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**pycellfit**  
*Release 0.0.1*

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# CHAPTER 1

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pycellfit

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## 1.1 pycellfit package

### 1.1.1 Submodules

### 1.1.2 pycellfit.utils module

Top-level utility functions for pycellfit module.

`pycellfit.utils.contains_triple_junction(linestring, list_of_points)`

helper function that tells you if a shapely LineString contains a triple junction

#### Parameters

- **linestring** (*shapely.geometry.LineString*) – the LineString of interest
- **list\_of\_points** (*list*) – list containing a bunch of points of type *shapely.geometry.Point*

**Returns** if the linestring contains a point in the list\_of\_points, the first point is returned; else, None.

**Return type** *shapely.geometry.Point*

`pycellfit.utils.extract_all_points(dataframe_of_cells, visualize=False)`

generate list of all points in mesh

#### Parameters

- **visualize** (*bool*) – boolean to indicate if plot of all points should be made or not
- **dataframe\_of\_cells** (*geopandas dataframe*) – a dataframe where each row contains a unique cell

**Returns** *list\_of\_all\_points*: list of all points in the mesh

**Return type** list

`pycellfit.utils.locate_triple_junctions (dataframe_of_cells, visualize=False)`  
generate list of triple junctions in mesh

**Parameters**

- **visualize** (`bool`) – boolean to indicate if plot of all points should be made or not
- **dataframe\_of\_cells** (`geopandas DataFrame`) – a dataframe where each row contains a unique cell

**Returns** list\_of\_tjs: list of all triple junctions in the mesh

**Return type** list

`pycellfit.utils.make_segments (cell_boundary, list_of_triple_junctions)`  
recursive function that splits up a cell boundary based on triple junctions

**Parameters**

- **cell\_boundary** (`shapely.geometry.LineString`) – boundary of a cell that needs to be broken up into segments
- **list\_of\_triple\_junctions** (`list`) – list of all triple junctions (of type `shapely.geometry.Point`) in the mesh

**Return results** list of segments (of type `shapely.geometry.LineString`) that make up the cell boundary

**Return type** list

`pycellfit.utils.read_segmented_image (file_name, visualize=False)`  
Displays the segmented image using matplotlib

**Parameters**

- **file\_name** (`str`) – file name of a segmented image in .tif format
- **visualize** (`bool`) – if true, then image will be plotted using matplotlib

**Raises** `TypeError` – only accepts tif/tiff files as input

**Returns** array of pixel values

**Return type** numpy.ndarray

### 1.1.3 pycellfit.junction module

```
class pycellfit.junction.Junction(coordinates)
Bases: object

add_edge (edge)
    Adds edge to list of edges – make sure no repeat edges

coordinates

degree

edges
    List of edges connected to this node

id_iter = count(0)

remove_edge (edge)
    Remove an edge and tension vector connected to this node :param edge:
```

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**tension\_vectors**  
returns list of Tension vectors connected to this node

**x**

**y**

#### 1.1.4 pycellfit.edge module

```
class pycellfit.edge.Edge(start_node, end_node, radius, center)
Bases: object

center
corresponding_tension_vector
end_node
id_iter = count(0)
radius
start_node
xc
yc
```

#### 1.1.5 pycellfit.tension\_vector module

A class to define tension vectors in CellFIT

```
class pycellfit.tension_vector.TensionVector(edge)
Bases: object

corresponding_edge
The corresponding Edge for this tension vector

    Returns corresponding edge
    Return type edge.Edge

direction
returns the direction of the tension vector in radians (or degrees) from the horizontal

    Parameters units (str) – units for the direction, either ‘rad’ or ‘deg’
    Raises ValueError – if units is not ‘rad’ or ‘deg’

    Returns direction
    Return type float

id_iter = count(0)

label
returns the label (id number) for this tension vector

    Returns label
    Return type int

magnitude
Magnitude of the tension vector
```

**Returns** magnitude

**x\_component**

returns the x-component of the tension vector

**Returns** x-component of the vector

**Return type** float

**y\_component**

returns the y-component of the tension vector

**Returns** y-component of the vector

**Return type** float

## 1.1.6 pycellfit.cell module

```
class pycellfit.cell.Cell
    Bases: object

    add_edge_point(edge_point)
    id_iter = count(0)
    remove_duplicate_edge_points()
    sort_edge_points_ccw()
```

## 1.1.7 pycellfit.mesh module

```
class pycellfit.mesh.Mesh
    Bases: object

    add_cell(cell)
    remove_cell(cell)
```

## 1.1.8 pycellfit.constrained\_circle\_fit module

Constrained Circle Fit. Fit points to a circular arc when the two end points are fixed.

