- `void update_node`: updates the given node selected by its $L \times L$ grid coordinates `row_i` and `column_j` according to the turnover probabilities

- `void grid_update_linear`: calls the `update_node` function for each node in order of their grid position

- `void grid_update_stochastic`: calls `update_node` for L^2 randomly chosen nodes

- `double ratio_infected`: calculates the ratio of infected individuals with respect to the total grip population for a given grid

- `double average_ratio_infected`: applies `T` simulation steps to the grid by calling the stochastic grid updater with passed turnover probabilities and averages the above infection rate over each simulation step

3.2.4 Structure of the Main Function and General Workflow

The main function is divided into sections for each individual analysis step, where every section is an enclosed space in order to prevent the variables from interfering with each other.

Overall a running time of around three minutes should be expected after the interactive part is finished.

4 Results and Discussion

4.1 Model for the Spread of Infectious Diseases

4.2 Expected Ratio of Infected People averaged over Time

4.3 Vaccinated People without Participation in the Spread

4.4 Time Evolution of the Expected Ratio of Infected People

While previously the average of the ratio of infected individuals has been taken over time, the focus should now be layed on the time development of th einfection rate $\langle I \rangle_t$ for $N = 20$ samples. As grid size $L = 64$ was chosen for appropriate balance between running time and accuracy, the number of simulation steps again was set to $T = 1000$.
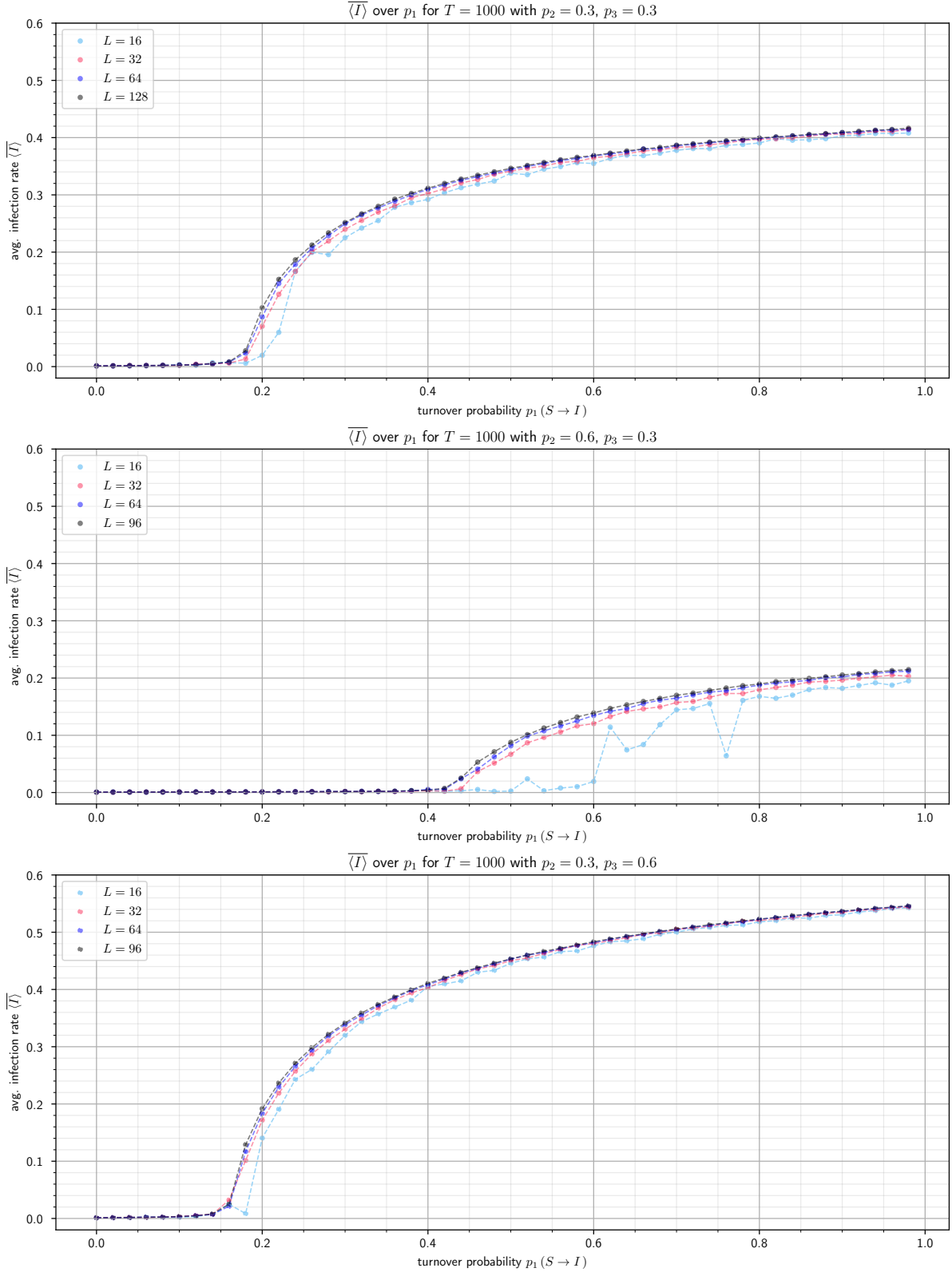
