Week 03, Laboratory 03

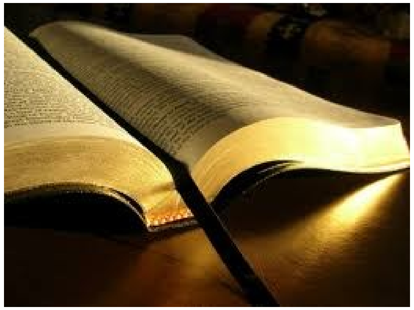
Summary:

Processing of kinematic data obtained from the Laboratory of Biomechanics of Lisbon in Matlab.

Kinematic analysis of a gait cycle in Matlab.

Suggested bibliography:

P. Nikravesh, *Computer-Aided Analysis of Mechanical Systems*, Prentice-Hall, Englewood-Cliffs, New Jersey, 1988.



Week 03, Laboratory 03

1st Assignment:
Kinematic Analysis of a Biomechanical Model

In this work, the Group is asked to study a gait cycle of one of its members (data collected in the Biomechanics Laboratory). The motion should be analyzed from the kinematics point of view and should be described using the directional terms and joint movement terminology presented in this course.

For the computational kinematic analysis of the human motion, the Group should:

- Define, using Cartesian coordinates, a 2D multibody model suitable for the motion under analysis.
- Identify the vector of generalized coordinates for the proposed model.
- Define the data driver constraints needed for the motion under analysis.
- Carry on the complete kinematic analysis of the model for the acquired motion.

Week 03, Laboratory 03

Kinematic Analysis of Multibody Systems

Laboratory data:

EMG data
The root-mean-square (RMS) envelopes of the EMG signals are provided along the raw data.

Kinematic and kinetic data
The coordinates of the bony landmarks and the ground reaction forces measured at the laboratory are provided.

Note: The ground reaction forces are provided in the local reference frame of each force plate (f_1, f_2, and f_3). The tsv2mat.m script must be used to transform the data to the same reference frame of the coordinates of the bony landmarks.

Foot pressure data
The distribution of foot pressures along the gait cycle are provided.

Gait parameters
The parameters most frequently used to characterize gait are provided.

Week 03, Laboratory 03

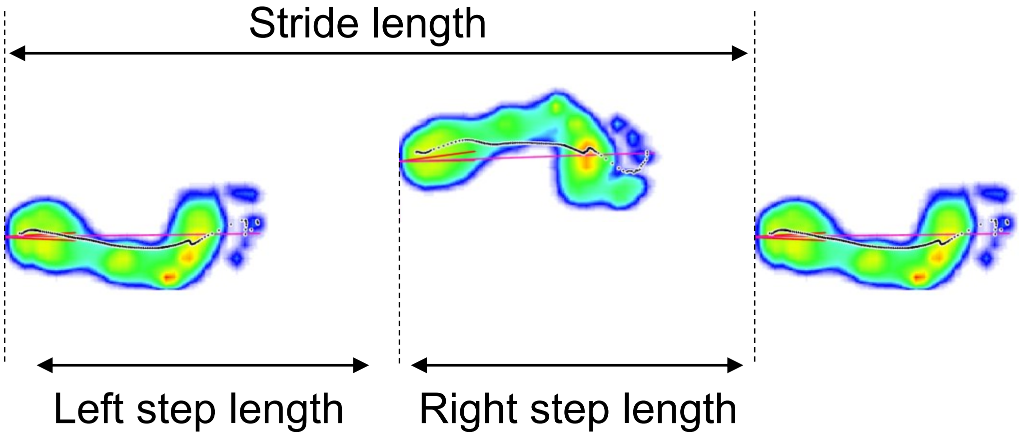
Kinematic Analysis of Multibody Systems

Laboratory data (gait parameters examples):

Step length is the distance between the heel contact point of one foot and that of the other foot.

Stride length is the distance between the successive heel contact points of one foot.

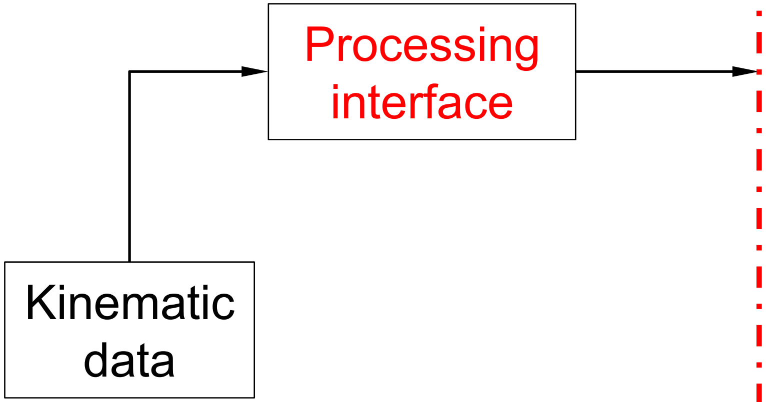
Cadence is the walking rate expressed in steps per minute. The average cadence is 100 – 115 steps/min.



Week 03, Laboratory 03

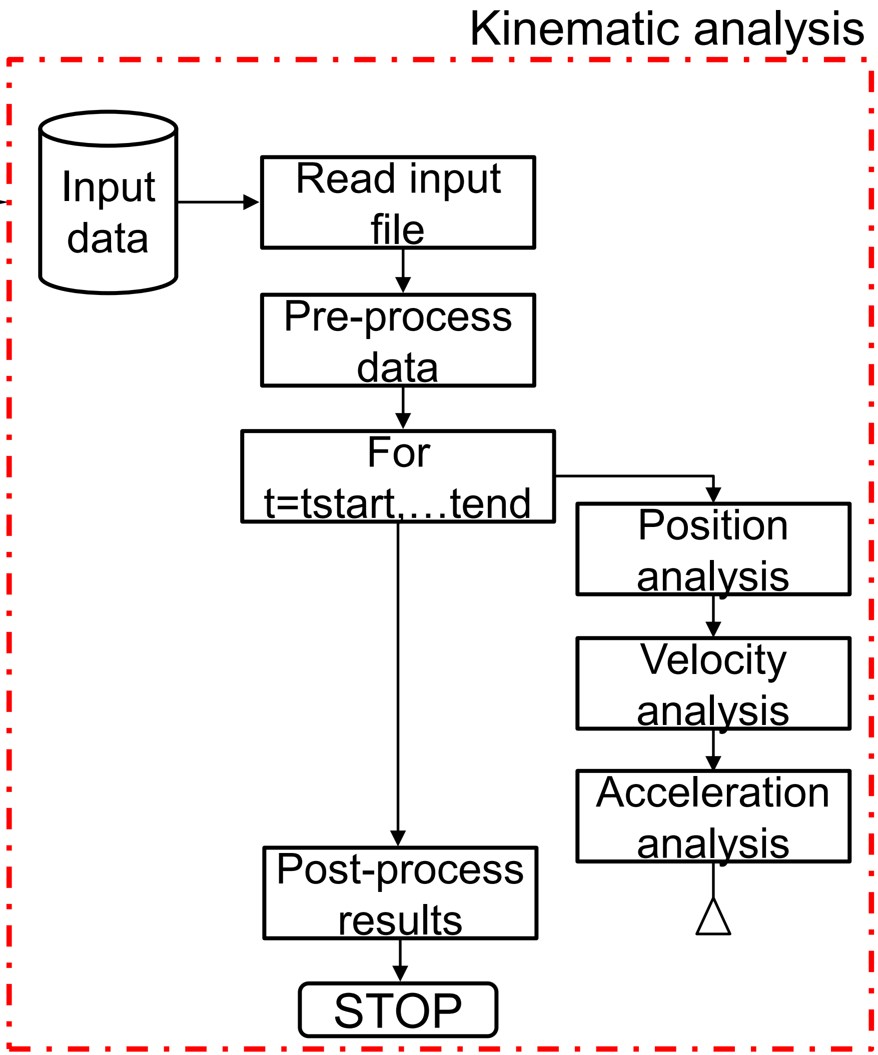
Kinematic Analysis of Multibody Systems

Laboratory data application:



Processing interface

Kinematic data



Kinematic analysis

Input data

Read input file

Pre-process data

For t=tstart,…,tend

Position analysis

Velocity analysis

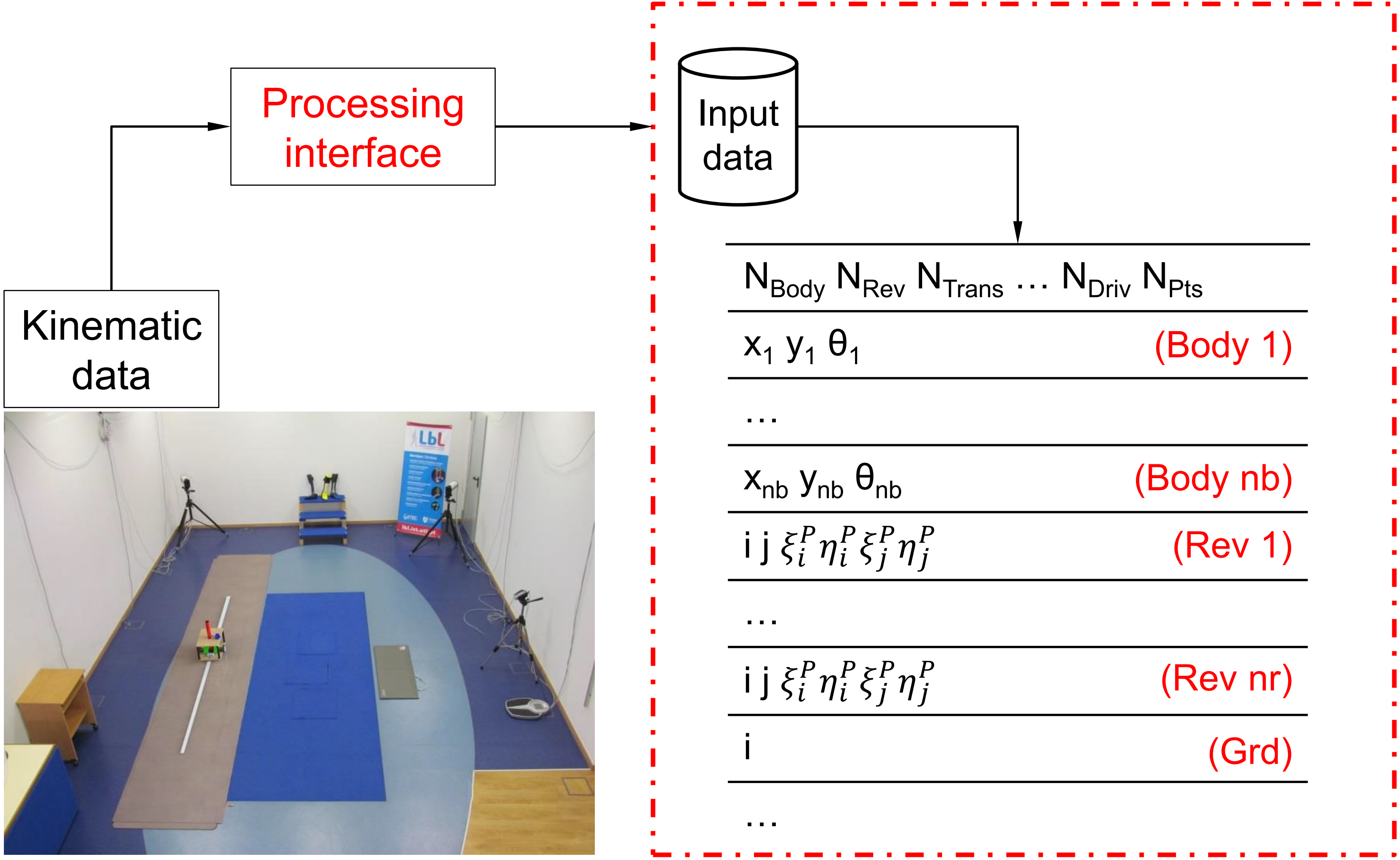
Acceleration analysis

Post-process results

STOP

Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

Laboratory data application:



