Supplementary Appendix: The role of scale in public goods problems: from pandemics to climate change

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1 Supplementary Material

1.1 Network model description

To instantiate our framework, we built an agent-based simulation of a small-world network [1] of N individuals, each with an average of Q neighbours. Networks were generated with the Watts-Strogatz generator of the NetworkX package [2], with rewiring probability 0.1. This generator joins each node to its $\lfloor Q/2 \rfloor$ nearest neighbours on each side of a ring before rewiring, so Q is only a network average: the mean degree is $2\lfloor Q/2 \rfloor$, which equals Q for even Q and $Q-1$ for odd Q, and individual nodes can have a higher or lower degree after rewiring. Each node has a state corresponding to their behavior, well-being, and presence or absence of agent:

- The behavioral state of node i is either mitigator (M) or non-mitigator (N) and is denoted $B_i \in \{M, N\}$. A node can change behavior in each timestep depending on how attractive mitigation or non-mitigation appears to them at that time.
- The state of well-being of node i is either well (W) or impacted (I) and is denoted $H_i \in \{W, I\}$. Impacted individuals have been infected, or have suffered a climate change impact, but they recover after some period of time.

- The agent status indicating whether agent is present (1) or absent (0) at node i is denoted $A_i \in \{1, 0\}$. Agent can be transferred to or from neighbouring nodes, and also decays. The presence of agent at a node can cause impacts.

Individuals can move from impacted back to well according to a parameter D governing the duration of impact. The prevalence of the natural agent that node i is subject to in a given timestep is denoted A_i^{risk} (which is the local prevalence of virus for an infectious disease, or greenhouse gas (GHG) concentration for climate change). This quantity influences the probability of impact. Individuals transition between behavioral states with a specified probability per timestep, as described by Equations (1)–(6) of the main text.

1.2 Simulation design

In each timestep, the following updates occur:

1. Generation, decay, and recovery: running through each node in the population from $i = 0$ to $i = N - 1$,
   - A non-mitigating node with agent status '0' transitions to agent status '1' with probability p_{gen}.
   - A node with agent status '1' transitions to '0' with probability δ.
   - A node with an impacted status becomes well with probability $1/D$.
2. Behaviour: running through each node in the population from $i = 0$ to $i = N - 1$,
   - Determine local risk to each node, A_i^{risk}.
   - With probability σ, the node decides whether to change its behaviour. A non-mitigator switches to mitigator if $e_{i,M} \geq e_{i,N}$, and a mitigator switches to non-mitigator if $e_{i,N} \geq e_{i,M}$.
3. Agent spread, and impacts: running through each node in the population from $i = 0$ to $i = N - 1$,
   - A node with agent status '0' transitions to agent status '1' due to spread from neighbours, with probabilities $p_i^{inf,M}$ or $p_i^{inf,N}$ depending on their behavioral state.
   - A node with agent status '1' transitions from well to impacted with probability β.
   - Nodes are updated in sequence, so that the local risk of a node in this step reflects any natural agent acquired earlier in the same pass by neighbours with a lower index.

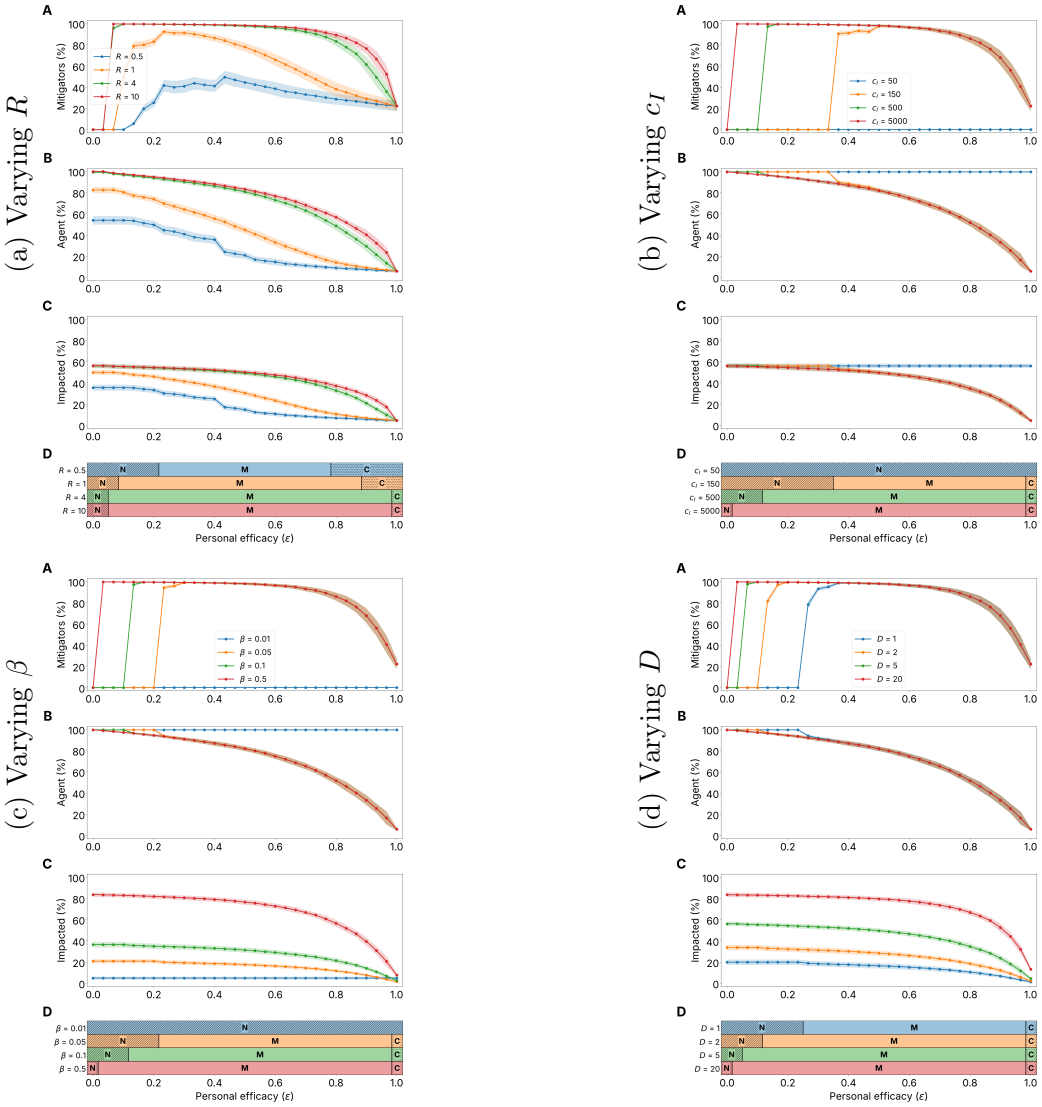
We initialize a population where 50% of the population are mitigators, each non-mitigator carries the natural agent with probability 0.01 (so that approximately 0.5% of nodes initially

