

## Code and data manual

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This document contains a short manual of how to use the c code `cyto.c` and Mathematica plotting file `cytoskeleton_plots.nb` that have been used to create and plot the data in the article "Mechanical interplay between cell shape and actin cytoskeleton organization" by Schakenraad *et al.*

### Performing simulations

A simulation, or a sequence of simulations, is performed by running the "`gcyto.pl`" file in a terminal. This file contains the values of all input parameters. This file calls on "`cyto`", "`cyto.c`", "`cyto.h`", and "`makefile`", and automatically creates new folders for storing the generated data. The final subfolders contain the following files: The file "`vertex`" contains the location of the cell edge, "`bulk`" contains the location and nematic tensor of the cell interior, "`force`" contains the forces on the adhesion sites, and "`global`" contains a number of global parameters that are defined in `cyto.c`. The number behind each of these names in the file name indicates the time during the simulation, with the last number indicating the final configuration. Finally, the file whose name starts with "`input`" stores all the input parameters as defined in "`gcyto.pl`", and the "`prints.dat`" contains the output of the terminal.

### Choosing the simulation

The parameter "`shape_number`", which is defined on top of "`gcyto.pl`", determines which type of simulation is performed. `shape_number = 8` defines a square cell and `shape_number = 9` a rectangular cell. The shape numbers 100-105 define the real cell shapes. They correspond to the figures in the article as follows:

cell number simulations	Displayed in figure
100	Fig. 6
101	Fig. 8d,i,n
102	Fig. 8c,h,m
103	Fig. 8e,j,o
104	Fig. 8b,g,l
105	Fig. 8a,f,k

The experimental cell shape simulations have been performed with a range of anchoring numbers. The table below shows which anchoring number is used for each figure:

Figure	Anchoring W	W/K (1/ $\mu\text{m}$ )	K/W( $\mu\text{m}$ )	An
6c	1	0.0141	70.656	0.333796
6d	5	0.0708	14.1312	1.66898
6e	24	0.3397	2.944	8.0111
8k	18	0.2548	3.92533	4.41137
8l	12	0.1698	5.888	4.13717

8m	33	0.4671	2.14109	18.6125
8n	13	0.1840	5.43508	4.57433
8o	13	0.1840	5.43508	4.65224

In order to translate this to a dimensionless anchoring number, the area of the cells have been calculated by counting how many pixels are inside the experimental cell, multiplied by the area 0.138 micron x 0.138 micron of a pixel. A typical length scale  $R$  has than be extracted using the square root of this area.

Figure	Area	Length scale $R$
6	556.237	23.5847
8a	299.848	17.3161
8b	593.392	24.3596
8c	1588.1	39.8509
8d	618.111	24.8618
8e	639.345	25.2853

### Plotting cells in Mathematica

The figures are created by plotting the data using `cytoskeleton_plots.nb`. In that file, three different plotting functions are defined which are used for different types of plots. More details are found in the Mathematica file. The file also contains an example for each of these plotting functions. The data required to run these examples can be found in the folder “example data”.