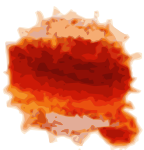


BasilLab User Manual



<https://xkcd.com/1247/>



Mark van Turnhout, 21st December 2015

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The use of an ovine model circumvents the ethical and financial problems associated with the use of bipedal animal models.

Armstrong, Read & Price [1]

1

Introduction

Pressure ulcers are localised injuries to the skin and/or underlying tissue due to mechanical loading. Deep Tissue Injury is a severe type of pressure ulcer originating subcutaneously. To better understand the aetiology of Deep Tissue Injury, [our group](#) studies physiological changes due to mechanical loading in a rat model [2, 3, 6–8, 10–14]. In this rat model, the animal's tibialis anterior muscle is deformed with an indenter inside a magnetic resonance (MR) imaging scanner. MR imaging allows for assessment of physiological changes, e.g. (re)perfusion and tissue damage, due to the deformation of the muscle. Animal specific finite element (FE) models are used to assess the relationship between the mechanical internal tissue state and tissue damage in the rat model.

Until recently, (animal specific) FE analysis of the experiments was restricted to cross sectional (2D) FE models. In the current project *Non-invasive monitoring of deep tissue injury* [15] the aim is to extend a previously developed cross sectional (2D) FE models [8] to a FE model of the complete leg (i.e. 3D) [16]. The first objective of these animal specific full leg 3D models is to assess the shortcomings of cross sectional 2D modelling (or: to assess what extra information can be obtained by switching to full leg 3D modelling).

BasilLab is a collection of scripts to facilitate the animal specific full leg 3D modelling of these experiments.

1.1 Software

BasilLab consists of a number of (pre-processing) Matlab-scripts that extract information from the MR images of the experiments and subsequently write a python script that can be fed to Abaqus: the FE software that runs the analysis. Parts of the pre-processing, in particular the segmentation of the MR images, rely on the GIBBOn toolbox¹ developed by Kevin Moerman [9, <http://kevinmoerman.org/portfolio/gibbon/>].

Next to the pre-processing Matlab scripts, a number of python scripts is provided to extract model results from the Abaqus output file. These results can be easily fed back to Matlab for post-processing purposes².

¹“The Geometry and Image-Based Bioengineering add-On”. Source available from <https://github.com/Kevin-Mattheus-Moerman/GIBBON>

²Other than these python scripts to write the Abaqus results to a Matlab- and human-readable text file, no post-processing is provided in BasilLab.

Table 1.1: Software used for development and testing of BasilLab.

Name	author	tested with version
Abaqus/Simulia	Dassault Systèmes	Abaqus 6.14-1
Matlab	MathWorks	MATLAB Version: 8.1.0.604 (R2013a) MATLAB Version: 8.2.0.701 (R2013b)
GIBBOn	Kevin Mattheus Moerman	See listing 1.1

Listing 1.1: First three lines of the Git log for GIBBOn, showing the version ('commit') that was used to develop and test BasilLab.

```
mark@telab11:~/git/gibbon$ git log | head -n 3
commit c060143843d1d6f30ee39ddab1d65c6731a0c83e
Author: Kevin Mattheus Moerman <Kevin-Mattheus-Moerman@users.noreply.github.com>
Date: Tue Jul 7 15:09:39 2015 +0200
```

Both Matlab and Abaqus suffer from (in)compatibility issues between software versions. The GIBBOn toolbox does not work well with Matlab R2012b or lower; and the Matlab command `DeLaunayTri` will be removed from a future release. Abaqus recently changed the formulation of some python commands that we use and the current scripts e.g. do not work with Abaqus version 6.11. See table ([1.1](#)) and listing ([1.1](#)) for the software versions that were used to develop and test BasilLab.

1.2 License and availability

BasilLab is released under a [Creative Commons Attribution-NonCommercial 2.5 License](#). Feel free to copy and share this software.



Note that there is ABSOLUTELY NO WARRANTY; not even for FITNESS FOR A PARTICULAR PURPOSE, and certainly not for MERCHANTABILITY.

BasilLab is available from the [author](#). BasilLab is maintained in a Git repository that is hosted at [BitBucket](#). If you wish to have access to that Git repository, again: contact the [author](#).

I have pointed out these things because the more you see how strangely Nature behaves, the harder it is to make a model that explains how even the simplest phenomena actually work. So theoretical physics has given up on that.

Richard P Feynman [5]

2

Conventions

2.1 Spatial dimensions

All spatial dimensions of the FE model are in mm, both for input and output. Thus, if you supply e.g. a stiffness parameter, you should convert it from N/m² to N/mm²:

$$E = 15.6 \text{ kPa} = 15600 \text{ N/m}^2 = 0.0156 \text{ N/mm}^2 \quad (2.1)$$

And when you read the element volume from the Abaqus output, this volume is in mm³.

See also section ‘1.2.2 Conventions’ in the Abaqus Analysis User’s Guide of the [Abaqus documentation](#) and the [Conversion Tables, Constants, and Material Properties](#) provided by Abaqus.