Kinematic data

Processing interface

Kinematic analysis

Input data

N_{Body} N_{Rev} N_{Trans} … N_{Driv} N_{Pts}

x_1 y_1 θ_1 (Body 1)

…

x_{nb} y_{nb} θ_{nb} (Body nb)

i j $\xi_i^P \eta_i^P \xi_j^P \eta_j^P$ (Rev 1)

…

i j $\xi_i^P \eta_i^P \xi_j^P \eta_j^P$ (Rev nr)

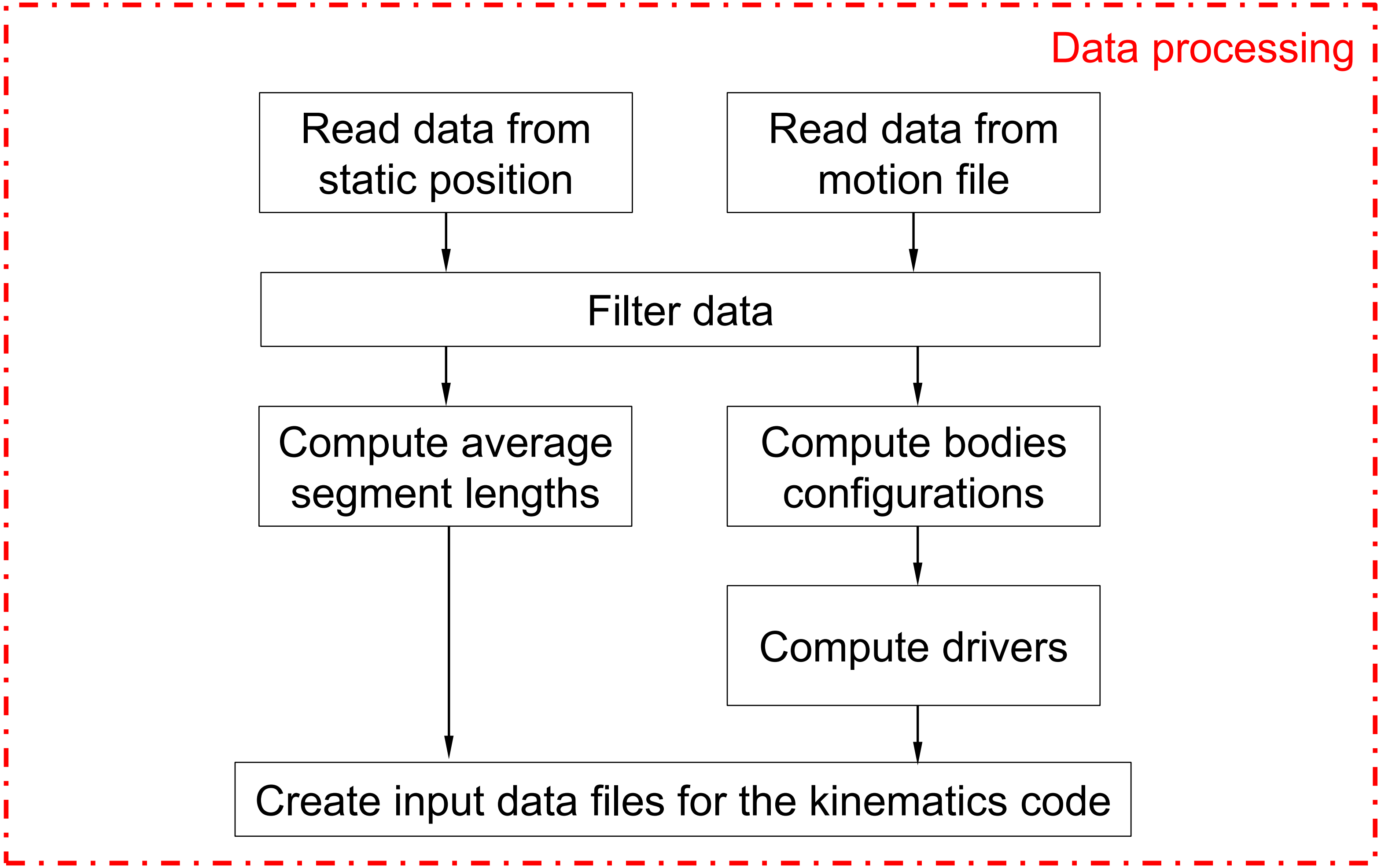
i (Grd)

…

Week 03, Laboratory 03

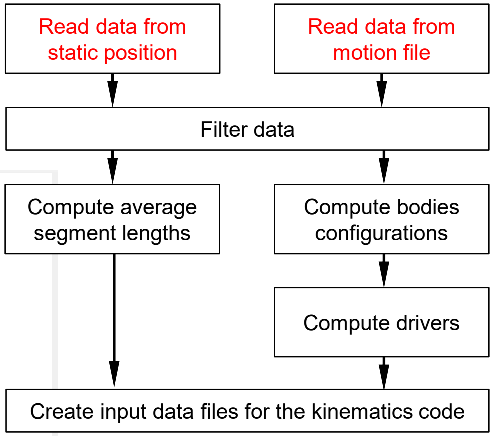
Kinematic Analysis of Multibody Systems

Flowchart of the data processing for the kinematic analysis:



Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

Data structure:


Read data from static position

Read data from motion file

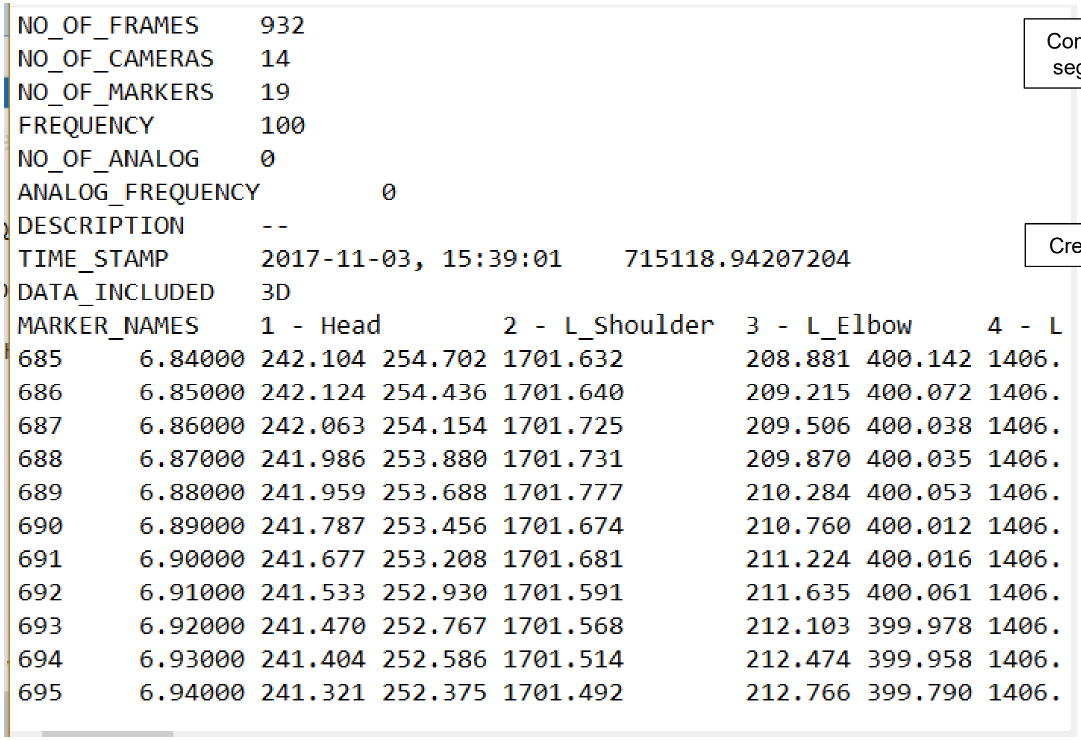
Filter data

Compute average segment lengths

Compute bodies configurations

Compute drivers

Create input data files for the kinematics code



```
NO_OF_FRAMES    932
NO_OF_CAMERAS   14
NO_OF_MARKERS   19
FREQUENCY       100
NO_OF_ANALOG    0
ANALOG_FREQUENCY        0
DESCRIPTION     --
TIME_STAMP      2017-11-03, 15:39:01    715118.94207204
DATA_INCLUDED   3D
MARKER_NAMES    1 - Head        2 - L_Shoulder  3 - L_Elbow     4 - L
685     6.84000 242.104 254.702 1701.632        208.881 400.142 1406.
686     6.85000 242.124 254.436 1701.640        209.215 400.072 1406.
687     6.86000 242.063 254.154 1701.725        209.506 400.038 1406.
688     6.87000 241.986 253.880 1701.731        209.870 400.035 1406.
689     6.88000 241.959 253.688 1701.777        210.284 400.053 1406.
690     6.89000 241.787 253.456 1701.674        210.760 400.012 1406.
691     6.90000 241.677 253.208 1701.681        211.224 400.016 1406.
692     6.91000 241.533 252.930 1701.591        211.635 400.061 1406.
693     6.92000 241.470 252.767 1701.568        212.103 399.978 1406.
694     6.93000 241.404 252.586 1701.514        212.474 399.958 1406.
695     6.94000 241.321 252.375 1701.492        212.766 399.790 1406.
```

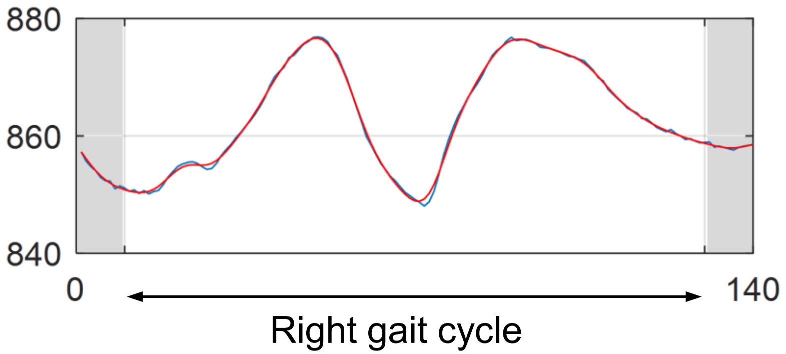
Notice that the coordinates are in the 3D space. For the application in the 2D space, the coordinates must be projected onto the sagittal plane.

