Network Dynamics – Homework 3

18 January 2025

Abstract

In this report we present our solution to Homework 3. This report is the result of active collaboration between: Kevin Elezi (s316685), Marco Conte (s346753), Melika Ghasemi (s309495), Mohamed Hatem (s346906) and Xiangxi Li (s336719).

Problem 1.1: Epidemic on a known graph

This exercise focuses on simulating the spread of the H1N1 virus (swine-flu) based on data from the 2009 pandemic in Sweden. The goal is to understand network structure characteristics and disease dynamics. Specifically, we simulate a discrete-time simplified SIR (Susceptible-Infected-Recovered) model on a symmetric k-regular undirected graph.

The graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ consists of $n = 500$ nodes, where every node is connected to $k = 4$ neighbors (the nodes with indices closest modulo n). The dynamics are governed by the infection probability $\beta = 0.3$ and the recovery probability $\rho = 0.7$.

The transition probabilities for a node i at time t are defined as:

$$\mathbb{P}\left(X_i(t+1) = \mathrm{I} \mid X_i(t) = \mathrm{S}, \sum_{j \in \mathcal{V}} W_{ij}\delta^{\mathrm{I}}_{X_j(t)} = m\right) = 1 - (1 - \beta)^m$$

$$\mathbb{P}(X_i(t+1) = \mathrm{R} \mid X_i(t) = \mathrm{I}) = \rho$$

where $\sum_{j \in \mathcal{V}} W_{ij}\delta^{\mathrm{I}}_{X_j(t)}$ is the number of infected neighbors for node i.

Task 1) Simulate the epidemic for 15 weeks (where 1 time unit = 1 week) over $N = 100$ runs. Initialize with 10 randomly selected infected nodes.

Task 2) Plot the **average number of newly infected individuals** each week.

Task 3) Plot the **average total number** of Susceptible (S), Infected (I), and Recovered (R) individuals at each week.
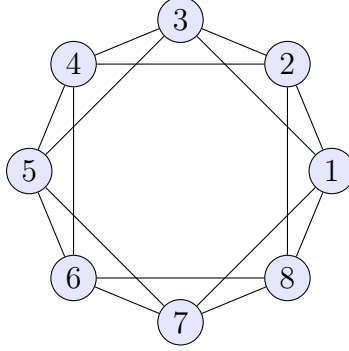
Figure 1: Example of a symmetric k-regular graph with $n = 8$ and $k = 4$, where each node is connected to its two nearest neighbors on either side.

Task 1: Epidemic Simulation on a Regular Graph

In this section, we implement a discrete-time SIR epidemic model on a symmetric k-regular undirected graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ with cardinality $n = |\mathcal{V}| = 500$ and constant degree $k = 4$. The network topology is constructed such that the neighborhood $\mathcal{N}_i$ of any node i comprises the k nodes with indices closest to i modulo n. The global state of the system at time t is described by the vector $X(t) \in \{S, I, R\}^n$, evolving according to a stochastic process governed by the infection probability $\beta = 0.3$ and the recovery probability $\rho = 0.7$.

Initial Configuration: The Clustered Outbreak

To emulate a realistic pandemic scenario characterized by spatial locality rather than a uniform random distribution, we initialize the simulation using a "clustered focolare" approach. We define a seed node v^*, or "Patient Zero", selected uniformly at random from $\mathcal{V}$. Around this seed, we establish a localized potential outbreak window $\mathcal{W} \subset \mathcal{V}$ defined as:

$$\mathcal{W} = \left\{ (v^* + \ell) \pmod{n} : \ell \in \mathbb{Z}, -\frac{\Delta}{2} \leq \ell < \frac{\Delta}{2} \right\}$$

where $\Delta = 20$ represents the spatial extent of the cluster. The initial set of infected nodes $\mathcal{I}(0)$ is then constructed by sampling $n_{\text{init}} = 10$ unique nodes from $\mathcal{W}$, while the remaining population $\mathcal{V} \setminus \mathcal{I}(0)$ is initialized as susceptible.

Task 2: Analysis of New Infections

We analyze the temporal evolution of the epidemic by observing the average number of newly infected individuals at each time step. The results, averaged

over $N = 100$ independent realizations, indicate a rapid suppression of the outbreak.
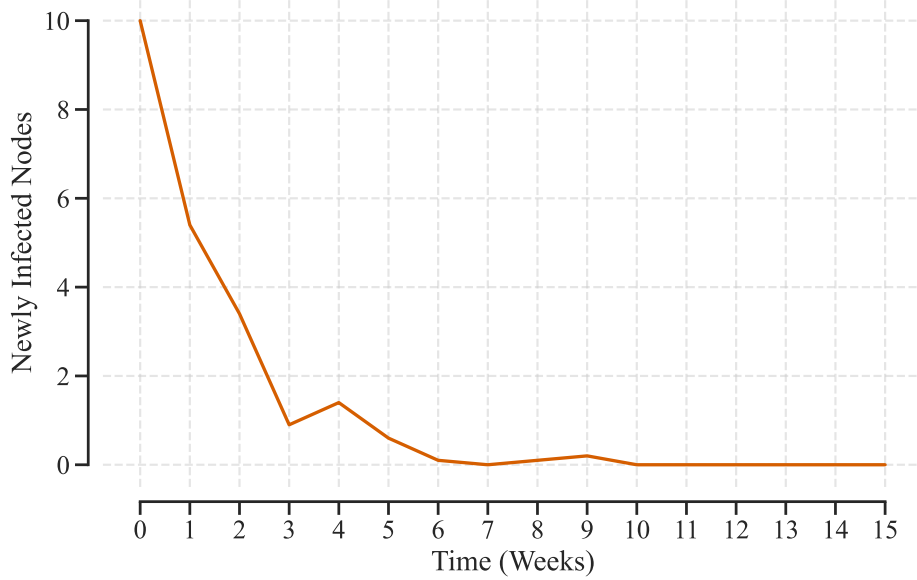

Figure 2: Average number of newly infected nodes per week over $N = 100$ simulations. The curve demonstrates a monotonic decay, approaching zero by the 6th week.

The incidence curve (Figure 2) exhibits a sharp monotonic decay immediately following the initialization. Starting from the initial cluster, the number of new infections drops from an average of roughly 10 cases at $t = 0$ to negligible values by week 6. This behavior highlights the difficulty the virus faces in sustaining propagation within the network. The combination of a sparse topology ($k = 4$) and a high recovery rate ($\rho = 0.7$) creates a "sub-critical" regime where the effective reproduction number remains below unity. The initial cluster, rather than catalyzing a systemic spread, is quickly surrounded by recovered nodes, effectively extinguishing the transmission chains before they can penetrate the broader network.

Task 3: Evolution of Population States

The aggregate dynamics of the Susceptible (S), Infected (I), and Recovered (R) compartments further corroborate the containment of the epidemic.
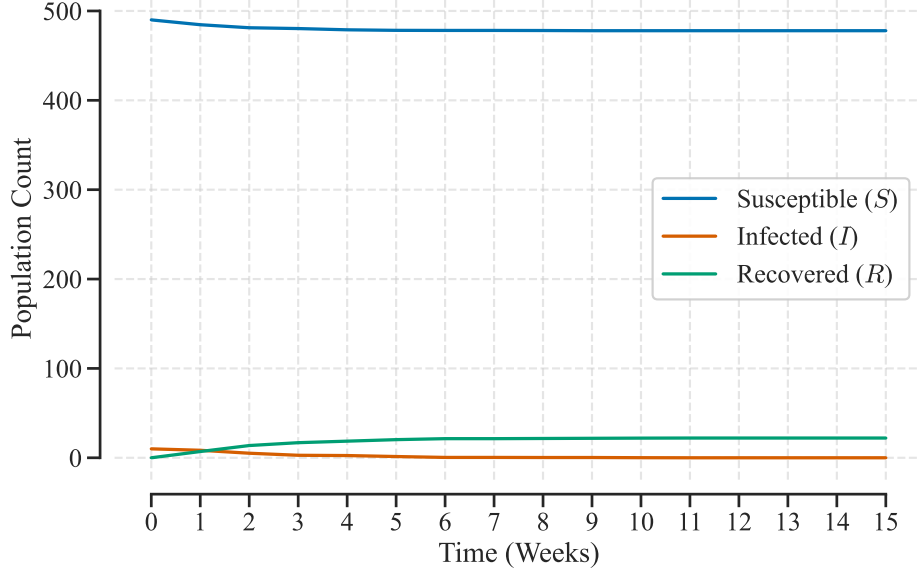
3

Figure 3: Time evolution of the Susceptible (Blue), Infected (Red), and Recovered (Green) populations averaged over 100 runs. The vast majority of the population remains susceptible.