2.2 Large displacements and logarithmic strain

The FE models are analysed with Abaqus’ ‘Large Displacement’ option for geometrically non-linear problems. As a result, Abaqus will output *logarithmic* strains ‘LE’:

$$LE = \epsilon^L = \ln V = \sum_{i=1}^3 \ln \lambda_i \mathbf{n}_i \mathbf{n}_i^T \quad (2.2)$$

When you use a hyperelastic material law (such as the Ogden material model that is used in BasilLab), Abaqus will also output the logarithmic strains ‘LE’. See section ‘1.2.2 Conventions’ in the Abaqus Analysis User’s Guide of the [Abaqus documentation](#).

2.3 Directory structure

BasilLab requires knowledge on two directories: one <MRI-root> where the (raw) MRI-data can be found, and one <basilhome> where the processed MRI-data and model data can be found. Raw MRI-data for each individual experiment/animal should be stored in a unique folder *inside* <MRI-root>. Processed MRI-data and model data is stored *inside* a unique folder in <basilhome>.

2.3 Directory structure

The link between the unique raw MRI-data folder inside <MRI-root> and the unique folder for model data inside <basilhome> is *hard-coded* in `bas_getMeta.m`. When you add animals/experiments or rename certain directories, you will have to adapt this file.

Each animal/experiment should have unique *numerical* identifier <basilid>. BasilLab calls `bas_getMeta.m` to find out where the raw MRI-data is stored for <basilid>, and it will look for <basilhome>/<basilid>/ to store and read modelling data. Currently, the unique <basilid> is the date of the experiment in `yymmdd`-format.

Thus, for the experiment performed on June 11th 2015

experiment identifier <basilid> = 140611

model data is stored and sought in <basilhome>/140611/

raw MRI-data is stored in <MRI-root>/140611.qd1/

the link between ‘<basilid> = 140611’ and ‘raw MRI-data is stored in <MRI-root>/140611.qd1/’ is hard-coded in `bas_getMeta.m`

BasilLab provides `bas_setMRIroot.m` to set <MRI-root>, and `bas_setDataRoot.m` to set <basilhome> (see section [3.0](#)).

In the computer model, all the microfilaments were given certain quantitative properties with names that mean something to physicists: a ‘viscous damping coefficient’ and an ‘elastic spring constant’. Never mind exactly what these mean: they are the kind of things physicists like to measure in a spring.

Richard Dawkins [4]

3

Work flow

After initialisation of BasilLab, the work flow can be roughly divided into four steps:

0. Initialise BasilLab (once)
1. Pre-processing of (raw) MRI-data. Including reading and copying (raw) MRI-data, segmentation of MR images, and processing (segmented) MRI-data. Requires Matlab (and human intervention).
2. Building the FE model. Requires Matlab and Abaqus.
3. Running the FE model, Requires Abaqus.
4. Post-processing of FE results. Requires Abaqus.

3.0 Initialise BasilLab

Matlab needs to be aware of the location of the BasilLab-scripts, so you first have to add the directory that contains the (Matlab) scripts, possibly `<basilhome>` to your Matlab search path, e.g. go (in Matlab) to that directory and issue `addpath(pwd)`; on the command line.

As a matter of principle and for philosophical reasons, BasilLab leaves the raw MRI-data completely untouched. You have to initialise BasilLab *once* by defining the path to the raw MRI-data (`<MRI-root>`), and the path to the BasilLab work directory (`<basilhome>`, see also section 2.3). The necessary MRI (meta) data will be copied from `<MRI-root>` to a unique folder `<basilid>` inside `<basilhome>` for each animal. All (model) information that is extracted from the MRI-data by BasilLab will be written to, and sought in, that folder: `<basilhome>/<basilid>`.

`<MRI-root>` is defined (hard-coded) in `bas_getMRIroot.m`. This script is called by BasilLab when it needs to know the path to the `<MRI-root>`-folder. You can edit this script manually, or you can use `bas_setMRIroot.m` to update this script to your local situation. When you call `bas_setMRIroot.m`, the `bas_getMRIroot.m`-script is overwritten with a new version that provides the `<MRI-root>` that you provided as an argument to `bas_setMRIroot.m`.

Similarly, `<basilhome>` is defined in `bas_getDataRoot.m` and updated with `bas_setDataRoot.m`. The argument for `bas_setDataRoot.m` or `bas_setMRIroot.m` is the *full* path to the folder that you wish to define, e.g.:

```
1 >> bas_setMRIroot('/home/mark/BrukerData');  
2 >> bas_setDataRoot(pwd);
```

3.1 Pre-processing of MRI-data

All steps that are required to prepare the model data can be performed with `bas_prepFEM.m`. Briefly, these steps are

1. Copy MRI-data from `<MRI-root>/experiment-folder` to `<basilhome>/<basilid>`
2. Segment MRI-data to obtain skin- and bone contours
3. Determine bone movement and rotation due to indentation from segmented bone contours
4. Determine indenter orientation and displacements from MRI-data

Only step 2. requires user interaction, the rest is performed 'under the hood', automatically.

3.1.1 Copying MRI data

Extracting and copying MRI (meta) data is done by `bas_MRIToMat.m`. This function calls `bas_getMRIroot.m` for the path to the raw MRI-data, `bas_getDataRoot.m` for the path to the BasilLab work directory, and `bas_getMeta.m` for the experiment specific sub-folders within these two directories.

3.1.2 Segment MRI-data

3.1.3 Map bone movement

3.1.4 Map indenter movement

3.2 Building the FE model

3.3 Running the FE model

3.4 Post-processing of FE results

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