USER MANUAL

BIOFORM

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1. Acknowledgements

This project was made possible through the guidance and support from our supervisor and client, Professor Michelle Kuttel, and our tutor Vincent Moloi.
The main contributors of this project include: Daniel Holgate, Thalia Hawthorn and Tziyona Cohen.

2. Welcome to BioForm

BioForm is a standalone desktop application that can be used as simulation and visualisation tool to show the lifecycle of bacteria and their formation of biofilms.

2.1. Key Features of BioForm

User input is accepted (EPS monomers, bacteria, width, height, duration) that is given as starting parameters that runs the simulation model and produces a textfile output of the simulation activities. This textfile is submitted to the program to be read and produce the visualization of the simulation activities. The added benefit of using a standardised textfile format is that the user is able to edit the contents (providing it follows the correct format) and thereafter run visualisations of their own choice.

One can generate the dataset by running their own simulation or provide a valid textfile to just produce the visualisation. After every animation is completed, an MP4 video of its graphics are saved to the user's local repository. This allows the user to go through the simulation at their own speed and leisure by pausing, rewinding and replaying it.

3. Getting started

3.1. Setup and Installation

3.1.1. Requirements

The prerequisites to run the BioForm is at least Python version 3.x and it requires the following Python packages:

- Matplotlib - embeds plots in GUI
- Numpy
- Tkinter - creates the GUI
- Ffmeg
- PIL (Pillow) - handles images
- Pathlib - for file paths
- Subprocess - runs external commands
- Threading

To install the tkinter module run:

On Ubuntu/Debian:

```
sudo apt-get update
sudo apt-get install python3-tk
```

On Fedora:

```
sudo dnf install python3-tkinter
```

On Arch Linux:

```
sudo pacman -S tk
```

For MacOS via Homebrew:

```
brew install python-tk
```

To ensure all the other libraries are installed you can run the following command in the terminal:

For Windows:

Navigate to ‘biofilm’ folder and run to get into Linux:

```
wsl
```

For Ubuntu/Debian:

```
sudo apt-get install python3 python3-pip
```

For MacOS via Homebrew:

```
brew install python3
```

Navigate to ‘biofilm’ folder and run:

```
pip3 install -r requirements.txt
```

3.1.2. Running the project

Navigate to the directory containing the ‘biofilm/frontEnd’ folder and run the following command:

```
python3 BiofilmSimulationApp.py
```

Makefile use directly:

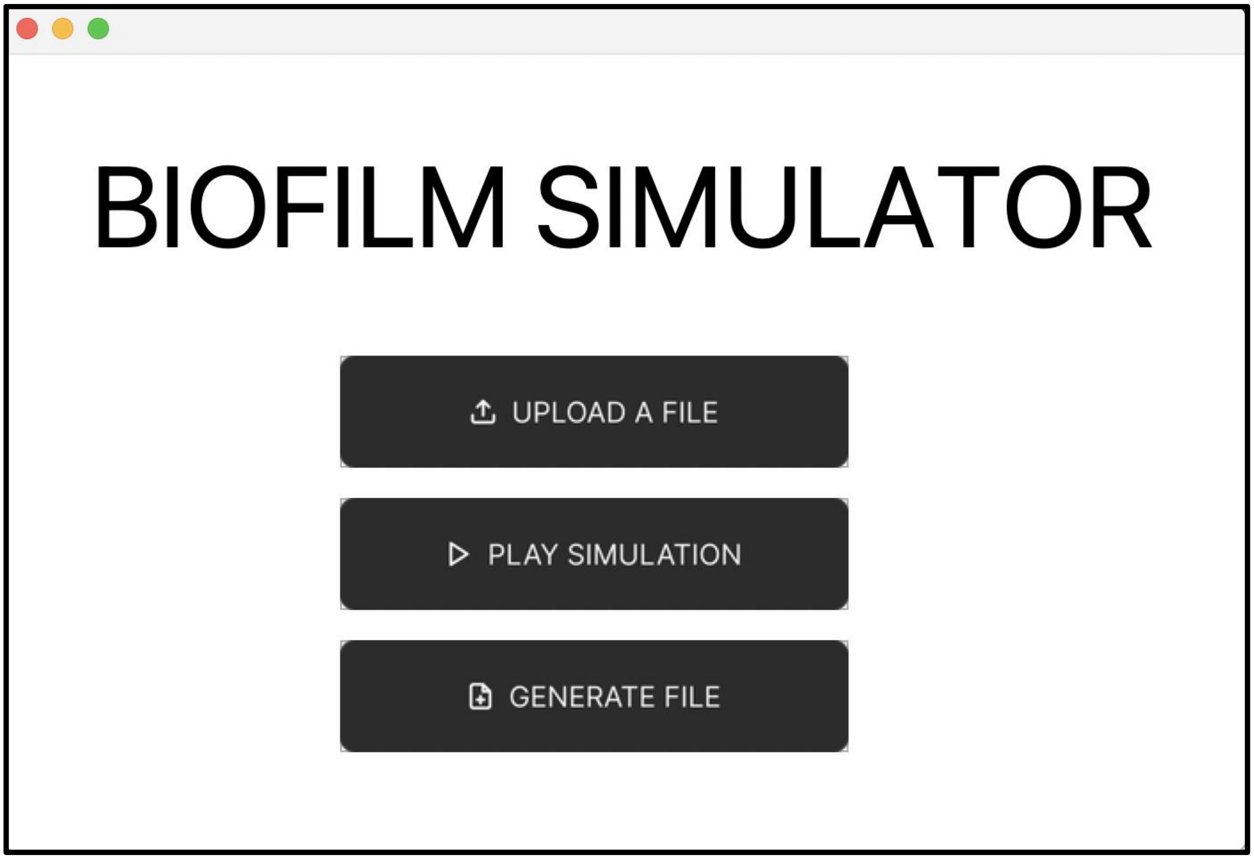
One can run the backend i.e. the simulation model which produces a textfile output of the simulation activities through use of the makefile directly. Navigate to the directory containing the ‘biofilm/frontEnd’ folder and run the following command in the terminal:

```
make run ARGS=”{number of eps monomers} {number of bacteria} {width} {height} {duration} {textfile name}”
```

E.g. make run ARGS="100 3 100 100 20 test.txt"

