**AsciiSection Instructions v3.1**

*Instructions written by Thomas Davies in ~2014, and updated (to an extent) in 2016. Hopefully these cover a lot of issues, but feel free to contact me if you run into any problems.*

**Introduction**

These are instructions for the latest (Feb 2016, v3.1) version of AsciiSection software. This version should enable you to do the following[[1]](#footnote-1):

* Calculate cross-sectional properties at set intervals of % of bone length (e.g. every 1% of bone length from 20-80%).
* Calculate cross-sectional properties at a single cross-section location of your choice (e.g. 50%).
* Calculate cross-sectional properties on fragments of a complete bone, where you set up a text file to tell the code an estimate of bone length, and the distance from the distal end of the bone (if it had existed) to the start of the fragment. [Be very careful with this version that when the results actually run, the correct max length is used for the correct bone (i.e. that the sequence matches). See further notes below.]

*I have placed some notes about producing cross-sectional images first below, as this is useful context to be aware of before running AsciiSection software. The main instructions for installing and running AsciiSection follow subsequently.*

**Producing cross-sectional images (via Gnuplot)**

AsciiSection calculates cross-sectional properties directly from coordinates (using maths based on polygons), and therefore it never has any need to create image files of the cross-sections – as would be the normal basis of results calculated via BoneJ or MomentMacro. However, it is obviously useful to have images, and therefore the bashscript does use code that invokes the freeware software gnuplot to produce images. The programme works without gnuplot, but you will not have any images. I recommend installing gnuplot and then you will be much better placed to pick up any potential errors in the results that are produced. Once installed, running AsciiSection will automatically create the image files as it calculates the cross-sectional results. There are separate instructions I wrote as a guide to install gnuplot on Mac OS X via macports (in ~2014), however, I believe there are now contributed MacOSX executables (http://ricardo.ecn.wfu.edu/pub/gnuplot/) although I’ve yet to try this myself.

If you don’t want to install gnuplot, or run into problems, then you can always just take the coordinate files generated by AsciiSection and copy them into excel and create a scatterplot manually.

***Amending the gnuplot outputs***

By default, this version of AsciiSection produces three different types of image for each cross-section. This can be useful, but if you are taking lots of cross-sections, you will end up with a lot of files very quickly, and it also means the programme runs slower (producing all the plots). It is fairly straightforward to prevent some of these plots, by making a couple of quick changes to the text of the biomechanics\_bashscript file:

* Open the script in a text editor (e.g. TextEdit, Xcode).
* Scroll down to lines 133 -137 (five lines that all start with the symbol #).
* On lines you want to inhibit, insert a hashtag at the start of the line to inhibit the software reading those lines of the code.
* To stop any one type of plot you need to insert hashtags on each of the lines of code for that style of plot. That’s a section of about 16 lines in each case, all starting with the word “cat” and ending “EOF”.
* You should not amend the lines that say “for file in …..” (line 139) at the start, or the “done” at the end (line 209).
* Now just save the file, and then next time you run it, it will only produce the plots that you have not inhibited.

**Instructions for AsciiSection v3.1 (Mac OS X).**

**Installation**

***Pre-requisites***

It may be necessary to install the XCode Developer tools before trying to run AsciiSection (or at least if using Gnuplot to produce images). You can download Xcode Developer tools for free from the AppStore, although it is quite a big package of tools. (~a few Gb). Previously it was not possible to install to Xcode without being on the most recent OS X – so you may have to update that as well (or try and see how far you get without this).

***AsciiSection Install/Set-up Summary.***

AsciiSection (v3.1) is packaged as a .dmg file.