carry the natural agent), and 100% of the population are well. For COVID-19, our baseline values assumed a small neighborhood (Q), a rapid decay of the natural agent (δ) and a high personal efficacy (ε). Similarly, other timescale variables reflected the faster timescales of infectious disease spread, with R and σ relatively large and D relatively small for COVID-19. For climate change, our baseline values assumed a neighborhood size equal to the entire population ($Q = N - 1$), a slow decay rate (δ), and a low personal efficacy (ε), while R and σ were relatively small and D relatively large. Other parameter values were the same for the baseline climate and COVID-19 scenarios. Baseline parameter values appear in Table 1). The simulation was coded in Python (see Supplementary File). Each point in Figures 2–4 of the main text is a single simulation, and each simulation uses a different network realization and sequence of random numbers. Plotted values in these figures are means over the final 70% of time steps, and shaded regions denote one standard deviation over the same window. Our sensitivity analyses with 50 independent realizations per point give the same regimes as these single simulations, and the system appears to be ergodic, so time averages over a single long simulation are representative of averages over independent realizations. Each point in Supplementary Figures 1–9 and 11–13 is instead the mean, over 50 independent runs (random seeds 0–49) that each have their own network realization and initial conditions, of the value at the final time step of a 500-step simulation; shaded regions denote one standard deviation across runs, and the regime of each point is assigned from these means. For the Supplementary Figures we also used two other network types generated with NetworkX: random regular networks, in which every node has exactly Q neighbours, and scale-free networks from the Barabási-Albert generator [3], in which each new node attaches to $\lfloor Q/2 \rfloor$ existing nodes. Supplementary Figure 10 uses a single simulation per point, with the same network realization and random numbers for every point, averaged over the final 20% of time steps.

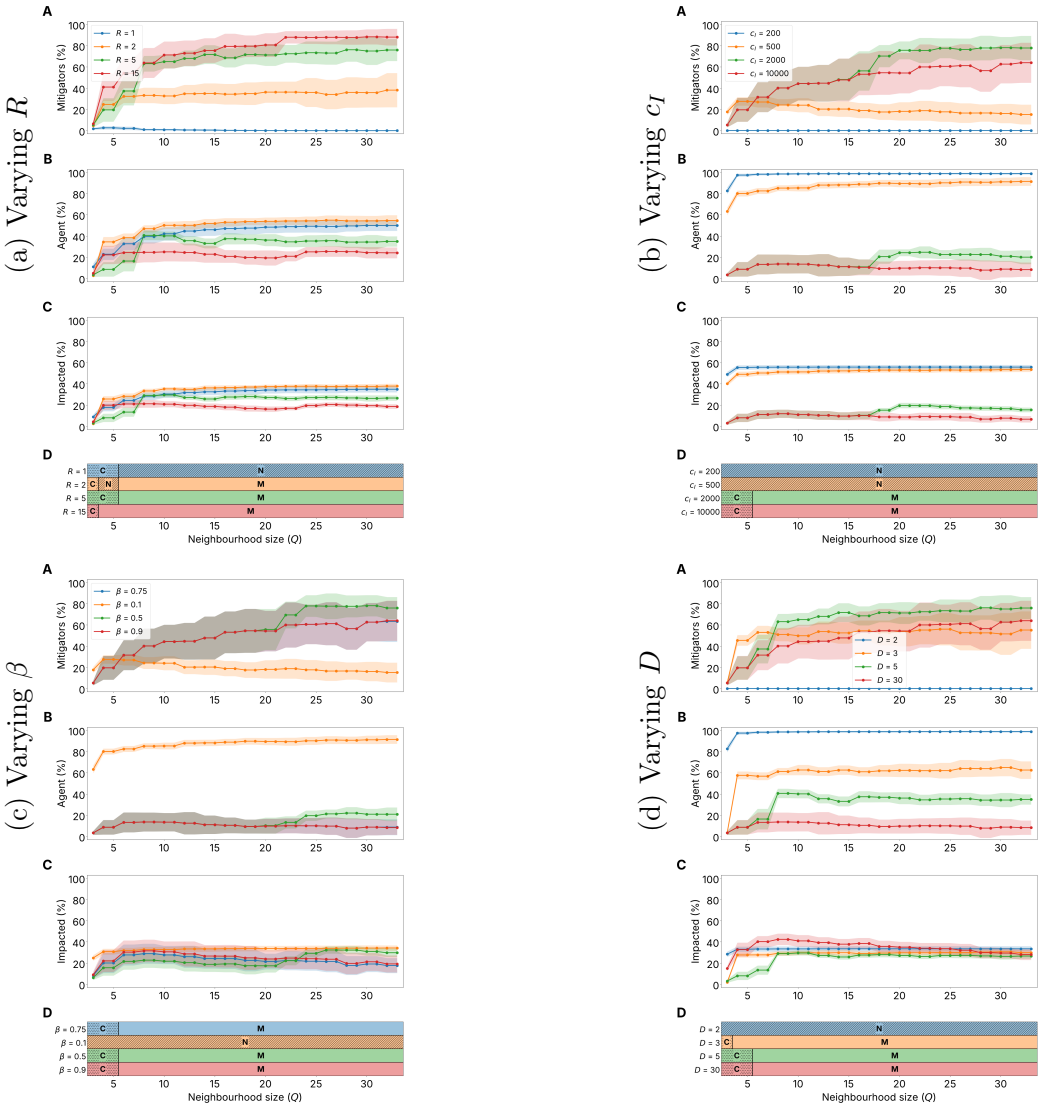
Parameters	Description	Values
Q	Neighbourhood size (mean node degree) (COVID/Climate)	5 / 999
ε	Personal efficacy of mitigation (COVID/Climate)	0.95 / 0.01
δ	Agent decay probability, per timestep (COVID/Climate)	0.5 / 0.01
R	Proportionality constant for rate of spread (COVID/Climate)	5 / 0.001
D	Duration of impact, in timesteps (COVID/Climate)	5 / 50
σ	Probability of changing behavior (COVID/Climate)	0.9 / 0.2
c_M	Cost of being a mitigator	50
c_I	Cost of being impacted	1000
β	Impact probability	0.2
p_{gen}	Agent generation probability, per timestep	0.02
N	Total number of individuals	1000
p_{rw}	Rewiring probability of the small-world network	0.1
Function	Description	
$A_i^{risk} = \frac{1}{k_i}\sum_{j\in\mathcal{N}_i} A_j$	proportion of neighbours of node i that carry agent	
$p_i^{inf,M} = (1-\varepsilon)(1-e^{-RA_i^{risk}})$	Probability of mitigating node i receiving agent from neighbors	
$p_i^{inf,N} = 1-e^{-RA_i^{risk}}$	Probability of non-mitigating node i receiving agent from neighbors	
$p_i^M = \beta p_i^{inf,M}$	Probability of node i being impacted, if a mitigator	
$p_i^N = \beta p_i^{inf,N}$	Probability of node i being impacted, if a non-mitigator	
$e_{i,M} = -p_i^M c_I D - c_M$	Payoff to node i for being a mitigator	
$e_{i,N} = -p_i^N c_I D$	Payoff to node i for being a non-mitigator	