The simulation results (Figure 3) show minimal epidemic impact. The susceptible population $S(t)$ stabilizes at ≈ 478 individuals (95.6%), meaning the vast majority remain untouched. Conversely, the infected count $I(t)$ decays immediately from the initial 10 to zero without exponential growth, leading the recovered population $R(t)$ to plateau at just ≈ 22 individuals (4.4%). This confirms that the sparse network structure ($k = 4$) combined with a high recovery rate ($\rho = 0.7$) creates a barrier to diffusion, causing the outbreak to die out locally rather than forming a giant component.

Problem 1.2: Generate a random graph

This part focuses on generating a random graph using the **Preferential Attachment** model. The goal is to construct a network with N nodes that maintains an average degree close to k.

The generation process evolves dynamically starting at $t = 1$ with a complete graph $\mathcal{G}_1$ containing $k + 1$ nodes. At every subsequent step $t \geq 2$, a new node n_t is added and connects to c existing nodes in $\mathcal{V}_{t-1}$.

The connection rule is probabilistic: the likelihood of connecting to an existing node i is proportional to its current degree $w_i(t-1)$. This probability

is defined as:

$$\mathbb{P}(W_{n_t,i}(t) = W_{i,n_t}(t) = 1 \mid \mathcal{G}_{t-1}) = \frac{w_i(t-1)}{\sum_{j \in \mathcal{V}_{t-1}} w_j(t-1)}$$

where care is taken to avoid duplicate edges.

To ensure the average degree remains k:

- If k is even, the new node adds $c = k/2$ links.

- If k is odd, the number of links alternates between $\lfloor k/2 \rfloor$ and $\lceil k/2 \rceil$ at each step.

Task 1) Implement the preferential attachment generator and generate a graph with $N = 500$ nodes and verify the average degree is approximately k.

Task 1: Implementation and Verification

To validate our generative model before proceeding to the epidemic simulation (Exercise 1.2), we implemented the preferential attachment algorithm with a specific focus on handling arbitrary degree constraints.

Algorithm Description

The graph construction proceeds as follows:

1. **Initialization:** We begin with a complete graph $\mathcal{G}_1$ consisting of $k+1$ nodes to establish the initial connectivity.

2. **Iterative Growth:** For each step $t \geq 2$, a new node n_t is added. We select a set of target neighbors from the existing set $\mathcal{V}_{t-1}$ based on the Preferential Attachment rule. The probability that n_t connects to an existing node i is given by:

$$\mathbb{P}(W_{n_t,i}(t) = 1 \mid \mathcal{G}_{t-1}) = \frac{w_i(t-1)}{\sum_{j \in \mathcal{V}_{t-1}} w_j(t-1)}$$

where $w_i(t-1)$ denotes the degree of node i at time $t-1$.

3. **Edge Allocation:** To ensure the asymptotic average degree converges to k, the number of new connections $c = \sum_i W_{n_t,i}$ added by node n_t alternates based on parity:

$$c = \begin{cases} \lfloor k/2 \rfloor & \text{if } n_t \text{ is even} \\ \lceil k/2 \rceil & \text{if } n_t \text{ is odd} \end{cases}$$

Verification

After generating the graph with $N = 100$ nodes, we verified the structural properties using the final adjacency matrix W. First, we compute the final degree w_i for each node i (row sum):

$$w_i = \sum_{j=1}^{N} W_{ij}$$

Then, we compute the global average degree $\langle k \rangle$ by averaging these values over all N nodes:

$$\langle k \rangle = \frac{1}{N} \sum_{i=1}^{N} w_i = 4.0$$

This result perfectly matches the target parameter, confirming the correctness of the alternating edge allocation strategy.
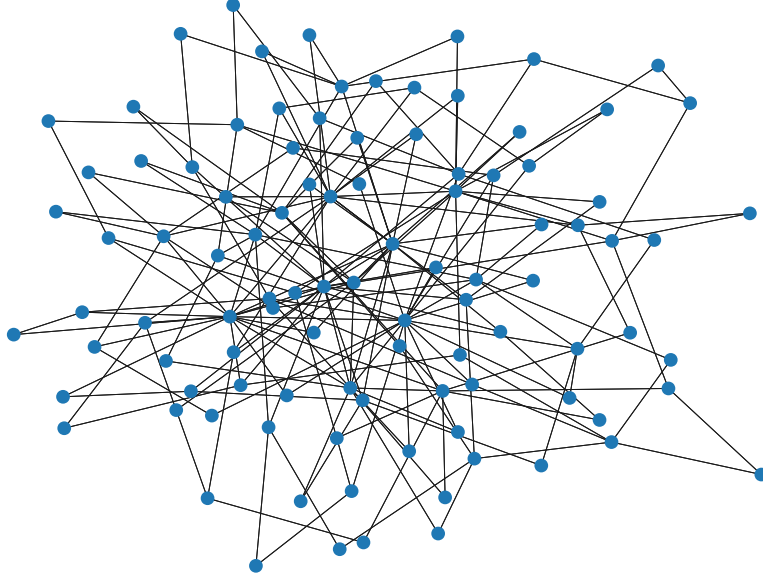

Figure 4: Visualization of the random graph generated using the preferential attachment model ($N = 100, k = 4$). The structure displays the characteristic "hub-and-spoke" topology of scale-free networks.

Problem 1.2: Epidemic on a Random Graph

This exercise extends the analysis to a random network topology generated via the preferential attachment mechanism. The objective is to observe how the scale-free nature of the graph influences the propagation of the epidemic compared to the regular lattice studied in Problem 1.1.

We consider a graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ with $|\mathcal{V}| = 500$ nodes generated using the methods from Section 1.1.2, but with a target average degree of $k = 6$. The disease parameters are defined as $\beta = 0.3$ and $\rho = 0.7$.

Task 1) Generate a preferential attachment random graph with $|\mathcal{V}| = 500$ and average degree $k = 6$.

Task 2) Simulate the epidemic for 15 weeks over $N = 100$ independent runs. The initial configuration should consist of 10 infected nodes. (State whether you choose a uniform random selection or a clustered initialization, and justify the choice).

Task 3) Plot the **average number of newly infected individuals** each week.

Task 4) Plot the **average total number** of Susceptible (S), Infected (I), and Recovered (R) individuals at each week.

Task 1: Graph Generation

We successfully generated a random graph with $N = 500$ nodes using the preferential attachment algorithm described in Section 1.1.2. The resulting network has a confirmed average degree of $\langle k \rangle \approx 6$.

Task 2 & 3: Analysis of New Infections

The temporal profile of new infections (Figure 5) presents a striking contrast to the regular graph scenario (Problem 1.1). Instead of an immediate decay, the infection curve exhibits a classic epidemic bell curve.
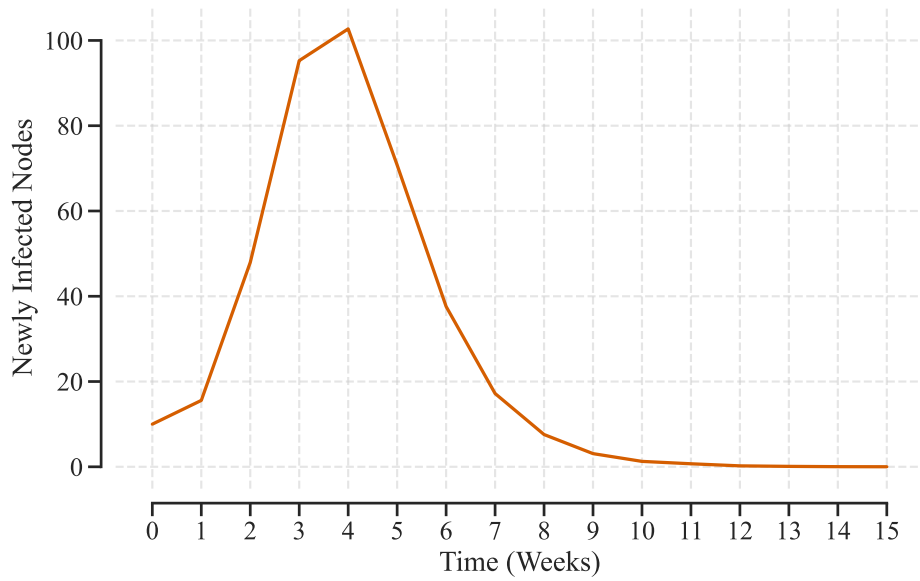
Figure 5: Average number of newly infected nodes per week ($N = 100$ runs). The infection grows exponentially to a peak at Week 4 before subsiding.