`pycellfit.constrained_circle_fit.algebraic_circle_fit(point_1, point_2, point_3)`  
finds center and radius of a circle that contains three points on its edge

**Parameters**

- `point_1` –
- `point_2` –
- `point_3` –

**Returns**

`pycellfit.constrained_circle_fit.center_point_to_t_alpha_beta(center, point_p)`  
converts from standard form (center, point on circle) to parametric form (t, alpha, beta)

**Parameters**

- `center` –

- `point_p` –

**Returns**

```
pycellfit.constrained_circle_fit.constraint(ans)
first constraint for the solver: alpha^2 + beta^2 = 1
```

**Parameters** `ans` –**Returns**

```
pycellfit.constrained_circle_fit.constraint2(ans, point_a, point_p)
second constraint for the solver: distance from center to point_a = distance from center to point_p
```

**Parameters**

- `ans` –
- `point_a` –
- `point_p` –

**Returns**

```
pycellfit.constrained_circle_fit.f(ans, x, y, point_a, point_p)
cost function that needs to be minimized See https://arxiv.org/pdf/1504.06582.pdf (page 9)
```

**Parameters**

- `ans` –
- `x` –
- `y` –
- `point_a` –
- `point_p` –

**Returns**

```
pycellfit.constrained_circle_fit.fit(x, y, start_point, end_point)
performs a constrained circle fit based on points around an arc and the start and end points of the arc
```

**Parameters**

- `x` –
- `y` –
- `start_point` –
- `end_point` –

**Returns**

```
pycellfit.constrained_circle_fit.plot_data_and_circle_fit(x, y, xc, yc, radius,
                                                               start_point, end_point)
plots the results of the circular fit
```

**Parameters**

- `x` – nparray of all x coordinates of data
- `y` – nparray of all y coordinates of data
- `xc` – float of x coordinate of center of fit circle
- `yc` – float of y coordinate of center of fit circle

- **radius** – radius of fit circle
- **start\_point** –
- **end\_point** –

**Returns** None

```
pycellfit.constrained_circle_fit.r(point_a, point_p, alpha, beta, t)
calculate radius of circle
```

**Parameters**

- **point\_a** –
- **point\_p** –
- **alpha** –
- **beta** –
- **t** –

**Returns**

```
pycellfit.constrained_circle_fit.t_alpha_beta_to_center_radius(ans, point_a,
                                                               point_p)
converts from parametric form (t, alpha, beta) to standard form (radius, center)
```

**Parameters**

- **ans** –
- **point\_a** –
- **point\_p** –

**Returns**

```
pycellfit.constrained_circle_fit.test1()
pycellfit.constrained_circle_fit.test2()
```

## 1.1.9 pycellfit.circle\_fit\_helpers module

```
pycellfit.circle_fit_helpers.M(g, h, x, y)
pycellfit.circle_fit_helpers.a0(point_a, point_p, x, y)
pycellfit.circle_fit_helpers.a1(point_a, point_p, alpha, beta, x, y)
pycellfit.circle_fit_helpers.a2(point_a, alpha, beta, x, y)
pycellfit.circle_fit_helpers.b0(point_a, point_p)
pycellfit.circle_fit_helpers.b1(point_a, point_p, alpha, beta)
pycellfit.circle_fit_helpers.b2()
pycellfit.circle_fit_helpers.distance(point_1, point_2)
calculates the euclidian distance between two points
```

**Parameters**

- **point\_1** –
- **point\_2** –

**Returns**

```
pycellfit.circle_fit_helpers.q(point_a, x, y)
pycellfit.circle_fit_helpers.qx(point_a, x, y)
pycellfit.circle_fit_helpers.qxx(point_a, x, y)
pycellfit.circle_fit_helpers.qxy(point_a, x, y)
pycellfit.circle_fit_helpers.qy(point_a, x, y)
pycellfit.circle_fit_helpers.qyy(point_a, x, y)
```

### 1.1.10 pycellfit.segmentation\_transform module

functions to convert between watershed and skeleton segmented images

```
pycellfit.segmentation_transform.skeleton_to_watershed(skeleton_image_array,
                                                       region_value=0,
                                                       boundary_value=255,
                                                       keep_boundaries=False)
```

converts a segmented skeleton image (all regions are same value with region boundaries being a second value) to a watershed segmented image (each region has a unique value and there are no boundary pixels, background region has value of zero)

