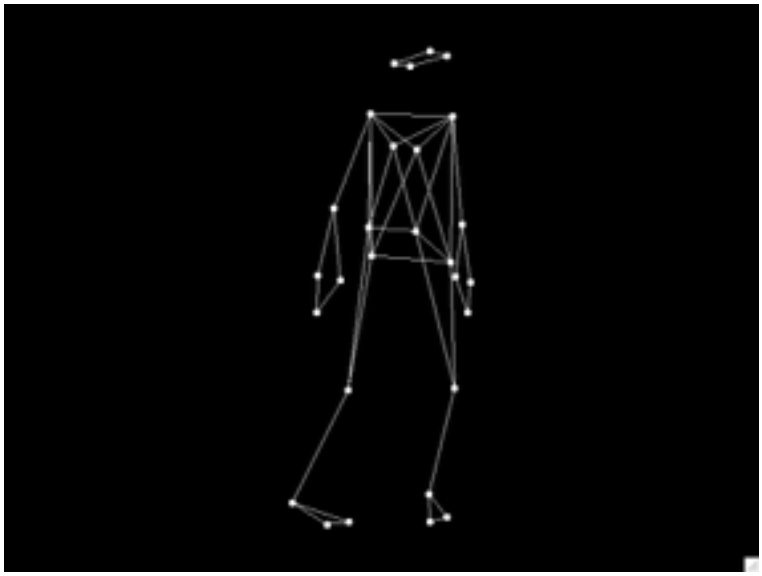
```
mapar.scrsize
ans =
   400   300
```

For the purpose of making the frame plots look nicer on this manual, let us increase the screen size:

```
mapar.scrsize = [800 600];
```

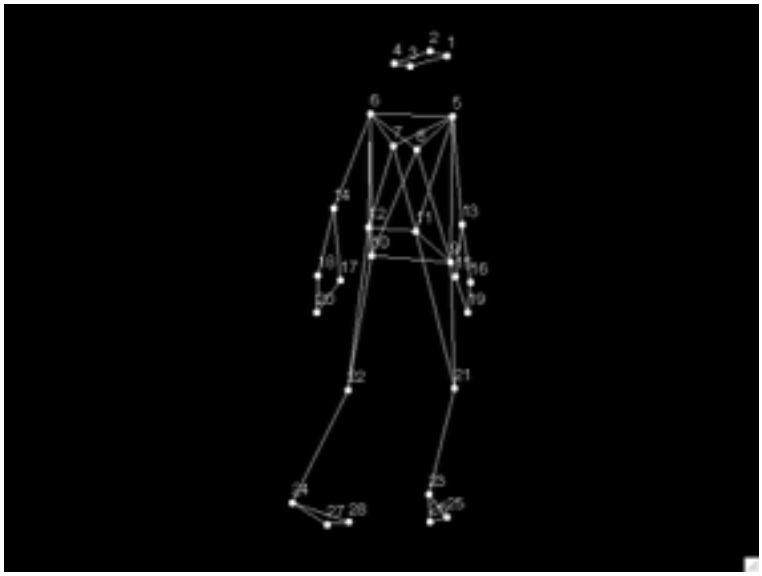
Using the parameter structure `mapar`, we get the following visualization:

```
mcplotframe(walk1, 160, mapar);
```



We can add marker numbers to the plot by setting the field `.showmnum` to have the value 1:

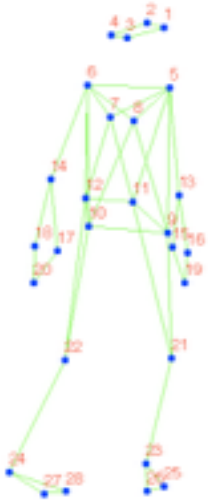
```
mapar.showmnum = 1;
mcplotframe(walk1, 160, mapar);
```



Different colors can be used by changing the value of the field `.colors`:

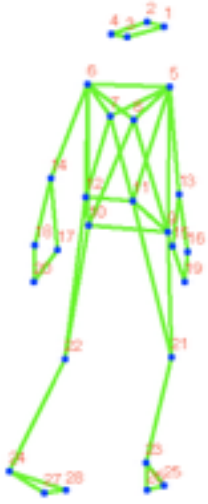
```
mapar.colors='wbgcr';
mcplotframe(walk1, 160, mapar);
```

Changing individual marker, connector, and number colors is explained in section Colored animations.



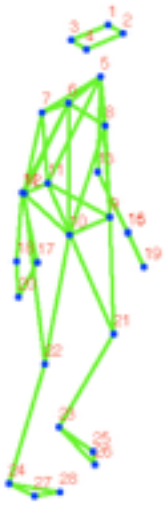
The connector widths and marker sizes can be adjusted by changing the values of the fields `.cwidth` and `.msize`, respectively:

```
mapar.cwidth = 3;
mapar.msize=6;
mcplotframe(walk1, 160, mapar);
```



The viewing azimuth and elevation can be changed by changing the values of the fields `.az` and `.el`, respectively:

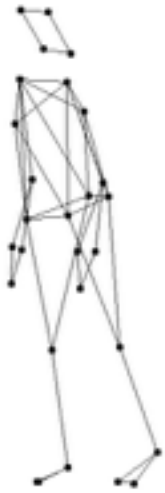
```
mapar.az = 45;
mapar.el = 20;
mcplotframe(walk1, 160, mapar);
```



Transforming MoCap data (mcdemo2)

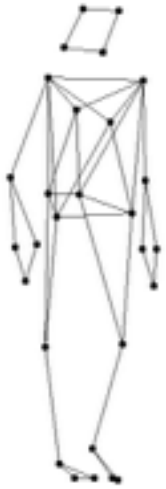
This example shows how you can do various coordinate transformations to MoCap data and merge data collected at different motion capture sessions. Let us plot a motion-capture frame:

```
load mcdemodata
mapar.scrsize=[800 600];
mapar.colors = 'wkkkk';
mcplotframe(dance1, 50, mapar);
```



Let us next rotate the data contained in the variable `dance1` by 90 degrees counterclockwise around the z (vertical) axis and plot the same frame:

```
d1rot1 = mcrotate(dance1, 90, [0 0 1]);
mcplotframe(d1rot1, 50, mapar);
```



Next, let us rotate the data in `dance1` by 90 degrees counterclockwise around the x axis:

```
d1rot2 = mcrotate(dance1, 90, [1 0 0]);
mcplotframe(d1rot2, 50, mapar);
```

Finally, let us rotate the data in `dance1` by 90 degrees counterclockwise around the y axis:

```
d1rot3 = mcrotate(dance1, 90, [0 1 0]);
mcplotframe(d1rot3, 50, mapar);
```

To add data from several *MoCap data structures* to one visualization, the functions `mctranslate` and `mcmerge` are useful:

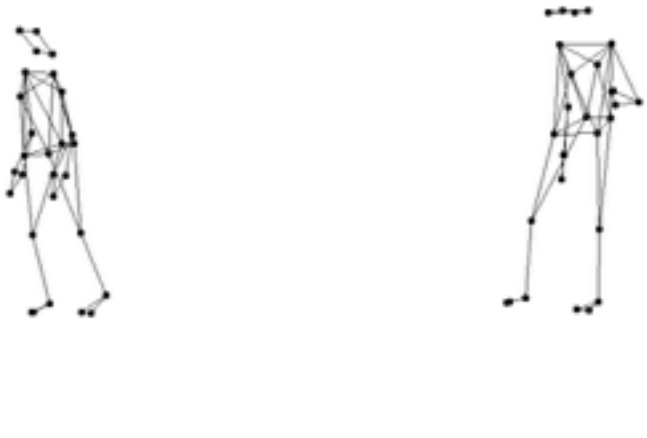
```
all = dance1;
% translate 'd1rot1' 2000 mm to the right and merge with 'all'
% merge also the parameter structures
[all, allparams] = mcmerge(all, mctranslate(d1rot1, [2000 0 0]),...
 mapar, mapar);
% Same with 'd1rot2' and 'd1rot3', but with different translations
[all, allparams] = mcmerge(all, mctranslate(d1rot2, [0 0 2000]),...
 allparams, mapar);
[all, allparams] = mcmerge(all, mctranslate(d1rot3, [2000 0 2000]),...
 allparams, mapar);
```

Next, let us plot one frame from the merged data:

```
allparams.msize=6;
mcplotframe(all, 50, allparams);
```

Let us now take excerpts from the variables `dance1` and `dance2` and merge them for visualization

```
d1 = mctrim(dance1, 0, 2);
d2 = mctrim(dance2, 0, 2);
d2 = mctranslate(d2, [2000 0 0]);
[d, par] = mcmerge(d1, d2, mapar, mapar);
mcplotframe(d, 60, par);
```



Several frames can be plotted with one command by using a vector as the second parameter

```
mcplotframe(d, 1:10:71, par);
```

(In Matlab the frames will be plotted as separate figures.)

Chapter *Creating Animations* explains how these frames can be used to create an animation.

Kinematic analysis (mcdemo3)

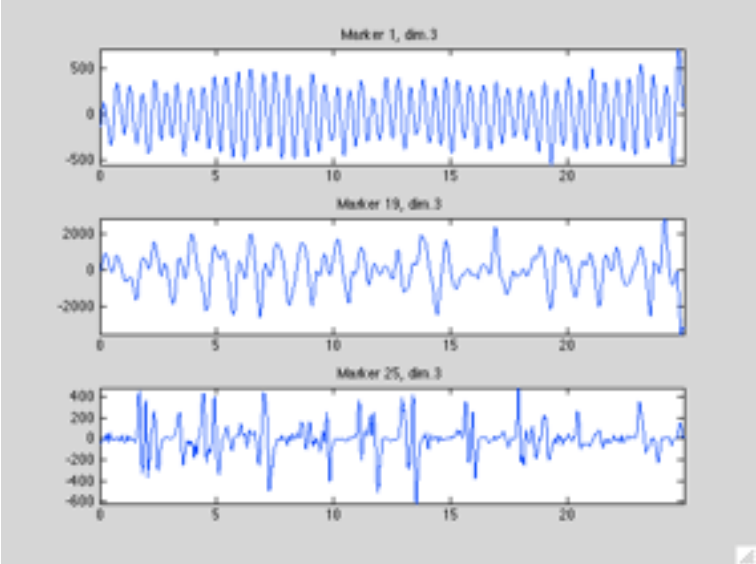
This example shows how you can estimate kinematic variables from MoCap data and visualize them.

Time derivatives of motion-capture data can be estimated using the function `mctimeder`:

```
load mcdemodata
d2v = mctimeder(dance2, 1); % velocity
d2a = mctimeder(dance2, 2); % acceleration
```

Let us have a look at the vertical velocity component of markers 1, 19, and 25 (left front head, left hand, and left foot):

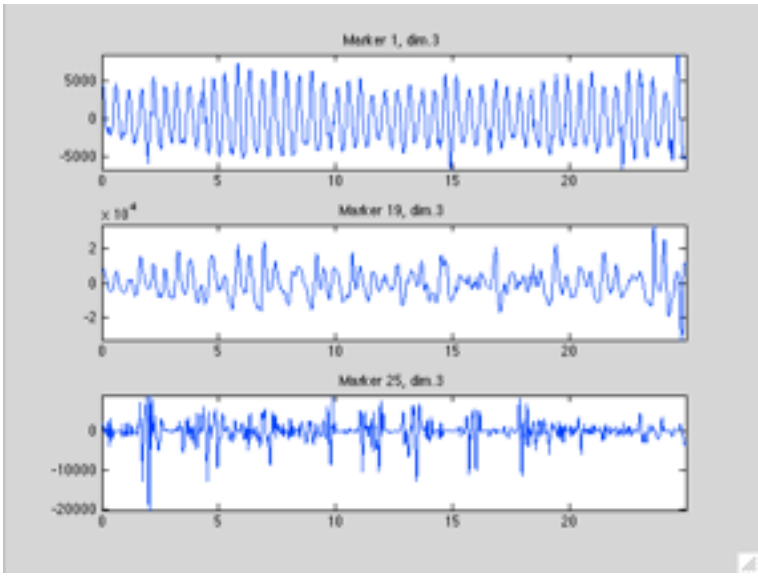
```
mcplottimeseries(d2v, [1 19 25], 'dim', 3)
```



The subplots display the vertical velocities of markers 1, 19, and 25, from top to bottom.

Next, let us plot the vertical acceleration components of the same markers:

```
mcplottimeseries(d2a, [1 19 25], 'dim', 3)
```



The phase plane plots for velocity and acceleration can be produced as follows:

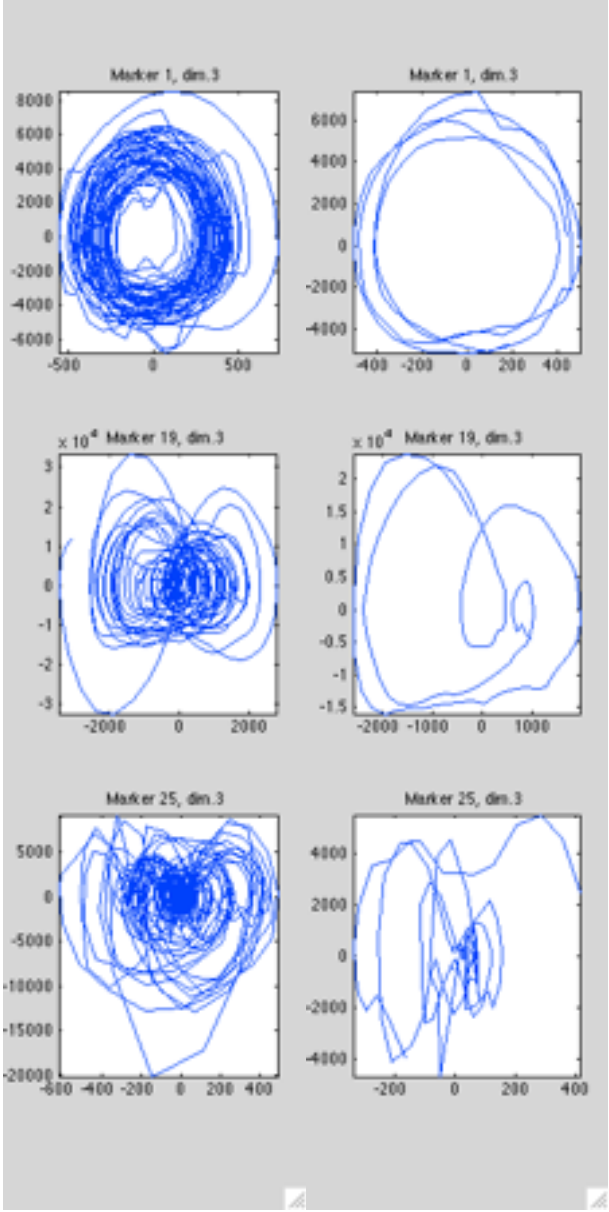
```
figure, set(gcf,'Position',[40 40 200 800])
% change the shape of the figure to make the subplots rectangular
mcplotphaseplane(d2v, d2a, [1 19 25], 3)
```

This figure is below on the left.

The same phase plane plot, but for the interval between 5 and 7 seconds can be produced as follows:

```
mcplotphaseplane(mctrim(d2v,5,7), mctrim(d2a,5,7), [1 19 25], 3)
```

This figure is below on the right.