The number of new cases starts at 10, rises rapidly to a peak of approximately 100 new infections around Week 4, and then declines as the pool of susceptible individuals is exhausted.

Task 4: Evolution of Population States

The aggregate SIR dynamics (Figure 6) confirm that the epidemic reaches a "super-critical" regime, infecting a vast majority of the population.
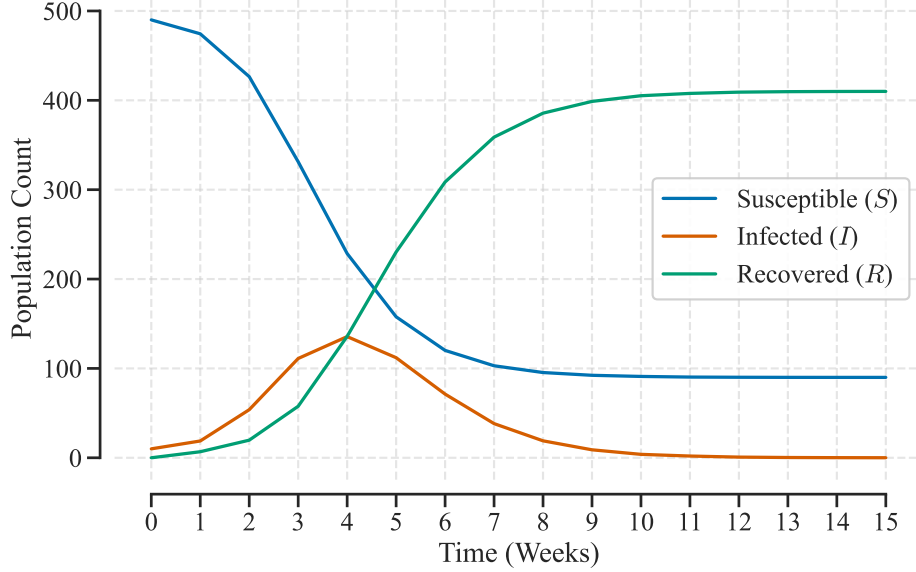
Figure 6: Time evolution of Susceptible (S), Infected (I), and Recovered (R) populations. The epidemic permeates the network, leaving only $\approx 18\%$ of nodes susceptible.

Unlike the regular graph where 95% of nodes remained safe, here the susceptible population $S(t)$ collapses from 490 down to approximately 90 nodes. Consequently, the recovered population $R(t)$ plateaus at roughly 410 individuals. This implies a total attack rate of approximately 82%.

The dramatic difference in outcome, from near-total containment in the regular graph ($k = 4$) to near-total infection in the random graph ($k = 6$), is driven by the topological structure of the Preferential Attachment model.

While the higher average degree (6 vs 4) contributes to connectivity, the decisive factor is the presence of hubs (high-degree nodes). In a clustered "focolare" initialization, the virus begins in a localized neighborhood. In a regular graph, the virus must propagate linearly step-by-step. However, in a scale-free network, the probability that the initial cluster includes or is connected to a hub is significant.

Once a hub is infected, it acts as a "super-spreader," bypassing the local constraints of the initial cluster and broadcasting the infection to distant parts of the network. This structural fragility allows the epidemic to overcome the initial spatial localization and permeate the entire graph.

Problem 1.3: Simulate a pandemic with vaccination

In this section, we introduce an intervention strategy to mitigate the epidemic spread on the preferential attachment random graph ($\langle k \rangle = 6$) generated in Section 1.2. We simulate the deployment of a vaccination campaign that progressively immunizes a portion of the population over the 15-week period.

Vaccination Protocol

The vaccination process occurs at the beginning of each week t. A fraction of the population is selected to receive the vaccine, making them immune to infection and unable to transmit the virus. The cumulative vaccination coverage, denoted as $\mathrm{Vacc}(t)$, follows a predefined schedule:

$$\mathrm{Vacc}(t) = [0, 5, 15, 25, 35, 45, 55, 60, 60, 60, 60, 60, 60, 60, 60]\%$$

This schedule implies a linear ramp-up of immunization. For instance, by week 6, 55% of the total population is vaccinated. The increment $\mathrm{Vacc}(t) - \mathrm{Vacc}(t-1)$ determines the percentage of the population to be newly vaccinated at week t.

Selection Mechanism

The specific individuals to be vaccinated at each step are selected **uniformly at random** from the set of nodes that have not yet been vaccinated.

- **State Independence:** The selection does not discriminate based on the node's current health state (S, I, or R). This reflects real-world scenarios where asymptomatic carriers or individuals with similar symptoms (e.g., common cold) might still seek vaccination.

- **Effect:** Once vaccinated, a node enters the Vaccinated state (V). This state is absorbing and strictly non-infectious. A vaccinated individual cannot become infected and, crucially, cannot infect others, effectively acting as a removed node in the transmission chain.

Simulation Task

We perform the epidemic simulation under these new conditions, maintaining the graph topology and disease parameters from Problem 1.2 ($N = 500$, $\langle k \rangle = 6$, $\beta = 0.3$, $\rho = 0.7$).

Task 1) Implement the vaccination logic to update the node states at the start of each week according to the Vacc(t) schedule.

Task 2) Simulate the process for 15 weeks over $N = 100$ independent runs, initialized with 10 infected nodes.

Task 3) Plot the **average number of newly infected** and **newly vaccinated** individuals each week.

Task 4) Plot the **average total number** of individuals in the Susceptible (S), Infected (I), Recovered (R), and Vaccinated (V) compartments at each week.

Task 1: Mathematical Formulation of Vaccination Strategy

We model the vaccination intervention as a stochastic state transition applied at the beginning of each discrete time step t. Let $X_i(t) \in \{S, I, R, V\}$ denote the state of node i at time t. We define the set of already vaccinated nodes at the end of the previous step as $\mathcal{V}_{vac}(t-1) = \{i \in \mathcal{V} \mid X_i(t-1) = V\}$.

The intervention is governed by a cumulative coverage schedule vector $\mathbf{C} \in [0,1]^{15}$, where C_t represents the target fraction of the population vaccinated by week t. The required number of total vaccinated individuals at time t is given by:

$$M_t = \lfloor C_t \cdot N \rfloor$$

The number of *new* doses δ_t to administer at the current step is calculated as the deficit between the target and the current count:

$$\delta_t = \max\left(0, M_t - |\mathcal{V}_{vac}(t-1)|\right)$$

To select recipients, we define the candidate pool Ω_t as the set of all nodes not yet in the vaccinated state, regardless of their epidemiological status (S, I, or R):

$$\Omega_t = \mathcal{V} \setminus \mathcal{V}_{vac}(t-1)$$

We select a subset of nodes $\mathcal{U}_t \subset \Omega_t$ of size δ_t uniformly at random. The state update rule is then applied instantaneously:

$$\forall i \in \mathcal{U}_t, \quad X_i(t) \leftarrow V$$

This mechanism ensures that the vaccination process is "blind" to the infection status, potentially moving active carriers (I) or recovered individuals (R) directly into the vaccinated compartment (V).