**Parameters**

- **skeleton\_image\_array** (*np.ndarray*) – 2D numpy array with pixel values of a skeleton segmented image
- **region\_value** (*float*) – value of pixels in regions in skeleton\_segmented images (default is 0)
- **boundary\_value** (*float*) – value of boundary pixels of regions in skeleton\_segmented images (default is 255)
- **keep\_boundaries** (*bool*) – if True, watershed image will keep boundaries in returned result

**Returns** watershed\_image\_array

**Rtype** watershed\_image\_array np.ndarray

```
pycellfit.segmentation_transform.watershed_to_skeleton(watershed_image_array,
                                                       region_value=0,      bound-
                                                       ary_value=255)
```

converts a watershed segmented image (no boundaries between regions and each region has a different pixel value, background region has value of zero) to a skeleton segmented image (each region has the same pixel value and are separated by boundaries of a second value)

**Parameters**

- **watershed\_image\_array** (*numpy.ndarray*) – 2D numpy array with pixel values of a watershed segmented image
- **region\_value** (*float*) – desired value of all regions in the output (skeleton segmented) array
- **boundary\_value** (*float*) – desired value of boundary pixels in the output (skeleton segmented) array

**Returns** skeleton\_image\_array

**Rtype** `skeleton_image_array` `np.ndarray`

### 1.1.11 `pycellfit.segmentation_transform_utils` module

`pycellfit.segmentation_transform_utils.fill_region(array_of_pixels, position, new_value)`  
fills a region of a 2D numpy array with the same value

#### Parameters

- `array_of_pixels` (`np.ndarray`) – 2D numpy array of all pixel values
- `position` (`tuple`) – tuple with (row, col) location of pixel in the region to modify
- `new_value` (`float`) – new value for pixel at `position` and all pixels in same region

#### Returns

`None`

`pycellfit.segmentation_transform_utils.pad_with(vector, pad_width, iaxis, kwargs)`  
helper function that is called by `np.pad` to surround a nparray with a constant value Example: `[[0,0],[0,0]]` becomes `[[-1,-1,-1, -1],[-1, 0, 0, -1],[-1, 0, 0, -1],[-1,-1,-1, -1]]`

### 1.1.12 Module contents

# CHAPTER 2

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## README

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### 2.1 pycellfit

#### 2.1.1 Project Description

**pycellfit:** an open-source Python implementation of the CellFIT method of inferring cellular forces developed by Brodland et al.

**Author:** Nilai Vemula, Vanderbilt University (working under Dr. Shane Hutson, Vanderbilt University)

**Project Goal:** To develop an open-source version of CellFIT, a toolkit for inferring tensions along cell membranes and pressures inside cells based on cell geometries and their curvilinear boundaries. (See<sup>1</sup>.)

**Project Timeline:** Initial project started in August 2019 with work based off of XJ Xu. This repository was re-made in May 2020 in order to restart repository structure.

**Project Status:** Early development

#### 2.1.2 Getting Started

This project is available on [PyPI](#) and can be installed using pip.

It recommended that users make a virtual environment and install the package as such:

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<sup>1</sup> Brodland GW, Veldhuis JH, Kim S, Perrone M, Mashburn D, et al. (2014) CellFIT: A Cellular Force-Inference Toolkit Using Curvilinear Cell Boundaries. PLOS ONE 9(6): e99116. <https://doi.org/10.1371/journal.pone.0099116>

```
pip install pycellfit
```

Full documentation for this package can be found on [readthedocs](#).

## Dependencies

One of the goals of this project is to avoid dependencies that are difficult to install such as GDAL. This project primarily depends on numpy, scipy, matplotlib, and other common python packages common in scientific computing. A full list of dependencies is available in the [requirements.txt](#) file. All dependencies should be automatically installed when running pip install.

### 2.1.3 Development

This project is under active development and not ready for public use. The project is built using Travis CI, and all tests are run with every commit or merge.

### 2.1.4 Features

This section will include a list of features available in the package and maybe a check-list of things to add...

### 2.1.5 Examples

A example walk-through of how to use this module is found in [quickstart](#).

### 2.1.6 Future Goals

The final implementation of pycellfit will be as a web-app based on the Django framework. See (add link to django-pycellfit repo).

### 2.1.7 References

# CHAPTER 3

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