Figure 1: Plots showing the time-averaged infection rates $\overline{\langle I \rangle}$ in dependence of the turnover probability $p_1 \left(S \rightarrow I \right)$ for the different grid sizes $L = 16$, $L = 32$, $L = 64$ and $L = 128$ with $T = 1000$ simulation steps each. The upper plot shows has now been generated using the turnover rates $p_2 \left(S \rightarrow I \right) = 0.3$ and $p_3 \left(S \rightarrow I \right) = 0.5$, the middle one using $p_2 = 0.6$ and $p_3 = 0.3$, and the lower one $p_2 = 0.3$ and $p_3 = 0.6$.
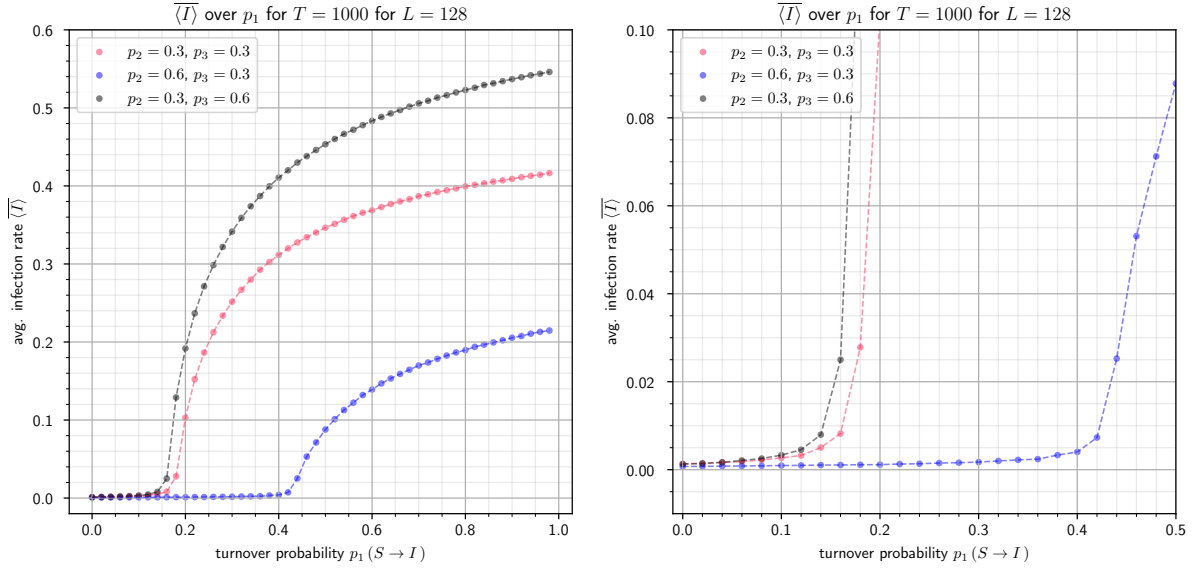
Figure 2: Detailed view of the time-averaged infection rates $\overline{\langle I \rangle}$ over $p_1\,(S \to I)$ for $L = 128$ and $T = 1000$ simulation steps. On the left the different trends for the respective choices of $p_2\,(S \to I)$ and $p_3\,(S \to I)$ can be observed, while on the right the critical values of p_1 for $\overline{\langle I \rangle}$ approaching zero are visible.
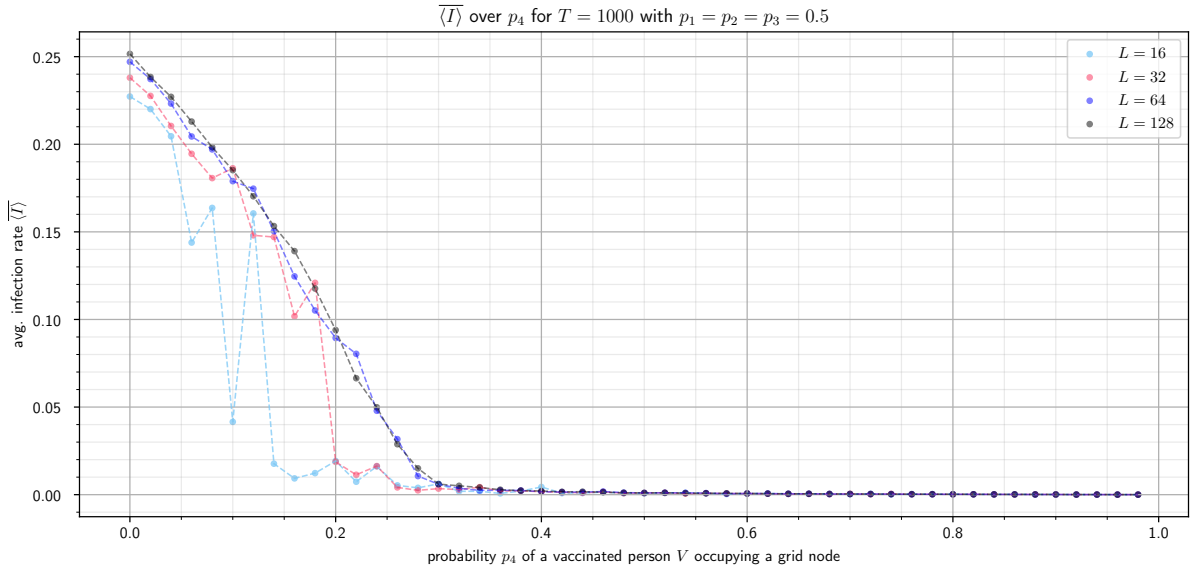

