

The Delft Shoulder and Elbow Model (DSEM) User's Guide

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1 Introduction

The Delft Shoulder and Elbow Model (DSEM) is a finite-element, musculoskeletal model of the upper limb based on the SPACAR software for mechanical analysis (Jonker (1988)). In this model each anatomical structure is represented by an appropriate element type (van Der Helm (1994)). Bones are modelled as rigid bodies, muscles as active trusses (tensile force generating elements) and ligaments as passive trusses (passive elements which can only be loaded in tension). Each node of the finite element model represents an anatomically important structure, such as a joint rotation centre, ligament attachment point or muscle attachment point. More information about the structure can be obtained by examining the parameter file *.dsp.

The inverse version of the model uses the motions of the bones as input, together with the external loading, and internal forces and moments are calculated using an inverse-dynamic optimisation method. Output from the model consists of the resulting joint contact forces, ligament forces and muscle forces, lengths and moment arms.

This is a brief guide to the use of the inverse model. The package also contains some source files from a forward-dynamic version, but these are not discussed further here.

For details of changes made since the last version, see changelog.txt.

2 Structure of the model

To run the shoulder model, you need the following directory structure (directories shown in bold; files in italics):

dsem

c files	C source files
dasp	cadaver data: *.dsp, *.num, *.spc filter parameters: <i>filter.par</i>
docs	documentation files such as this one
f files	Fortran source files
input	motion data: *.inp (contains two sample files: <i>abduction.inp</i> and <i>anteflexion.inp</i>)
o files	object files
output	output files
sasp	main program: <i>inverse.exe</i> input arguments: *.input other files such as compiler setup (<i>newfortran.bat</i>)

Makefile and common variable declarations (*.txt and *.com) are in main directory **dsem**

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3 Input files

3.1 The *.input file

The *.input file contains run-time arguments for the model and must be of the form:

```
'../output/output_file'  
'header'  
'mode'  
'filter.par'          *** only for 'dyn' mode ***  
'../input/motion_file'  
a b c d  
'y/n'  
input option  
'parameter file code'  
'../dasp/parameter_file.dsp'  
'../dasp/parameter_file.num'  
'../dasp/parameter_file.spc'  
cost
```

where:

output file name for output files (no extension) containing the results of the simulation;

header here you should insert meaningful comments about the simulation;

mode 'stat' or 'dyn' (for static or dynamic modes);

filter.par name of file containing filter parameters (only for 'dyn' mode, for 'stat' mode this line should be omitted); see Section 3.2;

motion file is the name of the file containing the motion data;

a is the number of the first usable frame of motion data;

b is the number of frames of motion data (0 = use all frames);

c is the step size in frames i.e. 1 = use every frame, 2 = use every other frame, etc.; can also be set to zero in 'dyn' mode, in which case c is chosen such that output is produced at a frequency of twice the maximum cut-off frequency;

d no. of steps to first position (in moving from anatomical position to first step try to limit joint rotations to around 30° i.e. if first simulated position is 90° from anatomical position no. of steps should be 3);

y/n indicates whether retroflexion of the gleno-humeral joint occurs during the motion ('y' for yes; 'n' for no);

input option numeric input giving the format for the motion data and must be one of the following:

1 input 17 generalised co-ordinates, including thorax position;

2 input 6 generalised co-ordinates (ACy, ACz, TSx, GHy, GHz, GHy) and direction vector of gravity (fixed thorax approach);

3 input thorax and joint rotations, ACy, ACz and TSx are calculated;

4 input AA rotations, which are transformed to cadaver AC rotations ;

***.dsp** cadaver parameter file (geometrical data);

***.num** muscle element numbering;

***.spc** node-naming scheme;

cost number of cost function to use in muscle-force optimisation (constants c1 to c5 can be changed in objffsqp.f); default values give equal contributions to cost from linear and non-linear terms at 50% activation.

$$J = \sum_{i=1}^n \left(\frac{F_i}{PCSA_i} \right)^2 \quad (1)$$

$$J = \sum_{i=1}^n m_i \left(c_1 \frac{F_i}{PCSA_i} + c_2 \left(\frac{F_i}{F_{imax}(l)} \right)^2 \right) \quad (2)$$

$$J = \sum_{i=1}^n c_3 F_i l_i + m_i \left(c_4 \frac{F_i}{F_{imax}(l)} + c_5 \left(\frac{F_i}{F_{imax}(l)} \right)^2 \right) \quad (3)$$

3.2 The filter parameter file ('dyn' mode only)

The file is a text file consisting of eight numbers (or groups of numbers), A - H, each on a separate line, where:

A X-column (Column in data file which represents X data, or 0 if only the time interval is known.)

