

AmoePy

A Python-based toolbox for analyzing and simulating amoeboid cell motility

1. Installation

Requirements: Anaconda/Miniconda ([Link](#))

- **Installation via conda command lines**^{1,2,3}

```
# Initiatilize conda environment/installing packages
$ cd B02/src
$ conda update conda           # Updates conda packages
$ conda env create -n AmoePy -f environment.yml
# After installation use following command:
$ cd B02/src
$ conda activate AmoePy
$ python -m run.run_amoepy    # Alternatively: python3
```

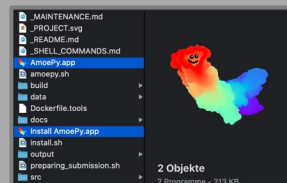
- **Alternative 1: Shell script**^{1,2}

```
$ cd B02
$ sh install.sh    # Also updates conda environmet
# After installation use following command:
$ sh amoepy.sh    # Opens AmoePy
```

- **Alternative 2: AmoePy.app**¹

- Click on “Install AmoePy.app”
- After installation click on “AmoePy.app”

¹ MacOS ² Linux ³ Windows



2. Documentation

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Documentation for the entire AmoePy **Code base** ([Link](#)) is generated by **Sphinx**

3. Import Contour Data

- Contour data must be imported as ***.txt** file
- 1st line starts with **#** and is reserved for **comments**
- Each line stands for **one contour**, starting with a **time** coordinate followed by alternating **X** and **Y** coordinates, representing neighboring segmentation points

Time (s)

```
# Comments in first line
0 0.0 0.0 1.0 0.0 1.0 1.0
1 0.0 0.1 1.0 0.1 1.0 1.1
2 0.0 0.2 1.0 0.2 1.0 1.2
3 0.1 0.2 1.1 0.2 1.1 1.2
4 0.2 0.2 1.2 0.2 1.2 1.2
```

Alternating X and Y (μm)

Delimiters:
' ' (spaces) and line breaks

File format:
*.txt

Prerequisites:
Equal number of points for all contours

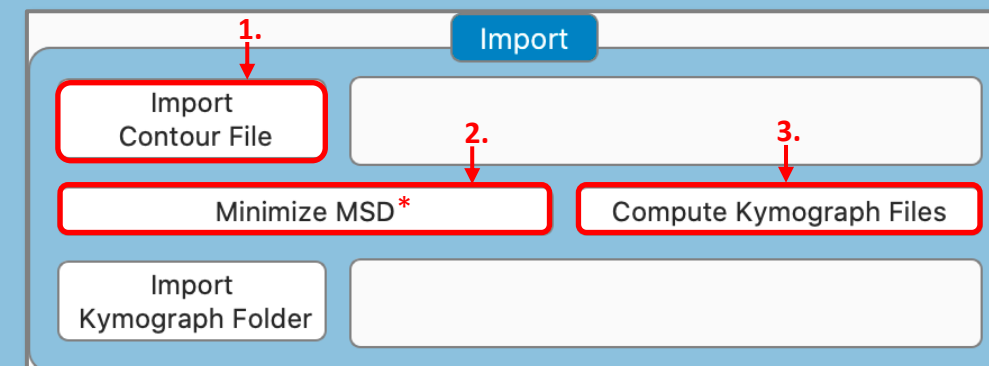
Creating file from NumPy array:

```
np.savetxt('contour.txt', data, delimiter=' ', header='comments ...')
```

Paths of example contour data:

B02/data/testing_data	D. discoideum
b02-data/dictyostelium_data_2016/original_data	D. discoideum
b02-data/keratocyte_data/original_data	Hypophrys nicaraguensis
b02-data/embryonic_killifish_data/original_data	Fundulus heteroclitus

4. Data Processing/Analysis



* Pre-sorting virtual markers based on **Mean Square Displacement** (recommended)