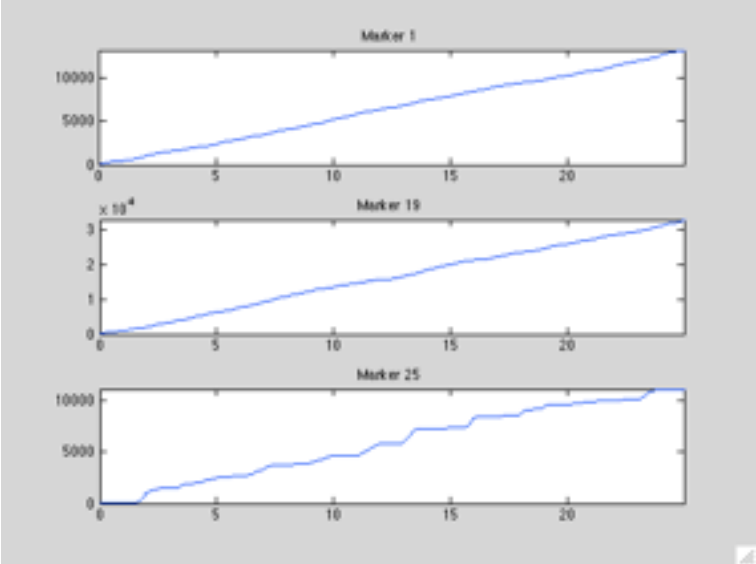


The cumulative distance tavelled by a marker can be calculated with the function `mccumdist`.

```
d2dist=mccumdist(dance2);
```

Let us have a look at the distance travelled by markers 1, 19, and 25 (left front head, left hand, and left foot):

```
mcplottimeseries(d2dist, [1 19 25])
```



As we can see, the head has travelled ca. 13 meters, the hand ca. 33 meters, and the foot ca. 11 meters.

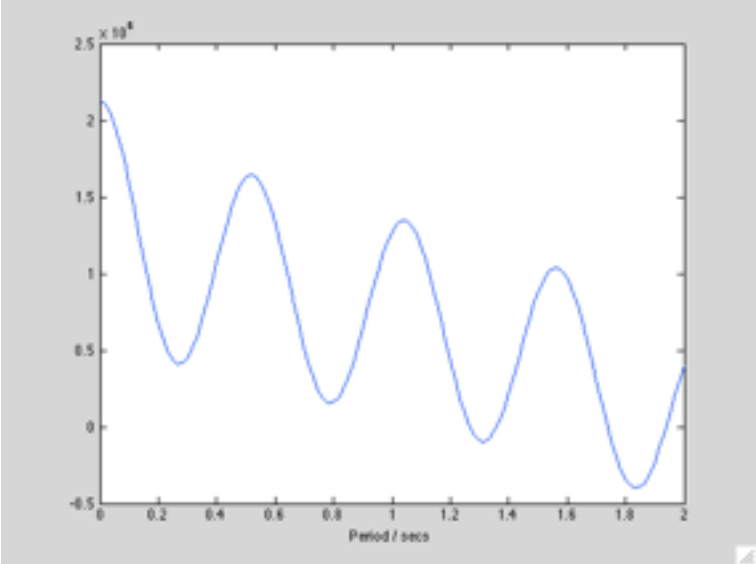
Periodicity of movement can be estimated using the function `mcperiod`. Let us estimate the periodicity of the movement of marker 1 (left front head) in the three dimensions.

```
d2m1 = mcgetmarker(dance2, 1);
[per, ac, eac, lag] = mcperiod(d2m1, 2); % maximal period=2 sec

per
per =
       NaN       NaN    0.5167
```

There is thus no periodic movement along the horizontal dimensions (dimensions 1 and 2), but a period of 0.51 seconds in the vertical direction.

The autocorrelation function for the vertical location of marker 1 looks like this:

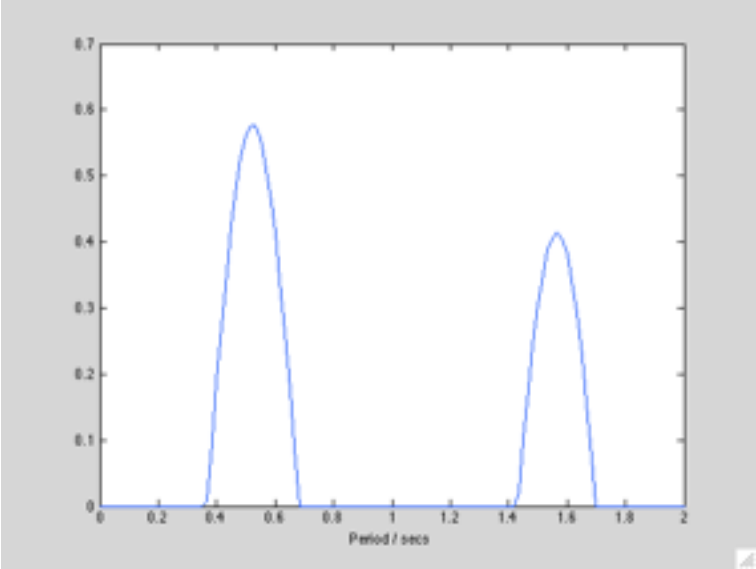
```
plot(lag, ac(:,3)), xlabel('Period / secs')
```



The first maximum at non-zero lag can be found at 0.51 secs, corresponding to the previous result.

The enhanced autocorrelation function for the same data looks like this:

```
plot(lag, eac(:,3)), xlabel('Period / secs')
```



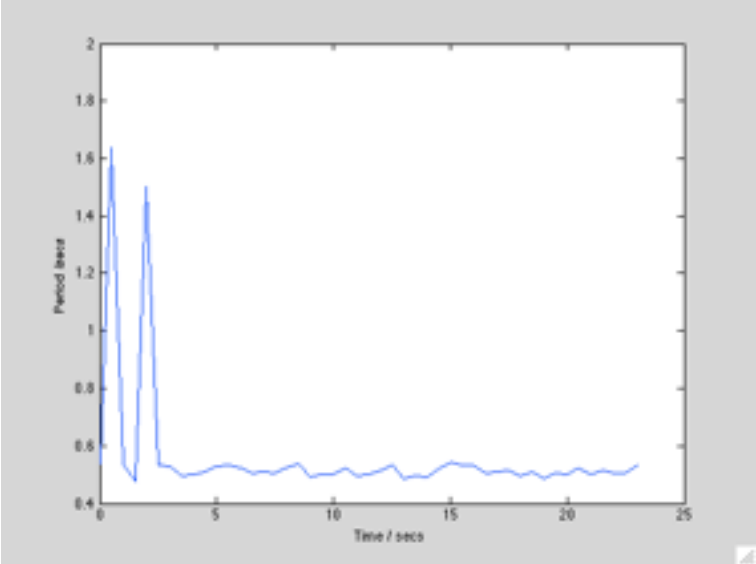
Again, there is a clear maximum at the period of 0.51 secs.

More accurate periodicity analysis can be done using windowed autocorrelation:

```
[per, ac, eac, lags, wtime] = mcwindow(@mcperiod, d2m1, 2, 0.25);
```

Let us plot the periodicity estimates for the vertical dimension for each of the windows

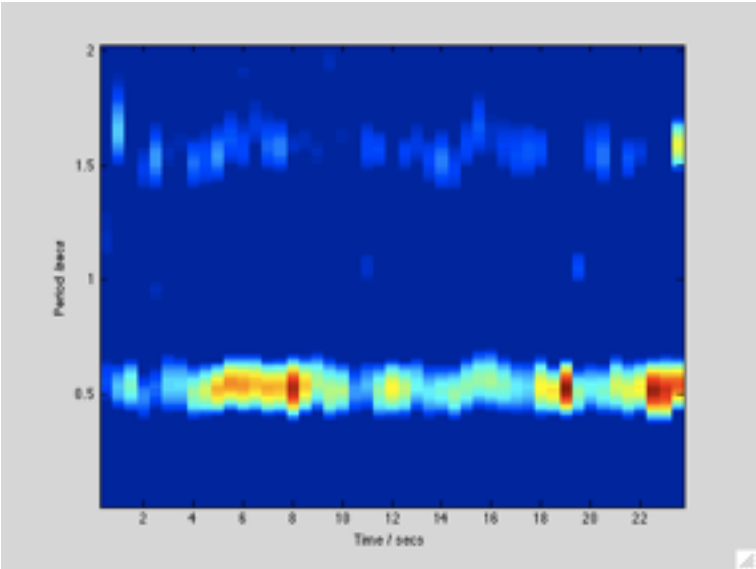
```
plot(wtime, per(:,3))
xlabel('Time / secs')
ylabel('Period /secs')
```



After displaying some initial transients, the period settles at the vicinity of 0.5 secs.

The enhanced autocorrelation matrix can be plotted as an image to allow visual inspection of the time development of periodicity. The colors provide an indication of the regularity of periodic movement, with warm colors corresponding to regions of highly regular periodic movement.

```
imagesc(eac(:,:,3)), axis xy
set(gca,'XTick',0:4:46)
set(gca,'XTickLabel',0.5*(0:4:46))
set(gca,'YTick',[0 30 60 90 120])
set(gca,'YTickLabel',[0 0.5 1 1.5 2.0])
xlabel('Time / secs')
ylabel('Period /secs')
```



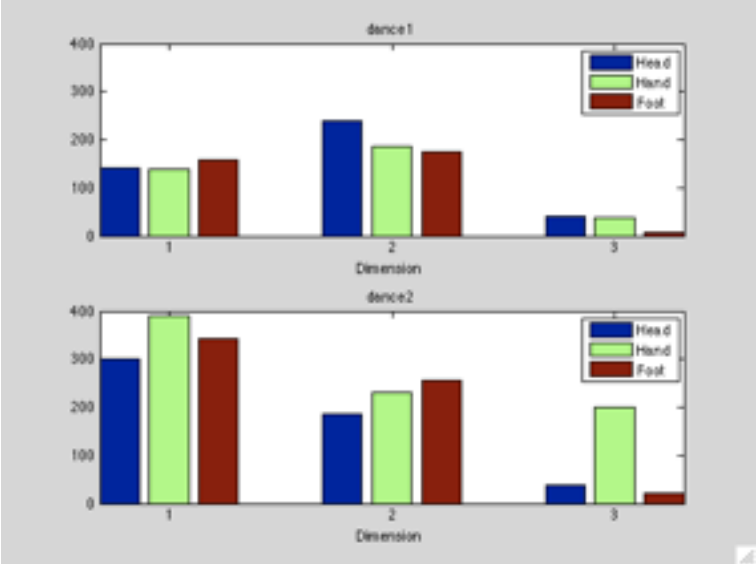
Time-series analysis (mcdemo4)

This example shows how you can perform various statistical analyses on time-series data using the functions provided in the MoCap toolbox.

The first statistical moments, mean, standard deviation, skewness, and kurtosis, can be calculated using the functions `mcmean`, `mcstd`, `mcskewness`, and `mckurtosis`, respectively. These functions ignore eventual missing frames. The function `mcstatmoments` can be used to calculate these statistical moments with one function call.

Standard deviations provides a measure for the extent of movement. Let us calculate the standard deviations for the markers 1, 19, and 25 (left front head, left hand, and left foot) in the *MoCap data structures* `dance1` and `dance2`:

```
load mcdemodata
std1 = mcstd(mcgetmarker(dance1, [1 19 25]));
std2 = mcstd(mcgetmarker(dance2, [1 19 25]));
figure, set(gcf,'Position',[40 200 560 420])
subplot(2,1,1)
bar(reshape(std1,3,3)), xlabel('Dimension')
legend('Head', 'Hand', 'Foot'), axis([-Inf Inf 0 400])
title('dance1')
subplot(2,1,2)
bar(reshape(std2,3,3)), xlabel('Dimension')
legend('Head', 'Hand', 'Foot'), axis([-Inf Inf 0 400])
title('dance2')
```

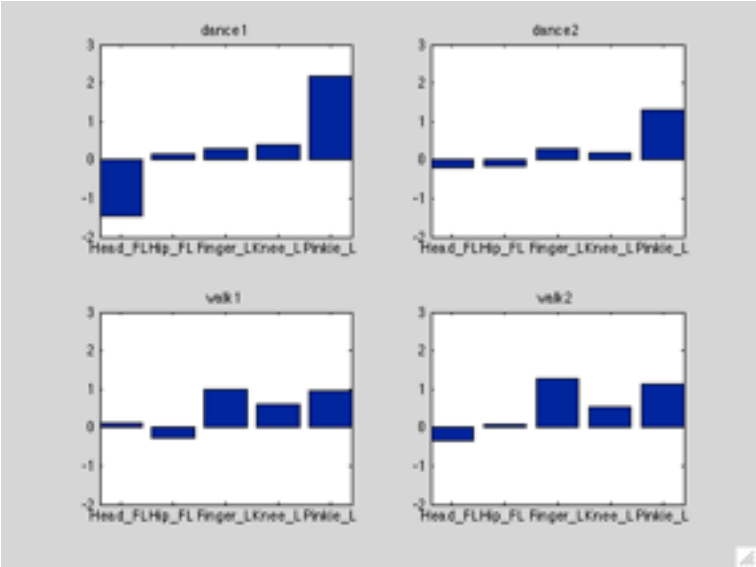


The standard deviations for the dimensions 1 and 2 are larger for `dance1` than for `dance2`, suggesting that dancer 1 occupies a larger area horizontally. The standard deviation for dimension 3 for the hand marker is larger for `dance1`, suggesting that dancer 1 uses larger vertical hand movements than dancer 2.

Let us calculate and plot the skewness values for the vertical dimension of selected markers in variables `dance1, dance2, walk1` and `walk2`.

```
marker = [1 9 19 21 25];
d1skew = mcskewness(mcgetmarker(dance1, marker));
w1skew = mcskewness(mcgetmarker(walk1, marker));
d2skew = mcskewness(mcgetmarker(dance2, marker));
w2skew = mcskewness(mcgetmarker(walk2, marker));
mn = mcgetmarkername(dance1);
subplot(2,2,1)
bar(d1skew(3:3:end)), set(gca,'XTickLabel', [mn{marker}])
title('dance1'), axis([-Inf Inf -2 3])
subplot(2,2,2)
bar(d2skew(3:3:end)), set(gca,'XTickLabel', [mn{marker}])
title('dance2'), axis([-Inf Inf -2 3])
subplot(2,2,3)
bar(w1skew(3:3:end)), set(gca,'XTickLabel', [mn{marker}])
title('walk1'), axis([-Inf Inf -2 3])
subplot(2,2,4)
```

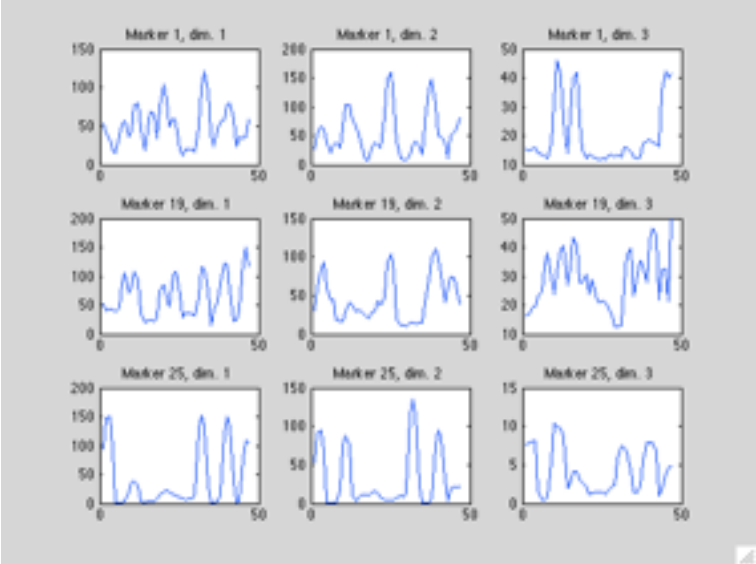
```
bar(w2skew(3:3:end)), set(gca,'XTickLabel', [mn{marker}])
title('walk2'), axis([-Inf Inf -2 3])
```



There are some differences between dancing and walking with respect to the skewness values. The interpretation of these differences will be left to the user.