1. Double click the .dmg file, and then drag the folder “AsciiSection\_v3.1” onto your Applications folder.
2. Open a ‘Terminal’ window (search ‘Terminal’ in Spotlight search or find it in /Applications/Utilities/)
3. Navigate to the AsciiSection folder in your Applications and:
   1. Copy paste your files (.asc or .xyz files of a whole bone mesh) into the folder ‘asciifiles’ [see notes below ‘preparing input data’]
   2. Then, select the file ‘biomechanics\_bashscript.sh’ and drag and drop this onto the terminal window. Then press Enter to start the programme.
4. If it is working correctly it should ask you a couple of questions and then will start calculating the biomechanics and outputting them into folders ‘Boneresults’ and ‘results’ in the ‘Applications/Asciisection\_v3.1’ folder.
5. If you need to cancel the programme while running you can press ctrl+c at any time to stop it.
6. It is best to remove all previously run results out of the Boneresults & results folders manually yourself before running the programme again.

*Further notes on these various stages in process follow below.*

**Preparing Input data.**

As above, you will need to copy-paste your input files (coordinate files of a 3D mesh) into the folder “asciifiles”. There can be as many as you want all together – but they should not be separated out into any further folders (files in folders don’t run). The files need to have been saved with the extension .asc or .xyz. The file names should not contain any spaces.

***A. Creating these files:***

You can create .xyz files directly in ScanStudio (if using NextEngine):

1. Once you’ve got a fused and orientated bone model, select ‘Export’.
2. Choose the option .xyz filetype.

If using Rapidworks/Rapidform (and perhaps other software), export as a .asc file.

***B. Bone orientation***

It is important that the 3D mesh of the bone is orientated correctly before you export the .xyz or .asc files. AsciiSection assumes that the x-axis is parallel to the mediolateral, and the y-axis is anteroposterior, and the z-axis parallel to the long axis of the bone (i.e. perpendicular to the planes of the sections you want). (the names of the axes are sometimes interchanged in different software, e.g. between y and z axes) – check against my notes below if unsure).

In Scanstudio:

1. Use CADtools/Orient.
2. Set up the orientation such that when you click on the mesh in the toolbar at the bottom of the screen (to reset the view), the distal end of the bone is at the bottom, the proximal end at the top of the viewer, and that the posterior surface is facing the screen. Mediolateral should run parallel to the screen (if that makes sense).
3. (N.B. you need to actually orientate it in one of the modes where you are given a bounding box – you can’t just rotate the bone in normal view and save the file. The position of the bone in relation to the bounding box needs to change, so that the default view position is changed. I’ve used the instructions from Ruff, 2002 as a guide to getting the exact orientations correct.

In Rapidform (or other software with better capabilities):

1. You can reorientate the bones much more precisely using, e.g. the ScanTools/Align/ options – either “global alignment” or “datum match alignment”. Alison Macintosh has created detailed instructions from when I first taught her the process I followed, for how to do this correctly by drawing planes and vectors which can then be used to apply the correct transformations to the bone such that the planes map onto the x,y,z axes. It’s a cumbersome process, but ultimately only takes 3-4 minutes per bone once you’ve got used to it. The aim is that in the set views within Rapidform the positioning of the bone becomes meaningful. The Alt-1 view (Front) should show the posterior surface of the bone, Alt-2 the anterior, Alt-3 and Alt-4 the medial and lateral surfaces (depending on whether bone is a left or right), and Alt-5 the proximal surface, Alt-6 the distal surface. Once orientated like this, then go File/Export and save as an “ascii points file .asc”.

**Running the programme**

*Select the file ‘biomechanics\_bashscript.sh’ and drag and drop this onto the terminal window. Then press Enter to start the programme.*

Once you’ve started the programme, now just read the text and enter in your responses, followed by pressing return. You have choice over:

* The number of sections to take.
* If 1 section per bone, then you can specify the location at which to take it.
* The cross-section range (e.g. 20-80%) – so you just get the diaphysis
* The slice thickness (see Davies & Stock 2012)
* Whether to read max length from the scan, or from a separate file with an estimate of max length listed (needed for fragmentary or incomplete bones – see further instructions below). Note: if a scan does not encompass the complete max length of the bone (e.g. if it is not preserved) then you cannot use the default (calculating max length automatically), but instead should set up a file with the lengths (xlfile.txt). If you do select auto, the programme still works, and the results will be run and output, but they will be largely meaningless.