Table 1: Baseline model parameters and functions, as used for Figures 2 and 3 of the main text. Figure 4 of the main text and the Supplementary Figures use the parameter values stated in their captions. All parameters are dimensionless, and the model is discrete in time.

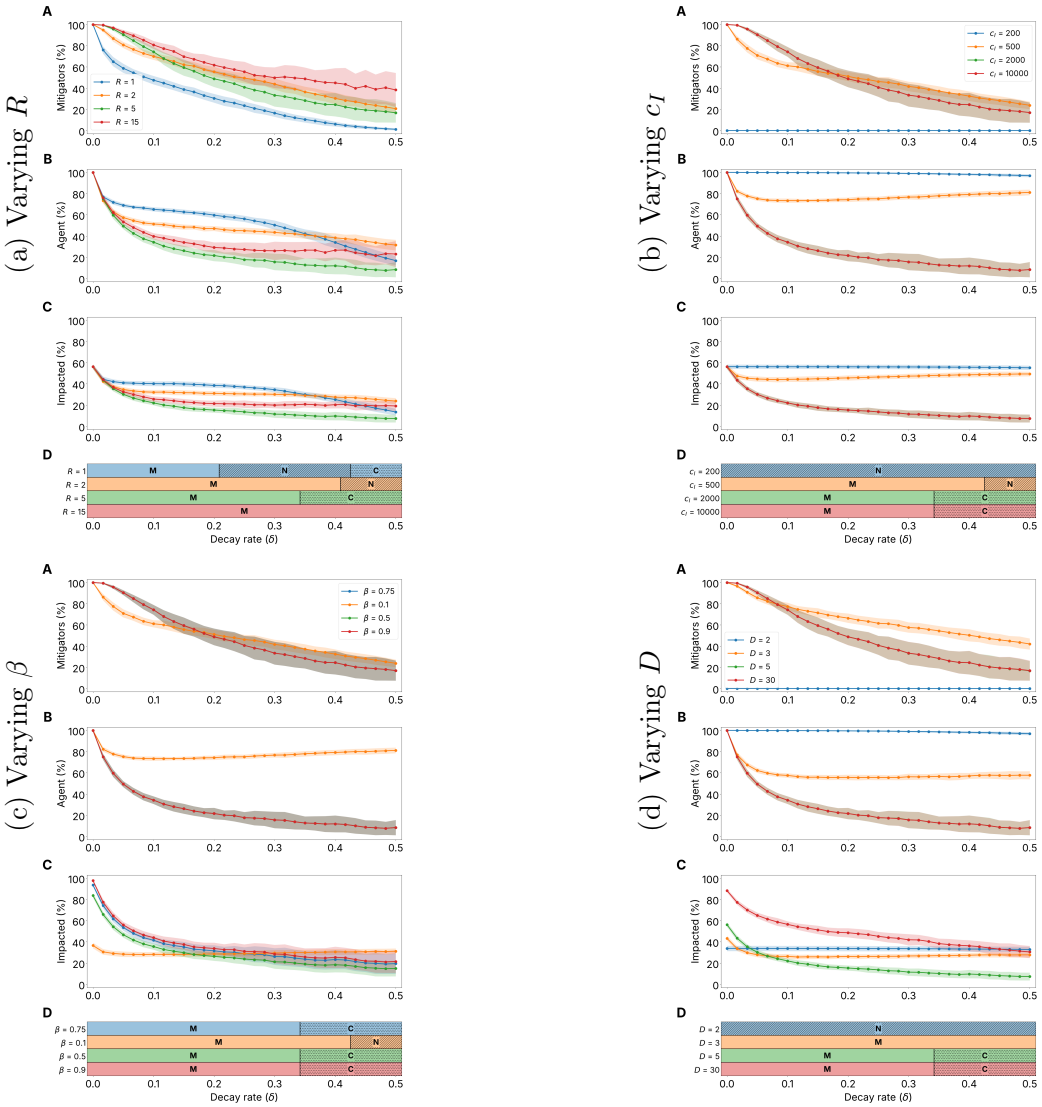
1.3 Supplementary Figures



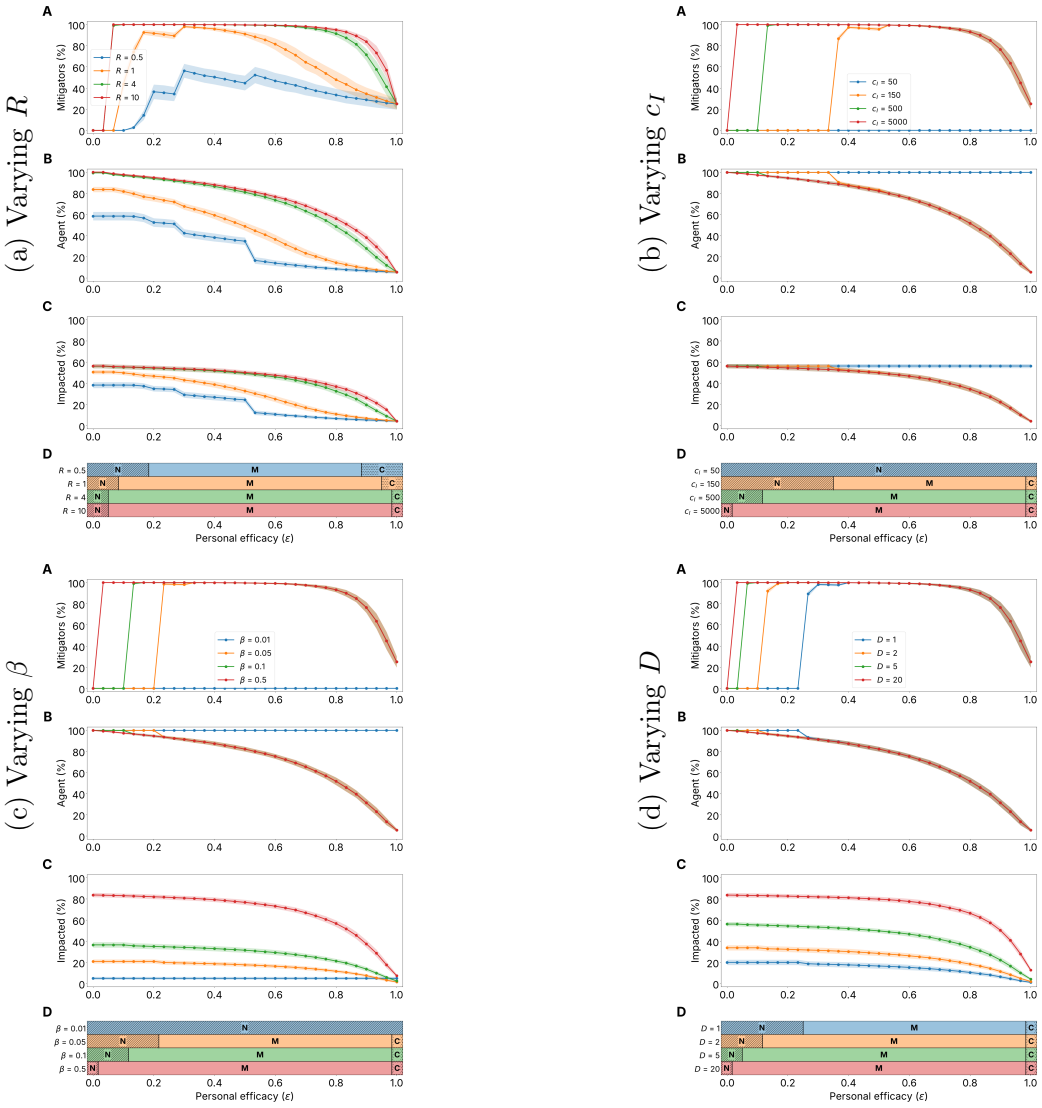
Supplementary Figure 1: Univariate analysis of model outcomes against personal efficacy ϵ (31 values from 0 to 1), varying (a) rate of spread $R \in \{0.5, 1, 4, 10\}$, (b) cost of infection $c_I \in \{50, 150, 500, 5000\}$, (c) impact probability $\beta \in \{0.01, 0.05, 0.1, 0.5\}$ and (d) duration of impact $D \in \{1, 2, 5, 20\}$. Other parameters are at values: $R = 5$, $c_I = 1000$, $\beta = 0.2$, $D = 5$, mitigation cost $c_M = 50$, decay rate $\delta = 0.2$, $Q = 5$ (neighbourhood size $Q - 1 = 4$), agent generation probability 0.02, $N = 300$ individuals on a small-world network (rewiring probability 0.1), initial prevalence 1% of non-mitigators, initial mitigators 50%, behavioural update probability $\sigma = 1$, 500 time steps. Panels A–C show the percentage of the population that are mitigators (A), carry the natural agent (B) and are impacted (C); each dot is the mean over 50 independent runs (random seeds 0–49, each with its own network and initial conditions) of the value at the final time step, shaded bands show one standard deviation across runs, and lines join points with the same value of the varied parameter. Panel D gives the regime of each point, assigned from the means over runs, one strip per line in that line's colour: *mitigation* (M, plain), more than 30% mitigators; *containment* (C, dotted), at most 30% mitigators and at most 30% carrying the natural agent; *non-control* (N, hatched), at most 30% mitigators and more than 30% carrying the natural agent. Regime boundaries lie halfway between adjacent simulated values of ϵ. Lines not visible coincide with others.