Windowed analysis of the statistical time-series descriptors can be carried out using the `mcwindow` command. Let us compute the windowed standard deviation of markers 1, 19, and 25 (left front head, left hand, and left foot) in the variable `dance1`:

```
marker = [1 19 25];
d1std=mcwindow(@mcstd, mcgetmarker(dance1, marker), 2, 0.25);
for k=1:9
 subplot(3,3,k), plot(d1std(:,k)),
 title(['Marker ' num2str(marker(1+floor((k-1)/3)))...
 ', dim. ' num2str(1+rem(k-1,3))])
end
```



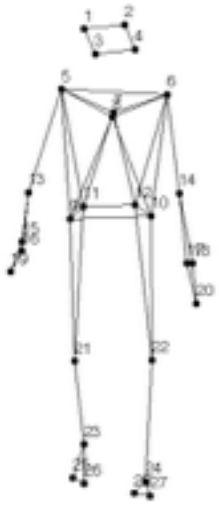
High values in these graph correspond to temporal regions where the particular marker shows wide movements for the respective dimension.

Kinetic analysis (mcdemo5)

This example shows how the toolbox can be used to calculate kinetic variables from MoCap data using Dempster's body-segment model.

Let us estimate various forms of mechanical energy in walking movement (variable `walk1`). To start with, we plot a MoCap frame with marker numbers:

```
load mcdemodata
mapar.colors = 'wkkkk';
mapar.showmnum = 1;
mapar.msize=6;
mapar.az=90;
mcplotframe(walk2,160, mapar);
```



The first thing to do is to reduce the set of markers to make the data compatible with Dempster's model. This can be accomplished using the marker-to-joint transformation, implemented in function `mcm2j`. The parameters needed for this conversion are in the variable `m2jpar`:

```
m2jpar
m2jpar =

          type: 'm2jpar'
       nMarkers: 20
     markerNum: {1x20 cell}
    markerName: {1x20 cell}
```

The information concerning which markers correspond to each joint is contained in the field `m2jpar.markerNum`. The names of the new joints are in `m2jpar.markerName`. For instance, ...

```
m2jpar.markerName{1}
ans =
root

m2jpar.markerNum{1}
ans =
     9    10    11    12
```

... the joint 'root' is obtained by calculating the centroid of markers 9, 10, 11 and 12

The marker-to-joint conversion is carried out as follows:

```
walk2j = mcm2j(walk2, m2jpar)
```

```
walk2j =
            type: 'MoCap data'
        filename: '25-Walking.tsv'
         nFrames: 401
        nCameras: 8
        nMarkers: 20
            freq: 60
         nAnalog: 0
         anaFreq: 0
    timederOrder: 0
      markerName: {1x20 cell}
            data: [401x60 double]
      analogdata: []
           other: [1x1 struct]
```

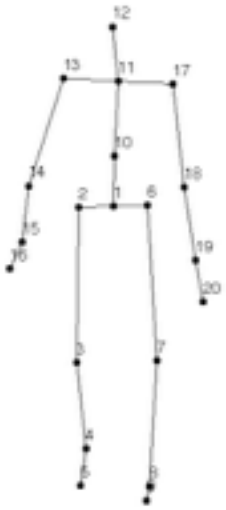
The parameters for the visualization of the joint representation are in the variable `japar`:

```
japar
japar =
            type: 'animpar'
         scrsize: [400 300]
          limits: []
              az: 0
              el: 0
           msize: 6
         colors: 'kwwww'
    markercolors: []
      conncolors: []
     tracecolors: []
    numbercolors: []
          cwidth: 1
          twidth: 1
            conn: [19x2 double]
           conn2: []
             trm: []
             trl: 0
```

```
        showmnum: 0
        numbers: []
        showfnum: 0
         animate: 0
             fps: 30
          output: 'tmp'
     videoformat: 'avi'
    createframes: 0
       getparams: 0
     perspective: 0
            pers: [1x1 struct]
```

Let us visualize a frame from the new variable `walk2j` with marker numbers visible:

```
japar.colors = 'wkkkk';
japar.scrsize = [800 600];
japar.showmnum = 1;
japar.msize=6;
japar.az=90;
mcplotframe(walk2j,160, japar);
```



The next step is to make a joint-to-segment transformation. The parameters needed for the transformation are in the variable `j2spar`:

```
j2spar =
            type: 'j2spar'
      rootMarker: 1
```

```
    frontalPlane: [6 2 10]
          parent: [0 1 2 3 4 1 6 7 8 1 10 11 11 13 14 15 11 17 18 19]
     segmentName: {1x19 cell}
```

The transformation can be accomplished using the function `mcj2s`:

```
walk2s = mcj2s(walk2j, j2spar)
```

The parameters for each body segment can be obtained using the function `mcgetsegmpar`:

```
segmindex = [0 0 8 7 6 0 8 7 6 13 12 10 11 3 2 1 11 3 2 1];
spar = mcgetsegmpar('Dempster', segmindex);
```

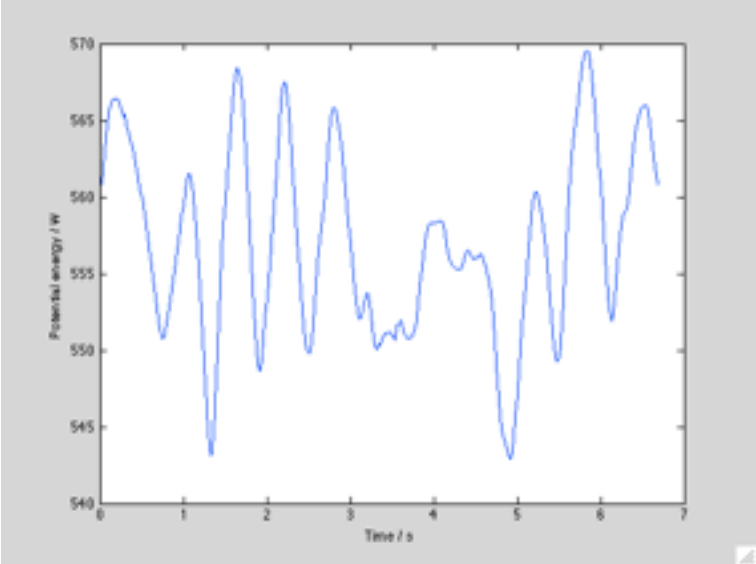
The second argument in the function call, `segmindex`, associates each joint in `walk1j` and `walk1s` with a segment type. The numbers refer to the distal joint of the respective segment. Joints that are not distal to any segment have zero values. Segment number values for model 'Dempster' are as follows: no parameter=0, hand=1, forearm=2, upper arm=3, forearm and hand=4, upper extremity=5, foot=6, leg=7, thigh=8, lower extremity=9, head=10, shoulder=11, thorax=12, abdomen=13, pelvis=14, thorax and abdomen=15, abdomen and pelvis=16, trunk=17, head, arms and trunk (to glenohumeral joint)=18, head, arms and trunk (to mid-rib)=19. For instance, the third component, 8, tells that the body segment whose distal joint is joint number 3, is a 'thigh'.

Now that we have a body-segment representation of the movement, we can estimate various kinetic variables. The potential energy for each body segment can now be calculated as follows:

```
pot = mcpotenergy(walk2j, walk2s, spar);
```

The resulting variable `pot` is a matrix where each column corresponds to one of the body segments. Let us plot the total potential energy as a function of time:

```
time = (1:walk2.nFrames)/walk2.freq;
plot(time, sum(pot,2))
xlabel('Time / s')
ylabel('Potential energy / W')
```



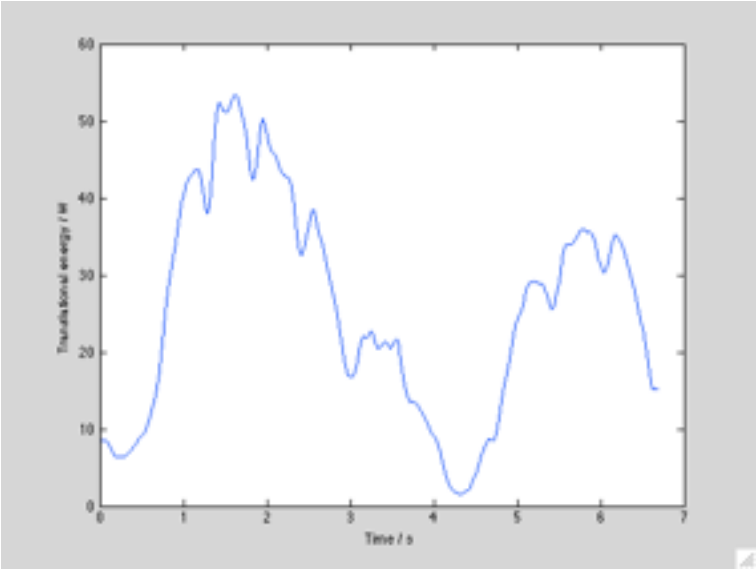
We can see a relatively regularly oscillating pattern, with the exception of the region between 3.0 and 4.5 seconds, where the walker turns around.

The translational and rotational energy for each body segment can be calculated as follows:

```
[trans, rot] = mckinenergy(walk2j, walk2s, spar);
```

Let us plot the total translational energy:

```
plot(time, sum(trans,2))
xlabel('Time / s')
ylabel('Translational energy / W')
```



We can observe a region of low translational energy in the region between 3.0 and 4.5 seconds, where the walker is turning.

Creating animations (mcdemo6 - mcdemo9)

Basics (mcdemo6)

This example shows how you can create animations with the MoCap toolbox.

You can either produce an animation video (.avi or .mp4 format) or animation frames (single .png files) with the MoCap toolbox. The frames would have to be compiled into a movie using some other software. On a Macintosh you can use, for instance, the QuickTime Pro software. Should you happen to use the Windows operating system, you can use, for instance the Movie Maker software.

Let us create an animation from the variable `walk2`. The *animpar* structure `mapar` contains the connector information for this variable:

```
load mcdemodata
mapar
mapar =
            type: 'animpar'
          scrsize: [400 300]
           limits: []
               az: 0
               el: 0
            msize: 6
           colors: 'kwwww'
      markercolors: []
        conncolors: []
       tracecolors: []
      numbercolors: []
           cwidth: 1
           twidth: 1
             conn: [43x2 double]
            conn2: []
              trm: []
              trl: 0
         showmnum: 0
          numbers: []
         showfnum: 0
```

```
          animate: 0
              fps: 30
           output: 'tmp'
      videoformat: 'avi'
     createframes: 0
        getparams: 0
      perspective: 0
             pers: [1x1 struct]
```

Let us change the frames-per-second value to 15

```
mapar.fps = 15;
```

The animation will be stored into the current directory with the filename `tmp.avi`. If needed, the current directory should be changed before creating the animation.

The animation is produced as follows:

```
newpar = mcanimate(walk2, mapar);
```

If you wish to plot consecutive frames (png files) instead of creating a video file, set the animation parameter `createframes` to 1:

```
mapar.createframes = 1;
```

You will then find the png files in a folder called `tmp` in the current directory.

Merging data for animations (mcdemo7)

The next example shows how MoCap data from different sessions can be combined into the same animation. It also shows how the viewing angle can be changed dynamically. Let us create a 10-second animation with two dancers and a dynamically moving viewing angle. The variable `dance1` has some missing frames, so we shall fill them first.

```
dance1 = mcfillgaps(dance1);
```

Next, we extract the first ten seconds from the variables `dance1` and `dance2`:

```
d1 = mctrim(dance1, 0, 10);
d2 = mctrim(dance2, 0, 10);
```

We make the viewing azimuth change dynamically from zero to 180 degrees and the elevation angle from 45 to -45 degrees during the animation:

```
mapar.az = [0 180];
mapar.el = [45 -45];
```

We set the movie to have 15 frames per second and give a name for the file:

```
mapar.fps = 15;
mapar.output = 'twodancers';
```

The next step is to translate the data in `d2` by two meters to the right and merge this with the data in `d1`:

```
[d, par] = mcmerge(d1, mctranslate(d2, [2000 0 0]), mapar, mapar);
```

Next, if needed, we change the current directory. Now we are ready to create the animation frames.

```
newpar = mcanimate(d, par);
```

There should be now a file called `twodancers.avi` in the current directory.

Colored animations (mcdemo8)

This example shows how to color plots and animations.

We will create a colored animation from the variable `dance2`. The animpar structure `mapar` looks like this:

```
load mcdemodata
mapar
mapar =
            type: 'animpar'
         scrsize: [400 300]
          limits: []
              az: 0
              el: 0
           msize: 6
          colors: 'kwwww'
    markercolors: []
      conncolors: []
     tracecolors: []
    numbercolors: []
          cwidth: 1
          twidth: 1
            conn: [43x2 double]
           conn2: []
             trm: []
```

```
            trl: 0
       showmnum: 0
        numbers: []
       showfnum: 0
        animate: 0
            fps: 30
         output: 'tmp'
    videoformat: 'avi'
   createframes: 0
      getparams: 0
    perspective: 0
           pers: [1x1 struct]
```

Let us change the frames-per-second value to 15

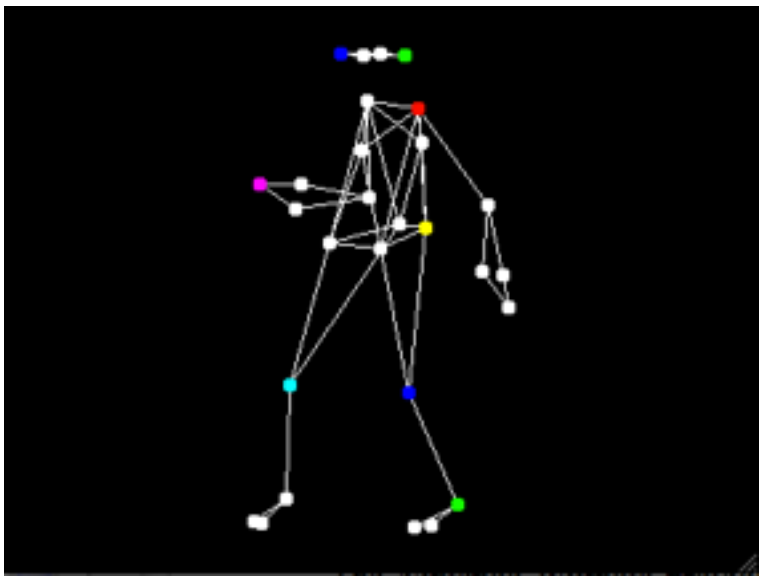
```
mapar.fps = 15;
```

Let us set individual colors for six markers (head front left, head back right, shoulder left, hip left back, finger right, knee left, knee right, heel left)

```
mapar.markercolors='bwwgwrwwwwwywwwwwwmwcbwg';
```

and let us have a look at the new colors:

```
mcplotframe(dance2, 150, mapar);
```



Now let us set the markers that we want to trace and the trace length (in seconds):

```
mapar.trm=[1 6 12 19 21 24];
```

```
mapar.trl=3;
```

And let us set individual colors for the traces:

```
mapar.tracecolors='grymcb';
```

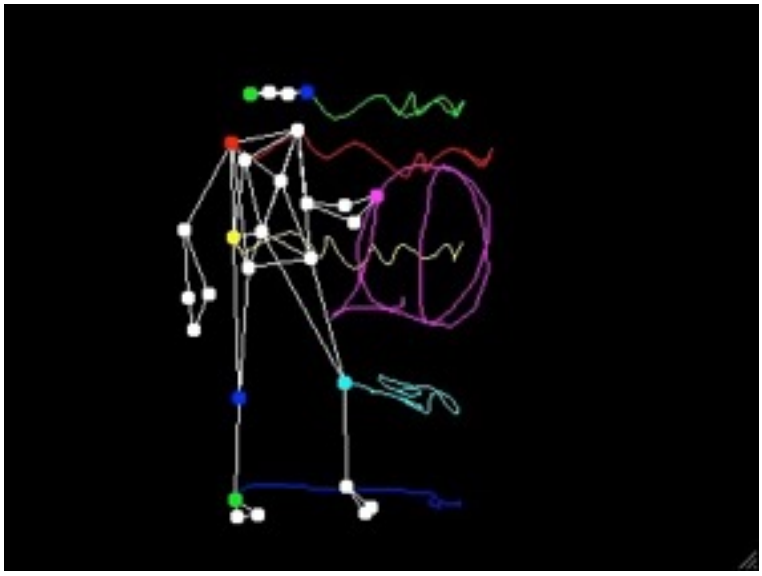
We rotate the figure to be frontal on average

```
dance2=mc2frontal(dance2,9,10);
```