B X-interval (If A is NOT zero, then B is omitted.)

C Resampling options

- 1 Constant X-interval (same time range as input)
- 2 Minimal distance between successive samples
- 3 Normalisation to constant number of samples
- 4 Same X-values as input file
- 5 Constant X-interval (choice of X-range)
- 6 Constant number of samples (choice of X-range)

D is dependent on the value of C:

- 1 X-interval for output file
- 2 Minimum RMS distance
- 3 Number of output samples
- 4 D is omitted
- 5 StartX, endX, and interval
- 6 StartX, endX, and no. of samples

E Upper limit for valid data

F Spline order

G Smoothing options:

- 1 Generalised crossvalidation
- 2 Use RMS noise level
- 3 Use cutoff frequency

H is dependent on the value of **G**:

- 1 If $G = 1$, **H** is omitted.
- 2 RMS noise
- 3 Cutoff frequency (Hz)

NB. Real values (**B**, **D**, **E**, **H**) must be given with at least one decimal place.

4 Compiling and using the model

The model is shipped as a package of source files, which need to be compiled into an executable before the model can be run. The recommended compiler is currently gcc-2.95.2 (<http://www.gnu.org/software/gcc/gcc.html>), which can be downloaded from the dsem ftp site. Email me for details of this. To compile the model, change into the dsem directory and type

```
make inverse
```

In some cases it may also be necessary to add the location of the compiler to your path, which if you have installed gcc-2.95.2 in c: you can do with

```
newfortran
```

If you have installed gcc-2.95.2 somewhere else, you will have to edit *newfortran.bat*.

The program is run from DOS (in the directory containing the inverse.exe file) with the following command (with all options shown):

```
inverse -f filename -sa filename -sm filename -simm -fout -p <file.input
```

where (options):

- f** use file to read in the relative force (interval [0,1]) of each muscle (in file *filename*; each relative force on a separate line)
- sa** constrain all elements of the muscles flagged with 1 in *filename* to have the same activation
- sm** constrain the muscles with the same flag number in *filename* to have the same activation
- simm** SIMM input files will be written
- fout** files with segment loads will be generated
- p** produce expanded output in the *.out file
- kin** omit force-optimisation stage: produces kinematic output but no muscle or joint forces

and:

file.input is the file containing input arguments (eg. *dyn.input* or *stat.input*).

5 Output files

The following (text) output files are always generated:

- *.out file for progress information and results
- *.m results file to be read by PlotDSM (Matlab)
 - kinematic output (rotations, positions, lengths)
 - potential moment vectors about joint axes
 - muscle and ligament forces, joint reaction forces

The following file can be generated with the -simm option:

- *.mot: motion file in SIMM format
- *.ktx: kinetics file for SIMM

The following files can be generated with the -fout option (see Section 5.1):

- *thor.m: Matlab readable file with thoracic loads
- *clav.m: Matlab readable file with clavicular loads
- *scap.m: Matlab readable file with scapular loads
- *hum.m: Matlab readable file with humerus loads

5.1 Segment loading files

The file **segment.m* is a text file containing the all the forces acting on the segment (thorax, clavicle, scapula or humerus), during a certain motion. See **.inp* file for exact motion used. The global co-ordinate system (GCS) has its origin at IJ (Incisura Jugularis), with x left to right, y vertically upwards and z front to back. For further definitions of coordinate systems, see: <http://www.internationalshouldergroup.org>

The file contains the following data (can be loaded into Matlab as 3D arrays):

Xi 3 x 3 x istep array with orientation of local co-ordinate system (LCS) of segment, per step, with respect to GCS