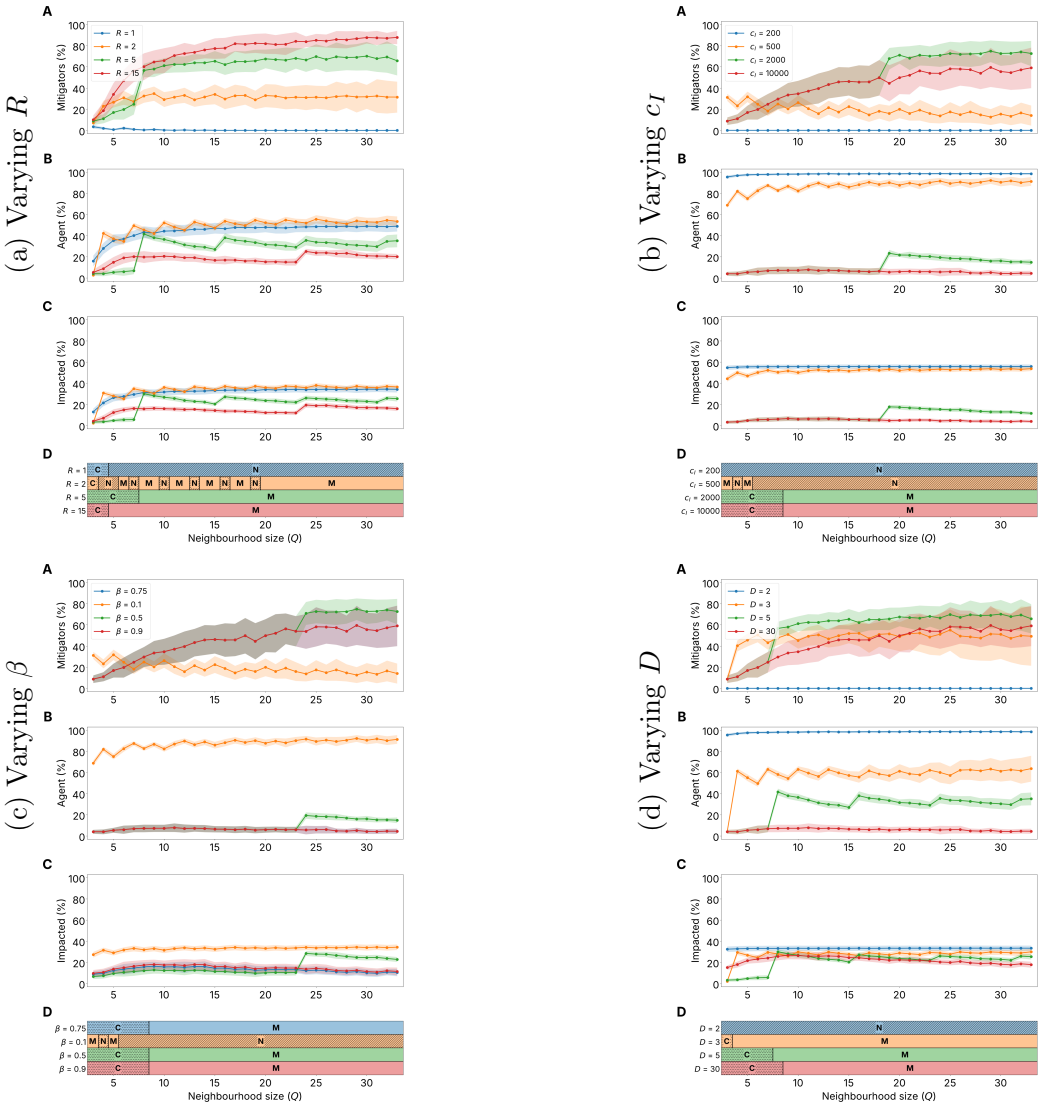
Supplementary Figure 2: Univariate analysis of model outcomes against Q (integers from 3 to 33), varying (a) rate of spread $R \in \{1, 2, 5, 15\}$, (b) cost of infection $c_I \in \{200, 500, 2000, 10000\}$, (c) impact probability $\beta \in \{0.1, 0.5, 0.75, 0.9\}$ and (d) duration of impact $D \in \{2, 3, 5, 30\}$. Neighbourhood size is $Q - 1$ for odd Q and Q for even Q, so outcomes at $Q = 2k$ and $Q = 2k + 1$ coincide. Other parameters are at values: $R = 5$, $c_I = 1000$, $\beta = 0.2$, $D = 5$, personal efficacy $\epsilon = 0.95$, mitigation cost $c_M = 450$, decay rate $\delta = 0.46$, agent generation probability 0.02, $N = 300$ individuals on a small-world network (rewiring probability 0.1), initial prevalence 1% of non-mitigators, initial mitigators 50%, behavioural update probability $\sigma = 1$, 500 time steps. Panels A–C show the percentage of the population that are mitigators (A), carry the natural agent (B) and are impacted (C); each dot is the mean over 50 independent runs (random seeds 0–49, each with its own network and initial conditions) of the value at the final time step, shaded bands show one standard deviation across runs, and lines join points with the same value of the varied parameter. Panel D gives the regime of each point, assigned from the means over runs, one strip per line in that line's colour: *mitigation* (M, plain), more than 30% mitigators; *containment* (C, dotted), at most 30% mitigators and at most 30% carrying the natural agent; *non-control* (N, hatched), at most 30% mitigators and more than 30% carrying the natural agent. Regime boundaries lie halfway between adjacent simulated values of Q. Lines not visible coincide with others.