Now we make the animation:

```
newpar = mcanimate(dance2, mapar);
```

For plotting a figure with traces, just select one frame that was calculated during the animation, for instance frame number 100 of `dance2`:



Perspective Projection `(mcdemo9)`

Next, the possibility of creating an animation with a perspective (three-dimensional) effect will be explained. We will create a couple of animations of the walk2 data, with and without the perspective projection to see the differences. Let us load the `mcdemodata` and change a couple of parameters of the animpar structure `mapar`

```
load mcdemodata
mapar.scrsize=[600 400];
mapar.msize=8;
mapar.fps=15;
mapar.colors='wkkkk';
```

And we also set the azimuth parameter in the animpar structure `mapar`, so that the walker will walk towards us

```
mapar.az=270;
```

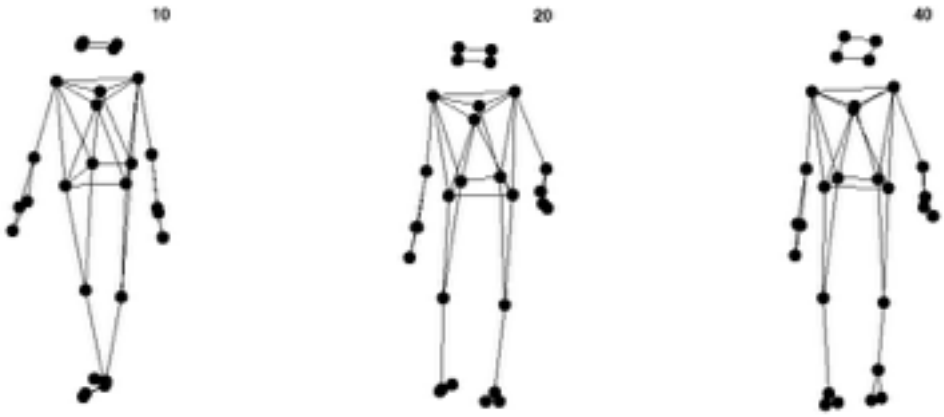
We do not want to create a video this time, but have a look at the separate frames (to better see the differences in the projection), we set the createframes parameter accordingly and re-name the default file name, which will serve as the folder name now, into which the frames (i.e., png files) are saved

```
mapar.createframes = 1;
mapar.output = 'pers0';
```

Now we create an animation out of that:

```
mcanimate(walk2, mapar);
```

If we have a look at the animation frames, the figure appears to walk on the spot, although she is actually walking forwards. As an example, have a look at the 10th, 20th, and 40th frame:



The idea of the perspective projection is to visualize that the figure is actually walking forward. To activate the perspective projection, we set the perspective parameter in the animpar structure to 1 and call the `mcanimate` function again:

```
mapar.perspective = 1;
mapar.output = 'pers1';
mcanimate(walk2, mapar);
```

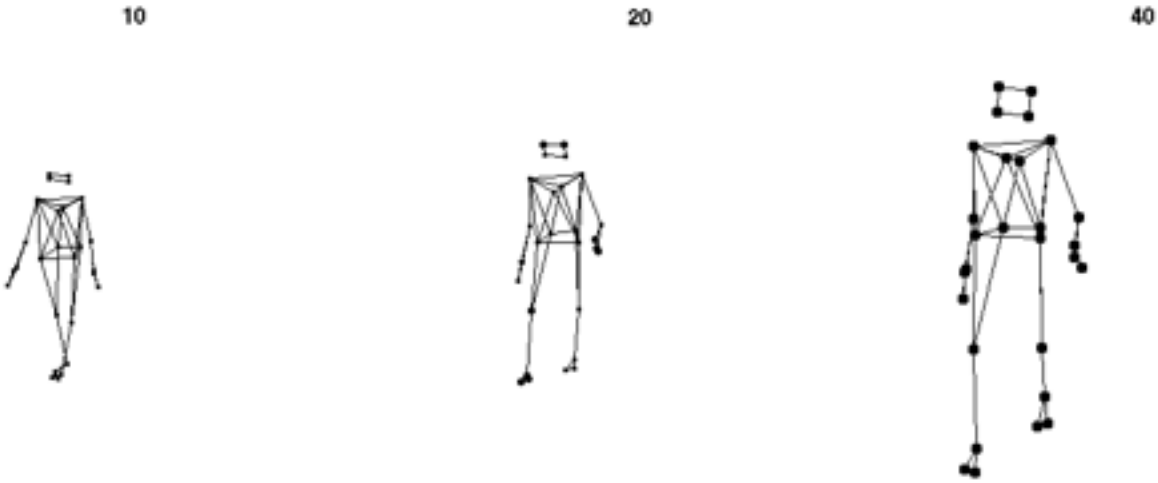
This animation looks far more natural regarding the movement direction of the walker

The parameters for the perspective projection are set in the `pers` part of the animpar structure `mapar`

```
mapar.pers
mapar.pers =
   c: [0 -4000 0]
  th: [0 0 0]
   e: [0 -2000 0]
```

The field `c` sets the 3D position of the camera, `th` is the orientation of the camera, and `e` stores the viewer's position relative to the display surface. We can now change, for example, the camera position and create another animation to see what happens.

```
mapar.pers.c = [1000 -4000 1000];
mapar.output = 'pers2';
mcanimate(walk2, mapar, 1);
```



Principal Components Analysis (mcdemo10)

Principal components analysis can be used to decompose Motion Capture data into components that are orthogonal to each other.

Let us extract the first four seconds from the structure `dance2`,

```
load mcdemodata
d=mctrim(dance2,0,4);
```

and convert it into a joint representation

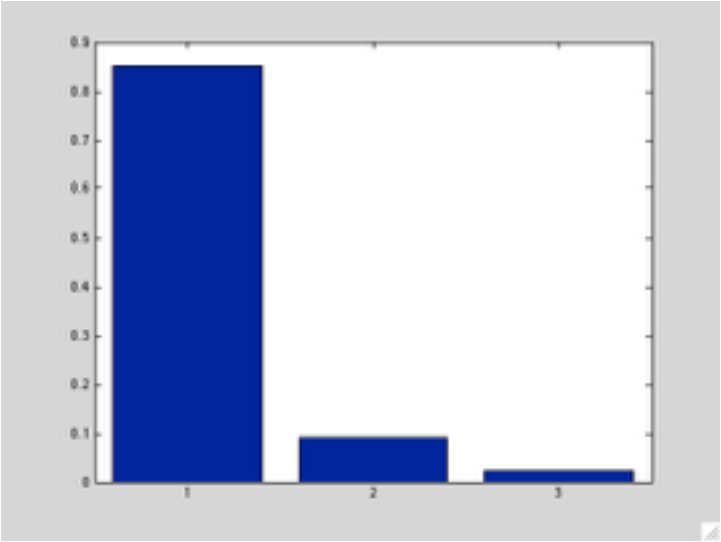
```
j=mcm2j(d, m2jpar);
```

Next, we calculate the first three principal component projections of the structure `j`,

```
[pc,p]=mcpcaproj(j,1:3);
```

and plot the amount of variance contained in these principal components.

```
bar(p.l(1:3))
```



We see that the first PC contains ca. 85% of the variance, while the next two components contain only 9% and 2%.

The PC projections can be investigated, for instance, by creating animations:

```
mcanimate(pc(1), japar);
```

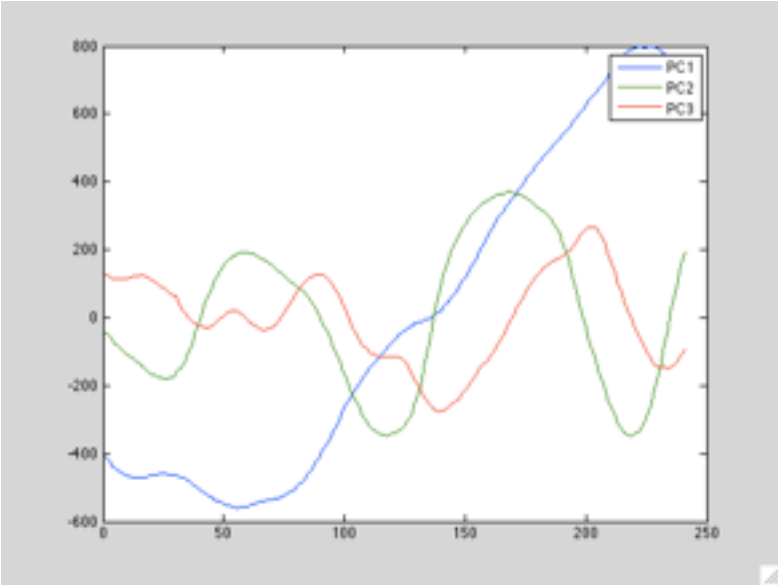
The animations show that the principal component distort the body segment relations, in particular, the lengths of certain body segments vary. Often better results can be obtained by performing the PCA on the segment representation

```
s=mcj2s(j,j2spar); % convert to segment structure
```

```
[pcs,ps]=mcpcaproj(s,1:3); % perform PCA
for k=1:3 % convert PC projections back to joint structures
    pcj(k) = mcs2j(pcs(k), j2spar);
end
```

Next, let us plot the first three PC projections:

```
plot(ps.c(1:3,:)'), legend('PC1','PC2','PC3')
```



The plot reveals that the first PC correspond to non-periodic motion, while PCs 2 and 3 correspond to (almost) periodic motion. Animation of `pcj(k)` shows that the first three PCs correspond to translation of the body, periodic anti-phase movement of arms, and periodic rotation of torso.

Analyzing Wii data (mcdemo11)

The Nintendo Wiimote provides an inexpensive means for simple motion capture. This example shows how movement data collected with the Nintendo Wii controller can be analyzed using the MoCap Toolbox.

The MoCap Toolbox supports the file format used by the WiiDataCapture software, available at www.jyu.fi/music/coe/materials.

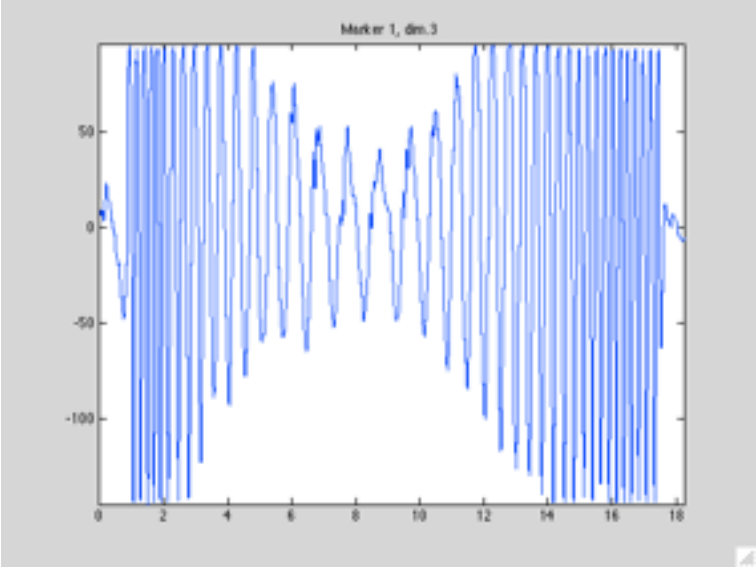
In the file `mcdemodata`, the variable `wiidata` contains acceleration data captured using the Nintendo Wii controller and the WiiDataCapture software:

```
load mcdemodata
```

```
wiidata
wiidata =
            type: 'MoCap data'
        filename: 'data.wii'
         nFrames: 1826
        nCameras: []
        nMarkers: 1
            freq: 100
         nAnalog: 0
         anaFreq: []
    timederOrder: 2
      markerName: {}
            data: [1826x3 double]
      analogdata: []
           other: []
```

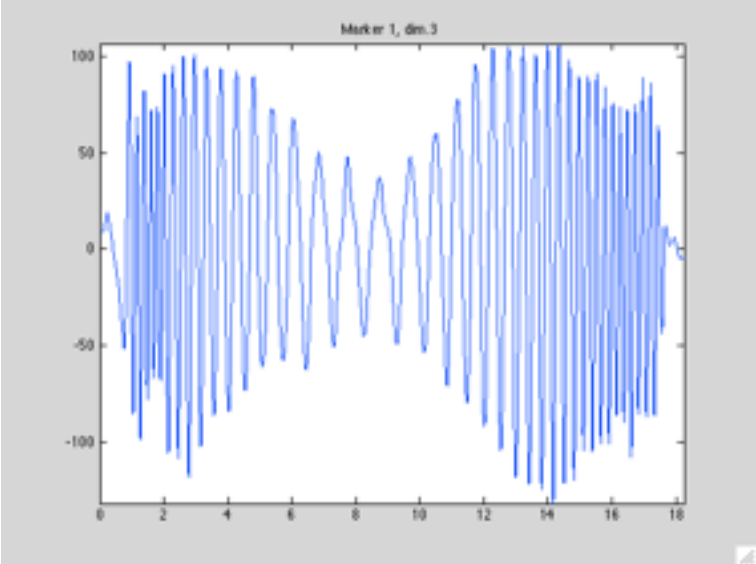
As the field `.timederOrder` indicates, this variable holds acceleration data. Let us plot the third (vertical) component of the acceleration data:

```
mcplottimeseries(wiidata,1, 'dim', 3)
```



The data is somewhat noisy, so we smoothen it a bit:

```
wd2 = mcsmoothen(wiidata,25);
mcplottimeseries(wd2,1,'dim',3)
```

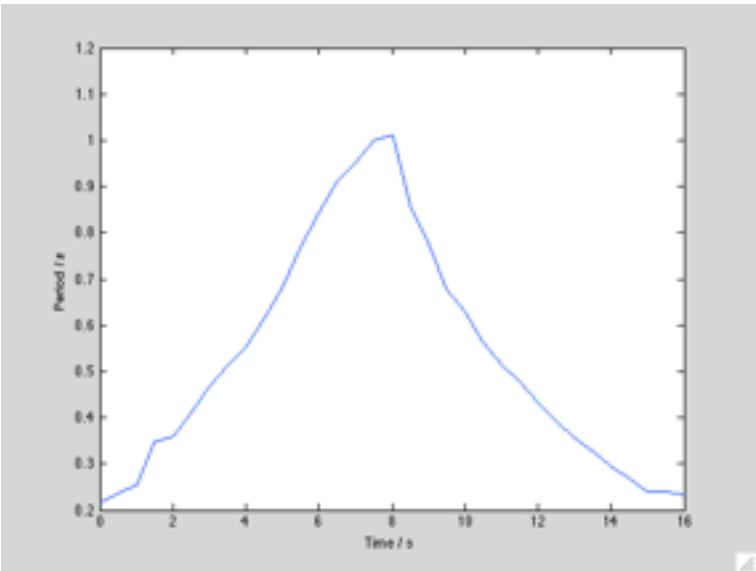


Let us do a windowed analysis of the period of this acceleration component using a window length of two seconds and a hop factor of 0.25:

```
[per, ac, eac, lags, wstart] = mcwindow(@mcperiod, wd2, 2, 0.25);
```

Next, let us plot the estimated period of the third component as a function of the starting point of the window:

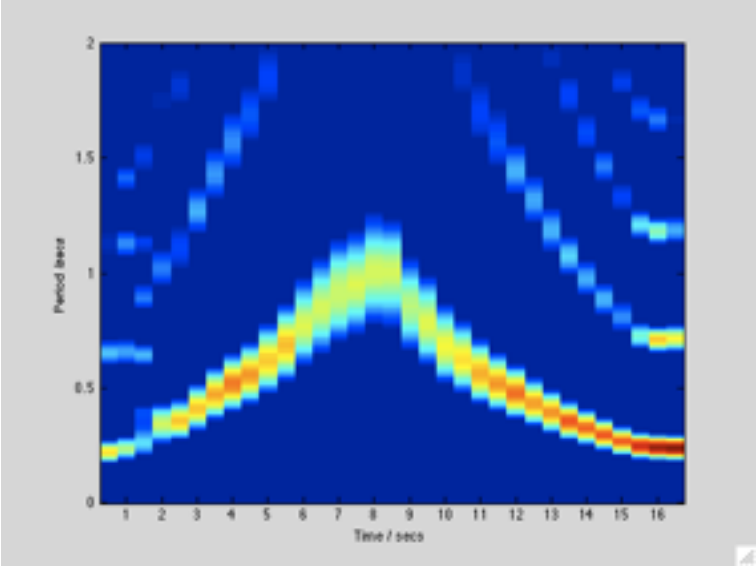
```
plot(wstart,per(:,3))
set(gcf,'Position',[40 200 560 420])
xlabel('Time / s')
ylabel('Period / s')
```



We observe a periodic motion that starts with a period of ca. 0.2 seconds, slows down to a period of ca. 1 second, and speeds again up to a period of ca. 0.2 seconds.