Oxi 3 x istep array with position of origin of LCS

Cxmusi maxmus x 3 x istep array with point of application of muscle forces in GCS (only muscles with segment attachment are non-zero)

Fxmusi maxmus x 3 x istep array with muscle force vectors in GCS

Cxpasi n x 3 x istep array with point of application of n passive forces in GCS

Fxpasi n x 3 x istep array with n passive force vectors in GCS

where the letter x in the array names is to be replaced by the appropriate letter for the segment (t - thorax, c - clavicle, s - scapula, h - humerus), istep is the maximum number of steps in the file and maxmus is the maximum number of muscle elements.

Passive forces are as follows for each segment:

Thorax:

1. SC joint reaction force
2. TS scapulothoracic reaction force (acts at TS)
3. AI scapulothoracic reaction force (acts at AI)
4. Costo-clavicular ligament
5. Generalised force at IJ
6. Gravitational and inertia forces at Center of Gravity

Clavicle:

1. SC joint reaction force
2. AC joint reaction force
3. Costo-clavicular ligament
4. Ligamentum Conoideum
5. Ligamentum Trapezoideum
6. Gravitational and inertia forces at Center of Gravity

Scapula:

1. GH joint reaction force
2. AC joint reaction force
3. TS scapulothoracic reaction force (acts at TS)
4. AI scapulothoracic reaction force (acts at AI)
5. Ligamentum Conoideum
6. Ligamentum Trapezoideum
7. Gravitational and inertia forces at Center of Gravity

Humerus:

1. GH joint reaction force
2. HU joint reaction force
3. Gravitational and inertia forces at Center of Gravity
4. Elbow 3 x istep array with resultant elbow moment
5. Phu_a 3 x istep array with position of elbow moment

6 Muscle numbering

The following shows the elements which belong each muscle for cadaver I1091. Zeros in both columns indicate that the muscle is not present.

No.	Muscle name	First element	Last element
1	M.TRAPEZIUS, SCAP. PART	44	54
2	M.TRAPEZIUS, CLAV. PART	55	56
3	M.LEVATOR SCAPULAE	57	58
4	M.PECTORALIS MINOR	59	62
5	M.RHOMBOIDEUS	63	67
6	M.SERRATUS ANTERIOR	68	79
7	M.DELTOIDEUS, SCAP. PART	80	90
8	M.DELTOIDEUS, CLAV. PART	91	94
9	M.CORACOBRAHIALIS	95	97
10	M.INFRASPINATUS	98	103
11	M.TERES MINOR	104	106
12	M.TERES MAJOR	107	110
13	M.SUPRASPINATUS	111	114
14	M.SUBSCAPULARIS	115	125
15	M.BICEPS, CAPUT LONGUM	126	126
16	M.BICEPS, CAPUT BREVE	127	128
17	M.TRICEPS, CAPUT LONGUM	129	132
18	M.LATISSIMUS DORSI	133	138
19	M.PECT. MAJOR, THOR. PART	139	144
20	M.PECT. MAJOR, CLAV. PART	145	146
21	M.BICEPS, CAPLONG.ELBOW	147	147
22	M.TRICEPS, MEDIAL PART	148	152
23	M.BRACHIALIS	153	159
24	M.BRACHIORADIALIS	160	162
25	M.PRONATOR TERES, hum-rad	163	163
26	M.PRONATOR TERES, uln-rad	164	164
27	M.SUPINATOR, hum-rad	0	0
28	M.SUPINATOR, uln-rad	165	169
29	M.PRONATOR QUADRATUS	170	172
30	M.TRICEPS, LATERAL PART	173	177
31	M.ANCONEUS	178	182

References

- Jonker, B., 1988. A FINITE ELEMENT DYNAMIC ANALYSIS OF FLEXIBLE SPATIAL MECHANISMS AND MANIPULATORS. Ph.D. thesis, Technical University of Delft.
- van Der Helm, F. C. T., 1994. A finite element musculoskeletal model of the shoulder mechanism. *Journal of biomechanics* 27 (5), 551–69.
URL <http://www.ncbi.nlm.nih.gov/pubmed/8027090>