Week 03, Laboratory 03

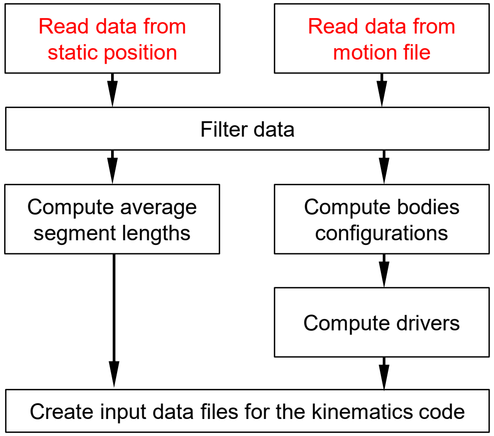
Kinematic Analysis of Multibody Systems

Data structure:

Note: The kinematic data provided for gait include 10 time steps before the beginning of the gait cycle and 10 time steps after.



These time steps are included to have data for the filtering and spline interpolation steps before and after the gait cycle.


Read data from static position

Read data from motion file

Filter data

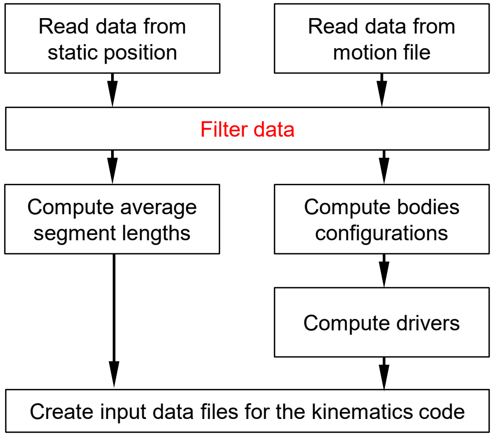
Compute average segment lengths

Compute bodies configurations

Compute drivers

Create input data files for the kinematics code

Data filtering:



Read data from static position

Read data from motion file

Filter data

Compute average segment lengths

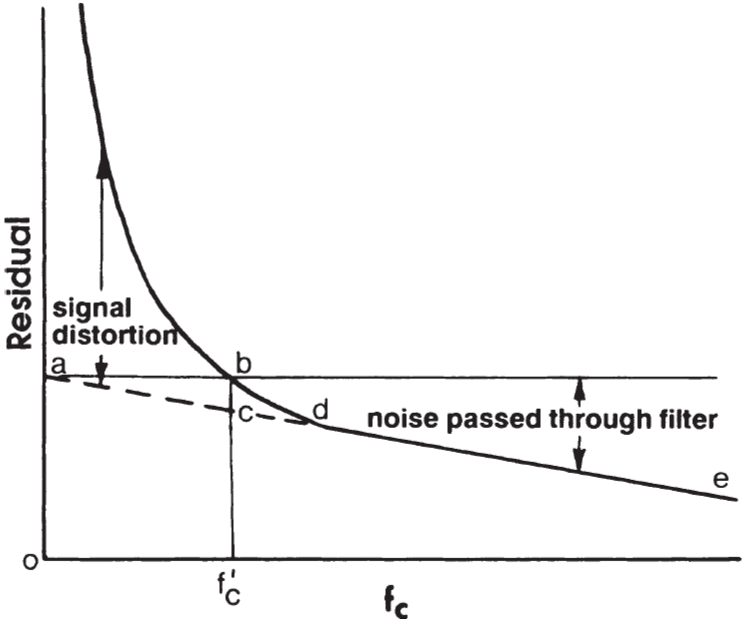
Compute bodies configurations

Compute drivers

Create input data files for the kinematics code

Low-pass filters are widely used to reduce noise levels in reconstructed trajectories.

Several methods exist to define the cut-off frequency (e.g., harmonic analysis, residual analysis).



$$R(f_c) = \sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(X_i - \hat{X}_i\right)^2}$$

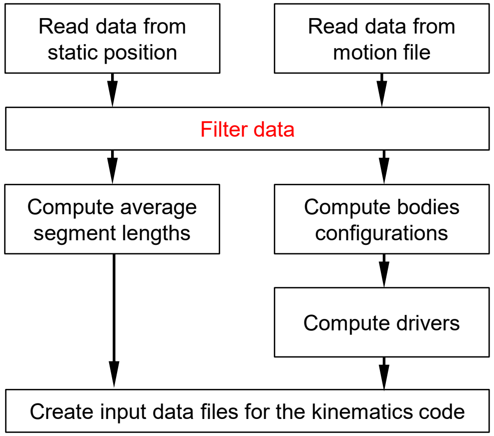
Plot of the residual between a filtered and an unfiltered signal as a function of the filter cutoff frequency; in Winter, 2009, Biomechanics and motor control of human movement**.**

Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

Data filtering:

Low-pass filters are widely used to reduce noise levels in reconstructed trajectories.

Several methods exist to define the cut-off frequency (e.g., harmonic analysis, residual analysis).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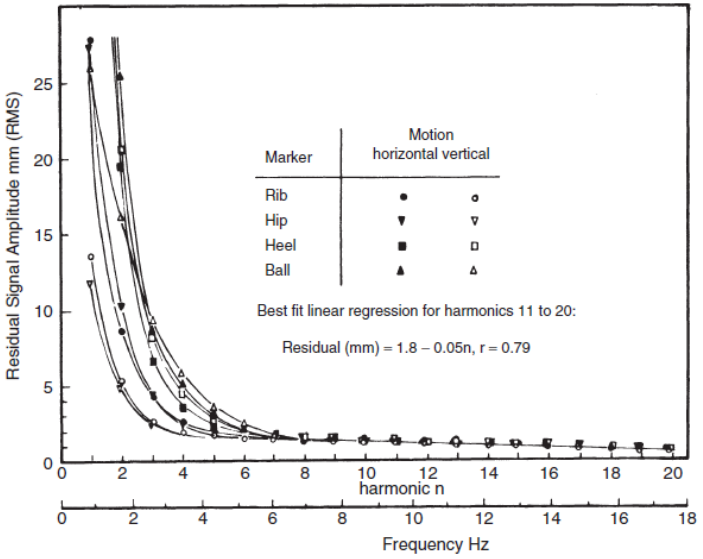
Compute bodies configurations

Compute drivers

Create input data files for the kinematics code



$$R(f_c) = \sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(X_i - \hat{X}_i\right)^2}$$

Plot of the residual of four markers from a walking trial; in Winter, 2009, Biomechanics and motor control of human movement**.**

The cut-off frequencies for a gait cycle are expected to range between 2 and 6 Hz.

Week 03, Laboratory 03

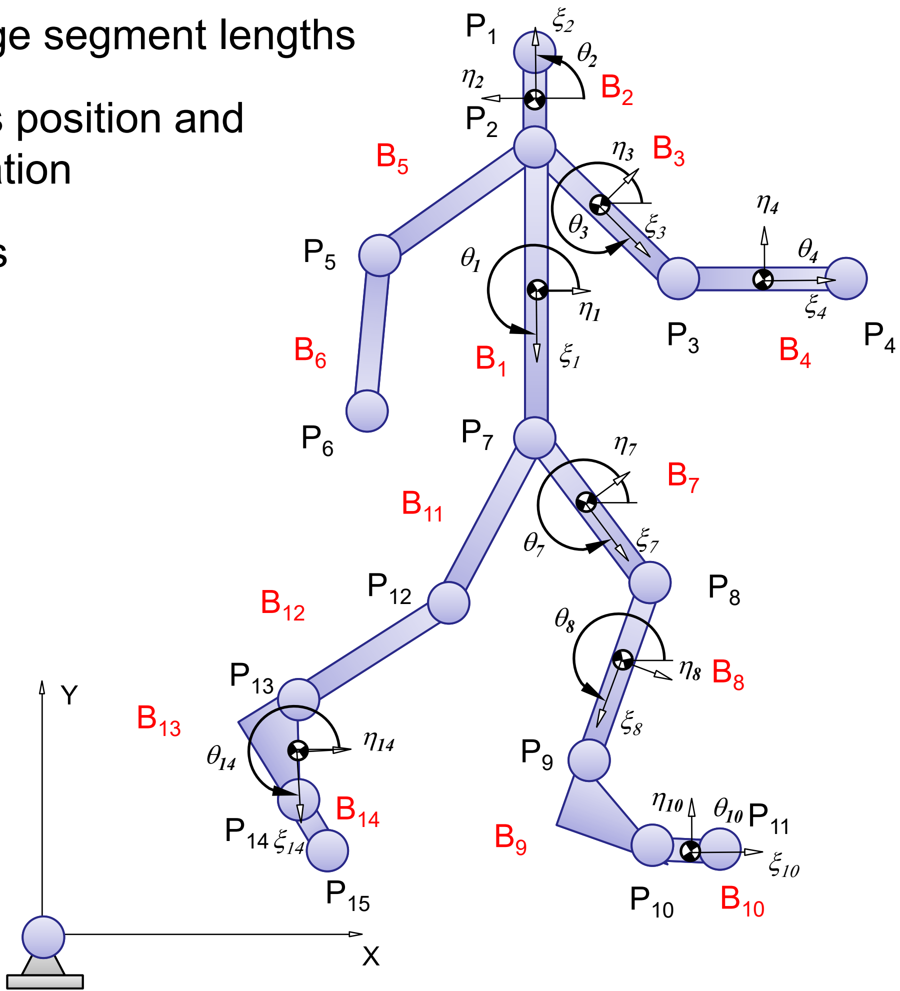
Kinematic Analysis of Multibody Systems

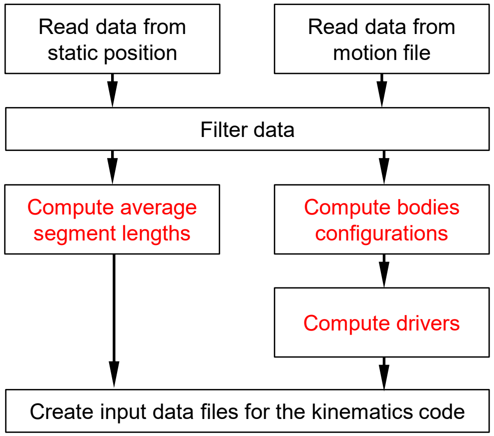
Compute biomechanical data:

Average segment lengths

Bodies position and orientation

Drivers





Read data from static position

Read data from motion file

Filter data

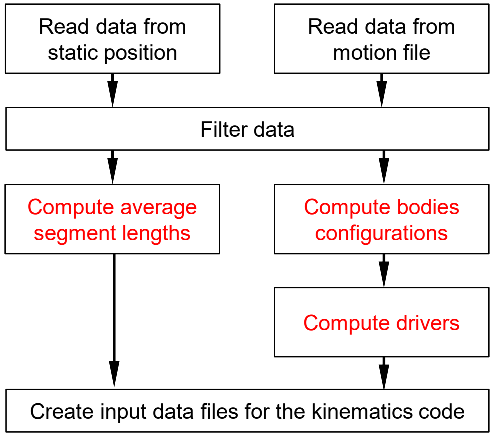
Compute average segment lengths

Compute bodies configurations

Compute drivers

Create input data files for the kinematics code

Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems


Read data from static position

Read data from motion file

Filter data

Compute average segment lengths

Compute bodies configurations

Compute drivers

Create input data files for the kinematics code

Segment lengths:

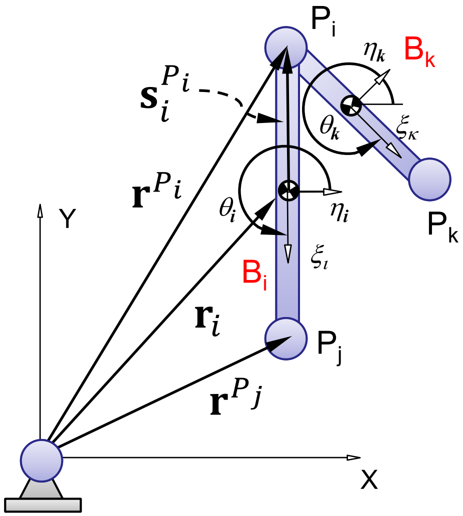
The length of body *i* is given by:

$$L_i = \sqrt{\left(\mathbf{r}^{P_j} - \mathbf{r}^{P_i}\right)^{\mathrm{T}}\left(\mathbf{r}^{P_j} - \mathbf{r}^{P_i}\right)}$$

Due to measuring errors, the length of a segment will be different in each time frame. Therefore, an average length must be computed for each body:

$$L_i = \frac{\sum_{t=0}^{t_f} L_i^t}{n_f}$$

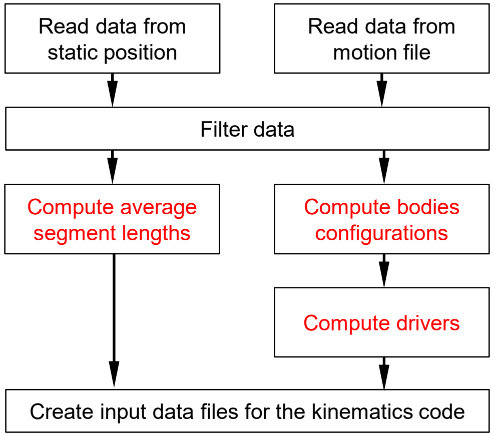
where n_f is the total number of frames.



Week 03, Laboratory 03

Kinematic Analysis of Multibody Systems

Position and orientation of the bodies:



Read data from static position

Read data from motion file

Filter data

Compute average segment lengths

Compute bodies configurations

Compute drivers

Create input data files for the kinematics code

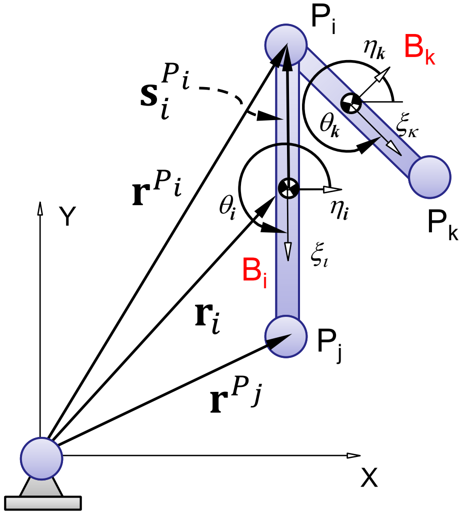
When using Cartesian coordinates, the coordinates required to define the position and orientation of a body are the position and orientation of a body-fixed reference frame:

$$\mathbf{q}_i = \begin{Bmatrix} \mathbf{r}_i \\ \theta_i \end{Bmatrix} = \begin{Bmatrix} x_i \\ y_i \\ \theta_i \end{Bmatrix}$$

The orientation of body i can be defined from points P_i and P_j:

$$\xi\ axis\text{:}\ \frac{\left(\mathbf{r}^{P_j} - \mathbf{r}^{P_i}\right)}{\sqrt{\left(\mathbf{r}^{P_j} - \mathbf{r}^{P_i}\right)^{\mathrm{T}}\left(\mathbf{r}^{P_j} - \mathbf{r}^{P_i}\right)}}$$

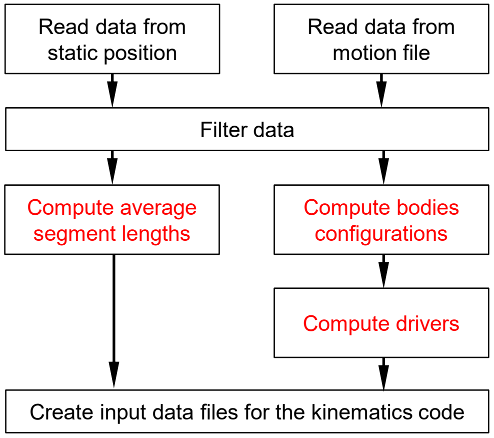
$$\eta\ axis\text{:}\ \perp\ \xi\ axis$$



Week 03, Laboratory 03

Kinematic Analysis of Multibody Systems

Position and orientation of the bodies: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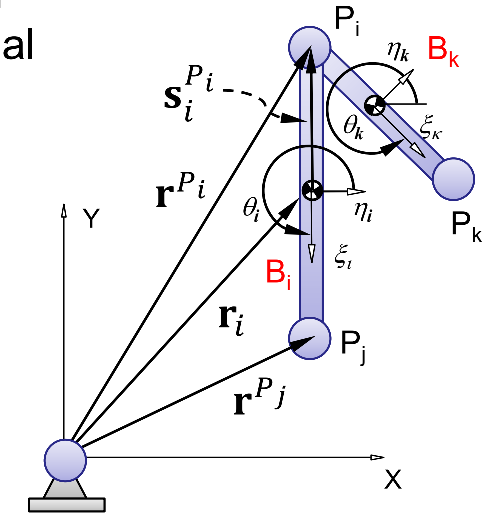
$$\mathbf{q}_i = \begin{Bmatrix}\mathbf{r}_i\\ \theta_i\end{Bmatrix} = \begin{Bmatrix}x_i\\ y_i\\ \theta_i\end{Bmatrix}$$

The position of the center of mass (CoM) can be defined using the relationships between the CoM and the proximal or distal points of the body:

$$\mathbf{r}^{P_i} = \mathbf{r}_i + \mathbf{A}_i \mathbf{s}_i'^{P_i}$$

$$\Rightarrow \mathbf{r}_i = \mathbf{r}^{P_i} - \mathbf{A}_i \mathbf{s}_i'^{P_i}$$

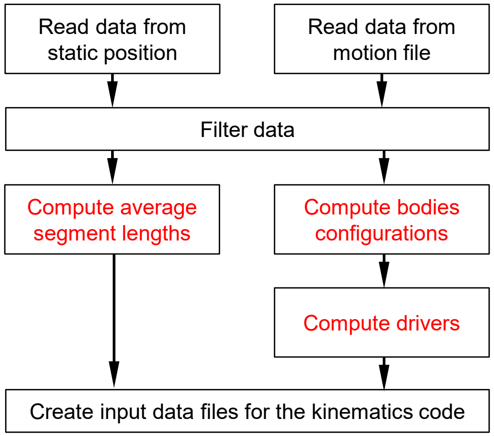


Note: Use an anthropometric table to define the relationships between CoM and the proximal or distal points of a body.

Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

Drivers:

All degrees of freedom (dof) of the biomechanical model must be driven using the data measured in the laboratory.


Read data from static position

Read data from motion file

Filter data

Compute average segment lengths

Compute bodies configurations

Compute drivers

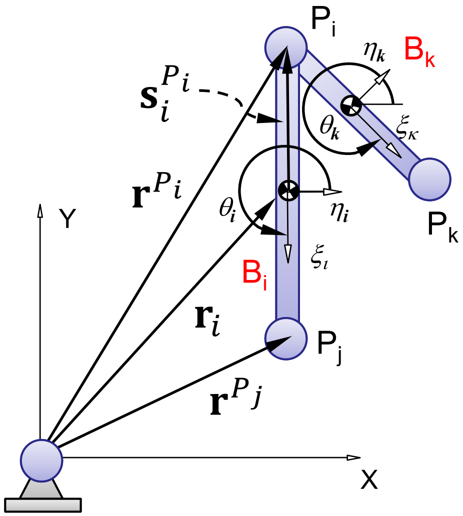
Create input data files for the kinematics code

Drivers' data should be computed considering the driver joints implemented in MuboKAP and MuboDAP.

The following drivers are particularly relevant:

$$\mathbf{\Phi}^{(driv_3,1)} = z - z^*(t),$$

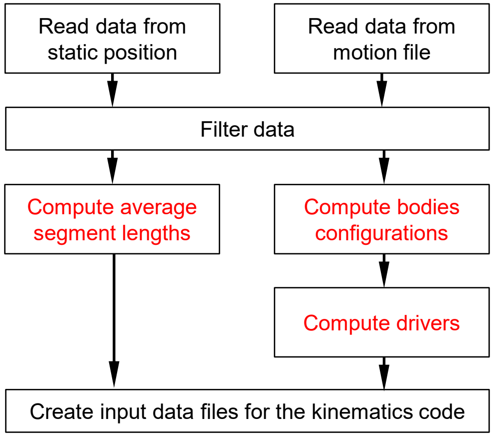
$$\mathbf{\Phi}^{(driv_4,1)} = \theta_j - \theta_i - \theta_{ij}^*(t)$$



Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

Drivers:

All degrees of freedom (dof) of the biomechanical model must be driven using the data measured in the laboratory.



Read data from static position

Read data from motion file

Filter data

Compute average segment lengths

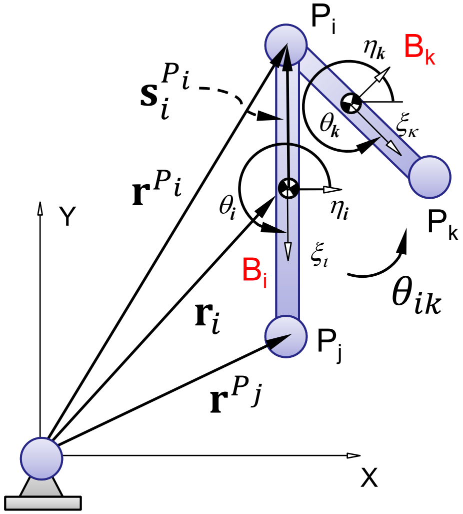
Compute bodies configurations

Compute drivers

Create input data files for the kinematics code

Drivers' data should be written in *.txt files for the kinematics code to read. For instance, for the relative angle between bodies i and k:

t (s)	θ_{ik}^{t} (rad)
0	θ_{ik}^{0}
…	…
t_f	$\theta_{ik}^{t_f}$

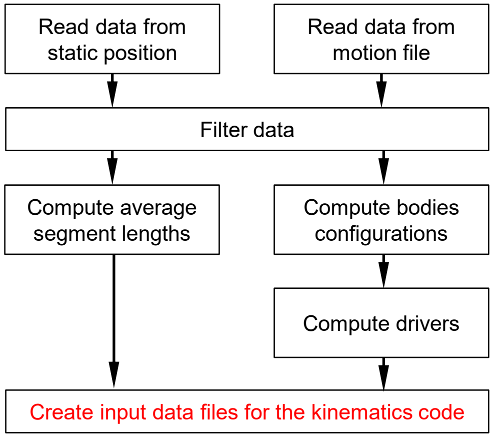


Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

Create input data files:

The input file of the biomechanical system to be read by the kinematic analysis and the drivers must be written:

N_{Body} N_{Rev} N_{Trans} … N_{Driv} N_{Pts}	
x_1 y_1 θ_1	(Body 1)
…	
x_{nb} y_{nb} θ_{nb}	(Body nb)
i j $\xi_i^P \eta_i^P \xi_j^P \eta_j^P$	(Rev 1)
…	
i j $\xi_i^P \eta_i^P \xi_j^P \eta_j^P$	(Rev nr)
i	(Grd)
…	


Read data from static position

Read data from motion file

Filter data

Compute average segment lengths

Compute bodies configurations

Compute drivers

Create input data files for the kinematics code

t (s)	θ_{ik}^{t} (rad)
0	θ_{ik}^{0}
…	…
t_f	$\theta_{ik}^{t_f}$

Week 03, Laboratory 03

Kinematic Analysis of Multibody Systems

Implementation tips (1):

Define the bodies and joints of the biomechanical model.