A similar representation can be obtained by plotting the enhanced autocorrelation image:

```
imagesc(eac(:,:,3)), axis xy
set(gcf,'Position',[40 200 560 420])
set(gca,'XTick',0:2:32)
set(gca,'XTickLabel',0.5*(0:2:32))
set(gca,'YTick',[1 51 101 151 201])
set(gca,'YTickLabel',[0 0.5 1 1.5 2.0])
xlabel('Time / secs')
ylabel('Period /secs')
```



Data and Parameter Structure Reference

MoCap data structure

synopsis

Data structure for motion capture data. Created by the function `mcread`.

structure

type: structure type ('MoCap data')
filename: name of the file from where the data were read
nFrames: number of frames
nCameras: number of cameras
nMarkers: number of markers
freq: sampling frequency (frame rate) of motion data
nAnalog: number of analog devices
anaFreq: sampling frequency of analog data
timederOrder: order of time differentiation of data (0 = location, 1 = velocity, 2 = acceleration, 3 = jerk/jolt/surge/lurch, 4 = jounce/snap, 5 = crackle, 6 = pop, 7 = you-name-it)
markerName: marker names (cell structure)
data: motion capture data (nFrames x 3nMarkers matrix)
analogdata: analog data (nFrames x nAnalog matrix)
other: other data read from the file (depends on equipment and file format used)
for mocap data read from a .tsv file, the fields are:
other.descr: some description string
other.timeStamp: some time stamp string
other.dataIncluded: '3D'

comments

see also

`mcread`

norm data structure

synopsis

Data structure for vector norms. Created by `mcnorm`.

structure

type: structure type ('norm data')
filename: name of the file from where the data were read
nFrames: number of frames
nCameras: number of cameras
nMarkers: number of markers
freq: sampling frequency (frame rate) of motion data
nAnalog: number of analog devices
anaFreq: sampling frequency of analog data
timederOrder: order of time differentiation of data (0 = location, 1 = velocity, 2 = acceleration, 3 = jerk/jolt/surge/lurch, 4 = jounce/snap, 5 = crackle, 6 = pop, 7 = you-name-it)
markerName: marker names (cell structure)
data: motion capture data (nFrames x nMarkers matrix)
analogdata: analog data (nFrames x nAnalog matrix)
other: other data read from the file (depends on equipment and file format used)

comments

The data structure is identical to MoCap data structure, except that the data field contains only one column per marker.

see also

`mcnorm`

segm data structure

synopsis

Data structure for body segment data. Created by `mcj2s`.

structure

type: structure type ('segm data')
filename: name of the file from where the data were read
nFrames: number of frames
nCameras: number of cameras
nMarkers: number of markers
freq: sampling frequency (frame rate) of motion data
nAnalog: number of analog devices
anaFreq: sampling frequency of analog data
timederOrder: order of time differentiation of data (0 = location, 1 = velocity, 2 = acceleration, 3 = jerk/jolt/surge/lurch, 4 = jounce/snap, 5 = crackle, 6 = pop, 7 = you-name-it)
analogdata: []
other: [1x1 struct]
parent: vector containing the number of the parent joint (proximal joint in kinematic chain) of each joint; zero means no parent joint
roottrans: matrix (nFrames x 3) containing the coordinates of body root
rootrot: [1x1 struct]
  rootrot.az: azimuth angle of the normal vector of the frontal plane (see the j2spar structure)
  rootrot.el: elevation angle of the normal vector of the frontal plane (see the j2spar structure)
segm: [1 x nMarkers struct]
  segm(k).eucl: euclidean vector pointing from proximal to distal joint of the segment
  segm(k).r: length of the segment (averaged over time)
  segm(k).quat: quaternion representing rotation from (0 -1 0) to segm(k).eucl
  segm(k).angle: angle between segments k and k-1
segmentName: cell structure containing the names of the segments

comments

The number of each segment is identical to the number of the marker representing the distal joint of the segment in the MoCap data structure from which the segm data structure was derived. That means the first segment is empty.

see also

`mcj2s`

m2jpar parameter structure

synopsis

Parameters for conversion from markers to joints.

structure

type: structure type ('m2jpar')
nMarkers: number of joints
markerNum: cell structure containing, for each joint, the numbers of the markers whose centroid defines the location of that joint; for instance, if markerNum{k} = [m1 m2 m3 m4], the location of joint k is calculated as the centroid of markers m1, m2, m3, and m4
markerName: cell structure containing the names of the joints

comments

see also

`mcinitm2jpar`

j2spar parameter structure

synopsis

Parameters for conversion from joints to segments.

structure

type: structure type ('j2spar')
rootMarker: number of the root joint
frontalPlane: numbers of three joints that define the frontal plane
parent: vector containing the number of the parent joint (proximal joint in kinematic chain) of each joint; zero means no parent joint
segmentName: cell structure containing the names of each segment

comments

The parent number of the root joint is zero.

see also

`mcinitj2spar`

animpar parameter structure

synopsis

Parameters for creating frame plots and animations.

structure

type: structure type ('animpar')
scrsize: two-component vector containing the size of frames in pixels [width height]
limits: four-component vector containing the limits of x and z coordinates for plotting [xmin xmax zmin zmax]
az: azimuth angle (in degrees) of viewing point
el: elevation angle (in degrees) of viewing point
msize: size of markers
colors: five-character string or RGB triple (5x3) containing the colors of background, markers, connections, traces, and marker numbers, respectively
markercolors: string or RGB triple (nx3) containing the individual colors for the markers
conncolors: string or RGB triple containing the individual colors for the connector lines
tracecolors: string or RGB triple containing the individual colors for the trace lines
numbercolors: string or RGB triple containing the individual colors for numbers
cwidth: width of connection lines
twidth: width of trace lines
conn: matrix (nMarkers x 2) indicating the connections between markers; each row represents one connection, with the numbers indicating the markers to be connected
conn2: matrix (nMarkers x 4) indicating the connections between midpoints of two marker pairs; each row represents one connection, with the first two numbers and the last two numbers indicating the markers whose midpoints are to be connected
trm: vector indicating the markers with a trace
trl: length of trace in seconds
showmnum: flag indicating whether marker numbers are shown (1=yes, 0=no)
numbers: array indicating the markers for which number is to be shown
showfnum: flag indicating whether frame numbers are shown (1=yes, 0=no)
animation: flag indicating whether animation is created (1=yes, 0=no); this is set by the mcanimate function before it calls the mcplotframe function
fps: frames per second used in animation
output: either file name for video file, of folder for pgn frames (‘tmp’)
videoformat: specifies video file format, either 'avi' or 'mpeg4' ('avi')
createframes: create png frames instead of video file, 1=frames, 0=video file (0)
getparams: return animation parameters, without plotting or animating frames, 1=yes, 0=no (0)
perspective: perform perspective projection, 0 = orthographic (default), 1 = perspective (0)
pers: perspective projection parameters:
    pers.c: 3D position of the camera [0 -4000 0]
    pers.th: orientation of the camera [0 0 0]
    pers.e: viewer's position relative to the display surface [0 -2000 0]

see also

`mcinitanimpar`

Function Reference

mc2frontal

synopsis

Rotates MoCap data to have a frontal view with respect to a pair of markers.

syntax

```
d2 = mc2frontal(d, m1, m2);
d2 = mc2frontal(d, m1, m2, method);
```

input parameters

d: MoCap data structure or data matrix
m1, m2: numbers of the markers that define the frontal plane
method: rotation method, possible values:
'mean' (default) rotates data in all frames with the same angle to have a frontal view with respect to the mean locations of markers m1 and m2
'frame' rotates each frame separately to have a frontal view with respect to the instantaneous locations of markers m1 and m2; with this method, each individual frame is centered as well

output

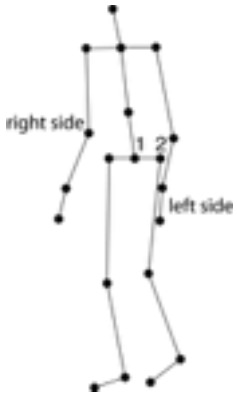
d2: MoCap data structure or data matrix

examples

```
d2 = mc2frontal(d, 3, 7);
d2 = mc2frontal(d, 3, 7, 'frame');
```

comments

The frontal plane is defined by the temporal mean of markers m1 and m2.
`mc2frontal(d, 1, 2)` would rotate to that view:



see also

`mcrotate`

mcaddframes

synopsis

Duplicates frames in a given mocap structure; either last frame in the end, first frames in the beginning, or at a given position in the middle.

syntax

```
d2 = mcaddframes(d, add);
d2 = mcaddframes(d, add, 'timetype', 'frame', 'location', 'beginning');
d2 = mcaddframes(d, add, 'location', 'middle', 'position', n);
```

input parameters

d: MoCap or norm data structure
add: total amount of frames to be added
timetype: amount of frames given in frames ('frame') or seconds ('sec') (default: sec)
location: location where frames are added: 'beginning', 'middle', or 'end' (default: end)
position: position where frames are added – only needed when using 'middle' as location. The timetype parameter applies to both add and position.

output

d2: MoCap or norm data structure

examples

```
d2 = mcaddframes(d, 60);
d2 = mcaddframes(d, 60, 'location', 'middle', 100);
```

comments

timetype, location, and position are optional. Default values are used if not specified.

see also

mcanimate

synopsis

Creates animation of mocap data and saves it to file (.avi or mpeg-4) or as consecutive frames (.png). Matlab's VideoWriter function is used to create the video file.

COMPATIBILITY NOTES (v. 1.5): The 'folder'-field (animpar structure, v. 1.4) has been changed to 'output' and is used as file name for the animation (and stored to the current directory) or as folder name in case frames are to be plotted.
Please use the function without the projection input argument, but specify it in the animation structure instead.

syntax

```
par = mcanimate(d);
par = mcanimate(d, par);
```

input parameters

d: MoCap data structure
par: animpar structure (optional)

output

par: animpar structure used for plotting the frames

examples

```
mcanimate(d, par);
```

comments

If the animpar structure is not given as input argument, the function creates it by calling the function `mcinitanimpar` and setting the `.limits` field of the animpar structure automatically so that all the markers fit into all frames.

If the `par.pers` field (perspective projection) is not given, it is created internally for backwards compatibility. For explanation of the `par.pers` field, see `help mcinitanimpar`

see also

`mcplotframe, mcinitanimpar`

mcbandpass

synopsis

Band pass filters data in a MoCap or norm structure using an FFT filter.

syntax

```
d2 = mcbandpass(d, f1, f2);
d2 = mcbandpass(d, f1, f2, method);
```

input parameters

d: MoCap or norm data structure
f1: lower frequency in Hz of passband
f2: higher frequency in Hz of passband
method: filtering window, ‘rect’ (default) or ‘gauss’

output

d2: MoCap or norm data structure containing band bass filtered data

examples

```
d2 = mcbandpass(d, 0.5, 3);
```

comments

see also

mcboundrect

synopsis

Calculates the bounding rectangle (the smallest rectangular area that contains the projection of the trajectory of each marker on the horizontal plane (i.e., floor).

syntax

```
br = mcboundrect(d);
br = mcboundrect(d, mnum);
br = mcboundrect(d, mnum, w, hop);
```

input parameters

d: MoCap data structure
mnum: marker numbers (optional; if no value given, all markers are used)
w: length of analysis window (optional; default: 4 sec)
hop: overlap of analysis windows (optional; default: 2 sec)

output

br: data matrix (windows x nMarkers)

examples

```
br = mcboundrect(d);
br = mcboundrect(d, [1 3 5]);
br = mcboundrect(d, [1:d.nMarkers], 3, 1);
```

comments

If the function is called with the mocap data structure as the only input parameter, the calculation is performed for all markers with the default parameters. If the window and overlap length are to be changed, the markers have to be always specified (e.g., all markers by [1:d.nMarkers]).

see also

references

Burger, B., Saarikallio, S., Luck, G., Thompson, M. R. & Toiviainen, P. (2013). Relationships between perceived emotions in music and music-induced movement. Music Perception 30(5), 519-535.

mcc3d2tsv

synopsis

Converts a c3d file into a tsv file.

syntax

```
mcc3d2tsv(fn, path);
```

input parameters

fn: name of c3d file
path: path to save the tsv file (optional). If no path is given, file is saved to current directory

output

tsv file, saved in the current or in the specified directory

examples

```
% mcc3d2tsv('file.c3d')
% mcc3d2tsv('file.c3d', 'folder')
% mcc3d2tsv('file.c3d', '/path/folder') %(Mac)
```

comments

see also

mcread

mccenter

synopsis

Translates motion capture data to have a centroid of [0 0 0] across markers and over time.

syntax

```
d2 = mccenter(d);
```

input parameters

d: MoCap data structure or data matrix

output

d2: MoCap data structure or data matrix

examples

comments

Missing data (NaN's) is ignored when calculating the centroid.

see also

mccomplexity

synopsis

Calculates the complexity of movement based on entropy of the proportion of variance contained in the principal components. A high value indicates a high complexity, whereas a low value indicated low complexity.

syntax

```
c = mccomplexity(d, mnum);
```

input parameters

d: MoCap data structure
mnum: marker numbers (optional; if no value given, all markers are used)

output

c: complexity value, between 0 and 1

examples

c = mccomplexity(d);
c = mccomplexity(d, 4:7);

comments

Data will be filled in case of missing frames.

see also

mcpcaproj

references

Burger, B., Saarikallio, S., Luck, G., Thompson, M. R. & Toiviainen, P. (2013). Relationships between perceived emotions in music and music-induced movement. Music Perception 30(5), 519–535.

mcconcatenate

synopsis

Concatenates markers from different MoCap or norm data structure.

syntax

```
d2 = mcconcatenate(d1, mnum1, d2, mnum2, d3, mnum3, ...);
```

input parameters

d1, d2, d3, ...: MoCap or norm data structure

mnum1, mnum2, mnum3, ...: vector containing the numbers of markers to be extracted from the preceding MoCap structure

output

d2: MoCap or norm data structure

examples

d2 = mcconcatenate(d1, [1 3 5], d2, [2 4 6]);

d2 = mcconcatenate(d1, 1, d2, 2, d1, 3, d3, 4, d2, 5);

comments

Each mocap structure must have a corresponding marker number or number array.