Figure 3: Display of the time-averaged infection rates $\overline{\langle I \rangle}$ depending on the vaccination rate p_4 at the beginning of the simulation and constant turnover probabilities $p_1 = p_2 = p_3 = 0.5$. The simulation was performed over $T = 1000$ simulation steps and th respective grid sizes $L = 16$, $L = 32$, $L = 64$ and $L = 128$.
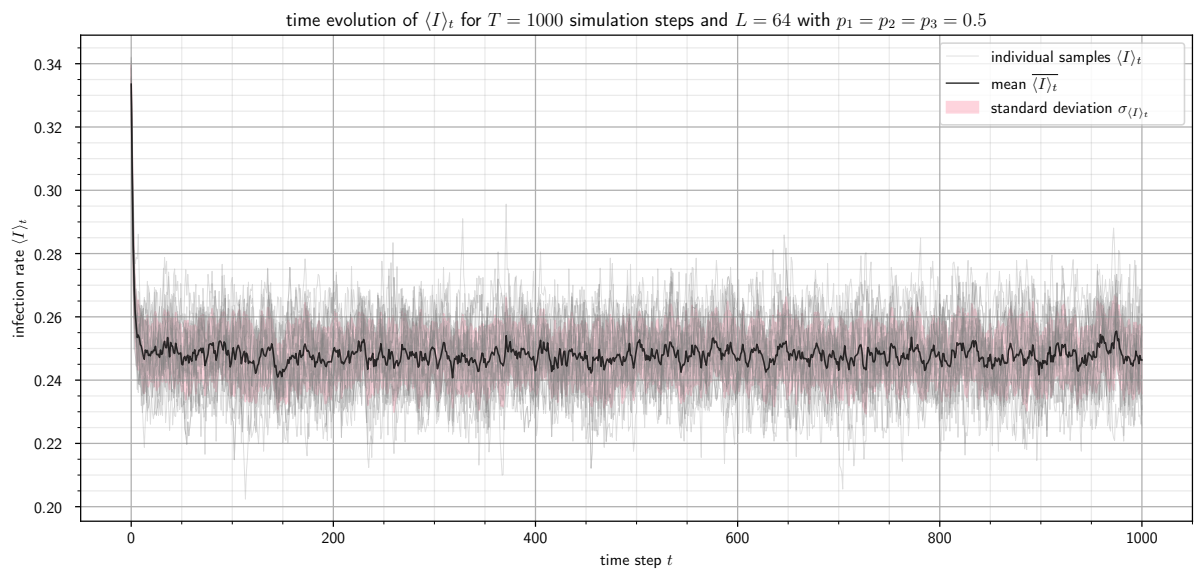
Figure 4: Time evolution of the infection rate $\langle I \rangle_t$ over each of the $T = 1000$ simulation steps for a total of 20 samples. At each timestep mean $\overline{\langle I \rangle_t}$ and standard deviation $\sigma_{\langle I \rangle_t}$ of the infection rate were calculated and are also displayed in the plot. The grid size was chosen as $L = 64$, the turnover probabilities as $p_1 = p_2 = p_3 = 0.5$, no vaccinated induviduals were used.
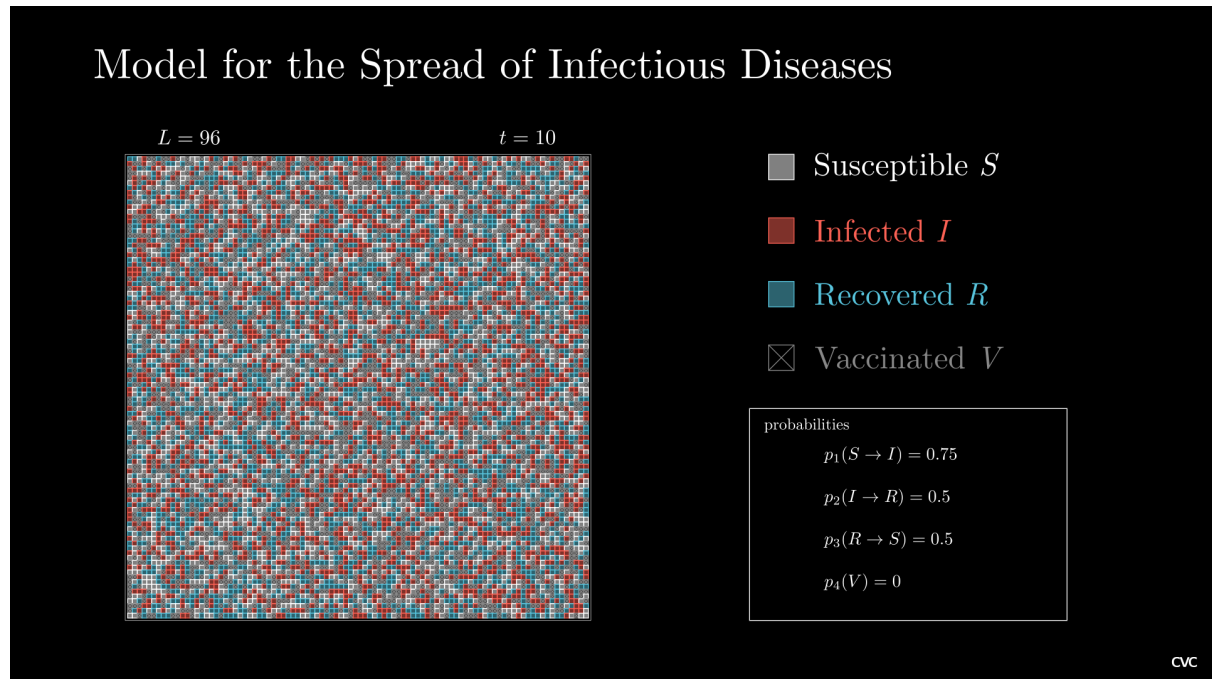
5 Supplementary Materials

Figure 5: Frame $t = 10$ of an animated simulation of the infectious disease model for the grid size $L = 96$. The grid was initialized with a vaccination rate $p_4 = 0.25$ and progressed with the turnover probabilities $p_1 = 0.75$ as well as $p_2 = p_3 = 0.5$. The total animation as well as variations in the probabilities can be found under `/soi_animations`.

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