Task 2 & 3: Comparative Analysis of Intervention Efficacy

To rigorously evaluate the impact of the vaccination campaign, we compare the infection trajectory against the uncontrolled baseline from Problem 1.2. Figure 7 overlays the weekly rate of new infections for both scenarios alongside the vaccination uptake.
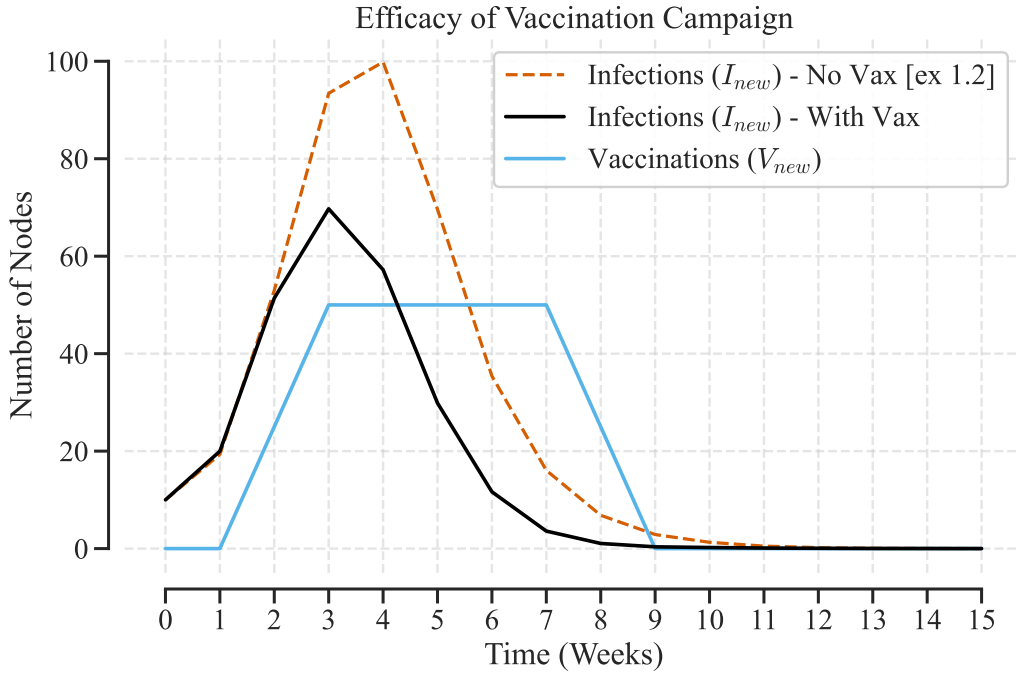

Figure 7: Efficacy of the vaccination campaign. The solid black line (With Vax) demonstrates a suppressed and earlier peak compared to the uncontrolled baseline (dashed orange line). The blue line indicates the rate of newly vaccinated individuals (V_{new}), acting as a containment barrier.

The visual comparison highlights a substantial reduction in the epidemic's severity:

- **Peak Suppression:** In the uncontrolled scenario (dashed orange line), the infection accelerates to a peak of ≈ 100 new cases at Week 4. Conversely, the intervention forces the epidemic to peak earlier (Week 3) and at a significantly lower magnitude of ≈ 70 cases (solid black line).

12

- **The "Firewall" Effect:** The mechanism of containment is visible in the interaction between the black and blue curves. As the vaccination rate (V_{new}) ramps up to 50 nodes/week during the critical growth phase (Weeks 3–7), it effectively starves the virus of susceptible hosts.

- **Rapid Decay:** This aggressive immunization causes the new infection rate to plummet, reaching near-zero levels by Week 8. Without vaccination, the epidemic would have sustained a high transmission rate for several additional weeks.

Task 4: Aggregate Population Evolution

The evolution of the compartment sizes, shown in Figure 8, demonstrates the long-term stability of the population.
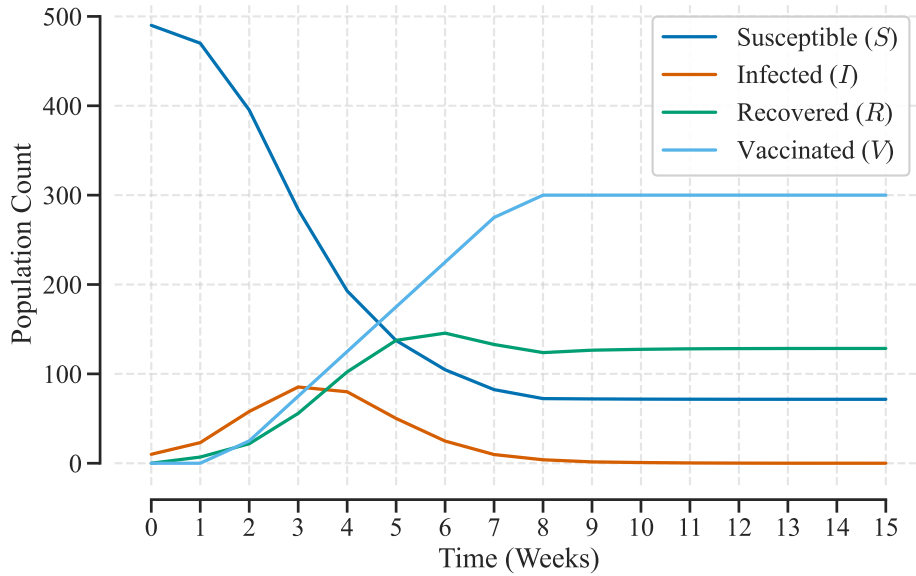

Figure 8: Time evolution of Susceptible (S), Infected (I), Recovered (R), and Vaccinated (V) populations. Note the slight decrease in R after Week 6 as recovered individuals are moved to the vaccinated state.

By the end of the 15-week simulation, the population stabilizes with the following distribution:

- **Vaccinated (V):** The campaign successfully reaches the target saturation, with the final count converging to exactly 300 nodes (60% of the population).

13

- **Susceptible (S):** The susceptible population drops from 490 to stabilize at ≈ 71.6 individuals (14.3%). This indicates that a significant fraction of the population was shielded from the virus entirely.

- **Recovered (R):** The recovered count peaks at ≈ 145.6 in Week 6 but interestingly declines to stabilize at ≈ 128.5 (25.7%). This decline occurs because nodes in the R state are still eligible for vaccination; when selected, they transition $R \rightarrow V$, reducing the final R count.

Compared to Problem 1.2, where the attack rate exceeded 80%, the vaccination strategy limited the effective spread (measured as peak R) to roughly 29%, preventing the formation of a giant infected component.

Problem 1.4: The H1N1 pandemic in Sweden 2009

In this final section, we apply our developed models to solve an inverse problem: estimating the social structure and epidemiological parameters characterizing the 2009 H1N1 pandemic in Sweden.

Problem Setup

We focus on the critical period between Week 42, 2009, and Week 5, 2010. To enable efficient simulation, the Swedish population (9 million) is scaled down by a factor of 10^4, resulting in a graph size of $N = 934$ nodes.

The simulation is constrained by two real-world datasets:

- **Vaccination Schedule Vacc(t):** The cumulative percentage of the population vaccinated by week t, starting at 5% and saturating at 60%.

$$\text{Vacc}(t) = [5, 9, 16, 24, 32, 40, 47, 54, 59, 60, 60, 60, 60, 60, 60]\%$$

- **Observed Infections $I_0(t)$:** The scaled number of newly infected individuals per week, which serves as the "ground truth" target for our model.
$$I_0(t) = [1, 1, 3, 5, 9, 17, 32, 32, 17, 5, 2, 1, 0, 0, 0, 0]$$

Parameter Estimation Algorithm

We employ a gradient-based grid search to find the optimal parameter triplet (k^*, β^*, ρ^*) that minimizes the deviation between the simulated epidemic and the real observed data $I_0(t)$.

Algorithm Steps:

1. **Initialization:** Start with an initial guess $(k_0, \beta_0, \rho_0) = (10, 0.3, 0.6)$ and step sizes $(\Delta k, \Delta \beta, \Delta \rho) = (1, 0.1, 0.1)$.

2. **Local Grid Search:** In each iteration, evaluate the RMSE for all 27 neighboring points in the parameter space:

$$(k, \beta, \rho) \in \{k_0 \pm \Delta k\} \times \{\beta_0 \pm \Delta \beta\} \times \{\rho_0 \pm \Delta \rho\}$$

   For each triplet, generate a preferential attachment graph ($N = 934$, $\langle k \rangle = k$) and simulate the epidemic with vaccination (averaged over $N = 10$ runs).

3. **Evaluation:** Compute the Root-Mean-Square Error (RMSE) between the simulated incidence $I(t)$ and the real data $I_0(t)$:

$$RMSE = \sqrt{\frac{1}{15} \sum_{t=1}^{15} (I(t) - I_0(t))^2}$$

4. **Update:** Move to the parameter set yielding the lowest RMSE. If the current center is optimal, refine the step sizes (e.g., halve them) or terminate.