All mocap structures must have identical frame rates.

If the numbers of frames are not equal, the output MoCap structure will be as long as the shortest input MoCap structure.

see also

`mcgetmarker, mcmerge`

mccreateconnmatrix

synopsis

Creates a connection matrix for the animation parameters (`.conn` field) by using the "bones" connections saved as a label list of the Qualisys track manager software (QTM).

syntax

```
par = mccreateconnmatrix(fn, par);
```

input parameters

fn: text file (ending: .txt) that contains the "bones" (connections) made in QTM
par: animpar structure

output

par: animpar structure with connection matrix

examples

par = mccreateconnmatrix('labellist.txt', par);

comments

This function works only with label list files created by Qualisys Track Manager.
This function works for marker representations (before any marker reduction or joint transformation has been applied). The markers in the MoCap structure must resemble the structure of the marker connections in the label list file.

see also

`mcinitanimpar`

mccumdist

synopsis

Calculates the cumulative distance traveled by each marker.

syntax

```
d2 = mccumdist(d);
```

input parameters

d: MoCap data or norm data structure

output

d2: norm data structure

examples

comments

If the input consists of one-dimensional data (i.e., norm data), the cumulative distance to the origin of the reference space/coordination system is calculated, which is not (necessarily) the cumulated distance traveled by the marker.

see also

mccut

synopsis

Cuts two MoCap structures to the length of the shorter one.

syntax

```
[d11, d22] = mccut(d1, d2);
```

input parameters

d1, d2: MoCap or norm structures

output

d11, d22: MoCap or norm structures, one shortened and one original (both with same number of frames)

examples

comments

see also

mcdecompose

synopsis

Decomposes a kinematic variable into tangential and normal components.

syntax

```
[dt, dn] = mcdecompose(d, order);
```

input parameters

d: MoCap data structure containing either location or velocity data (timederorder = 0 or 1)
order: time derivative order of the variable, must be at least 2 (2 = acceleration, 3 = jerk, etc.)

output

dt: norm data structure containing the tangential components
dn: norm data structure containing the normal components

examples

```
[dt, dn] = mcdecompose(d, 2); % acceleration
[dt, dn] = mcdecompose(d, 3); % jerk
[dt, dn] = mcdecompose(d, 4); % jounce / snap
[dt, dn] = mcdecompose(d, 5); % crackle
[dt, dn] = mcdecompose(d, 6); % pop
[dt, dn] = mcdecompose(d, 7); % you-name-it
```

comments

see also

mceigenmovement

synopsis

Constructs eigenmovements using PCA and a scaled sinusoidal projection.

syntax

```
e = mceigenmovement(d);
e = mceigenmovement(d, eigind);
e = mceigenmovement(d, eigind, len);
e = mceigenmovement(d, eigind, len, per);
```

input parameters

d: MoCap or segm data structure
eigind (optional): selected eigenmovements (if not given, projections onto the first PCs that contain a total of 90% of the variance are returned)
len (optional): length in seconds (default 0.5 sec)
per (optional): period in seconds (default 0.5 sec)

output

e: vector of MoCap or segm data structures

examples

```
e = mceigenmovement(d);
e = mceigenmovement(d, 1:3);
e = mceigenmovement(d, 1:4, 2);
e = mceigenmovement(d, 1:2, 1.2, 0.6);
```

comments

The sinusoidal projections are scaled to match the RMS amplitudes of the PC projections of respective degrees of freedom.

see also

`mcpcaproj`

mcfillgaps

synopsis

Fills gaps in motion capture data.

syntax

```
d2 = mcfillgaps(d);
d2 = mcfillgaps(d, maxfill);
d2 = mcfillgaps(d, method);
d2 = mcfillgaps(d, maxfill, method);
```

input parameters

d: MoCap, norm, or segm data structure
maxfill: maximal length of gap to be filled in frames (optional, default = 1000000)
method: three different options for filling missing frames in the beginning and/or end of a recording:
default (parameter empty): missing frames in the beginning and/or in the end are set to 0;
'fillall': fills missing frames in the beginning and end of the data with the first actual (recorded) value or the last actual (recorded) value respectively;
'nobefill': fills all the gap in the data, but not missing frames in the beginning or end of the data, but sets them to NaN instead.

output

d2: MoCap, norm, or segment data structure

examples

```
d2 = mcfillgaps(d);
d2 = mcfillgaps(d, 120);
d2 = mcfillgaps(d, 'nobefill');
d2 = mcfillgaps(d, 60, 'fillall');
```

comments

Uses linear interpolation. More sophisticated algorithms will be implemented in the future.

see also

mcfilteremg

synopsis

Filters EMG data.

syntax

```
out = mcfilteremg(emgdata);
out = mcfilteremg(emgdata, filterfreqs);
```

input parameters

emgdata: norm data structure containing EMG data

filterfreqs: cutoff frequencies (in Hz) for the Butterworth filters; first value for high-pass filter, second value for low-pass filter (default: [20 24])

output

out: norm data structure containing filtered data

examples

```
out = mcfilteremg(emgdata);
out = mcfilteremg(emgdata, [18 21]);
```

comments

Filters the data using a 4th order Butterworth high-pass filter (default cutoff frequency: 20 Hz), then full-wave rectifies it, then filters it using a 4th order Butterworth low-pass filter (default cutoff frequency: 24 Hz).

see also

`mcreademg`

mcfluidity

synopsis

Calculates the fluidity/circularity of mocap data, defined as the ratio between velocity and acceleration of the normed and averaged mocap data.

syntax

```
f = mcfluidity(d, mnum);
```

input parameters

d: MoCap data structure

mnum: marker numbers (optional; if no value given, all markers are used)

output

f: fluidity value (the higher the value, the higher the smoothness/fluidity)

examples

```
f = mcfluidity(d, 4:6);
```

comments

see also

references

Burger, B., Saarikallio, S., Luck, G., Thompson, M. R. & Toiviainen, P. (2013). Relationships between perceived emotions in music and music-induced movement. Music Perception 30(5), 519–535.

mcgetmarker

synopsis

Extracts a subset of markers.

syntax

```
d2 = mcgetmarker(d, mnum);
```

input parameters

d: MoCap or norm data structure
mnum: vector containing the numbers of markers to be extracted

output

d2: MoCap or norm data structure

examples

```
d2 = mcgetmarker(d, [1 3 5]);
```

comments

see also

mcsetmarker, mcconcatenate

mcgetmarkername

synopsis

Returns the names of markers.

syntax

```
mn = mcgetmarkernames(d);
```

input parameters

d: MoCap data or norm structure

output

mn: cell structure containing marker names

examples

comments

see also

mcgetsegmpar

synopsis

Get parameters for body segments.

syntax

```
spar = mcgetsegmpar(model, segmnum);
```

input parameters

model: string indicating the body-segment model used (possible value: 'Dempster', more to be added in the future)

segmnum: vector indicating numbers for each segment

output

spar: segmpar structure

examples

```
segmnum = [0 0 8 7 6 0 8 7 6 13 12 10 11 3 2 1 11 3 2 1];
spar = mcgetsegmpar('Dempster', segmnum);
```

comments

Returns the mass relative to total body mass (`spar.m`), relative distance of center of mass from proximal joint (`spar.comprox`) and distal joint (`spar.comdist`), and radius of gyration relative to center of gravity (`spar.rogcg`), proximal joint (`spar.rogprox`) and distal joint (`spar.rogdist`) of for body segments indicated in `segmnum` according to given body-segment model.

Segment number values for model 'Dempster': no parameter=0, hand=1, forearm=2, upper arm=3, forearm and hand=4, upper extremity=5, foot=6, leg=7, thigh=8, lower extremity=9, head=10, shoulder=11, thorax=12, abdomen=13, pelvis=14, thorax and abdomen=15, abdomen and pelvis=16, trunk=17, head, arms and trunk (to glenohumeral joint)=18, head, arms and trunk (to mid-rib)=19.

Note that the root needs its own segment being 0, so `segmnum` is of size segments+1. (The first zero in the `segmnum` vector above).

See the description of the segmpar structure.

see also

references

Robertson, D. G. E., Caldwell, G. E., Hamill, J., Kamen, G., & Whittlesley, S. N. (2004). *Research methods in biomechanics*. Champaign, IL: Human Kinetics.

mchilbert

synopsis

Calculates the Hilbert transform of data in a MoCap or norm structure.

syntax

```
[amp, phase, h] = mchilbert(d, wrap);
```

input parameters

d: MoCap or norm data structure

wrap: flag to indicate if phase is returned as wrapped or unwrap (default: unwrapped); 0 or empty: unwrap, 1: wrap

output

amp: amplitude of analytic function derived from zero-mean signal

phase: (unwrapped or wrapped) phase of analytic function derived from zero-mean signal

h: analytic function

examples

amp = mchilbert(d);

[amp, phase, h] = mchilbert(d, 1);

comments

See `help hilbert`

see also

mchilberthuang

synopsis

Performs a Hilbert-Huang transform of order N on MoCap, norm or segm data.

syntax

```
hh = mchilberthuang(d, N);
```

input parameters

d: MoCap, norm or segm data structure
N: order of the H-H transform

output

hh: vector of MoCap, norm or segm data structures containing H-H transforms

examples

comments

See `help hilberthuang`

see also

mcicaproj

synopsis

Performs an Independent Components analysis on MoCap, norm or segm data, using the FastICA algorithm, and projects the data onto selected components.

syntax

```
[di, p] = mcicaproj(d, pc, ic);
```

input parameters

d: MoCap, norm or segm data structure
pc: number of PCs entered into ICA
ic: number of ICs estimated

output

di: vector of MoCap, norm or segm data structures
p: structure containing the following fields:
- icasig: independent components
- A: mixing matrix
- W: separation matrix
- meanx: mean vector of variables

examples

```
[di, p] = mcicaproj(d, 6, 3);
```

comments

Uses the fastICA algorithm, implemented in the FastICA Package, which is available at http://www.cis.hut.fi/projects/ica/fastica/

see also

`mcpcaproj, mcsethares`

mcinitanimpar

synopsis

Initializes an animation parameter (animpar) structure.

syntax

```
ap = mcinitanimpar;
```

input parameters

(none)

output

ap: animation parameter (animpar) structure

examples

comments

See also description of the animpar structure (default values given in parentheses:)

scrsize: frame size in pixels ([800 600])
limits: plot limits [xmin xmax zmin zmax] ([])
az: azimuth vector in degrees (0)
el: elevation vector in degrees (0)
msize: marker size (12)
colors: [background marker connection trace markernumber] ('kwwww') or RGB triplet (5x3)
markercolors: String holding marker colors ([]) or RGB triplet
conncolors: String holding connector (line) colors ([]) or RGB triplet
tracecolors: String holding trace colors (only animations) ([]) or RGB triplet
numbercolors: String holding number colors (indicated in the numbers array) ([]) or RGB triplet
cwidth: width of connectors (either single value or vector with entries for different widths) (1)
twidth: width of traces (either single value or vector with entries for different widths) (1)
conn: marker-to-marker connectivity matrix (M x 2) - mccreateconnmatrix() can be used for creating the connection matrix ([])
conn2: midpoint-to-midpoint connectivity matrix (M x 4) ([])
trm: vector indicating markers for which traces are added ([])
trl: length of traces in seconds (0)
showmnum: show marker numbers, 1=yes, 0=no (0)
numbers: array indicating the markers for which number is to be shown ([])
showfnum: show frame numbers, 1=yes, 0=no (0)
animation: create animation, 1=yes, 0=no (0)
fps: frames per second for animation (30)
output: either file name for video file, of folder for pgn frames (‘tmp')

videoformat: specifies video file format, either 'avi' or 'mpeg4' ('avi')
createframes: create png frames instead of video file, 1=frames, 0=video file (0)
getparams: return animation parameters, without plotting or animating frames, 1=yes, 0=no (0)
perspective: perform perspective projection, 0 = orthographic (default), 1 = perspective (0)
pers: perspective projection parameters:
pers.c: 3D position of the camera [0 -4000 0]
pers.th: orientation of the camera [0 0 0]
pers.e: viewer's position relative to the display surface [0 -2000 0]

Colors can be given as strings if only the MATLAB string color options are used. However, any color can be specified by using RGB triplets - for example, plotting the first two markers in gray: `par.markercolors=[.5 .5 .5; .5 .5 .5];`

see also

`mccreateconnmatrix, mcplotframe, mcanimate`

mcinitj2spar

synopsis

Initialises the parameter structure for joint-to-segment mapping.

syntax

```
par = mcinitj2spar;
```

input parameters

(none)

output

par: j2spar structure

examples

comments

See explanation about the j2spar structure. The initialized values are as follows:

type: 'j2spar'
rootMarker: 0
frontalPlane: [1 2 3]
parent: []
segmentName: {}

The fields `par.parent` and `par.segmentName` have to be entered manually.

see also

`mcj2s`

mcinitm2jpar

synopsis

Initialises the parameter structure for marker-to-joint mapping.

syntax

```
par = mcinintm2jpar;
```

input parameters

(none)

output

par: m2jpar structure

examples

comments

See the explanation of the m2jpar structure. The initialized values are as follows:

type: 'm2jpar'
nMarkers: 0
markerNum: {}
markerName: {}

The fields `par.nMarkers, par.markerNum` and `par.markerName` have to be entered manually.

see also

`mcm2j`

mcinitstruct

synopsis

Initializes MoCap or norm data structure.

syntax

```
d1 = mcinitstruct;
d1 = mcinitstruct(type);
d1 = mcinitstruct(type, data);
d1 = mcinitstruct(type, data, freq);
d1 = mcinitstruct(type, data, freq, markerName);
d1 = mcinitstruct(type, data, freq, markerName, fn);
d1 = mcinitstruct(data, freq);
d1 = mcinitstruct(data, freq, markerName);
d1 = mcinitstruct(data, freq, markerName, fn);
```

input parameters

type: 'MoCap data' or 'norm data' (default: 'MoCap data')
data: data to be used in the .data field of the mocap structure (default: [])
freq: frequency / capture rate of recording (default: NaN)
markerName: cell array with marker names (default: {})
fn: filename (default: ' ')

output

d1: mocap or norm data structure with default parameters or parameter adjustment according to the parameter input.

examples

d1 = `mcinitstruct`;
d1 = `mcinitstruct`('norm data', data);
d1 = `mcinitstruct`(data, 120, markernames, 'mydata1.tsv');

comments

default parameters (for ' MoCap data '):
type: 'MoCap data'
filename: ''
nFrames: 0
nCameras: NaN
nMarkers: 0
freq: NaN
nAnalog: 0
anaFreq: 0
timederOrder: 0

markerName: {}
data: []
analogdata: []
other:
other.descr: 'DESCRIPTION --'
other.timeStamp: 'TIME_STAMP--'
other.dataIncluded: '3D'

see also

mcj2s

synopsis

Performs a joint-to-segment mapping.

syntax

```
d2 = mcj2s(d, par);
```

input parameters

d: MoCap data structure
par: j2spar structure

output

d2: segm data structure

examples

comments

See explanation of the j2spar structure.

see also

`mcinitj2spar, mcs2j`

mckinenergy

synopsis

Estimates the instantaneous kinetic energy of each body segment.

syntax

```
[te, re] = mckinenergy(d, segd, spar);
```

input parameters

d: MoCap data structure
segd: segm data structure calculated from `d`
spar: segmpar structure (see `mcgetsegmpar`)

output

te: matrix containing translational energy values for each body segment
re: matrix containing rotational energy values for each body segment

examples

```
segd = mcj2s(d, j2spar);
spar = mcgetsegmpar('Dempster', segmnum);
[te, re] = mckinenergy(d, segd, spar);
```

comments

The energy for a given segment is in the column corresponding to the number of the distal joint of the respective segment.

see also

`mcj2s, mcgetsegmpar, mcpotenergy`

mckurtosis

synopsis

Calculates the kurtosis of data, ignoring missing values.

syntax

```
m = mckurtosis(d);
```

input parameters

d: MoCap data structure, norm data structure, or data matrix.

output

m: row vector containing the kurtosis values of each data column

examples

comments

see also

`mcmean, mcstd, mcvar, mcskewness`

mcm2j

synopsis

Performs a marker-to-joint mapping.

syntax

```
d2 = mcm2j(d, par);
```

input parameters

d: MoCap data structure
par: m2jpar structure

output

d2: MoCap data structure

examples

comments

The fields the fields `par.nMarkers`, `par.markerNum` and `par.markerName` have to be entered manually.

