# 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/μm) | K/W(μm) | 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”.