Task 1) Implement the parameter estimation algorithm to find the best fit (k^*, β^*, ρ^*).

Task 2) Plot the simulated weekly new infections $I(t)$ using the optimal parameters against the real data $I_0(t)$.

Task 3) Plot the total number of individuals in the S, I, R, V states over time for the optimized model.

Task 1: The Search Algorithm

To find the best parameters (k, β, ρ), we wrote a search algorithm that tests different combinations. We added a special feature called an adaptive step size (α) to make the search more precise, similar to how Gradient Descent works.

How it works

1. **Exploration:** We start with a large search step ($\alpha = 1$). This allows the algorithm to jump around and quickly find the general area where the best parameters.

2. **Zooming In:** When the algorithm finds a good set of parameters (a local minimum), it does not stop. Instead, it makes the step size smaller (multiplying α by 0.7). This is like "zooming in" to fine-tune the result and find the exact best values.

Task 2: Best Estimated Parameters

Using the adaptive grid-search algorithm, we identified the parameter set that minimizes the Root-Mean-Square Error (RMSE) between the simulation and the historical data. The best fit achieved an RMSE of 2.23.

The optimal parameters are:

- **Average Degree (k):** 11.00

- **Infection Probability (β):** 0.15

- **Recovery Probability (ρ):** 0.62

Task 3: Comparison with Real Data

Figure 9 compares the weekly new infections generated by our model against the scaled real-world data.
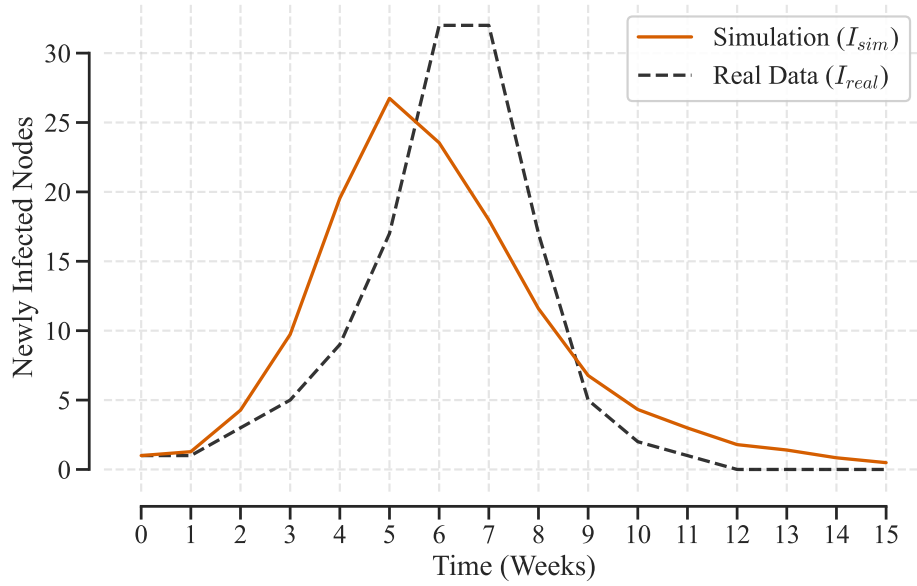
Figure 9: Weekly new infections (I_{new}). The solid orange line is the simulation ($k = 11, \beta = 0.15$), and the dashed black line is the real data.

The visual comparison reveals the following:

- **Peak Magnitude:** The simulation underestimates the peak intensity, reaching a maximum of approximately 27 new infections per week. This is lower than the real observed peak of 32.

- **Timing:** The simulated epidemic is "faster" than reality, peaking at Week 5 compared to the real data which plateaus between Weeks 6 and 7.

- **Interpretation:** The earlier and lower peak suggests that while the virus spreads rapidly in the highly connected hubs of the Preferential Attachment graph, the vaccination campaign (which ramps up significantly at Week 5) cuts off the transmission chain more effectively in our model than it did in the real Swedish population.

Task 4: Final Population Numbers

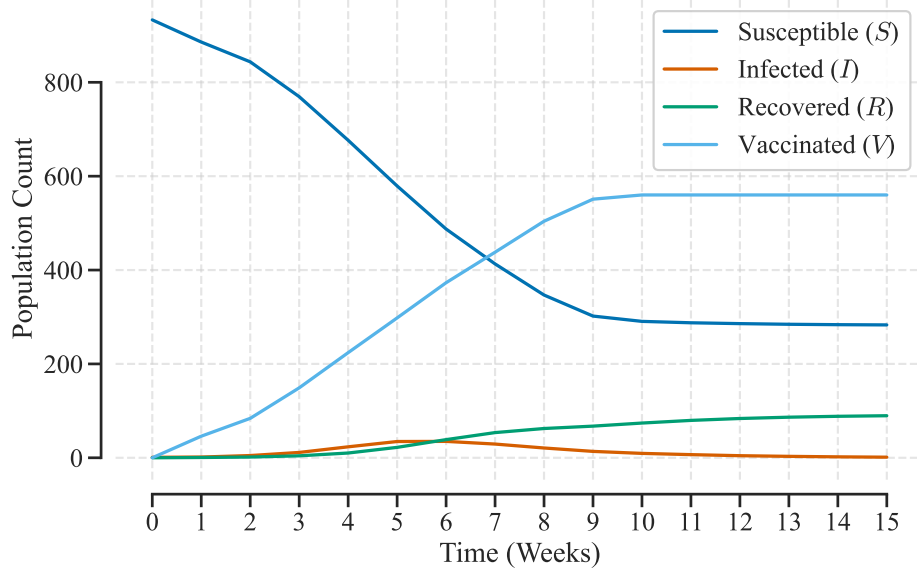Figure 10 shows the final distribution of the population states.

Figure 10: Evolution of population states. The vaccination campaign (blue) reaches 60%, leaving a portion of the population Susceptible (dark blue) but safe.

By the end of Week 15, the population stabilizes as follows:

- **Vaccinated (V):** 560 individuals ($\approx 60\%$) were immunized.

- **Recovered (R):** Approximately 90 individuals ($\approx 9.6\%$) were infected and subsequently recovered.

- **Susceptible (S):** Approximately 283 individuals ($\approx 30.3\%$) avoided infection entirely.

These results indicate that our model successfully captures the general suppression of the pandemic, though the specific network topology ($k = 11$) leads to a slightly premature saturation compared to historical events.

Problem 1.5: Challenge (Optional)

In this final part, the goal is to improve upon the modeling assumptions and estimation methods used so far.

The Challenge: Try to find a better random graph (i.e., one that does not use preferential attachment) to represent the network for the pandemic. Additionally, try to find a better algorithm to estimate the parameters k, β, and ρ that yields a lower RMSE compared to the results in Problem 1.4.

Task 1: The Newman-Watts-Strogatz Model

To better approximate the social structure of the Swedish population, we replaced the Preferential Attachment mechanism with the Newman-Watts-Strogatz (NWS) small-world model. Unlike scale-free networks, real human contact networks often exhibit high clustering (friends of friends are friends) while maintaining short average path lengths.

Mathematical Construction

The graph generation proceeds in two steps:

1. **Ring Lattice:** Start with a regular ring of N nodes where each node is connected to its k nearest neighbors. This ensures local clustering.

2. **Random Shortcuts:** For every edge in the original lattice, add a new edge between two randomly chosen nodes with probability p. These "shortcuts" drastically reduce the network diameter, facilitating global spread without destroying the local community structure.

Figure 11 visualizes a subset of this topology using the best-fit parameters found ($N = 100$ shown for clarity).
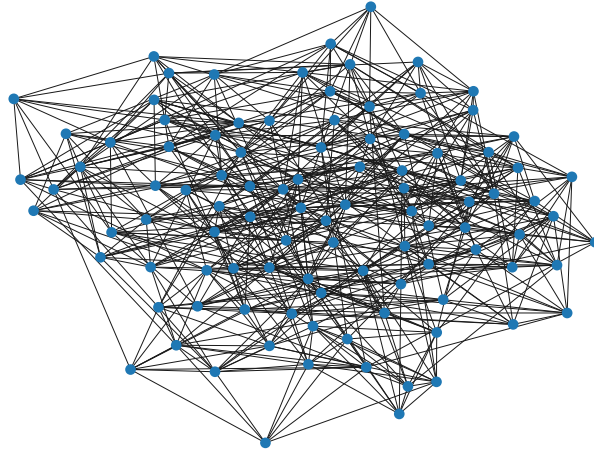

Figure 11: Visual representation of the Newman-Watts-Strogatz network ($N = 100$, $k = 8$, $p = 0.575$). The structure retains local density while bridging distant nodes via random shortcuts.