Identify the markers that define each body and its local reference frame:

P1 – Head

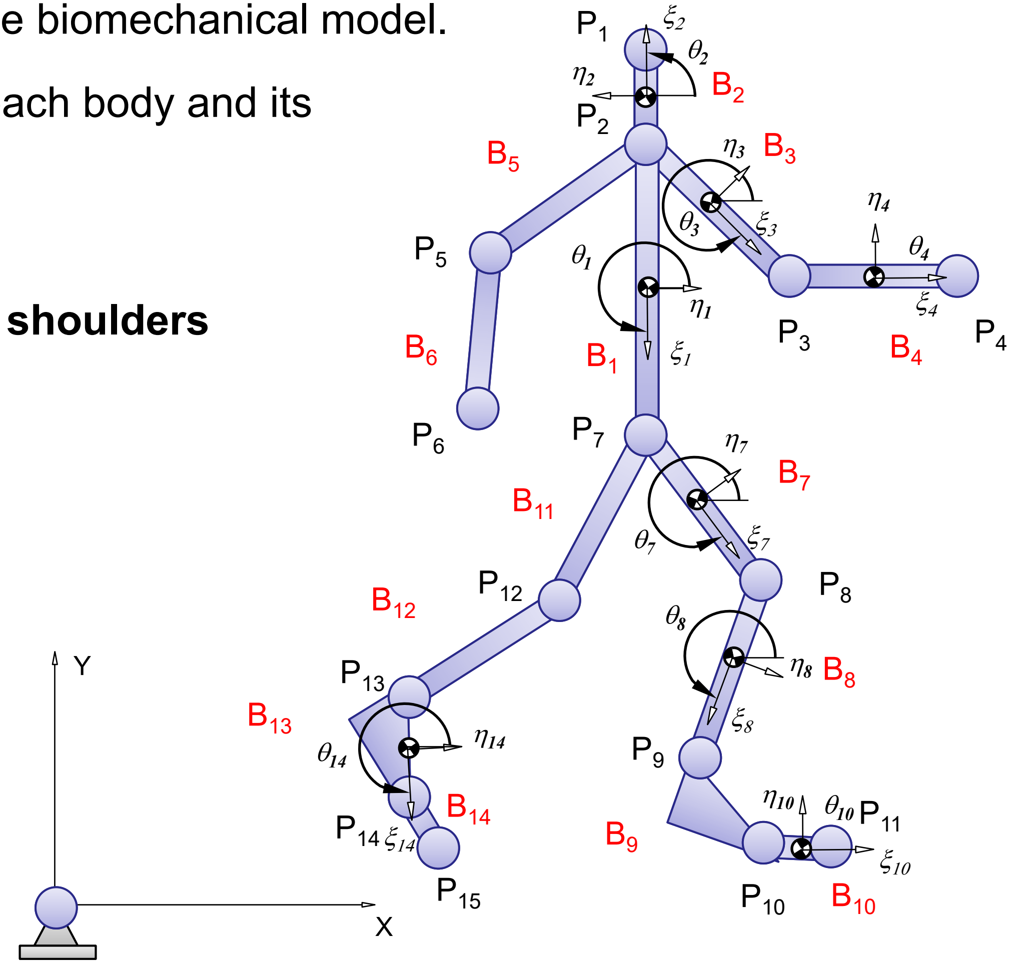
P2 – **Midpoint between shoulders**

P3 – Right elbow

P4 – Right wrist

P5 – Left elbow

…



Implementation tips (2):

Considering a similar structure as that of the input file of the kinematics code, build a processing file to organize the data for the processing code.

Compute average segment lengths

Compute the position and orientation of the bodies for all time frames

Compute drivers

Processing file

N_{Body} N_{Rev} N_{Trans} … N_{Driv} N_{Pts}

---

x_1 y_1 θ_1

…

x_{nb} y_{nb} θ_{nb}

---

i j $\xi_i^P \eta_i^P \xi_j^P \eta_j^P$

…

i j $\xi_i^P \eta_i^P \xi_j^P \eta_j^P$

---

i

…

Input file (kinematics code)

Week 03, Laboratory 03

Kinematic Analysis of Multibody Systems

Implementation tips (2):

Considering a similar structure as that of the input file of the kinematics code, build a processing file to organize the data for the processing code.

N_{Body} N_{Rev} N_{Trans} … N_{Driv} N_{Pts}

P_2 P_7 ξ_1^{CoM}/L_1
…
P_{m-1} P_m ξ_{nb}^{CoM}/L_{nb}

i j $\xi_i^P/L_i\ \ \eta_i^P/L_i\ \ \xi_j^P/L_j\ \ \eta_j^P/L_j$
…
k l $\xi_k^P/L_k\ \ \eta_k^P/L_k\ \ \xi_l^P/L_l\ \ \eta_l^P/L_l$

i

…

Processing file

N_{Body} N_{Rev} N_{Trans} … N_{Driv} N_{Pts}

x_1 y_1 θ_1
…
x_{nb} y_{nb} θ_{nb}

i j $\xi_i^P \eta_i^P \xi_j^P \eta_j^P$
…
i j $\xi_i^P \eta_i^P \xi_j^P \eta_j^P$

i

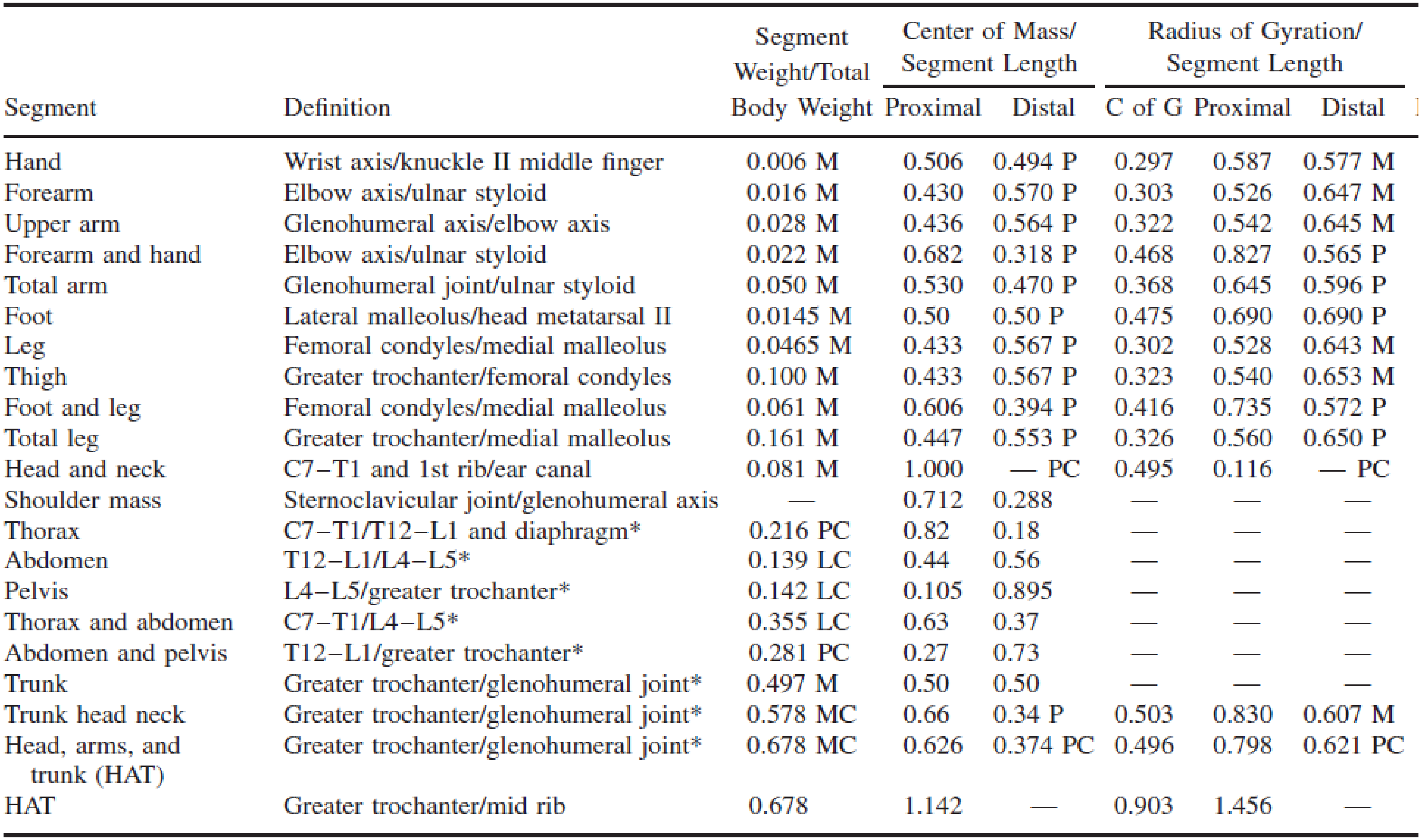
…

Input file (kinematics code)

Week 03, Laboratory 03

Kinematic Analysis of Multibody Systems

Anthropometry:



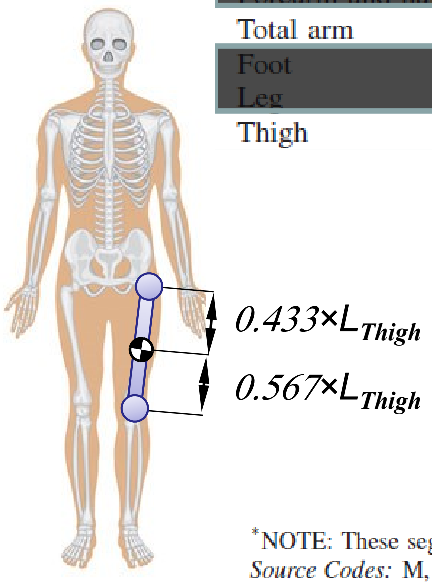
Segment	Definition	Segment Weight/Total Body Weight	Center of Mass/ Segment Length		Radius of Gyration/ Segment Length		
			Proximal	Distal	C of G	Proximal	Distal
Hand	Wrist axis/knuckle II middle finger	0.006 M	0.506	0.494 P	0.297	0.587	0.577 M
Forearm	Elbow axis/ulnar styloid	0.016 M	0.430	0.570 P	0.303	0.526	0.647 M
Upper arm	Glenohumeral axis/elbow axis	0.028 M	0.436	0.564 P	0.322	0.542	0.645 M
Forearm and hand	Elbow axis/ulnar styloid	0.022 M	0.682	0.318 P	0.468	0.827	0.565 P
Total arm	Glenohumeral joint/ulnar styloid	0.050 M	0.530	0.470 P	0.368	0.645	0.596 P
Foot	Lateral malleolus/head metatarsal II	0.0145 M	0.50	0.50 P	0.475	0.690	0.690 P
Leg	Femoral condyles/medial malleolus	0.0465 M	0.433	0.567 P	0.302	0.528	0.643 M
Thigh	Greater trochanter/femoral condyles	0.100 M	0.433	0.567 P	0.323	0.540	0.653 M
Foot and leg	Femoral condyles/medial malleolus	0.061 M	0.606	0.394 P	0.416	0.735	0.572 P
Total leg	Greater trochanter/medial malleolus	0.161 M	0.447	0.553 P	0.326	0.560	0.650 P
Head and neck	C7–T1 and 1st rib/ear canal	0.081 M	1.000	— PC	0.495	0.116	— PC
Shoulder mass	Sternoclavicular joint/glenohumeral axis	—	0.712	0.288	—	—	—
Thorax	C7–T1/T12–L1 and diaphragm*	0.216 PC	0.82	0.18	—	—	—
Abdomen	T12–L1/L4–L5*	0.139 LC	0.44	0.56	—	—	—
Pelvis	L4–L5/greater trochanter*	0.142 LC	0.105	0.895	—	—	—
Thorax and abdomen	C7–T1/L4–L5*	0.355 LC	0.63	0.37	—	—	—
Abdomen and pelvis	T12–L1/greater trochanter*	0.281 PC	0.27	0.73	—	—	—
Trunk	Greater trochanter/glenohumeral joint*	0.497 M	0.50	0.50	—	—	—
Trunk head neck	Greater trochanter/glenohumeral joint*	0.578 MC	0.66	0.34 P	0.503	0.830	0.607 M
Head, arms, and trunk (HAT)	Greater trochanter/glenohumeral joint*	0.678 MC	0.626	0.374 PC	0.496	0.798	0.621 PC
HAT	Greater trochanter/mid rib	0.678	1.142	—	0.903	1.456	—

Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

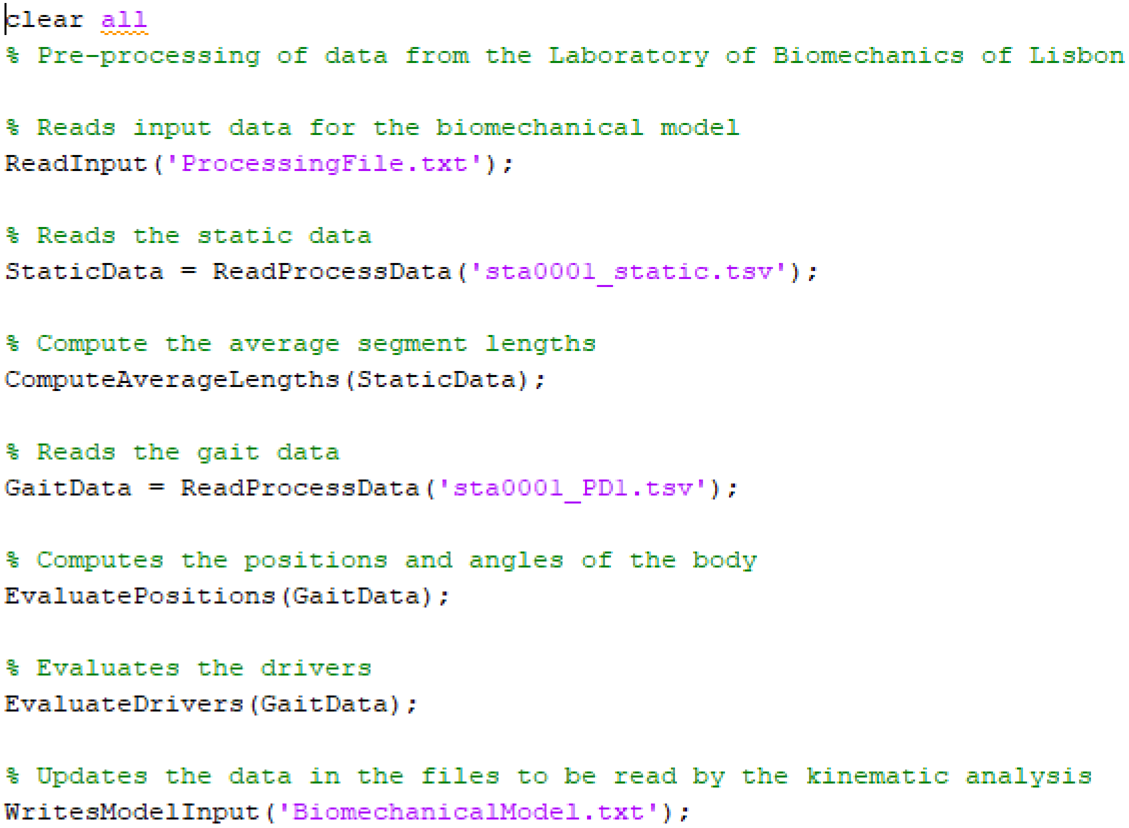
Anthropometry:

Segment	Definition	Segment Weight/Total Body Weight	Center of Mass/ Segment Length Proximal	Center of Mass/ Segment Length Distal	Radius of Gyration/ Segment Length C of G	Radius of Gyration/ Segment Length Proximal	Radius of Gyration/ Segment Length Distal
Hand	Wrist axis/knuckle II middle finger	0.006 M	0.506	0.494 P	0.297	0.587	0.577 M
Forearm	Elbow axis/ulnar styloid	0.016 M	0.430	0.570 P	0.303	0.526	0.647 M
Upper arm	Glenohumeral axis/elbow axis	0.028 M	0.436	0.564 P	0.322	0.542	0.645 M
Forearm and hand	Elbow axis/ulnar styloid	0.022 M	0.682	0.318 P	0.468	0.827	0.565 P
Total arm	Glenohumeral joint/ulnar styloid	0.050 M	0.530	0.470 P	0.368	0.645	0.596 P
Foot	Lateral malleolus/head metatarsal II	0.0145 M	0.50	0.50 P	0.475	0.690	0.690 P
Leg	Femoral condyles/medial malleolus	0.0465 M	0.433	0.567 P	0.302	0.528	0.643 M
Thigh	Greater trochanter/femoral condyles	0.100 M	0.433	0.567 P	0.323	0.540	0.653 M

*NOTE: These segments are presented relative to the length between the greater trochanter and the glenohumeral joint.
Source Codes: M, Dempster via Miller and Nelson; *Biomechanics of Sport*, Lea and Febiger, Philadelphia, 1973. P, Dempster via Plagenhoef; *Patterns of Human Motion*, Prentice-Hall, Inc. Englewood Cliffs, NJ, 1971. L, Dempster via Plagenhoef from living subjects; *Patterns of Human Motion*, Prentice-Hall, Inc., Englewood Cliffs, NJ, 1971. C, Calculated.

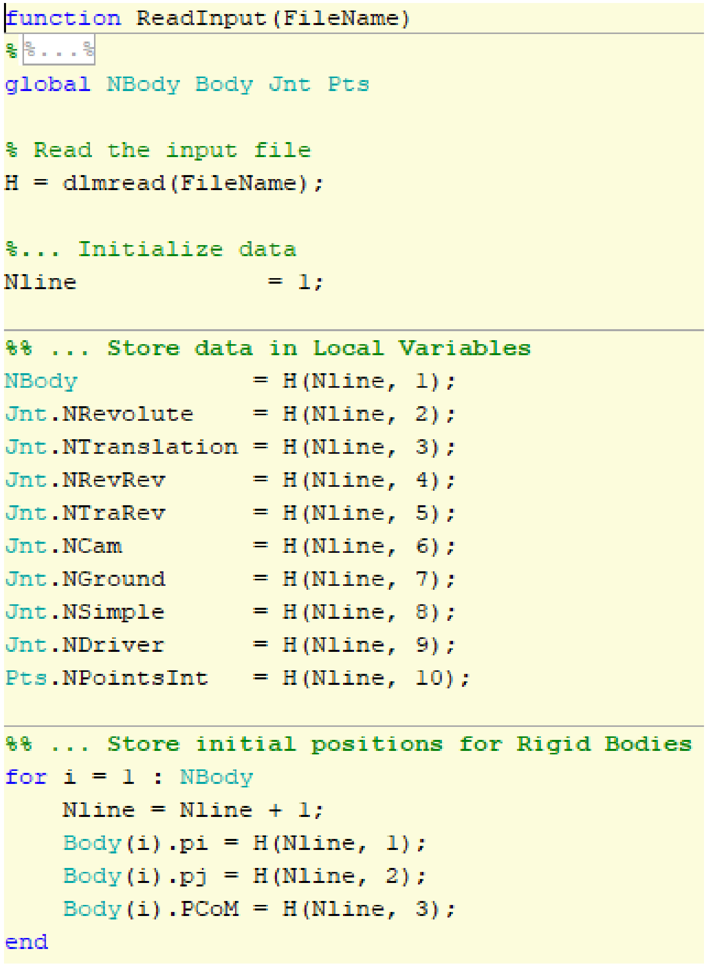


Matlab code – main function:

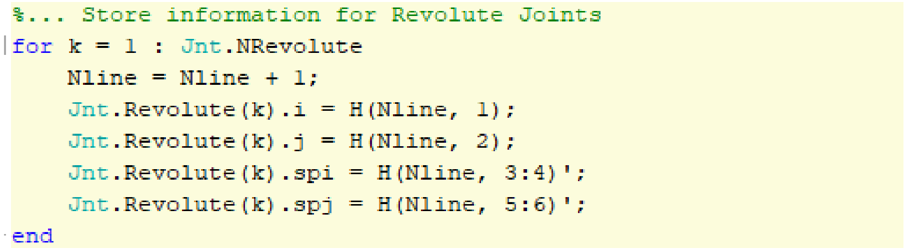


```
clear all
% Pre-processing of data from the Laboratory of Biomechanics of Lisbon

% Reads input data for the biomechanical model
ReadInput('ProcessingFile.txt');

% Reads the static data
StaticData = ReadProcessData('sta0001_static.tsv');

% Compute the average segment lengths
ComputeAverageLengths(StaticData);

% Reads the gait data
GaitData = ReadProcessData('sta0001_PD1.tsv');

% Computes the positions and angles of the body
EvaluatePositions(GaitData);

% Evaluates the drivers
EvaluateDrivers(GaitData);

% Updates the data in the files to be read by the kinematic analysis
WritesModelInput('BiomechanicalModel.txt');
```

