

Instructions for running the Agent Based Model (MATLAB)

Filename: ABM_RunSingle.m can be accessed on GitHub at:

https://github.com/frm3-st-andrews/EASTBIO_2022.git

1 Overview of model

The details included in the code are described below with any variable names used in the code given in purple with the corresponding line number in the code.

To run the code open the ABM_RunSingle.m file in MATLAB and press run, a pop-up will appear asking if the initial condition shall be rest - click yes is this is the first time running the code. All of the simulation data will be saved in a file called Data1.mat (this can be changed in line 263 of file).

1.1 Agents

The agent-based model simulates an infection spreading through a population. The following sub-populations of people exist:

- **S** - number of **S**usceptible people who can be infected
- **I** - number of **I**nfectious/infective who can infect others
- **R** - number of **R**ecovered, people who can no longer be infected

Total population = **S** + **I** + **R**

1.2 Rules:

The rules for each population are given below for ● **S**, ● **I** and ● **R** populations.

1. All people can move randomly in the domain (●, ●, ●)
 - This occurs at each time-step with probability **Mov** (defined on line 111 of code)
2. If an infected person meets a susceptible person they can infect them (●+●=●●)

- This occurs at each time-step with probability **Infection_Probability** if the infected and susceptible person are within a distance of **R** of each other (defined on line 103 and 109 of code, respectively)
3. If a person is infected they will become recovered after a certain time T_{rec} ($\bullet \rightarrow \bullet$)
- The recovery time is set as **Recovery_Time** (defined on line 105 of code)

1.3 Set up of spatial domain and initial conditions

- 2D grid (100×100 points) (defined on lines 22-36 of code)
- Closed boundary (everyone remains within the boundary)
- Ensure only one person can be on any spatial position at any time
- Total number of people **N** (defined on line 41 of code)
- Initial number of infected **Initial_No_Infected** (defined on line 83 of code)
- Initial number of recovered (e.g. vaccinated) **Vaccinated** (defined on line 85 of code)
- All people randomly distributed initially (the code will ask if you wish to use the same initial condition as previous runs)

2 Things to investigate with the code

When the code is run a figure will appear that shows the spatial positions of each person in a square grid and the total number of each population over the elapsed time in a plot below. This updates at every time-step.

- Run the simulation once with current values (if you wish you can save the figure either by uncommenting line 254 in code, or using file toolbar on the figure itself)
- Change some parameter settings to check what would change. For example:
 - Add vaccinations by increasing value of **Vaccinated** (defined on line 85 of code)
 - Change the total number of people in the simulation **N** (defined on line 41 of code)
 - Change the recovery time, **Recovery_Time** (defined on line 105 of code)

- You can also play around with other settings. **Tip: you may want to note down the original values of any parameter you change**

Optional: You can run the simulation more than once with the same parameter settings to see if the results are robust

- Note, in the same folder a file called Calculate_Averages.m allows you to plot the averaged results. To run this you need to have run the simulation 10 times ensuring that you change the filename you save the data to each time (e.g Data2.mat, Data3.mat,...Data10.mat on line 263 of original code)