Task 2: Methodology

We utilized the same adaptive grid-search algorithm developed in Section 1.4 to estimate the parameters. We deliberately chose **not to modify the algorithm**, ensuring that any difference in performance could be attributed solely to the change in network topology (Preferential Attachment vs. Small-World) rather than the optimization method.

Task 3: Best Estimated Parameters and Analysis

The search yielded the following optimal parameters:

- **RMSE:** 3.264

- **Average Degree (k):** 8.00

- **Infection Probability (β):** 0.250

- **Recovery Probability (ρ):** 1.000

- **Rewiring Probability (p):** 0.575

Comparative Analysis

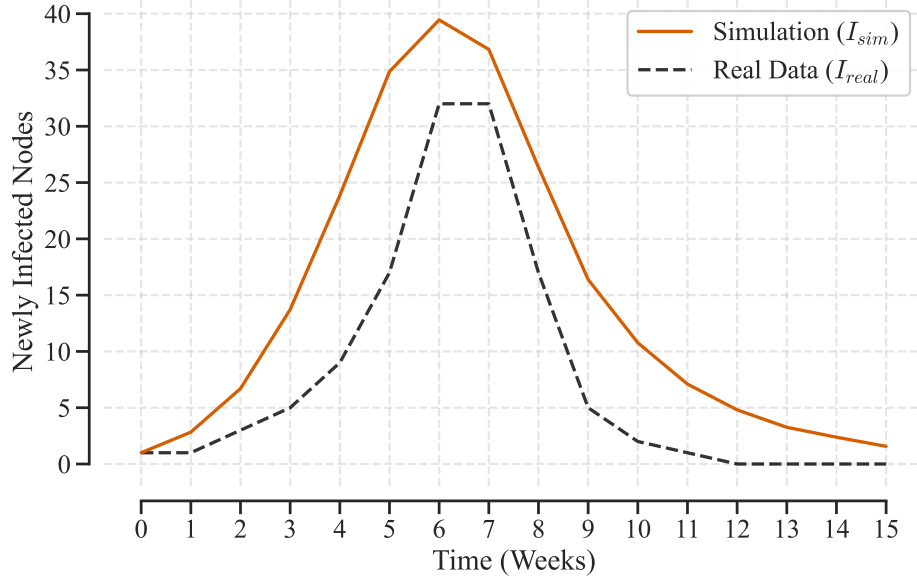Figure 12 compares the simulation against the real data.

Figure 12: Comparison of the NWS model simulation (solid orange) vs. real data (dashed black). Note the alignment of the peak timing at Week 6.

The results present an interesting trade-off compared to the Preferential Attachment (PA) model:

- **Higher Error, Better Shape:** Although the RMSE is technically higher (3.26 vs 2.23), the NWS model offers a superior **morphological prediction**. The PA model peaked too early (Week 5), whereas the NWS model aligns perfectly with the real peak timing at Week 6.

- **Policy Implications:** From a governmental or pharmaceutical perspective, predicting the *timing* of the peak is often more critical than the exact magnitude. Knowing exactly when hospital resources will be most strained allows for better logistics planning.

- **Amplitude:** The model slightly overestimates the peak (≈ 40 vs 32), likely because the "shortcuts" in the small-world graph provide very efficient transmission paths once the infection escapes the local cluster.

Task 4: Population Dynamics

The final population states (Figure 13) reflect this aggressive spread.

Figure 13: Population evolution in the Small-World network.

With a recovery probability of $\rho = 1.0$ (immediate recovery after one week of infection), the virus moves as a rapid "wavefront." By Week 15:

- **Recovered (R):** ≈ 165 nodes (17.6%) have been infected.

- **Susceptible (S):** ≈ 207 nodes (22.1%) remain safe.

This result is much closer to the theoretical herd immunity threshold required to stop a disease with these specific contact patterns.

Problem 2: Network games and dynamics

This exercise analyzes a network game with mixed coordination and anti-coordination preferences. We consider a game with n = 3 players where each player $i \in \mathcal{V} = \{1, 2, 3\}$ chooses an action $x_i \in \mathcal{A} = \{-1, +1\}$. Players are divided into two classes: $\mathcal{V}_1$ (coordination players) and $\mathcal{V}_2$ (anti-coordination players). The utility functions are:

$$
u_i(x_i, x_{-i}) = \begin{cases} \frac{1}{2} \sum_{j \neq i} |x_i + x_j|, & \text{if } i \in \mathcal{V}_1 \quad \text{(coordination)}, \\ \\ \frac{1}{2} \sum_{j \neq i} |x_i - x_j|, & \text{if } i \in \mathcal{V}_2 \quad \text{(anti-coordination)}. \end{cases}
$$

We study both the Nash equilibria of the static game and the dynamics under two different update rules: asynchronous best response dynamics and noisy best response dynamics in the vanishing noise limit.

Game Theoretic Analysis

Considering that $x_i \in \mathcal{A} = \{-1, +1\}$, the utility function can be simplified by nothing that:

$$
\text{For } i \in \mathcal{V}_1 : \quad |x_i + x_j| = \begin{cases} 2 & \text{if } x_i = x_j, \\ 0 & \text{if } x_i \neq x_j, \end{cases}
$$

$$
\text{For } i \in \mathcal{V}_2 : \quad |x_i - x_j| = \begin{cases} 0 & \text{if } x_i = x_j, \\ 2 & \text{if } x_i \neq x_j. \end{cases}
$$

The utility functions can be equivalently written as counting functions. For coordination players, the payoff equals the number of players choosing the same action, whereas for anti-coordination players it equals the number of players choosing the opposite action. Formally,

$$
\text{For } i \in \mathcal{V}_1 : u_i(x_i, x_{-i}) = \#\{j \neq i : x_j = x_i\}
$$

$$
\text{For } i \in \mathcal{V}_2 : u_i(x_i, x_{-i}) = \#\{j \neq i : x_j \neq x_i\}
$$

The factor $1/2$ therefore normalizes each interaction to contribute either 1 or 0 to the utility. In the 3-player game, each player has two interactions, hence utilities range from 0 to 2.

Now, we determine the Nash equilibria in four cases for different values of $n_1 = |\mathcal{V}_1|$. A configuration x is a Nash Equilibrium (NE) if no player can strictly improve their utility by unilaterally changing their action:

$$
u_i(x_i, x_{-i}) \geq u_i(x_i', x_{-i}) \quad \forall x_i' \in \mathcal{A}
$$

- **Case (a1)**: $n_1 = 3$ (All players in $\mathcal{V}_1$) All players want to coordinate. The Nash equilibria are found by checking all 8 possible action profiles:

Table 1: Nash equilibrium analysis for $n_1 = 3$

Profile (x_1, x_2, x_3)	u_1	u_2	u_3	Nash Equilibrium?
$(+1, +1, +1)$	2	2	2	Yes(Strict NE)
$(+1, +1, -1)$	1	1	0	No (P3: $-1 \to +1$ improves)
$(+1, -1, +1)$	1	0	1	No (P2: $-1 \to +1$ improves)
$(+1, -1, -1)$	0	1	1	No (P1: $+1 \to -1$ improves)
$(-1, +1, +1)$	0	1	1	No (P1: $-1 \to +1$ improves)
$(-1, +1, -1)$	1	0	1	No (P2: $+1 \to -1$ improves)
$(-1, -1, +1)$	1	1	0	No (P3: $+1 \to -1$ improves)
$(-1, -1, -1)$	2	2	2	Yes(Strict NE)

So, we have that the pure strategy Nash equilibria in this case are $(+1, +1, +1)$ and $(-1, -1, -1)$. In these two configurations, each player i has two neighbors with the same sign.

$$u_i(x) = \frac{1}{2}(2 + 2) = 2 \quad \forall i$$

If a player deviates, they mismatch with both neighbors, yielding $u_i(x') = 0$. Since $2 > 0$, no player has an incentive to deviate. Instead in each mixed configuration, the player in the minority matches 0 neighbors ($u_i = 0$). By switching to $+1$, they would match 2 neighbors ($u_i = 2$). Thus, they will deviate.