If you make a mistake in answering any of the questions you can just press ctrl+c to cancel the operation, and then just start again with “bash biomechanics\_bashscript” etc.

For reference, to calculate the bone length (and therefore the % section locations) the programme uses maximum bone length parallel to the long axis of the bone (i.e. perpendicular to the planes of the section). This is slightly different therefore from other measurements. The programme just looks for the range of z-coordinates, and uses that as the length. I recommend using this wherever possible (i.e. if you have complete bones), as it is definitely time saving, and avoids user errors). If you do not have complete bones, you have to run them with a max length estimate you list in a file (see instructions below). Inputting a max length manually via the xlfile.txt should really be an estimate of the same type of measurement (max length perpendicular to plane of sections) – because that is the most consistent with anything you run on the automatic settings. I’ve never tried anything different, but after a couple of minutes thought, I think if you really wanted the %locations to be of biomechanical length then it might work, if you list biomechanical lengths. The code would still be anchored at the distal end – taking the most distal point it sees of the scan as 0%, but section intervals would then be based on your biomechanical length, so would be at slightly smaller intervals than if using max bone length. Equally, you can give a negative number to the “distance to distal end of fragment” (e.g. for a tibia), to get it to start 0% at (say) the distal articular surface rather than the point of the medial malleolus. Personally, I think in the vast majority of cases different length estimates are largely irrelevant, and I would just use the automatic settings for complete bones, but it may be possible to do alternative things if you really needed to. I cannot say that I have considered this much, and I would recommend looking at sections across the whole bone (0-100%) to work out if the code is doing what you think it should be (re. what is a 0%, or 20%, 30% section etc etc etc). This paragraph may make more sense once you read the additional instructions below as well.

That’s about it. The program now does the work. (if you don’t have gnuplot installed it may give you a load of errors when it gets to that bit of the programme, but these can be ignored).

**Results**

If you look in the folder AsciiSection\_v3, two new folders should have been created within it: “Boneresults” and “results”.

Within “Boneresults” there will be a separate folder for every asciifile you had. Within each folder there will be lots of files:

The ones that begin “section\_” are the section coordinates files. The number indicates % of bone length. (without gnuplot, just copy the coordinates out of these files into say excel and plot to see the shape of your section ).

“lengths….” Lists the mm locations for the % sections if you need to know that.

“image…” files are your picture files if you have installed gnuplot.

The one file that begins “res…” contains your results for this bone.

If you go to the folder “results” this contains a copy of the results files for all the bones you just ran, and it also contains files that have extracted the results for the 5 variables \_ Imax, Imin, Ix , Iy, and TA. If you are doing lots of bones and lots of sections then this saves you a lot of manual copying and pasting of bits of results. You can take these text files and copy-paste into excel, and choose space-delimited text. It is sometimes useful to then copy the spreadsheet, and select paste-special , and tick “transpose” – to give you one row per individual.

If you have run the programme once, but then start it again in order to change the settings etc, I advise that you remove all the files from the “Boneresults” and “results” files prior to restarting. The programme mostly writes over any existing files with the same names, but if you say take sections at 5% intervals, and then go back to do it again but only for the 50% section, those previous 5% section files will still exist, and the programme will spend time replotting them all. Best to just clear out the folders every time so that you know everything you see in the results has appeared exactly from the latest set of settings you have specified.

That’s about it for the main programme, email me if you have any problems or questions.

