Variables.mat

Variables\_noSL.mat (separate file with disabled speed limit)

In this document I am going to present the different outputs saved in the *variables.mat.* The aim of *variables.mat* is to extract all the necessary data of BacStalk and reorder it. But also, to extract and save all the information about the intensity.

**BactID:** 3 columns matrix with:

|  |  |  |
| --- | --- | --- |
| TrackID | # frames tracked | # first track frame |

BactID: for moving cells  
BactID\_non\_moving: save info but for non-moving cells  
NOTE: when the speed limit is disabled there “non\_moving” cell is empty  
Comes from: filters.m function

**cell\_prop:** 13 columns cell:

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 |
| TrackID | # frames tracked | Center of Mass | Orientation [degree] | Poles coordinate | Mean Intensity of poles | List of tracked frames | Contour | Ratio Poles | Max intensity of poles | total polar intensity | mean cyto intensity | total cyto intensity |

- Center of Mass: for each bacterium *Center of Mass* is a vector of the length of *#frames tracked.* It contains the coordinate of center of mass at each time frame

-Orientation: for each bacterium *Orientation* is a vector of the length of *#frames tracked.* It contains the orientation angle at each time frame

-Poles coordinates: for each bacterium *Poles coordinates* is a cell of the length of *#frames tracked.* Each element of the cell is a matrix of 2 lines and 3 columns. Each line represents 1 pole. Column 1 & 2 are the center of the poles and column 3 is the radius of the circle. Poles are assigned randomly, not based on twitching direction or intensity. !!! A line is not always the same pole because BakStalk assigns them somehow randomly!!! Take labelled poles instead.

-Mean intensity of poles: for each bacterium *Mean intensity of poles* is a cell of the length of *#frames tracked.* Each element of the cell is a matrix of 2 columns. Column 1 is mean intensity of pole represented in line 1 at *Poles coordinates.* So, column 2 is line 2 in *Poles coordinates.*

-List of tracked frames: for each bacterium *List of tracked frames* is a matrix of the length of *#frames tracked.* (use?)

-Contour: for each bacterium *Contour* is a cell of the length of *#frames tracked.* Each length contains the contour of the bacterium corresponding to the time

-Ratio Poles: for each bacterium *Contour* is a matrix of the length of *#frames tracked.* The matrix contains the ratio of the poles at every time frame.

-Cyto: Intensities covering the cytoplasm. Cytoplasm is defined as the area of the whole cell body (contour) without the polar area circles (cf poles coordinates).

-Max intensity of poles: for each bacterium *Max intensity of poles* is a cell of the length of *#frames tracked.* Each element of the cell is a matrix of 2 columns. Column 1 is max intensity of pole represented if line 1 at *Poles coordinates.* So, column 2 is line 2 in *Poles coordinates.*

cell\_prop: for moving cells  
cell\_prop\_non\_moving: save info but for non-moving cells  
NOTE: when the speed limit is disabled there “non\_moving” cell is empty  
Comes from: Intensity.m function

**Data\_speed:** 6 columns cell:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 1 | 2 | 3 | 4 | 5 | 6 |
| TrackID | # frames tracked | Speed vector filtered by speed limit | Speed norm | Unitary speed vector | Raw speed vector |

The speed is calculated by the movement of the center of mass. The center of mass is taken from BacStalk.

-Speed vector filtered by speed limit: for each time if the speed is smaller than the speed limit then the speed is set to zero  
NOTE: when the speed limit is disabled the third column will be the unfiltered speed!  
  
- Unitary speed vector: speed vector filtered divided by the norm for each time frame  
  
-Raw speed vector: Speed data extracted from movement of center of mass not filtered by speed limit

Data\_speed: for moving cells  
Data\_speed\_non\_moving: save info but for non-moving cells  
Comes from: Speed.m function

**Data\_Intensity:** 5 columns cell:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| TrackID | # frames tracked | Gradient intensity vector | Gradient intensity norm | Unitary gradient intensity | total whole-cell intensity | mean whole-cell intensity |

The intensity is calculated by the traking the poles coordinates (with poles\_coordinates.m function) and then applying a mask of the poles coordinate on the fluo image, the intensity of each pole is extracted (with function poles\_intensity.m). Then with the intensity at each pole, the gradient of intensity can be calculated (with gradient\_intensity.m function).

Columns 6 and 7 include the whole-cell intensity as total and mean intensity, respectively.

- Unitary gradient intensity vector: speed vector filtered divided by the norm for each time frame  
  
Data\_intensity: for moving cells  
Data\_intensity\_non\_moving: save info but for non-moving cells  
NOTE: when the speed limit is disabled there “non\_moving” cell is empty  
Comes from: Intensity.m function

**Data\_Alignment:** 3 columns cell:

|  |  |  |
| --- | --- | --- |
| TrackID | # frames tracked | Alignment factor |

The alignment factor is calculated by taking the scalar product between the unitary speed vector and the unitary gradient intensity vector.   
  
- Alignment factor: for each bacterium *Alignment factor* is a vector of the length of *#frames tracked.*

Data\_alignment: for moving cells only  
Comes from: Alignment.m function

**“label\_the\_poles” function**

OUTPUT: Pole A: 3 ou 5 colums matrix depending on the option

1. column 1: X coordinate of pole center
2. column 2: Y coordinate of pole center
3. column 3: initial number of pole I think (MJK)
4. column 4: if option 2: corresponding mean intensity
5. column 5: if oprtion2: corresponding max intensity

NOT USED ANYMORE:

**Data\_projection:** 3 columns cell:

|  |  |  |  |
| --- | --- | --- | --- |
| TrackID | # frames tracked | Projection speed | Projection of intensity |

The scalar product between two consecutive speed vectors (or gradient intensity vector) is calculated. The aim was to see the change of direction. Never really used.   
   
  
- Projection speed: for each bacterium *Projection speed* is a vector of the length of *#frames tracked.*  
  
Data\_projection: for moving cells only  
Comes from: Projection\_factor.m function