5. Global Settings

- **General**
- **Graphics**
- **Video**

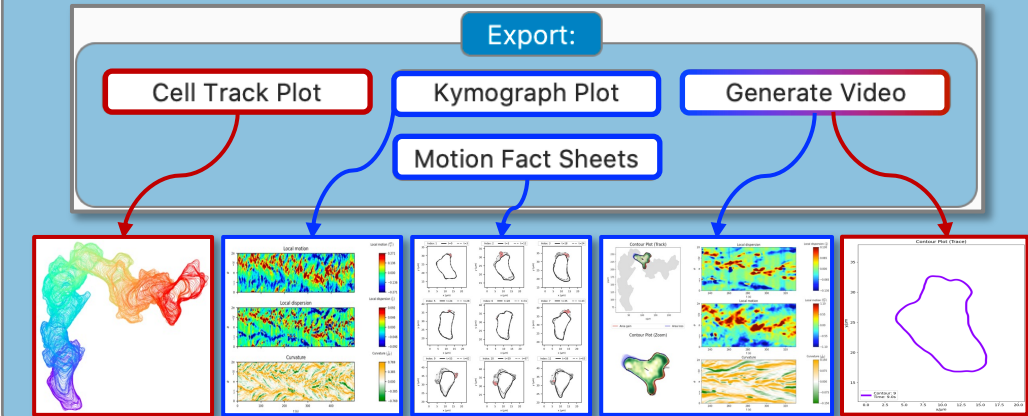
Terminal Output

End



6. Plotting Methods

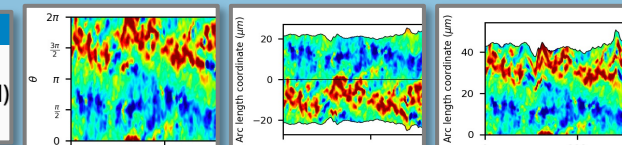
- **Methods which require contour file only**
- **Methods which require kymograph folder**



7. Kymograph Options

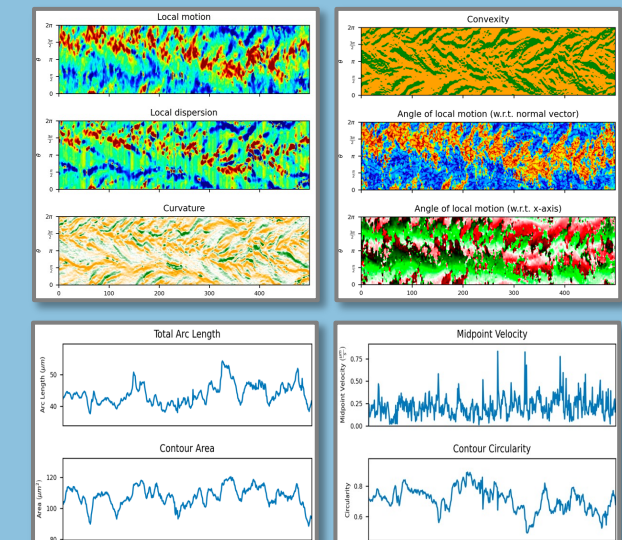
Kymograph Styles:

- ✓ **Conventional**
 - Conventional (Smoothed)
 - Varying arc length (double-sided)
 - Varying arc length (one-sided)



Kymograph Kinds:

- ✓ **Local Motion**
 - Local Dispersion
 - Curvature
 - Convexity
 - Shape
 - Angle (x-axis)
 - Angle (norm. vector)
 - Fluorescence Intensity
 - Protrusion Component
 - Perimeter
 - Area
 - Circularity
 - Midpoint velocity
 - MSD (centroid)
 - RMSD (centroid)