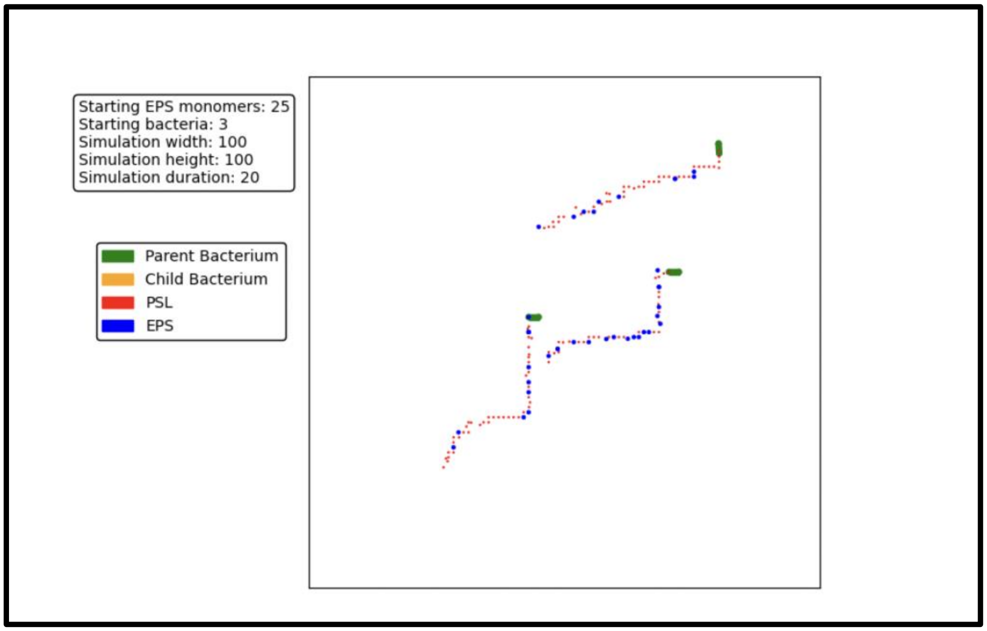
4. Quick start guide

4.1. Home Screen window



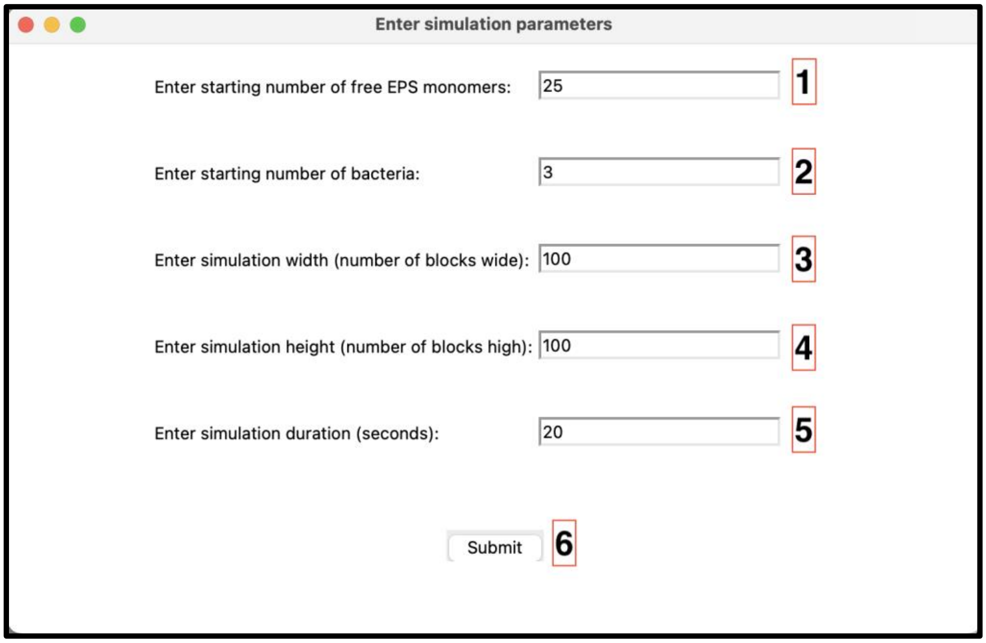
Label of button	Action on press of button
UPLOAD A FILE	This opens a file dialogue box that only accepts files with a .txt extension
PLAY SIMULATION	This will open the simulation window that has the embedded matplotlib canvas that will animate the simulation. An MP4 of the simulation will be saved to the user’s local repository.
GENERATE FILE	This will open the input window for the user to input their own values for the respective parameters.

4.2. Simulation window



Starting EPS monomers: 25
Starting bacteria: 3
Simulation width: 100
Simulation height: 100
Simulation duration: 20

4.3. Input Window



Enter simulation parameters

Enter starting number of free EPS monomers: 25

Enter starting number of bacteria: 3

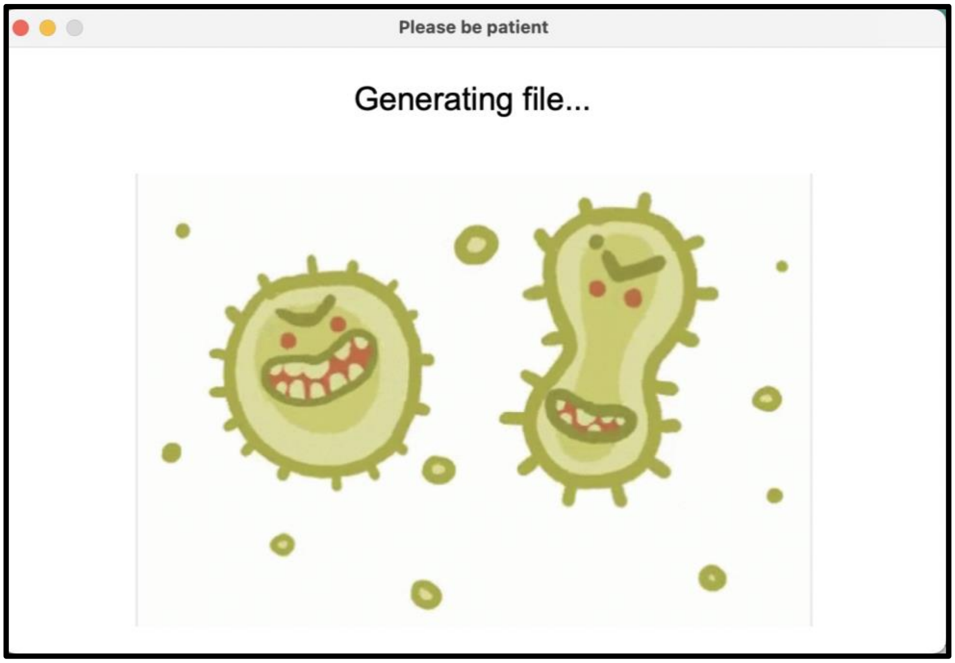
Enter simulation width (number of blocks wide): 100