See the explanation of the m2jpar structure.

see also

`mcinitm2jpar`

mcmarkerdist

synopsis

Calculates the frame-by-frame distance of a marker pair.

syntax

```
dist = mcmarkerdist(d, m1, m2);
```

input parameters

d: MoCap data structure
m1, m2: marker numbers

output

dist: column vector

examples

```
dist = mcmarkerdist(d, 1, 5);
```

comments

see also

mcmean

synopsis

Calculates the temporal mean of data, ignoring missing values.

syntax

```
m = mcmean(d);
```

input parameters

d: MoCap data structure, norm data structure, or data matrix.

output

m: row vector containing the means of each data column

examples

comments

see also

`mcstd, mcvar, mcskewness, mckurtosis`

mcmerge

synopsis

Merges two MoCap data structures and optionally the corresponding animation parameter files.

syntax

```
d3 = mcmerge(d1, d2);
[d3, p3] = mcmerge(d1, d2, p1, p2);
```

input parameters

d1, d2: MoCap or norm data structures
p1, p2: animpar structures for d1 and d2

output

d3: MoCap or norm data structure
p3: animpar structure

examples

comments

d1 and d2 must have identical frame rates. If the numbers of frames are not equal, the MoCap data structure with the higher number of frames will be cut before merging.

All animation parameters will be taken from the first animpar file, apart from any color, marker, trace definition, and connection matrices.

see also

mcconcatenate

mcmissing

synopsis

Reports missing data per marker and frame.

syntax

```
[mf, mm, mgrid] = mcmissing(d);
```

input parameters

d: MoCap or norm data structure.

output

mf: number of missing frames per marker
mm: number of missing markers per frame
mgrid: matrix showing missing data per marker and frame (rows correspond to frames and columns to markers

examples

comments

see also

mcmocapgram

synopsis

Plots mocapgram (shows positions of a large number of markers as projection onto a color-space).

syntax

```
h = mcmocapgram(d);
```

```
mcmocapgram(d);
```

```
mcmocapgram(d, timetype);
```

input parameters

d: MoCap or norm data structure.
timetype: time type used in the plot ('sec' (default) or 'frame')

output

h: figure handle

examples

```
mcmocapgram(d,'frame');
```

```
h = mcmocapgram(d);
```

comments

see also

mcnorm

synopsis

Calculates the norms of kinematic vectors.

syntax

```
n = mcnorm(d);
n = mcnorm(d, comps);
```

input parameters

d: MoCap data structure
comps: components included in the calculation (optional, default = 1:3)

output

n: norm data structure

examples

```
n = mcnorm(d);
n = mcnorm(d, 1:2); % calculates norm of horizontal projection
```

comments

see also

mcpcaproj

synopsis

Performs a Principal Components analysis on MoCap, norm or segm data and projects the data onto selected components.

syntax

```
[dp, p] = mcpcaproj(d);
[dp, p] = mcpcaproj(d, pc);
[dp, p] = mcpcaproj(d, pc, proj);
```

input parameters

d: MoCap, norm or segm data structure
pc (optional): selected Principal Components (if not given, projections onto the first PCs that contain a total of 90% of the variance are returned)
proj (optional): projection function (if not given, the PC projections of the data in d are used)

output

dp: vector of MoCap, norm or segm data structures
p: structure containing the following fields:
- l: proportion of variance contained in each PC
- q: PC vectors (columns)
- c: PC projections (rows)
- meanx: mean vector of variables

examples

```
[dp, p] = mcpcaproj(d);
[dp, p] = mcpcaproj(d, 1:3);
[dp, p] = mcpcaproj(d, 1:3, sin(2*pi*0:60/60);
```

comments

see also

`mcicaproj, mcsethares`

references

Burger, B., Saarikallio, S., Luck, G., Thompson, M. R., & Toiviainen, P. (2012). *Emotions Move Us: Basic Emotions in Music Influence People's Movement to Music.* In Proceedings of the 12th International Conference on Music Perception and Cognition (ICMPC) / 8th Triennial Conference of the European Society for the Cognitive Sciences of Music (ESCOM). Thessaloniki, Greece.

mcperiod

synopsis

Estimates the period of movement for each marker and each dimension.

syntax

```
[per, ac, eac, lag] = mcperiod(d);
[per, ac, eac, lag] = mcperiod(d, maxper);
[per, ac, eac, lag] = mcperiod(d, method);
[per, ac, eac, lag] = mcperiod(d, maxper, method);
```

input parameters

d: MoCap or norm data structure
maxper: maximal period in seconds (optional, default = 2 secs)
method: sets if 'first' or 'highest' maximal value of the autocorrelation function is taken as periodicity estimation (optional, default: 'first')

output

per: row vector containing period estimates for each column
ac: matrix containing autocorrelation functions for each column
eac: matrix containing enhanced autocorrelation functions for each column
lag: vector containing lag values for the (normal and enhanced) autocorrelation functions

examples

```
[per, ac, eac, lag] = mcperiod(d, 3);
per = mcperiod(d, 'highest');
```

comments

In ac and eac, each column corresponds to a dimension of a marker (or in case of norm data to a marker), and each row corresponds to a time lag.

see also

references

Eerola, T., Luck, G., & Toiviainen, P. (2006). *An investigation of pre-schoolers' corporeal synchronization with music.* Paper presented at the 9th International Conference on Music Perception and Cognition, Bologna, Italy.

mcplotframe

synopsis

Plots frames of motion capture data.

COMPATIBILITY NOTES (v. 1.5): Please use the function without the projection input argument, but specify it in the animation structure instead.

syntax

```
par = mcplotframe(d, n);
```

```
par = mcplotframe(d, n, par);
```

input parameters

d: MoCap data structure

n: vector containing the numbers of the frames to be plotted

par: animpar structure (optional)

output

par: animpar structure used for plotting the frames (if color strings were used, they will converted to RGB triplets)

examples

```
par = mcplotframe(d, 1);
```

```
mcplotframe(d, 500:10:600, par);
```

comments

If the animpar structure is not given as input argument, the function creates it by calling the function `mcinitanimpar` and setting the `.limits` field of the animpar structure automatically so that all the markers fit into all frames.

see also

`mcanimate, mcinitanimpar`

mcplotphaseplane

synopsis

Plots motion capture data on a phase plane.

syntax

```
mcplotphaseplane(d1, d2, marker, dim) % for MoCap data structure
mcplotphaseplane(n1, n2, marker) % for norm data structure
mcplotphaseplane(s1, s2, segm, var) % for segm data structure
```

input parameters

d1, d2, n1, n2, s1, s2: MoCap data structure, norm data structure, or segm data structure
marker: vector containing marker numbers to be plotted (for MoCap and norm data structure)
dim: vector containing dimensions to be plotted (for MoCap data structure)
segm: body segment number (for segm data structure)
var: variable to be plotted for segment segm (for segm data structure)

output

Figure.

examples

```
mcplotphaseplane(d1, d2, 1:3, 3) % for MoCap data structure
mcplotphaseplane(n1, n2, 5) % for norm data structure
mcplotphaseplane(s1, s2, [3 5 7], 'angle') % for segm data structure
mcplotphaseplane(s1, s2, 5:10, 'eucl') % for segm data structure
mcplotphaseplane(s1, s2, [12 14], 'quat') % for segm data structure
```

comments

see also

mcplottimeseries

synopsis

Plots motion capture data as time series. NEW SYNTAX IN VERSION 1.3.1

syntax

```
mcplottimeseries(d, marker) % for MoCap or norm data structure
mcplottimeseries(d, marker, 'dim', dim) % specifying dimensions
mcplottimeseries(d, marker, 'timetype', timetype) % axis unit
mcplottimeseries(d, marker, 'plotopt', plotopt) % combined or separate
plots
mcplottimeseries(d, marker, 'label', label) % y-axis label
mcplottimeseries(d, marker, 'names', names) % marker names
mcplottimeseries(s, segm, 'var', var) % for segm data structure
```

input parameters

d/s: MoCap data structure, norm data structure, or segm data structure
marker: vector containing marker numbers or cell array containing marker names (for MoCap or norm data structure)
segm: body segment numbers or cell array containing segment names (for segm data structure)
dim: dimensions to be plotted (for MoCap data structure - default: 1)
var: variable to be plotted for segment segm (for segm data structure - default: 1)
timetype: time type used in the plot ('sec' (seconds - default) or 'frame')
plotopt: plotting option (for MoCap or norm data structure); 'sep' (default) or 'comb':
 sep: all time series are plotted in separate subplots
 comb: all time series will be plotted into the same plot using different colors)
label: y-axis label (default: no y-axis label). X-axis label is always set, according to timetype (however, for plotting neither x-axis nor y-axis labels: 'label', 0)
names: if marker names (instead of numbers) are plotted in title and legend (0: numbers (default), 1: names)

output

Figure.

examples

```
mcplottimeseries(d, 2) % MoCap or norm data structure, marker 2, dim 1
mcplottimeseries(d, {'Head_FL','Finger_L'}) %marker names instead of num-
bers (works for segments as well)
mcplottimeseries(d, 1:3, 'dim', 1:3) % markers 1 to 3, dimensions 1 to 3
mcplottimeseries(d, 1:3, 'dim', 3, 'timetype', 'frame') % frames as x axis
unit
```

```
mcplottimeseries(d, 5, 'dim', 1:3, 'plotopt', 'comb') % all in one plot,
different colors per dim
mcplottimeseries(d, 5, 'dim', 1:3, 'plotopt', 'comb', 'label', 'mm') % y-
axis label: mm
mcplottimeseries(d, 5, 'dim', 1:3, 'timetype', 'frame', 'label', 0) % no x-
axis (and no y-axis) label
mcplottimeseries(d, 5, 'names', 1) % marker names (instead of numbers)
plotted in title and legend
mcplottimeseries(s, [3 6 20], 'var', 'angle') % for segm data structure
mcplottimeseries(s, 5:10, 'var', 'eucl', 'timetype', 'frame') % frames as x
axis unit
mcplottimeseries(s, [12 14], 'var', 'quat', 'dim', 2, 'plotopt', 'comb') %
all in one plot, component 2
```

comments

see also

mcpotenergy

synopsis

Estimates the instantaneous potential energy of each body segment.

syntax

```
pe = mcpotenergy(d, segd, segmpar)
```

input parameters

d: MoCap data structure
segd: segm data structure calculated from `d`
segmpar: segmpar structure (see `mcgetsegmpar`)

output

pe = matrix containing potential energy values for each body segment

examples

```
segd = mcj2s(d, j2spar);
spar = mcgetsegmpar('Dempster', segmnum);
pe = mckinenergy(d, segd, spar);
```

comments

The energy for a given segment is in the column corresponding to the number of the distal joint of the respective segment.

see also

`mcj2s, mcgetsegmpar, mckinenergy`

mcread

synopsis

Reads a motion capture data file and returns a MoCap data structure.

syntax

```
d = mcread(fn);
d = mcread;
```

input parameters

fn: file name, tsv, c3d, bvh, mat, or wii format. If no input parameter is given, a file open dialog opens.

output

d: MoCap data structure containing parameter values and data

examples

d = mcread('filename.tsv');
d = mcread('filename.c3d');
d = mcread('filename.bvh');
d = mcread('filename.mat');
d = mcread('filename.wii');
d = mcread;

comments

Currently the .c3d, .tsv (as exported by QTM), .bvh, .mat (as exported by QTM), and .wii (WiiDataCapture software) formats are supported. The file names must have postfixes '.c3d', '.tsv', '.bvh', '.mat', or '.wii', respectively. For reading .c3d files, the function provided at http://www.c3d.org/download_apps.html is used.

For exporting in `.tsv` format from Qualisys QTM, recommended export parameter are:
`3D data` and `Include TSV header` ticked
`Export time data for every frame` and `write column headers` will be ignored by `mcread` if ticked.

The `.c3d` format does not support more than 65535 frames per file (see www.c3d.org/HTML/default.htm → The C3D file format → Limitations). Therefore, if you happen to have longer recordings, export them either in `.tsv` or `.mat`, or in more than one `c3d` file. If further problems occur when reading in .c3d files, try to adapt the 'machinetype' parameters as indicated in the readc3d.m (in the folder 'private').

Reading in .bvh files requires additional toolboxes available here: http://staffwww.dcs.shef.ac.uk/people/N.Lawrence/mocap/ (mocap and ndlutil).

see also

mcreademg

synopsis

Reads emg files in .tsv format recorded with the Mega EMG system using QTM.

syntax

```
d = mcreademg(fn);
```

input parameters

fn: File name; tsv format (norm data structure)

output

d: norm data structure

examples

d = mcreademg('filename.tsv');

comments

see also

`mcfilteremg`

mcreorderdims

synopsis

Reorders the Euclidean dimensions in motion capture data.

syntax

```
d2 = mcreorderdims(d, dims);
```

input parameters

d: MoCap data structure
dims: vector containing the new order of dimensions

output

d2: MoCap data structure

examples

```
d2 = mcreorderdims(d, [1 3 2]);
```

comments

see also

mcrepovizz

synopsis

Exports MoCap structure as valid *repoVizz* `.csv` files, `.xml` *repoVizz* struct and optional `.bones` file.

syntax

```
mcrepovizz(d, path, p);
```

input parameters

d: MoCap data structure

path: path to save the .csv files (optional). If no path is given, files are saved in the current directory. If the chosen directory does not exist, it will be created.

p: animpar parameter structure (optional)

output

.csv files and *repoVizz* struct .xml file saved in the current or in the specified directory. Optional .bones file saved as well if animpar structure specified in the third argument

examples

```
mcrepovizz(d)
```

```
mcrepovizz(d, 'folder')
```

```
mcrepovizz(d, '/path/folder') %(only Mac)
```

```
mcrepovizz(d, 'folder', p)
```

```
mcrepovizz(d, p)
```

comments

For info about repoVizz: http://repovizz.upf.edu/

see also

mcread, mcwritetsv

mcresample

synopsis

Resamples motion capture data using interpolation.

syntax

```
d2 = mcresample(d, newfreq, method);
```

input parameters

d: MoCap data structure
newfreq: new frame rate
method: interpolation method (optional, default 'linear'; for other options, see `help interp1`)

output

d2: MoCap data structure

examples

```
d2 = mcresample(d, 240);
```

```
d2 = mcresample(d, 360, 'spline');
```

comments

see also

mcreverse

synopsis

Reverses dimensions of motion-capture data.

syntax

```
d2 = mcreverse(d, x);
```

input parameters

d: MoCap structure or data matrix
x: reverse vector (set 1 for each dimension to be reversed, otherwise 0)

output

d2: MoCap structure or data matrix

examples

```
d2 = mcreverse(d, [0 0 1]);
```

comments

see also

mcrotate

synopsis

Rotates motion-capture data.