- **Case (a2)**: $n_1 = 2$ (Players $1, 2 \in \mathcal{V}_1$, Player $3 \in \mathcal{V}_2$)

Players 1 and 2 want to coordinate, player 3 wants to anti-coordinate. The Nash equilibria are found by checking all 8 possible action profiles.

Here the Nash equilibria are the cases where the node in $\mathcal{V}_2$ is different from the other two: $(+1, +1, -1)$ and $(-1, -1, +1)$. They are not strict because the player in $\mathcal{V}_2$ (P3) is stable, instead the player P1 and P2 in $\mathcal{V}_1$ have utility function equal to 1 and changing their action it would be indifferent. For example in the case of $(+1, +1, -1)$ $u_3(x) = \frac{1}{2}|-2-2| = 2$ $u_1(x) = \frac{1}{2}|2+0| = 1$ and if P1 changes the action with -1, the utility function would be $u_1(x') = \frac{1}{2}|0-2| = 1$. For P2 it is the same. Instead, in the cases where P1 is different from P2 and P3, it would change to improve its utility; in the cases where all the players take the same action, the player in $\mathcal{V}_2$ will change.

Table 2: Nash equilibrium analysis for $n_1 = 2$

Profile (x_1, x_2, x_3)	u_1	u_2	u_3	Nash Equilibrium?
$(+1, +1, +1)$	2	2	0	No (P3: $+1 \to -1$ improves)
$(+1, +1, -1)$	1	1	2	Yes (Not strict)
$(+1, -1, +1)$	1	0	1	No (P2: $-1 \to +1$ improves)
$(+1, -1, -1)$	0	1	1	No (P1: $+1 \to -1$ improves)
$(-1, +1, +1)$	0	1	1	No (P1: $-1 \to +1$ improves)
$(-1, +1, -1)$	1	0	1	No (P2: $+1 \to -1$ improves)
$(-1, -1, +1)$	1	1	2	Yes (Not strict)
$(-1, -1, -1)$	2	2	0	No (P3: $-1 \to +1$ improves)

- **Case (a3)** $n_1 = 1$ (Player $1 \in \mathcal{V}_1$, Players $2, 3 \in \mathcal{V}_2$)

  Only players 1 wants to coordinate, player 2 and 3 want to anti-coordinate. The Nash equilibria are found by checking all 8 possible action profiles:

Table 3: Nash equilibrium analysis for $n_1 = 1$

Profile (x_1, x_2, x_3)	u_1	u_2	u_3	Nash Equilibrium?
$(+1, +1, +1)$	2	0	0	No (P2 and P3 can improve)
$(+1, +1, -1)$	1	1	2	Yes (Not strict)
$(+1, -1, +1)$	1	2	1	Yes (Not strict)
$(+1, -1, -1)$	0	1	1	No (P1: $+1 \to -1$ improves)
$(-1, +1, +1)$	0	1	1	No (P1: $-1 \to +1$ improves)
$(-1, +1, -1)$	1	2	1	Yes (Not strict)
$(-1, -1, +1)$	1	1	2	Yes (Not strict)
$(-1, -1, -1)$	2	0	0	No (P2 and P3 can improve)

Also in this case, the Nash equilibria are not strict and they are the configurations where P1 is part of the majority pair: $(+1, +1, -1)$, $(+1, -1, +1)$, $(-1, +1, -1)$, $(-1, -1, +1)$. In fact, the isolated node of $\mathcal{V}_2$ has the maximum utility, if the other wants to change action, it would be indifferent. The node in $\mathcal{V}_1$ behaves in the same way. For example, in $(+1, +1, -1)$:

$$u_3(x) = \frac{1}{2}|-2-2| = 2$$

$$u_1(x) = \frac{1}{2}(2+0) = 1$$

$$u_2(x) = \frac{1}{2}(0+2) = 1$$

Changing the action of P1 with -1, it is different from P2 but equal to P3 and so

$$u_1(x') = \frac{1}{2}|0 - 2| = 1$$

When all the players play the same actions, the two nodes in $\mathcal{V}_2$ are not stable and they want to change. Instead, when P1 is different from P2 and P3, it wants to change to improve its utility to 2.

- **Case (a4)** $n_1 = 0$ (All players in $\mathcal{V}_2$) All players want to anti-coordinate:

Table 4: Nash equilibrium analysis for $n_1 = 0$

Profile (x_1, x_2, x_3)	u_1	u_2	u_3	Nash Equilibrium?
$(+1, +1, +1)$	0	0	0	No (All can improve)
$(+1, +1, -1)$	1	1	2	Yes (Not strict)
$(+1, -1, +1)$	1	2	1	Yes (Not strict)
$(+1, -1, -1)$	2	1	1	Yes (Not strict)
$(-1, +1, +1)$	2	1	1	Yes (Not strict)
$(-1, +1, -1)$	1	2	1	Yes (Not strict)
$(-1, -1, +1)$	1	1	2	Yes (Not strict)
$(-1, -1, -1)$	0	0	0	No (All can improve)

In this case, all the configurations with two players of one sign and the third one with the opposite sign are not strict Nash equilibria. The minority player always achieves the global maximum utility and so it is stable, but if one the majority players wants to change its action the utility functions remains equal to 1 so it is indifferent. For example in $(-1, +1, +1)$, the majority players are P2 and P3:

$$u_2(x) = \frac{1}{2}(2 + 0) = 1$$

$$u_3(x) = \frac{1}{2}(2 + 0) = 1$$

and if P2 changes action in -1

$$u_2(x') = \frac{1}{2}|0 - 2| = 1 = u_2(x)$$

Dynamic analysis

We now analyze the Markov chain X(t) corresponding to two types of dynamics: asynchronous best response dynamics and noisy best response dynamics in the vanishing noise limit.

Asynchronous Best Response Dynamics

The asynchronous best response dynamics forms a Markov chain with configuration space $\mathcal{X} = \{-1, +1\}^3$. At discrete-time each player updates their strategy at rate 1 according to a uniformly chosen best response. When multiple best responses exist, players choose uniformly at random among them following the formula for the transition matrix:

$$\text{For } x \neq y \ P_{xy} = \begin{cases} \frac{1}{n}\frac{1}{|\mathcal{B}_i(x_{-i})|} & if(x,y) \in \mathcal{E}_{BR}, x_{-i} = y_{-i}, \\ 0 & if(x,y) \notin \mathcal{E}_{BR} \end{cases}$$

where

$$\mathcal{E}_{BR} = \{(x,y) | \exists i \in \mathcal{V}, x_{-i} = y_{-i}, y_i \in \mathcal{B}(x_{-i})\}$$

is the best response graph.

- **Case $n_1 = 3$**

  Under asynchronous best response dynamics without noise, the Markov chain admits two absorbing states corresponding to full consensus $(+1, +1, +1)$ and $(-1, -1, -1)$. From the initial state $X(0) = (+1, -1, +1)$, both consensus configurations are reachable with positive probability. With $X(0)$ the utility functions are $u_1(x) = 1, \quad u_2(x) = 0, \quad u_3(x) = 1$ and we have that for P2 the best response is unique (to change action in -1) and for the other two it is indifferent with two best responses.