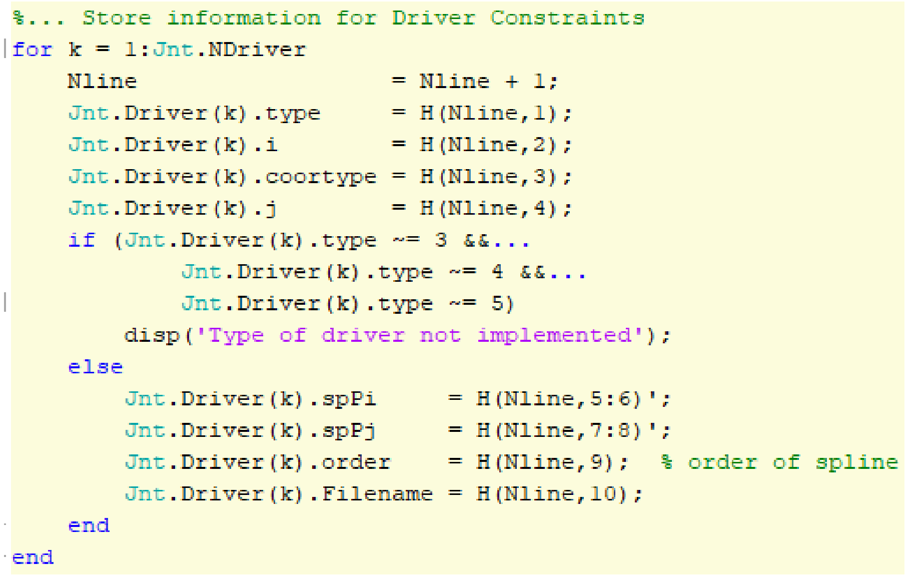
Matlab code – ReadInput (excerpts):



```
function ReadInput(FileName)
% %...%
global NBody Body Jnt Pts

% Read the input file
H = dlmread(FileName);

%... Initialize data
Nline              = 1;

%% ... Store data in Local Variables
NBody            = H(Nline, 1);
Jnt.NRevolute    = H(Nline, 2);
Jnt.NTranslation = H(Nline, 3);
Jnt.NRevRev      = H(Nline, 4);
Jnt.NTraRev      = H(Nline, 5);
Jnt.NCam         = H(Nline, 6);
Jnt.NGround      = H(Nline, 7);
Jnt.NSimple      = H(Nline, 8);
Jnt.NDriver      = H(Nline, 9);
Pts.NPointsInt   = H(Nline, 10);

%% ... Store initial positions for Rigid Bodies
for i = 1 : NBody
    Nline = Nline + 1;
    Body(i).pi = H(Nline, 1);
    Body(i).pj = H(Nline, 2);
    Body(i).PCoM = H(Nline, 3);
end
```



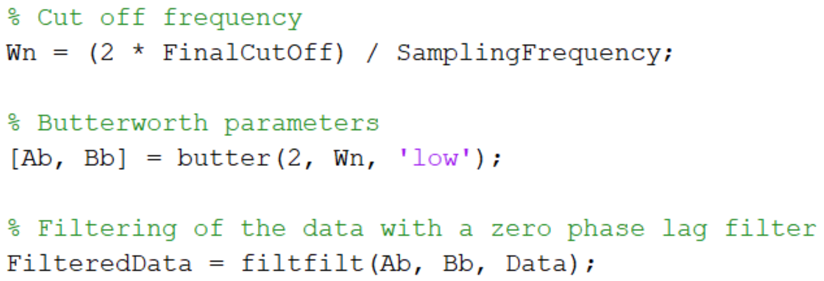
```
%... Store information for Revolute Joints
for k = 1 : Jnt.NRevolute
    Nline = Nline + 1;
    Jnt.Revolute(k).i = H(Nline, 1);
    Jnt.Revolute(k).j = H(Nline, 2);
    Jnt.Revolute(k).spi = H(Nline, 3:4)';
    Jnt.Revolute(k).spj = H(Nline, 5:6)';
end
```



```
%... Store information for Driver Constraints
for k = 1:Jnt.NDriver
    Nline                  = Nline + 1;
    Jnt.Driver(k).type      = H(Nline,1);
    Jnt.Driver(k).i         = H(Nline,2);
    Jnt.Driver(k).coortype = H(Nline,3);
    Jnt.Driver(k).j         = H(Nline,4);
    if (Jnt.Driver(k).type ~= 3 &&...
            Jnt.Driver(k).type ~= 4 &&...
            Jnt.Driver(k).type ~= 5)
        disp('Type of driver not implemented');
    else
        Jnt.Driver(k).spPi      = H(Nline,5:6)';
        Jnt.Driver(k).spPj      = H(Nline,7:8)';
        Jnt.Driver(k).order     = H(Nline,9);  % order of spline
        Jnt.Driver(k).Filename = H(Nline,10);
    end
end
```

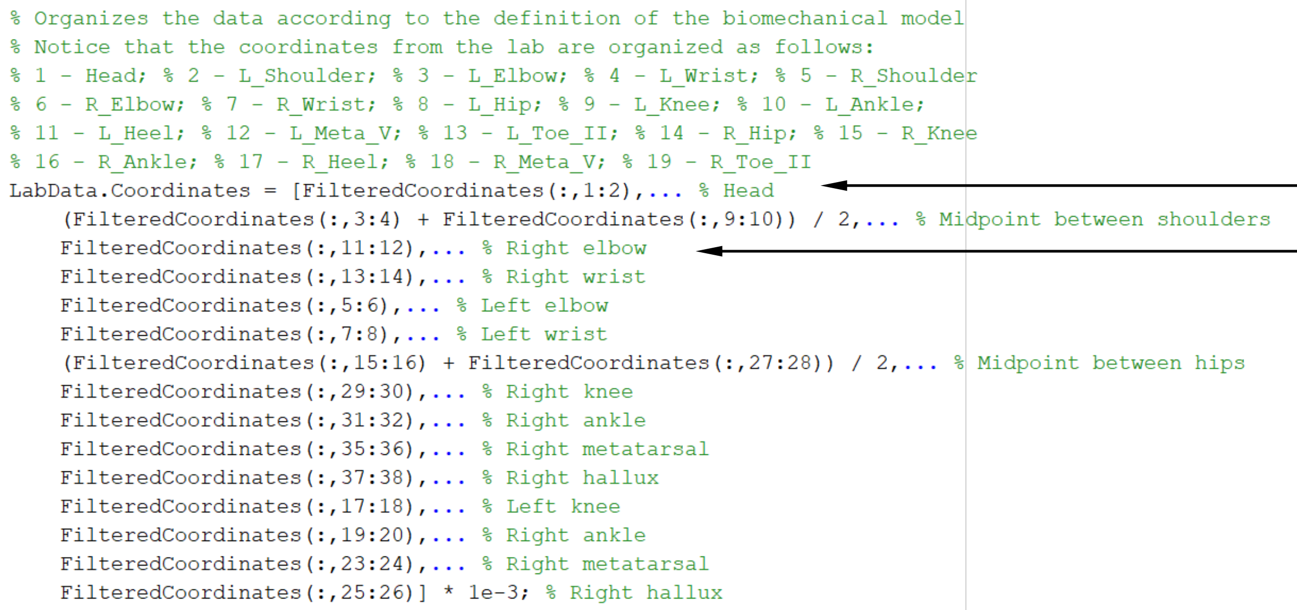
...

Matlab code – ReadProcessData (excerpts):



```
% Cut off frequency
Wn = (2 * FinalCutOff) / SamplingFrequency;

% Butterworth parameters
[Ab, Bb] = butter(2, Wn, 'low');

% Filtering of the data with a zero phase lag filter
FilteredData = filtfilt(Ab, Bb, Data);
```

Filtering



```
% Organizes the data according to the definition of the biomechanical model
% Notice that the coordinates from the lab are organized as follows:
% 1 - Head; % 2 - L_Shoulder; % 3 - L_Elbow; % 4 - L_Wrist; % 5 - R_Shoulder
% 6 - R_Elbow; % 7 - R_Wrist; % 8 - L_Hip; % 9 - L_Knee; % 10 - L_Ankle;
% 11 - L_Heel; % 12 - L_Meta_V; % 13 - L_Toe_II; % 14 - R_Hip; % 15 - R_Knee
% 16 - R_Ankle; % 17 - R_Heel; % 18 - R_Meta_V; % 19 - R_Toe_II
LabData.Coordinates = [FilteredCoordinates(:,1:2),... % Head
    (FilteredCoordinates(:,3:4) + FilteredCoordinates(:,9:10)) / 2,... % Midpoint between shoulders
    FilteredCoordinates(:,11:12),... % Right elbow
    FilteredCoordinates(:,13:14),... % Right wrist
    FilteredCoordinates(:,5:6),... % Left elbow
    FilteredCoordinates(:,7:8),... % Left wrist
    (FilteredCoordinates(:,15:16) + FilteredCoordinates(:,27:28)) / 2,... % Midpoint between hips
    FilteredCoordinates(:,29:30),... % Right knee
    FilteredCoordinates(:,31:32),... % Right ankle
    FilteredCoordinates(:,35:36),... % Right metatarsal
    FilteredCoordinates(:,37:38),... % Right hallux
    FilteredCoordinates(:,17:18),... % Left knee
    FilteredCoordinates(:,19:20),... % Right ankle
    FilteredCoordinates(:,23:24),... % Right metatarsal
    FilteredCoordinates(:,25:26)] * 1e-3; % Right hallux
```

P_1

P_2

P_3

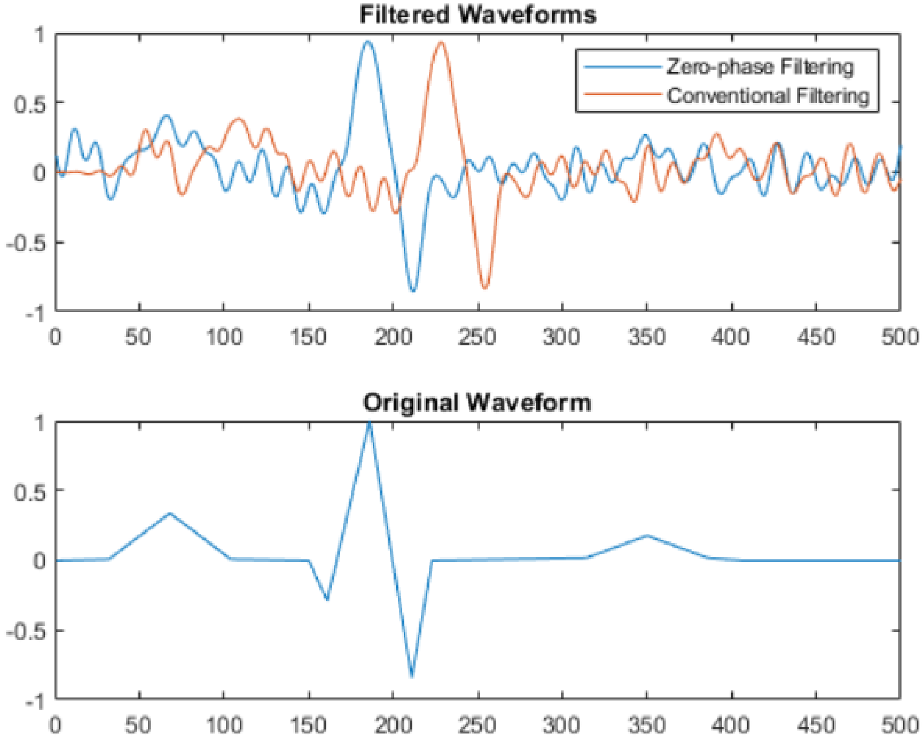
...