**A final word of caution**

To calculate cross-sectional properties from coordinates, the coordinates in each section file must be in either a clockwise or anticlockwise order, and with the first coordinate repeated at the end (to close the polygon). The code does this automatically by calculating an approximate central coordinate in the section, and then listing the individual coordinates in an order based on the angle created between a vertical line (0 degrees) and the line from the coordinate to this central point. For fairly simple shapes (e.g. rough circles, elipses etc) this is a very accurate way of getting a clockwise order. However, if you have much more complicated section shapes on whatever it is you have scanned, then the order may be incorrect, this is sometimes the case for section shapes around the epiphyses of long bones. If the order is wrong, the results will still be output, but will be meaningless. The way to check for any errors in the ordering is to look at the filled plots from gnuplot (solid white sections on a black background). Where there are errors, you can get a starburst type pattern radiating out from the centre, or across the section, as the plot struggles to work out what is the “inside” and what is the “outside”. Be aware to keep an eye out for this if you have any concerns about the complexity of the shape of your scans. For long bone diaphyses this should never be a problem. But if you are using the programme to look at epiphyseal section shapes or something, or other weird shaped bones etc, then be careful.

**Further instructions in the case of bones/fragments without a complete bone length in the scan (what I call the Input XL version).**

These are instructions for the version where you need to manually input a measurement (or estimate) of the bones’ maximum lengths. To activate this alternative part of the programme, just answer “1” to the question “Do you want to use bone lengths as calculated automatically ….”

By answering “1” you are acknowledging that there is a file which lists estimates of bone lengths – and so you need to have created a file and saved it with the name “xlfile.txt”. It must be a particular type of .txt file, however. If using excel, when saving as, you should select: .txt (windows formatted text file). Once you have this file, it should be copied into the “asciifiles” folder, before running the programme.

The format should be as follows:

bonexl\_maxl bonexl distancetobonefrag extra

430 0 0 01\_bone\_no\_1

463 0 0 02\_bone\_no\_2

450 52 0 03\_bone\_no\_3

etc.

To explain, the first column is the max bone length that you want the code to use as the bone length. The second column should be a zero if the bone is complete to the distal end, otherwise you should input here the distance from the supposed distal end of the bone (0%) to the position at which the fragment you have scanned actually starts). i.e. it is basically just how many mm are you missing from the distal end of the bone. The third column is defunct I think, so just make sure this is filled with zeros.…..The fourth column should be for your bone numbers/names. – just for you to know – the code doesn’t use this, it just goes through one line after another in order (so your asciifiles need to be in the exact same order – easiest to number them for this purpose.

The measurements should be listed in the order that the files will be read by the code. This is in most cases the order the files appear when viewed alphabetically in a Finder window – but I can’t guarantee there is an exact match. Hence why I recommend you number your asciifiles from 01, 02 onwards, and therefore cannot have any confusion.

Once done, the xlfile.txt should be put into the “asciifiles” folder.

The programme then just runs as normal (be sure to tell the programme to read max length from an xlfile (when it asks you that question).

I find I often make some mistake in running this version of the programme – mostly because the lines in the xlfile aren’t exactly matched up to the order in the folder, etc, so it is definitely worth checking that the images look about right, and that the numbers the code gives you seem about right (in amongst the output as it runs, it will tell you what it is reading as the max length – so you can check it against what you expect). Remember the code knows nothing about the association of a measurement to a particular bone name, it just takes the numbers it sees one line at a time, and runs them on the files it sees, one after the other. I had problems because 7-xxx and 70-xxx were interpreted differently to the order I thought they would be run in, and they ended up being allocated along with the wrong length measurements until I went back to fix it [I find it best to number sequentially, with zeros preceeding small numbers: 01, 02, …, 10, 11, etc]

Hopefully, I have covered everything I need to here. Note that there are separate instructions for installing gnuplot, and for creating the correct orientations in Rapidform prior to exporting asciifiles. If you have any questions feel free to email. If you do publish material based on results calculated in AsciiSection, I would be grateful if you could cite the Davies & Stock 2012 paper.

1. *There is one further alternative, where you take cross-sections at a set location (in mm) from the distal end of the fragment that you have a scanned. This is the only version that works without any estimate of bone length, but obviously you need some other information to equate the sections to, for example, a 50% location. This works, for example, to get a subtrochanteric femur section, as the morphology rather than bone length sets the location. Unfortunately, this cannot be done in this version of the software, however. If this is of particular interest, it would be best to email me to ask for a copy of this alternative, and its instructions.*  [↑](#footnote-ref-1)