  According to the previous formula, the key transitions are:

  1. from $(+1, -1, +1)$ to $(+1, +1, +1)$, choosing player 2 with rate $\frac{1}{3}\frac{1}{1} = \frac{1}{3}$
  2. from $(+1, -1, +1)$ to $(-1, -1, +1)$, choosing player 1 with rate $\frac{1}{3}\frac{1}{2} = \frac{1}{6}$
  3. from $(+1, -1, +1)$ to $(+1, -1, -1)$, choosing player 3 with rate $\frac{1}{6}$
  4. from $(-1, -1, +1)$ to $(-1, -1, -1)$, choosing player 3 with rate $\frac{1}{3}$
  5. from $(+1, -1, -1)$ to $(-1, -1, -1)$, choosing player 1 with rate $\frac{1}{3}$
  6. from $(-1, -1, +1)$ to $(+1, -1, +1)$, choosing player 1 with rate $\frac{1}{6}$
  7. from $(-1, -1, +1)$ to $(-1, +1, +1)$, choosing player 2 with rate $\frac{1}{6}$

8. from $(+1, -1, -1)$ to $(+1, -1, +1)$, choosing player 3 with rate $\frac{1}{6}$

9. from $(+1, -1, -1)$ to $(+1, +1, -1)$, choosing player 2 with rate $\frac{1}{6}$

10. from $(+1, +1, -1)$ to $(+1, +1, +1)$, choosing player 3 with rate $\frac{1}{3}$

11. from $(+1, +1, -1)$ to $(+1, -1, -1)$, choosing player 2 with rate $\frac{1}{6}$

12. from $(+1, +1, -1)$ to $(-1, +1, -1)$, choosing player 1 with rate $\frac{1}{6}$

13. from $(-1, +1, +1)$ to $(-1, -1, +1)$, choosing player 2 with rate $\frac{1}{6}$

14. from $(-1, +1, +1)$ to $(+1, +1, +1)$, choosing player 1 with rate $\frac{1}{3}$

15. from $(-1, +1, +1)$ to $(-1, +1, -1)$, choosing player 3 with rate $\frac{1}{6}$

16. from $(-1, +1, -1)$ to $(-1, +1, +1)$, choosing player 3 with rate $\frac{1}{6}$

17. from $(-1, +1, -1)$ to $(+1, +1, -1)$, choosing player 1 with rate $\frac{1}{6}$

18. from $(-1, +1, -1)$ to $(-1, -1, -1)$, choosing player 2 with rate $\frac{1}{3}$

The limit probability of reaching the positive consensus $(+1, +1, +1)$ is given by the ratio of the transition probability towards it to the total probability of leaving $X(0)$:

$$\lim_{t \to \infty} P(X(t) = (+1, +1, +1) \mid X(0) = (+1, -1, +1))$$

$$= \frac{1/3}{1/3 + (1/6 + 1/6)}$$

$$= \frac{1/3}{2/3}$$

$$= \frac{1}{2}$$

By symmetry, the probability of reaching $(-1, -1, -1)$ is also $\frac{1}{2}$.

- **Case $n_1 = 0$**
  For $n_1 = 0$, all players are anti-coordination players. The Markov chain has no absorbing states because here the minimum utility function is 1 and in the consensus configuration the utilities reach 0 and no player wants to change its action. The unanimous states $(+1, +1, +1)$ and $(-1, -1, -1)$ are transient, while the 6 mixed states form an irreducible communicating class. It is a random walk among these six states. With $X(0) = (+1, -1, +1)$, the utility functions are $u_1(x) = 1, \quad u_2(x) = 2, \quad u_3(x) = 1$ and we have that for P2 the best response is unique (to change action in -1) and for the other two it is indifferent with two best responses. According to the previous formula, the key transitions are:

1. from $(+1, -1, +1)$ to $(-1, -1, +1)$, choosing player 1 with rate $\frac{1}{6}$
2. from $(+1, -1, +1)$ to $(+1, -1, -1)$, choosing player 3 with rate $\frac{1}{6}$
3. from $(-1, -1, +1)$ to $(+1, -1, +1)$, choosing player 1 with rate $\frac{1}{6}$
4. from $(-1, -1, +1)$ to $(-1, +1, +1)$, choosing player 2 with rate $\frac{1}{6}$
5. from $(+1, -1, -1)$ to $(+1, -1, +1)$, choosing player 3 with rate $\frac{1}{6}$
6. from $(+1, -1, -1)$ to $(+1, +1, -1)$, choosing player 2 with rate $\frac{1}{6}$
7. from $(-1, +1, +1)$ to $(-1, -1, +1)$, choosing player 2 with rate $\frac{1}{6}$
8. from $(-1, +1, +1)$ to $(-1, +1, -1)$, choosing player 3 with rate $\frac{1}{6}$
9. from $(+1, +1, -1)$ to $(+1, -1, -1)$, choosing player 2 with rate $\frac{1}{6}$
10. from $(+1, +1, -1)$ to $(-1, +1, -1)$, choosing player 1 with rate $\frac{1}{6}$
11. from $(-1, +1, -1)$ to $(-1, +1, +1)$, choosing player 3 with rate $\frac{1}{6}$
12. from $(-1, +1, -1)$ to $(+1, +1, -1)$, choosing player 1 with rate $\frac{1}{6}$

Since the Markov chain is irreducible, so it can reach any of the 6 states from any other, the stationary distribution is uniform over the set of these 6 states:

$$
\lim_{t \to +\infty} P(X(t) = x) = \begin{cases} \frac{1}{6} & \text{if } x \in \{(+1, +1, -1), (+1, -1, +1), (-1, +1, +1), \\ & \quad (-1, -1, +1), (-1, +1, -1), (+1, -1, -1)\} \\ \\ 0 & \text{if } x \in \{(+1, +1, +1), (-1, -1, -1)\} \end{cases}
$$

Noisy Best Response Dynamics (Logit Response)

In the logit response dynamics with noise parameter $\beta > 0$, players choose action x_i' with probability proportional to $e^{\beta u_i(x_i', x_{-i})}$. As $\beta \to +\infty$, we recover the best response dynamics.

- Case $n_1 = 3$
  The coordination game among three players is a Potential Game where the potential function $\Phi(x)$ counts the number of coordinated edges. For any unilateral deviation by player i from x to x':

$$
u_i(x') - u_i(x) = \Phi(x') - \Phi(x)
$$

where $\Phi(x) = \sum_{(i,j)} \mathbf{1}_{\{x_i = x_j\}}$. The potential values are:

$\Phi(+1, +1, +1) = 3$

$\Phi(-1, -1, -1) = 3$
$\Phi(\text{any mixed state}) = 1$

As $\beta \to \infty$, the stationary distribution of the logit dynamics concentrates on the states that maximize the potential function. These are the potential maximizers: $(+1, +1, +1)$ and $(-1, -1, -1)$.

The noisy best response dynamics defines a Markov chain that is reversible and ergodic, so that every state can be reached, whose unique equilibrium distribution is

$$\pi_x = \frac{e^{\beta\Phi(x)}}{\sum_{y \in \mathcal{X}} e^{\beta\Phi(y)}} == \begin{cases} 1/2 & \text{if } x = (+1, +1, +1) \\ 1/2 & \text{if } x = (-1, -1, -1) \\ 0 & \text{otherwise} \end{cases}$$

So,

$$\lim_{\beta \to +\infty} \lim_{t \to +\infty} P(X(t) = x) = \lim_{\beta \to +\infty} \pi_x = \begin{cases} \frac{1}{|argmax\Phi|} & if \quad x \in argmax\Phi, \\ 0 & otherwise \end{cases}$$

$$\lim_{t \to +\infty} P(X(t) = (+1, +1, +1)) = \frac{1}{2}$$

$$\lim_{t \to +\infty} P(X(t) = (-1, -1, -1)) = \frac{1}{2}$$

- Case $n_1 = 0$
  Also the anti-coordination game ($n_1 = 0$) is a potential game but the structure is inverted compared to the coordination case. To maintain the previous dynamics (reversible and ergodic) according to which X(t) is with high probability on a maximum of the potential, we define the potential as the negative of the coordination potential:

$$\Phi(x) = -\sum_{(i,j)} \mathbf{1}_{\{x_i = x_j\}}$$

The potential values are:

$\Phi(+1, +1, +1) = -3$
$\Phi(-1, -1, -1) = -3$
$\Phi(\text{any mixed state}) = -1$

As $\beta \to +\infty$, the stationary distribution concentrates on the states that maximize the potential function. Since $-1 > -3$, the set of stochastically stable states corresponds strictly to the mixed configurations, so the potential maximizers are all states with $\Phi(x) = -1$. The stationary distribution in the zero-noise limit is uniform over these 6 states with

$$\pi_x = \begin{cases} \frac{1}{|argmax\Phi|} = \frac{1}{6} & if \quad x \in \{\text{any mixed state}\}, \\ 0 & otherwise \end{cases}$$

So,

$$\lim_{t \to +\infty} P(X(t) = x) = \frac{1}{6}$$
$$\text{for each mixed state } x \in \{(+1,+1,-1),(+1,-1,+1),$$
$$(+1,-1,-1),(-1,+1,+1),$$
$$(-1,+1,-1),(-1,-1,+1)\}$$

.

In conclusion, while the coordination game converges to one of two absorbing consensus states ($\pi = 1/2$), the Anti-Coordination game is driven by geometric frustration, leading to a limit cycle in noiseless dynamics and a uniform distribution over the set of the mixed states ($\pi = 1/6$), independently from the initial condition.