Enter simulation height (number of blocks high): 100

Enter simulation duration (seconds): 20

Label of component	Desired action
1. Initial EPS monomer value inputbox	A positive integer must be inputted.
2. Initial bacteria value inputbox	A positive integer must be inputted and the value must be greater or equal to the number of grid blocks (width x height).
3. Width value of grid (in blocks) inputbox	A positive integer value between 20 and 100 (inclusive).
4. Height value of grid (in blocks) inputbox	A positive integer value between 20 and 100 (inclusive).
5. Duration of simulation (in seconds) inputbox	A positive integer must be inputted
6. Submit button	This sends all the parameter values as arguments to run the make file command and thus start the simulation. It will produce a textfile that is stored in the local repository. A “generating file…” will be displayed as the simulation runs.

4.4. File generation window



Generating file...

This window will be displayed while the simulation runs and the textfile is being produced. Thereafter, it will be be destroyed when the simulation runs to completion.

5. Accepted textfile format

The accepted textfile format follows as below:

<u>The first 5 lines are for the parameters:</u>
Starting EPS monomers: [number]
Starting bacteria: [number]
Simulation width: [number]
Simulation height: [number]
Simulation duration: [number]

Thereafter the event log:

Event	**Format**	**Example**
Spawn	Bacterium:ID:Spawn:(xCoordinate,yCoordinate)	Bacterium:0:Spawn:(98,36)
Secrete	Bacterium:ID:Secrete:EPS	Bacterium:0:Secrete:EPS

Tumble	Bacterium:ID:Tumble:(xInitial,yInitial):(xFinal,yFinal)	Bacterium:2:Tumble:(89,66):(88,66)
Run	Bacterium:ID:Run:(xInitial,yInitial):(xFinal,yFinal)	Bacterium:2:Run:(87,66):(86,66)
Idle	Bacterium:ID:Idle:(xCoordinate,yCoordinate)	Bacterium:1:Idle(50,92)
Attach	Bacterium:ID:Attach:(xCoordinate,yCoordinate)	Bacterium:3:Attach:(60,54)
Die	Bacterium:ID:Die	Bacterium:1:Die
Reproduce	Bacterium:ID:Reproduce:Bacterium:IDofChild	Bacterium:0:Reproduce:Bacterium:3
Eat	Bacterium:ID:Eat	Bacterium:1:Eat

Between each timestep i.e. the period of activities that happen every frame update in the visualtion of the animation there is a delimiter “*”

Example textfile:

```
Starting EPS monomers: 25
Starting bacteria: 3
Simulation width: 100
Simulation height: 100
Simulation duration: 20

Bacterium:0:Spawn:(98,36)
Bacterium:1:Spawn:(47,92)
Bacterium:2:Spawn:(89,66)
Bacterium:0:Secrete:EPS
Bacterium:2:Tumble:(89,66):(88,66)
Bacterium:1:Tumble:(47,92):(48,92)
*
Bacterium:2:Tumble:(88,66):(87,66)
Bacterium:1:Secrete:EPS
Bacterium:0:Reproduce:Bacterium:3
*
Bacterium:2:Run:(87,66):(86,66)
Bacterium:0:Eat
Bacterium:1:Run:(48,92):(49,92)
Bacterium:3:Tumble:(80,25):(79,25)
*
Bacterium:1:Tumble:(49,92):(50,92)
Bacterium:3:Secrete
Bacterium:0:Run:(96,36):(95,36)
Bacterium:2:Idle
```