syntax

```
d2 = mcrotate(d, theta);
d2 = mcrotate(d, theta, axis);
d2 = mcrotate(d, theta, point);
d2 = mcrotate(d, theta, axis, point);
```

input parameters

d: MoCap data structure or data matrix
theta: rotation angle (in degrees)
axis: rotation axis (optional, default = [0 0 1])
point: point through which the rotation axis goes (optional, default is the centroid of markers over time)

output

d2: MoCap data structure or data matrix

examples

```
d2 = mcrotate(d, 130); % rotate 130 degrees counterclockwise around the vertical axis
d2 = mcrotate(d, 90, [1 0 0]); % rotate around the x axis
d2 = mcrotate(d, 45, [0 1 0], [0 0 500]); % rotate around the axis parallel to y axis going through point [0 0 500]
d2 = mcrotate(d, 20, [], [0 1000 0]); % rotate around the z (vertical) axis going through point [0 1000 0]
```

comments

If theta is a vector, its values are used as evenly-spaced break points in interpolation. This allows the creation of dynamic rotation of the data.
Rotation is performed according to the right-hand rule. For instance, if the rotation axis is pointing vertically upwards, positive rotation angle means counterclockwise rotation when viewed from up.

see also

mc2frontal

mcrotationrange

synopsis

Calculates the rotation range between two markers.

syntax

```
f = mcrotationrange(d, m1, m2);
```

input parameters

d: MoCap data structure
m1: marker one
m2: marker two

output

r: rotation range (the higher the value, the more rotation)

examples

```
r = mcrotation(d, 13, 17);
```

comments

see also

references

Burger, B., Saarikallio, S., Luck, G., Thompson, M. R. & Toiviainen, P. (2013). Relationships between perceived emotions in music and music-induced movement. Music Perception 30(5), 519-535.

mcs2j

synopsis

Performs a segment-to-joint mapping.

syntax

```
d2 = mcj2s(d, par);
```

input parameters

d: segm data structure
par: j2spar structure

output

d2: MoCap data structure

examples

comments

See the description of the j2spar structure.

see also

`mcinitj2spar, mcj2s`

mcs2posture

synopsis

Creates a posture representation from segm data by setting root transition and root rotation to zero values.

syntax

```
p = mcs2posture(d);
```

input parameters

d: segm data structure

output

p: segm data structure

examples

comments

see also

`mcj2s`

mcsegmangle

synopsis

Calculates the angles between two markers.

syntax

```
dn = mcsegmangle(d, m1, m2);
```

input parameters

d: MoCap data structure
m1: marker one
m2: marker two

output

dn: norm data structure containing the three angles

examples

dn = mcsegmangle(d, 1, 2);

comments

see also

mcsethares

synopsis

Performs either an m-best or a small-to-large Sethares transform on MoCap, norm or segm data.

Returns the basis functions for each DOF for given periods and, with the m-best transform, also the powers for the respective periods.

syntax

```
ds = mcsethares(d, per); %small-to-large Sethares transform
[ds, pers, pows] = mcsethares(d, per, nbasis);%m-best Sethares transform
```

input parameters

d: MoCap, norm or segm data structure

per: period in frames in case of small-to-large Sethares transform
maximum period in frames in case of m-best Sethares transform

nbasis: number of basis functions estimated (only for m-best Sethares transform)

output

ds: MoCap, norm or segm data structure - the only output in case of small-to-large Sethares transform

in case of m-best Sethares transform also:

per: best periods for each degree of freedom

pow: powers of respective periods

examples

comments

Dependent on the given input parameter, either the m-best or the small-to-large Sethares transform is chosen. See syntax above about in- and output argument structure.

Uses the Periodicity Toolbox downloadable at http://eceserv0.ece.wisc.edu/~sethares/downloadper.html

see also

`mcpcaproj, mcicaproj`

mcsetlength

synopsis

Sets mocap data to the length given.

syntax

```
d2 = mcsetlength(d, n)
d2 = mcsetlength(d, n, 'timetype', 'sec')
d2 = mcsetlength(d, n, 'position', 'location')
```

input parameters

d: MoCap or norm data structure
n: new length of mocap data
timetype: length given in frames ('frame') or seconds ('sec') (default: sec)
location: position where to add or trim frames ('beginning' or 'end' – default: end)

output

d2: MoCap or norm data structure

examples

d2 = mcsetlength(d, 1200);
d2 = mcsetlength(d, n, 'timetype', 'sec');
d2 = mcsetlength(d, 1200, 'location', 'beginning');

comments

If the given length is less than the number of frames in the mocap data, the data will be trimmed to the given length from either beginning or end. If the given length is more than the number of frames in the mocap data, data will be added by replicating with first or last frame.

see also

`mcaddframes, mctrim`

mcsetmarker

synopsis

Replaces a subset of markers in an existing mocap or norm structure.

syntax

```
d2 = mcsetmarker(d_orig, d_repl, mnum);
```

input parameters

d_orig: MoCap or norm data structure (the one to be changed)

d_repl: MoCap or norm data structure (the one that contains the replacement data). The data set must have the same amount of markers as indicated in mnum.

mnum: vector containing the marker numbers to be replaced in the original data set (order as in replacement mocap structure)

output

d2: MoCap structure

examples

```
d2 = mcsetmarker(d, d1, [1 3 5]);
```

comments

Use mcgetmarker to shorten the replacing data set to fit the mnum vector.

If the resulting mocap structure shall contain more markers than the original, the data will be appended at the specified marker number. Possible in-between markers will be set to NaN. Empty marker names will be set to EMPTY and can be adapted manually if desired.

see also

mccombine, mcgetmarker

mcsimmat

synopsis

Calculates self-similarity matrix from MoCap or segm data.

syntax

```
sm = mcsimmat(d);
sm = mcsimmat(d, metric);
```

input parameters

d: MoCap or segm data structure
metric: distance metric used, see `help pdist` (default: cityblock)

output

sm: self-similarity matrix

examples

```
sm = mcsimmat(d);
sm = mcsimmat(d, 'corr');
```

comments

see also

mcskewness

synopsis

Calculates the skewness of data, ignoring missing values.

syntax

```
m = mcskewness(d);
```

input parameters

d: MoCap data structure, norm data structure, or data matrix

output

m: row vector containing the skewness values of each data column

examples

comments

see also

`mcmean, mcstd, mcvar, mckurtosis`

mcsmoothen

synopsis

Smoothens motion capture data using a Butterworth (fast) or a Savitzky-Golay FIR (accurate) smoothing filter.

syntax

```
d2 = mcsmoothen(d);
d2 = mcsmoothen(d, filterparams);
d2 = mcsmoothen(d, method);
d2 = mcsmoothen(d, window);
```

input parameters

d: MoCap data structure or segm data structure
filterparams: order and cutoff frequency for Butterworth filter (optional, default [2, 0.2])
method: Butterworth filtering is default - if Savitzky-Golay filtering is to be used, use 'acc' as method argument
window: window length (optional, default = 7) for Savitzky-Golay FIR smoothing filter
(if input is scalar or a string, Savitzky-Golay filter is chosen - if input is vector, it is considered as parameters for Butterworth filter)

output

d2: MoCap data structure or segm data structure

examples

```
d2 = mcsmoothen(d); % Butterworth filter smoothing with default parameters
d2 = mcsmoothen(d, [2 .1]); % second order Butterworth filter with 0.1 Hz
cutoff frequency
d2 = mcsmoothen(d, 'acc'); % S-G filter smoothing with default frame length
d2 = mcsmoothen(d, 9); % S-G filter smoothing using a 9-frame window
```

comments

The default parameters for the Butterworth filter create a second-order zero-phase digital Butterworth filter with a cutoff frequency of 0.2 Hz.
For information about the Savitzky-Golay filter, see `help sgolayfilt`.

see also

`mctimeder`

mcsort

synopsis

sorts mocap data according to marker names (alphanumerical or according to given numeric or cell array indicating marker numbers or markers names as to how the output data is to be sorted).

syntax

```
d2=mcsort(d)
```

```
d2=mcsort(d, srt)
```

input parameters

d: MoCap data structure

srt: numeric or cell array containing markers numbers or marker names (optional)

output

d2: reordered mocap data structure

examples

```
d2=mcsort(d)
```

```
d2=mcsort(d, [1:5 7 6 9 8 10:20]);
```

```
d2=mcsort(d, d1.markerName);
```

comments

If the sort variable is not given, the data will be sorted alphanumerical according to the marker names.

The number of items in the sort array has to match the number of markers in the input mocap data structure.

see also

mcspectrum

synopsis

Calculates the amplitude spectrum of mocap time series.

syntax

```
s = mcspectrum(d);
```

```
[s f] = mcspectrum(d);
```

input parameters

d: MoCap structure, norm structure, or segm structure

output

s: MoCap structure, norm structure, or segm structure containing amplitude spectra in the .data field

f: frequencies in Hz for the frequency channels in the spectra

examples

comments

see also

mcstatmoments

synopsis

Calculates the first four statistical moments (mean, standard deviation, skewness, and kurtosis) of data, ignoring missing values.

syntax

```
mom = mcstatmoments(d);
```

input parameters

d: MoCap data structure, norm data structure, or data matrix.

output

mom: structure containing the fields .mean, .std, .skewness, and .kurtosis

examples

comments

Calls the functions `mcmean`, `mcstd`, `mcskewness`, and `mckurtosis`

see also

`mcmean`, `mcstd`, `mcskewness`, `mckurtosis`

mcstd

synopsis

Calculates the temporal standard deviation of data, ignoring missing values.

syntax

```
m = mcstd(d);
```

input parameters

d: MoCap data structure, norm data structure, or data matrix.

output

m: row vector containing the standard deviations of each data column

examples

comments

see also

`mcmean, mcvar, mcskewness, mckurtosis`

mctimeder

synopsis

Estimates time derivatives of motion capture data. Two options are available, the fast version uses differences between two successive frames and a Butterworth smoothing filter, whereas the accurate version uses derivation with a Savitzky-Golay FIR smoothing filter.

syntax

```
d2 = mctimeder(d);
d2 = mctimeder(d, order);
d2 = mctimeder(d, filterparams);
d2 = mctimeder(d, method);
d2 = mctimeder(d, order, filterparams);
d2 = mctimeder(d, order, method);
d2 = mctimeder(d, order, window, method);
```

input parameters

d: MoCap structure, norm structure, or segm structure
order: order of time derivative (optional, default = 1).
filterparams: order and cutoff frequency for Butterworth smoothing filter (optional, default [2, 0.2])
method: fast or accurate version; fast version is default, use 'acc' for accurate version (if no window length is given, the default lengths are used, see comment)
window: window length for Savitzky-Golay FIR smoothing filter (optional, default = 7 for first-order derivative)

output

d2: MoCap data structure or segm data structure

examples

```
d2 = mctimeder(d); % first-order time derivative using the fast method
(Butterworth filter with default parameters)
d2 = mctimeder(d, [2 .1]); % first-order time derivative using fast version
(second order Butterworth filter with 0.1 Hz cutoff frequency)
d2 = mctimeder(d, 'acc'); % first-order time derivative using the accurate
version (Savitzky-Golay filter)
d2 = mctimeder(d, 2, 9, 'acc'); % second-order time derivative with 9-frame
window using the accurate version (Savitzky-Golay filter)
```

comments

The default parameters for the Butterworth smoothing filter create a second-order zero-phase digital Butterworth filter with a cutoff frequency of 0.2 Hz.

The window length is dependent on the order of the time derivative and the given window length. It is calculated by 4*n+w-4. Thus, if the default window length of 7 is used, the window length for the second-order derivative will be 11, and the window length for the third-order derivative will be 15.

For information about the Savitzky-Golay filter, see `help sgolayfilt`.

The function updates the `d.timederorder` field as follows: `d2.timederorder = d.timederorder + order`.

see also

`mcsmoothen, mctimeintegr`

mctimeintegr

synopsis

Estimates time integrals of motion capture data using the rectangle rule.

syntax

```
d2 = mctimeder(d);
d2 = mctimeintegr(d, order);
```

input parameters

d: MoCap data structure or segm data structure
order: order of time integral (optional, default = 1)

output

d2: MoCap data structure or segm data structure

examples

```
d2 = mctimeintegr(d, 2); % second-order time integral
```

comments

The function updates the `d.timederorder` field as follows: `d2.timederorder = d.timederorder - order`.

see also

`mctimeder`

mctranslate

synopsis

Translates motion-capture data by a vector.

syntax

```
d2 = mctranslate(d, transvect);
```

input parameters

d: MoCap data structure or data matrix
transvect: translation vector

output

d2: MoCap data structure or data matrix

examples

```
d2 = mctranslate(d, [0 1000 0]);
```

comments

see also

mctrim

synopsis

Extracts a temporal section from a MoCap, norm, or segm data structure.

syntax

```
d2 = mctrim(d, t1, t2);
d2 = mctrim(d, t1, t2, timetype);
```

input parameters

d: MoCap data, norm, or segm data structure
t1: start of extracted section
t2: end of extracted section
timetype: either 'sec' (default) or 'frame'

output

d2: MoCap, norm, or segm data structure containing frames from t1 to t2 (if `timetype == 'frame'`) or frames between t1 and t2 seconds (if `timetype == 'sec'`) of MoCap data structure d.

examples

```
d2 = mctrim(d, 305, 1506, 'frame');
d2 = mctrim(d, 3, 5, 'sec');
```

comments

see also

mcvar

synopsis

Calculates the variance of data, ignoring missing values.

syntax

```
m = mcvar(d);
```

input parameters

d: MoCap data structure, norm data structure, or data matrix.

output

m: row vector containing the variance of each data column

examples

comments

see also

`mcmean, mcstd, mcskewness, mckurtosis`

mcvect2grid

synopsis

Converts a MoCap structure vector to a MoCap structure with three orthogonal views for each component.

syntax

```
[g, gpar] = mcvect2grid(c, par, dx, dy);
```

input parameters

c: MoCap structure vector
par: animpar structure
dx: horizontal offset between components (default: 2000)
dy: vertical offset between orthogonal views (default: 2000)

output

g: MoCap structure
gpar: animpar structure

examples

```
[g, gpar] = mcvect2grid(c, par, 1000, 2000);
```

comments

see also

mcwindow

synopsis

Performs a windowed time series analysis with a given function.

syntax

```
varargout = mcwindow(functionhandle, d);
varargout = mcwindow(functionhandle, d, wlen, hop);
varargout = mcwindow(functionhandle, d, wlen, hop, timetype);
```

input parameters

functionhandle: handle to function with which the windowed analysis is performed
d: MoCap data structure or norm data structure
wlen: length of window (optional, default = 2 sec)
hop: hop factor (optional, default = 0.5)
timetype: time type {'sec', 'frame'} (optional, default = 'sec')

output

When used with the functions `mcmean`, `mcstd`, `mcvar`, `mcskewness`, and `mckurtosis`, the output is a two-dimensional matrix where the first index corresponds to window number and the second index to marker/dimension.

When used with `mcperiod`, the function returns four output parameters `[per, ac, eac, lag]`, where `per` is a two-dimensional matrix with the first index corresponding to window number and the second to marker/dimension. Output parameters `ac` and `eac` are three-dimensional matrices, with the first index corresponding to window number, the second to lag, and the third to marker/dimension. The output parameter `lag` is a vector containing the lag values for the autocorrelations.

examples

```
stds = mcwindow(@mcstd, d, 3, 0.5);
[per, ac, eac, lags] = mcwindow(@mcperiod, d);
```

comments

see also

`mcmean`, `mcstd`, `mcvar`, `mcskewness`, `mckurtosis`, `mcperiod`

mcwritetsv

synopsis

Saves mocap structure as a tsv file.

syntax

```
mcwritetsv(d, path)
```

input parameters

d: MoCap data structure
path: path to save the tsv file (optional). If no path is given, file is saved to current directory

output

tsv file, saved in the current or in the specified directory

examples

```
mcwritetsv(d)
```

```
mcwritetsv(d, 'folder')
```

```
mcwritetsv(d, '/path/folder') %(Mac)
```

comments

see also

mcread

Never confuse motion with action.

— Benjamin Franklin —