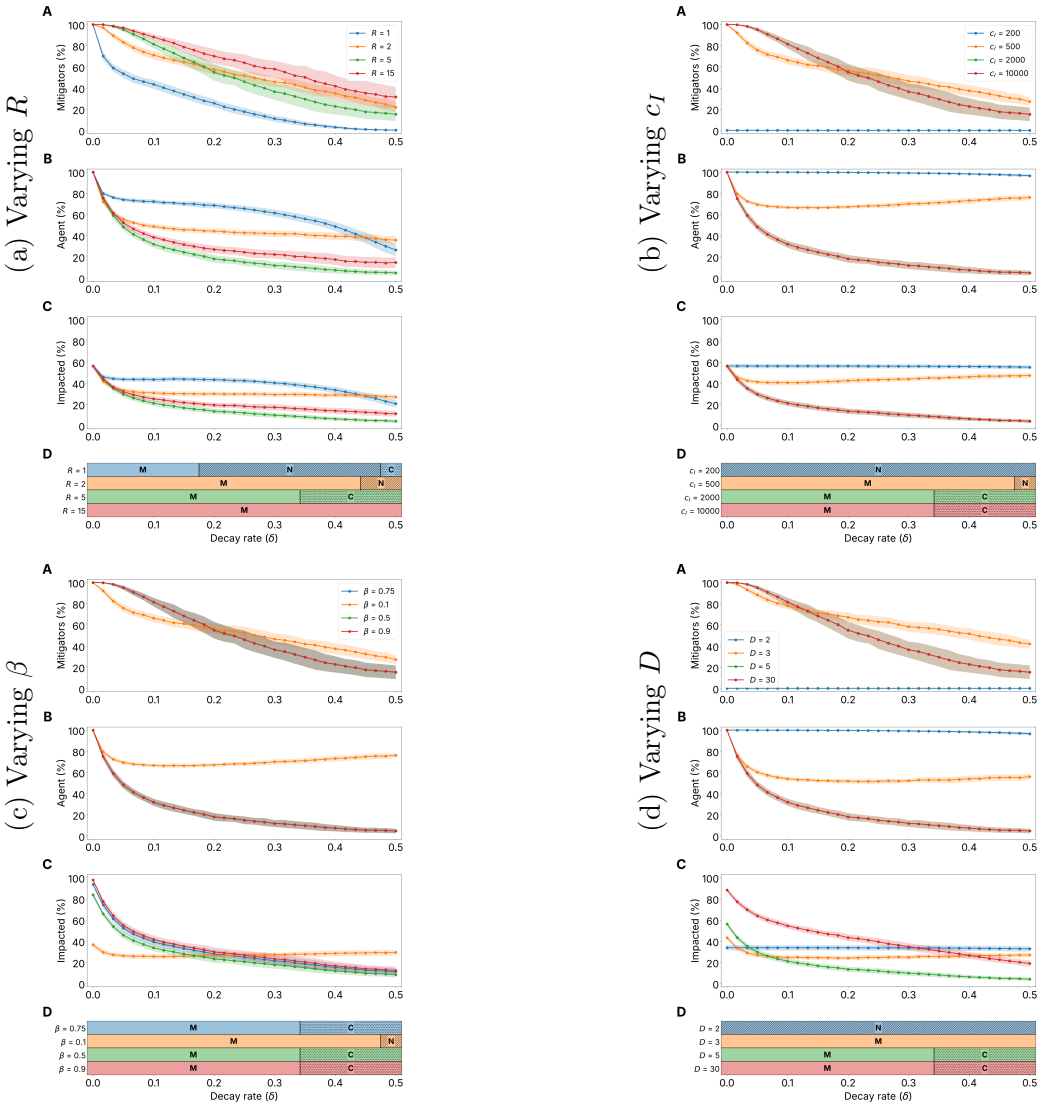
Supplementary Figure 3: Univariate analysis of model outcomes against decay rate δ (31 values from 0 to 0.5), varying (a) rate of spread $R \in \{1, 2, 5, 15\}$, (b) cost of infection $c_I \in \{200, 500, 2000, 10000\}$, (c) impact probability $\beta \in \{0.1, 0.5, 0.75, 0.9\}$ and (d) duration of impact $D \in \{2, 3, 5, 30\}$. Other parameters are at values: $R = 5$, $c_I = 1000$, $\beta = 0.2$, $D = 5$, personal efficacy $\epsilon = 0.95$, mitigation cost $c_M = 450$, $Q = 5$ (neighbourhood size $Q - 1 = 4$), agent generation probability 0.02, $N = 300$ individuals on a small-world network (rewiring probability 0.1), initial prevalence 1% of non-mitigators, initial mitigators 50%, behavioural update probability $\sigma = 1$, 500 time steps. Panels A–C show the percentage of the population that are mitigators (A), carry the natural agent (B) and are impacted (C); each dot is the mean over 50 independent runs (random seeds 0–49, each with its own network and initial conditions) of the value at the final time step, shaded bands show one standard deviation across runs, and lines join points with the same value of the varied parameter. Panel D gives the regime of each point, assigned from the means over runs, one strip per line in that line's colour: *mitigation* (M, plain), more than 30% mitigators; *containment* (C, dotted), at most 30% mitigators and at most 30% carrying the natural agent; *non-control* (N, hatched), at most 30% mitigators and more than 30% carrying the natural agent. Regime boundaries lie halfway between adjacent simulated values of δ. Lines not visible coincide with others.