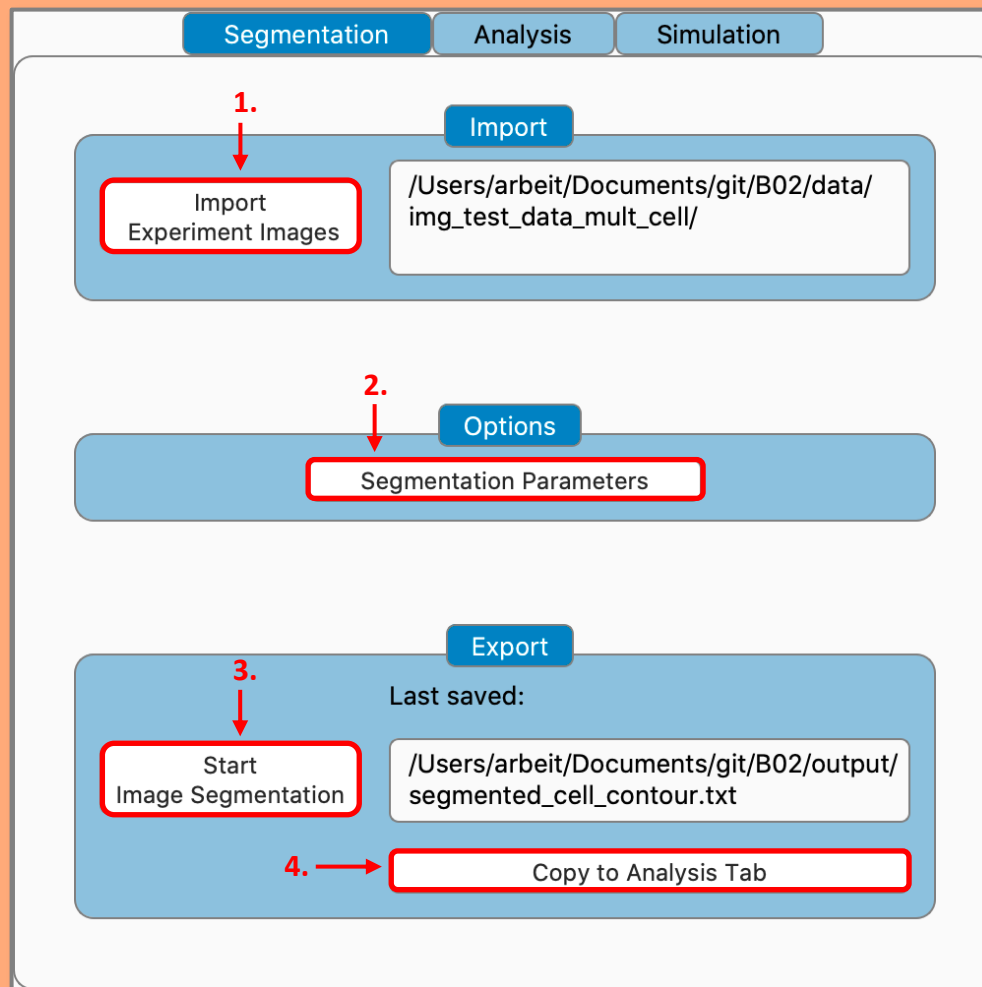
8. Video Settings

- Each frame will be saved as **png**
- For saving a **video** file, **FFmpeg** ([Link](#)) is required



9. Image Segmentation

- Extract cell contours from **microscopy images**
- Required file format: **.png, .tif, .tiff**



Path to segmentation algorithm:

`B02/src/amoepy/segmentation/segmentation`

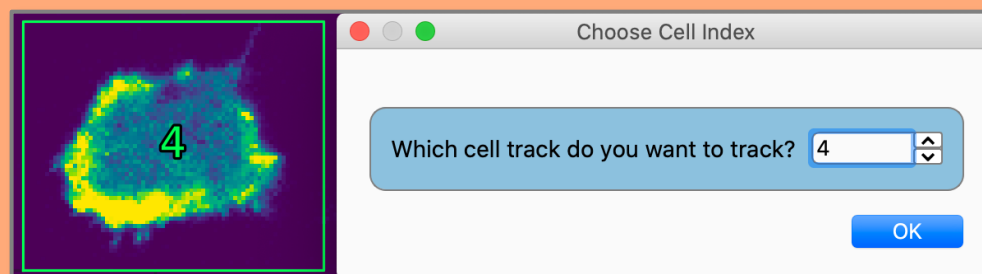
Paths to microscopy data:

`B02/data/testing_data/img_test_data`
`B02/data/testing_data/img_test_data_mult_cell`
`b02-data/fluorescence_data/...`

