

README file

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1 Introduction

This is the readme file for the open source code written for the paper submitted to MIG2021, Interactive Simulation of Disease Contagion in Dynamic Crowds.

The model combines a social force-based and contact-based crowd simulation with a diffusion model of disease spread to simulate disease spread in crowds. The model gives the user flexibility in generating groups of people, or agents, in a 2D grid, as well as setting their destinations. The model accounts for immunity, vaccinations, and other attributes.

The user can specify several attributes of the randomly generated crowds, as well as parameters which affect the randomly generated parameters of the individuals in these crowds. These attributes include spawning location, destinations of the individual agents, vaccinations and their effects on immunity, and the strength and influence range of the social force, contact force, disease spread, and immunity.

The code is C++ code in a cmake project. It was developed and run on Visual Studio Community 2019 on Windows 10.

Details of the algorithm can be found in the Interactive Simulation of Disease Contagion in Dynamic Crowds paper, particularly in section 3.

2 Parameters

The program reads from its base folder a description file, `description.txt`, which contains the parameters that specify the simulation. This file must be written by the user; it is the way that the user can specify the properties of groups and agents in the model. A sample description file appears below.

2.1 Sample `description.txt` file

```
5.0 social_force_strength
1.0 social_force_range_b
1.0 social_force_radius
10.0 contact_force_strength
0.05 particle_radius
```

```

10 disease_a
1.0 disease_s
2.0 disease_radius
1.0 disease_range_rs
0.0 mask_prob
0.5 healthy_life_prob
0.5 vaccine_factor
1.0 relaxation_time
1.0 desired_speed
0.01 dt
150 total_time
10 time_steps_per_frame
15.0 group_init_radius
500 people_per_group
2 num_groups
-30 0 init_coords
600 0 displacement_coords
30 0 init_coords
-600 0 displacement_coords

```

2.2 Explanations of the parameters in the description.txt file

- **social_force_strength**: A from the paper
- **social_force_range_b**: B from the paper
- **social_force_radius**: Maximum distance between agents for which the program calculates a social force
- **contact_force_strength**: Strength of the contact force between agents whose radii overlap
- **particle_radius**: Radius of each agent
- **disease_a**: a from the paper
- **disease_s**: s from the paper
- **disease_radius**: Maximum distance between agents for which the program calculates disease spread
- **disease_range_rs**: R_s from the paper
- **mask_prob**: The probability of agents wearing masks; for each agent, this value is the probability that it wears a mask, setting η_j (from the paper) for each agent j

- **healthy_life_prob**: This is the probability that an agent has a healthy lifestyle; for each agent this is the probability that an agent is healthy, which sets μ from the paper.
- **vaccine_factor**: ξ from the paper
- **relaxation_time**: τ_i from the paper
- **desired_speed**: v_i^0 from the paper
- **dt**: time step size
- **total_time**: total time that the simulation runs
- **time_steps_per_frame**: number of time steps skipped between frames, so if it is set to 10, the program generates a csv file every tenth time step
- **group_init_radius**: radius around a group's center, in which agents are generated for that group
- **people_per_group**: number of agents generated for each group
- **num_groups**: Sets the number of groups. It is expected that there will be one **init_coords** and one **displacement_coords** pair of lines below this parameter for each group in the simulation.
- **init_coords**: The x-axis and y-axis coordinates, respectively, for the center of the group being specified
- **displacement_coords**: The x-axis and y-axis values, respectively, for the displacement. An agent's initial position is added to this displacement value to produce the agent's destination. An agent sets the direction of its desired velocity to point towards its destination; this is the only influence on an agent which is not in range of any social force nor contact force.

3 Output

The code outputs a series of csv files, each detailing the agent attributes in a specific frame and being used for further rendering. The number of time steps skipped frame is specified in the description file. The agent attributes in the output files are:

- x-axis position
- y-axis position
- x-axis velocity
- y-axis velocity
- particle group ID (which specifies the group that the particle starts with)

- particle disease level (from 0=fully healthy to 1=fully infected)
- particle immunity level (from 0=no immunity to 1=maximum immunity)

4 Example visualizations of output

Using visualization software, we turned the data in the csv files into images which provide snapshots of the simulations presented in our paper and video. The following are two illustrative cases, more detailed results can be found in our paper and video.

4.1 Crowd Simulations



Figure 1: A visualization of one of the csv files generated from running the code for crowd simulations. Each agent is colored based on its group ID. Left: the groups at the start of their collision. Right: the groups post-collision.

4.2 Disease Spreading

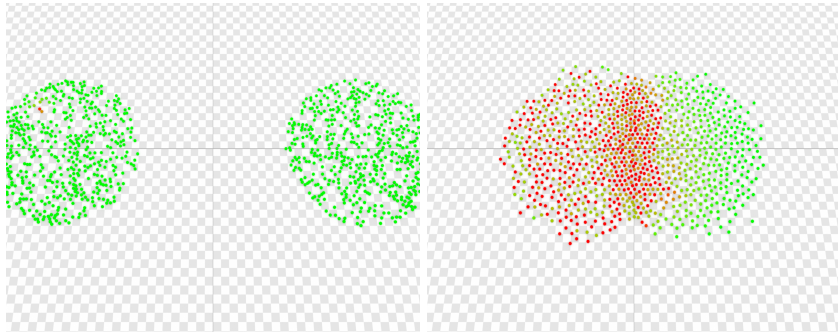


Figure 2: A visualization of one of the csv files generated from running the code for disease spreading simulations. Infectivity (disease level) quantities are visualized with colors from green (low) to red (high) for increasing values.