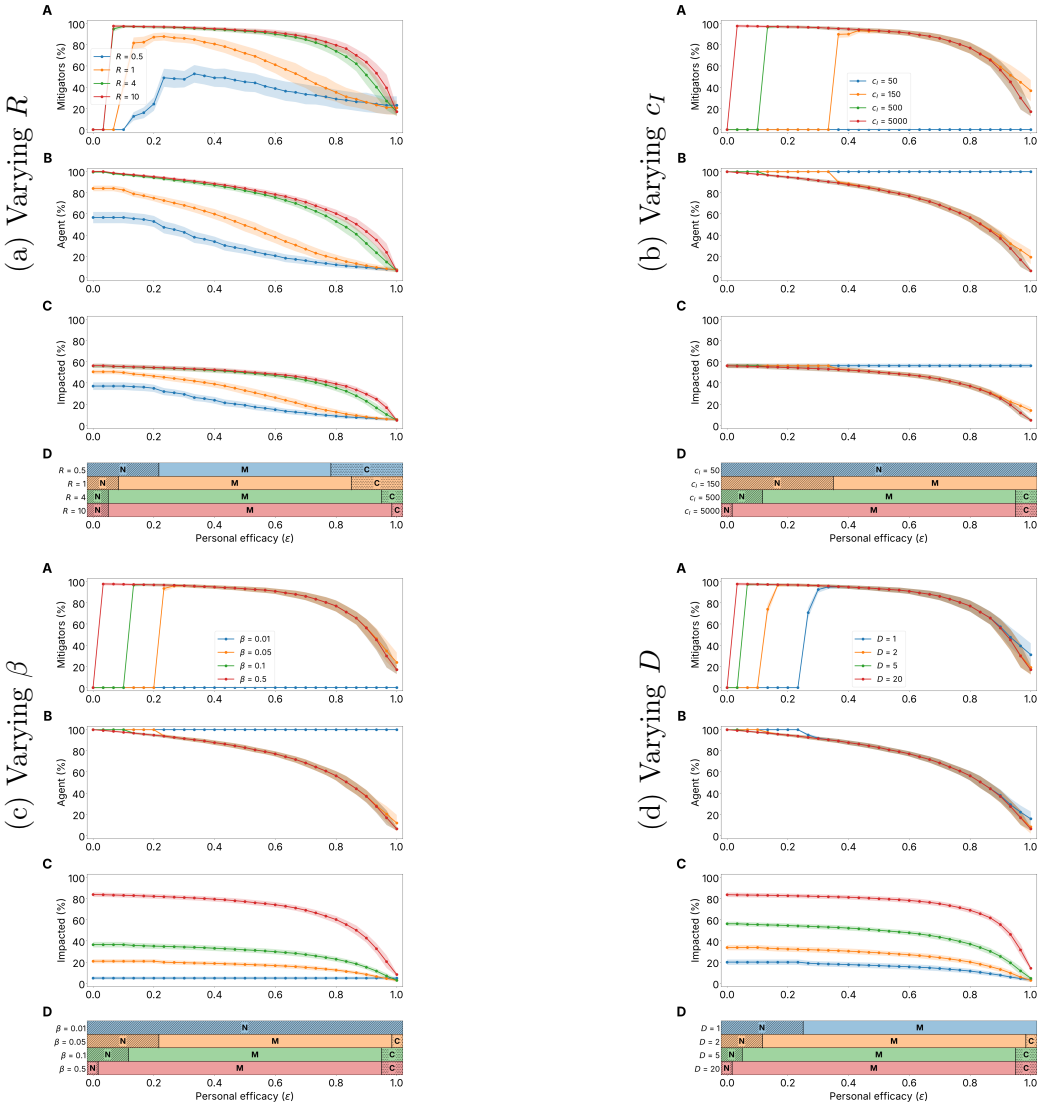
Supplementary Figure 4: Univariate analysis of model outcomes against personal efficacy ϵ (31 values from 0 to 1) on a random regular network, in which every node has exactly Q neighbours. The varied parameters (a)–(d), their values, all other parameter values (including $c_M = 50$, $\delta = 0.2$ and $Q = 5$), the statistics shown and the regime definitions are as in Supplementary Figure 1, which uses a small-world network.



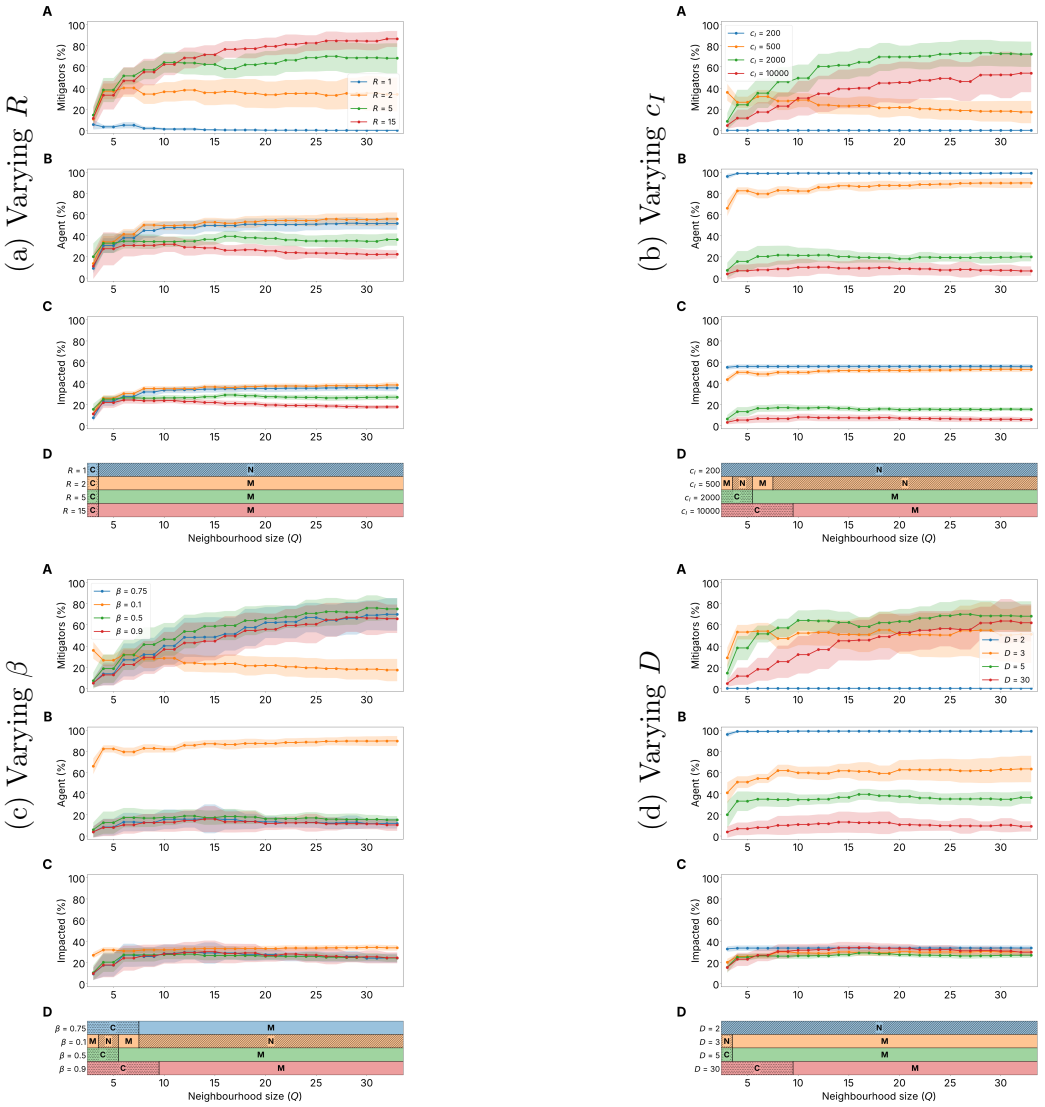
Supplementary Figure 5: Univariate analysis of model outcomes against Q (integers from 3 to 33) on a random regular network, in which every node has exactly Q neighbours. The varied parameters (a)–(d), their values, all other parameter values (including $c_M = 450$, $\delta = 0.46$ and $\epsilon = 0.95$), the statistics shown and the regime definitions are as in Supplementary Figure 2, which uses a small-world network.