D. discoideum
D. discoideum
diversus

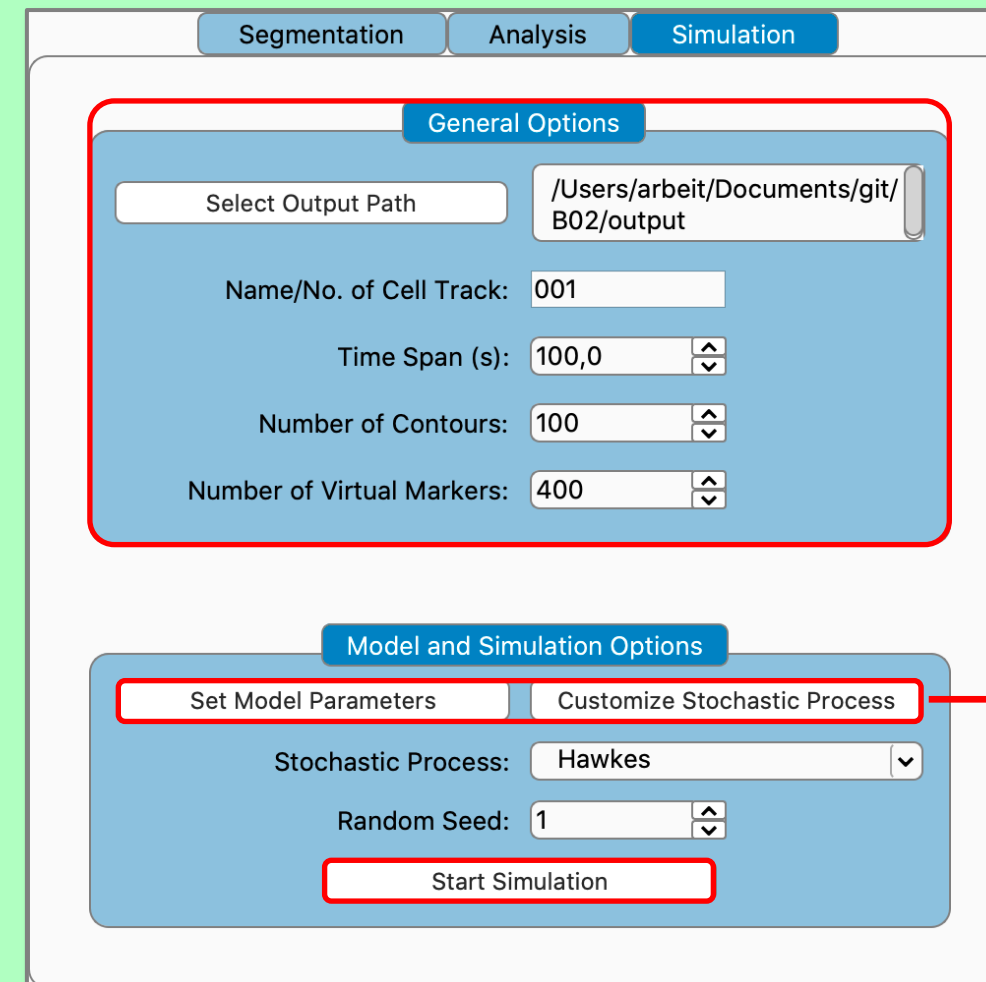
10. Segmentation Choice

- Initial request** after starting image segmentation:
Choice of cell to be tracked in segmentation routine



11. Simulating Cell Tracks

- Simulate cell tracks** based contour morphing model
- Choice between **two stochastic processes**:
 - Hawkes process
 - Ornstein-Uhlenbeck process
- Animation of contour dynamics** during simulation
- Final step: Contour data of simulated cell track is saved as ***.txt** file and is loaded to the analysis tab



Path to simulation routines:

`B02/src/amoepy/simulation/...`

Paths to simulated cell tracks:

`b02-data/artificial_data/...` **Simulated data**

12. General Options

- Choose **output path** and **name** of saved contour file
- Select **time span** of cell track (in seconds), **number of contours** and **number of virtual markers** per contour

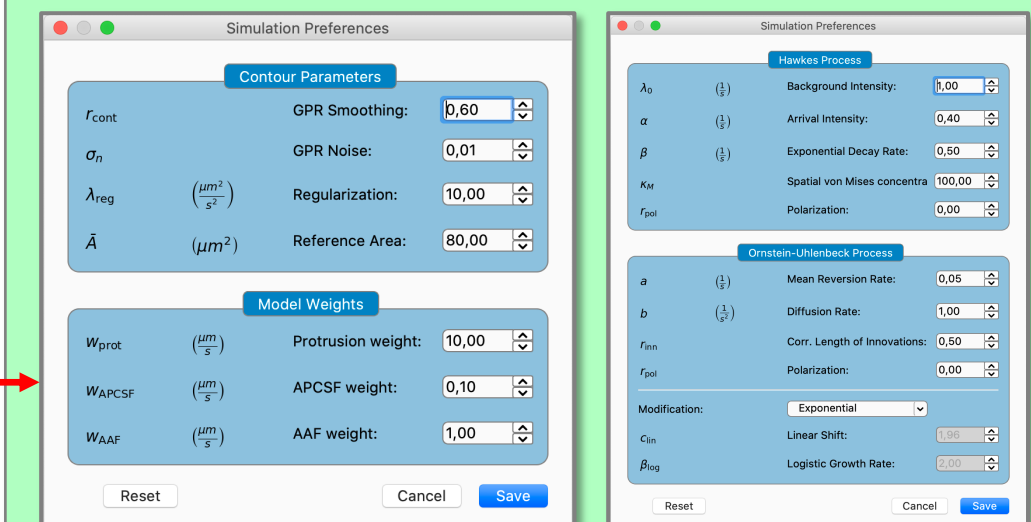
13. Advanced Options

Model Parameters:

- Select parameters regarding the contour smoothing and the regularization of the virtual marker flow
- Define contour size by choosing a reference area
- Select individual weights for each model component

Customize stochastic process:

- Select stochastic process to be used for simulations
- Customize the stochastic process by changing parameters and modifications
- Random seeds**: Change outcome of cell tracks by choosing different random seeds



14. Progress Bar/Terminal Output

Please, look carefully at the terminal output!