Organization of the data

Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

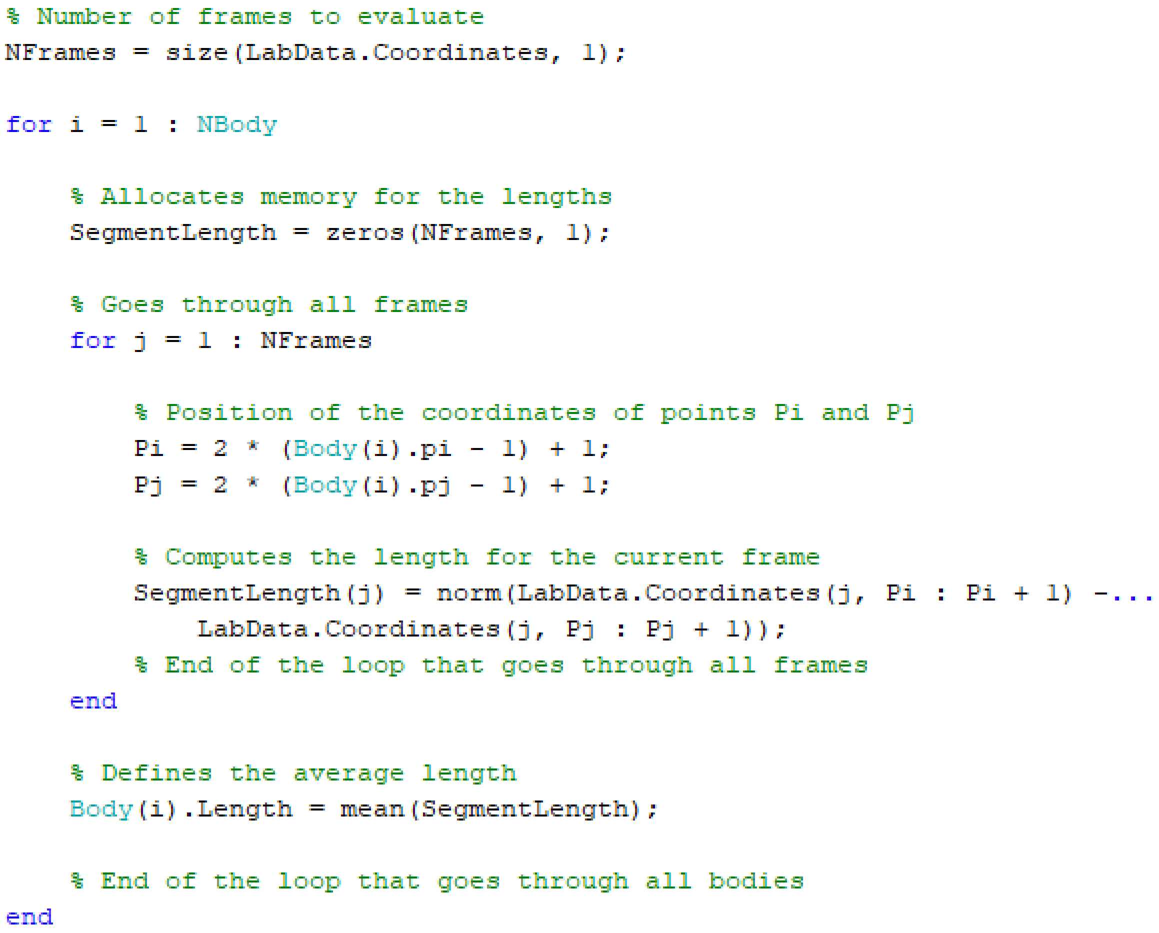
Matlab code – ReadProcessData:

A double filtering procedure (double pass) is required to remove phase shift.



Zero-phase filtering versus conventional filtering; in Mathworks documentation, filtfilt function.

Matlab code – ComputeAverageLengths (excerpt):



```
% Number of frames to evaluate
NFrames = size(LabData.Coordinates, 1);

for i = 1 : NBody

    % Allocates memory for the lengths
    SegmentLength = zeros(NFrames, 1);

    % Goes through all frames
    for j = 1 : NFrames

        % Position of the coordinates of points Pi and Pj
        Pi = 2 * (Body(i).pi - 1) + 1;
        Pj = 2 * (Body(i).pj - 1) + 1;

        % Computes the length for the current frame
        SegmentLength(j) = norm(LabData.Coordinates(j, Pi : Pi + 1) -...
            LabData.Coordinates(j, Pj : Pj + 1));
        % End of the loop that goes through all frames
    end

    % Defines the average length
    Body(i).Length = mean(SegmentLength);

    % End of the loop that goes through all bodies
end
```

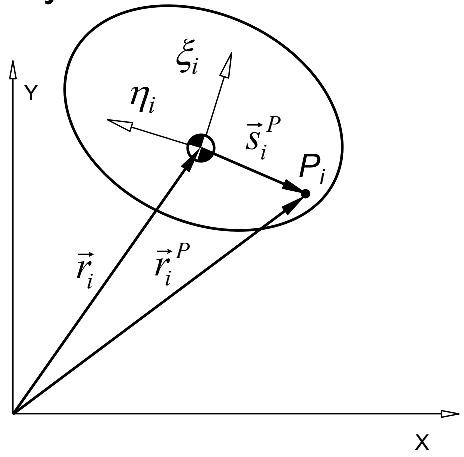
Week 03, Laboratory 03

Kinematic Analysis of Multibody Systems (Review)

Modeling with Cartesian coordinates:

The position of a point belonging to a rigid body *i* is described by:

$$\mathbf{r}_i^P = \mathbf{r}_i + \mathbf{s}_i^P$$



It is convenient to express positions of points of a rigid body in coordinates of the body-fixed coordinate frame

$$\mathbf{s}_i^P = \mathbf{A}_i \mathbf{s}_i'^P \Rightarrow s_i^P = \begin{bmatrix} \cos\theta_i & -\sin\theta_i \\ \sin\theta_i & \cos\theta_i \end{bmatrix} \begin{Bmatrix} \xi_i \\ \eta_i \end{Bmatrix}$$

The following quantities are broadly used in the formulation of all methods addressed in this course:

$\mathbf{r}_i^P = \{x_i^P \quad y_i^P\}^{\mathrm{T}}$	Global position of point P belonging to body *i*
$\mathbf{A}_i = \begin{bmatrix} \cos\theta_i & -\sin\theta_i \\ \sin\theta_i & \cos\theta_i \end{bmatrix}$	Transformation matrix of body *i*
$\mathbf{s}_i'^P = \{\xi_i^P \quad \eta_i^P\}^{\mathrm{T}}$	Position of point P in the body-fixed frame of body *i*

Week 03, Laboratory 03

Kinematic Analysis of Multibody Systems (Review)

Kinematic Analysis:

Position analysis (requires solving a system of nonlinear equations using, for instance, the Newton-Raphson Method):

$$\boldsymbol{\Phi}(\mathbf{q},t)=\mathbf{0}\Rightarrow\begin{cases}\mathbf{q}_{i+1}=\mathbf{q}_i-\left[\boldsymbol{\Phi}_{\mathbf{q}_i}\left(\mathbf{q}_i,t\right)\right]^{-1}\boldsymbol{\Phi}\left(\mathbf{q}_i,t\right)\\ \left|\mathbf{q}_i-\mathbf{q}_{i+1}\right|\leq\varepsilon\end{cases}$$

$$\boldsymbol{\Phi}_{\mathbf{q}}\left(\mathbf{q}_i\right)=\begin{bmatrix}\dfrac{\partial\Phi_1}{\partial q_1} & \cdots & \dfrac{\partial\Phi_1}{\partial q_n}\\ \vdots & \ddots & \vdots\\ \dfrac{\partial\Phi_n}{\partial q_1} & \cdots & \dfrac{\partial\Phi_n}{\partial q_n}\end{bmatrix}$$

Velocity analysis (requires solving a system of linear equations):

$$\dot{\boldsymbol{\Phi}}\left(\mathbf{q},t\right)\equiv\quad\boldsymbol{\Phi}_{\mathbf{q}}\dot{\mathbf{q}}=\boldsymbol{\nu}$$

$$\boldsymbol{\nu}=-\frac{\partial\boldsymbol{\Phi}}{\partial t}$$

Acceleration analysis (requires solving a system of linear equations):

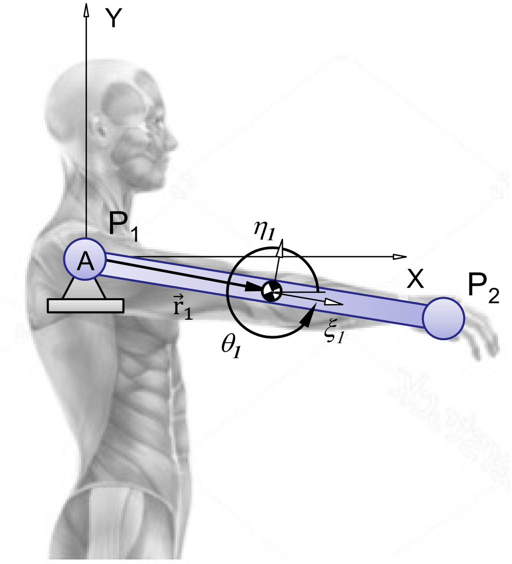
$$\ddot{\boldsymbol{\Phi}}\left(\mathbf{q},\dot{\mathbf{q}},t\right)\equiv\quad\boldsymbol{\Phi}_{\mathbf{q}}\ddot{\mathbf{q}}=\boldsymbol{\gamma}$$

$$\boldsymbol{\gamma}=-\frac{\partial^2\boldsymbol{\Phi}}{\partial t^2}-\left(\boldsymbol{\Phi}_{\mathbf{q}}\dot{\mathbf{q}}\right)_{\mathbf{q}}\dot{\mathbf{q}}$$

Week 03, Laboratory 03
Kinematic Analysis of Multibody Systems

Homework Exercise :

Considering the coordinates $\mathbf{r}_1 = \{x_1 \quad y_1\}^{\mathrm{T}}$, and *θ₁* for the arm segment:



a) If $\mathbf{r}_1 = \left\{\frac{\sqrt{2}}{4} \quad \frac{\sqrt{2}}{4}\right\}^{\mathrm{T}}$, $\theta_1 = \frac{\pi}{4}$, and $\boldsymbol{s}_1'^{\mathrm{P}_2} = \left\{\frac{1}{2} \quad 0\right\}^{\mathrm{T}}$, compute the global coordinates of point P_2.

b) If $\mathbf{r}^{\mathrm{P}_3} = \left\{\frac{\sqrt{2}}{16} \quad 0\right\}^{\mathrm{T}}$, determine the local coordinates of Point P_3.

c) Determine the number of dof of the system. Write the constraint equations. For the driver constraint, consider that the body is rotating with a frequency *w* ($\boldsymbol{\Phi}^{driv} = \theta_1 - wt$).

d) Determine the Jacobian matrix and write the velocity and acceleration equations for the system.