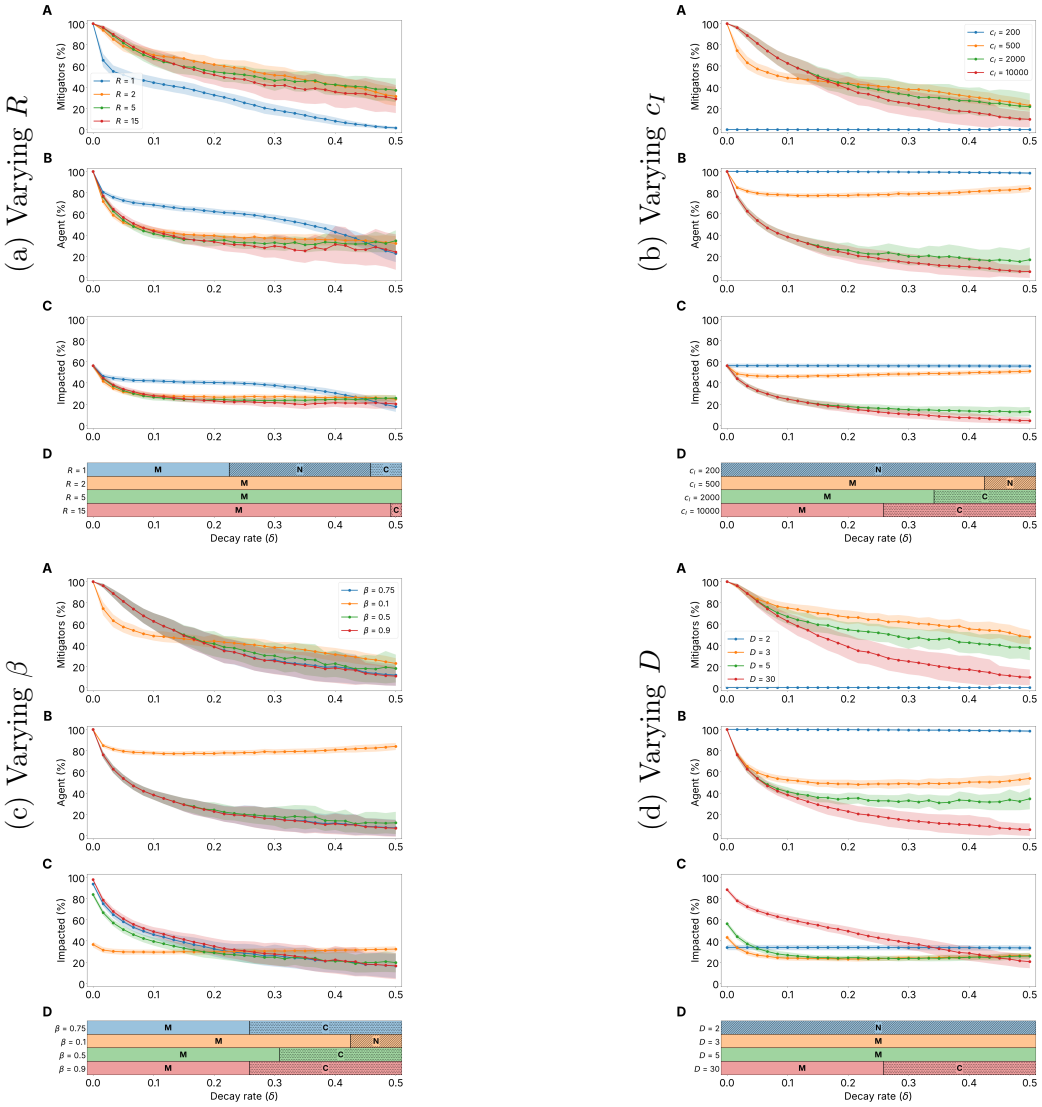
Supplementary Figure 6: Univariate analysis of model outcomes against decay rate δ (31 values from 0 to 0.5) on a random regular network, in which every node has exactly Q neighbours. The varied parameters (a)–(d), their values, all other parameter values (including $c_M = 450$, $Q = 5$ and $\epsilon = 0.95$), the statistics shown and the regime definitions are as in Supplementary Figure 3, which uses a small-world network.



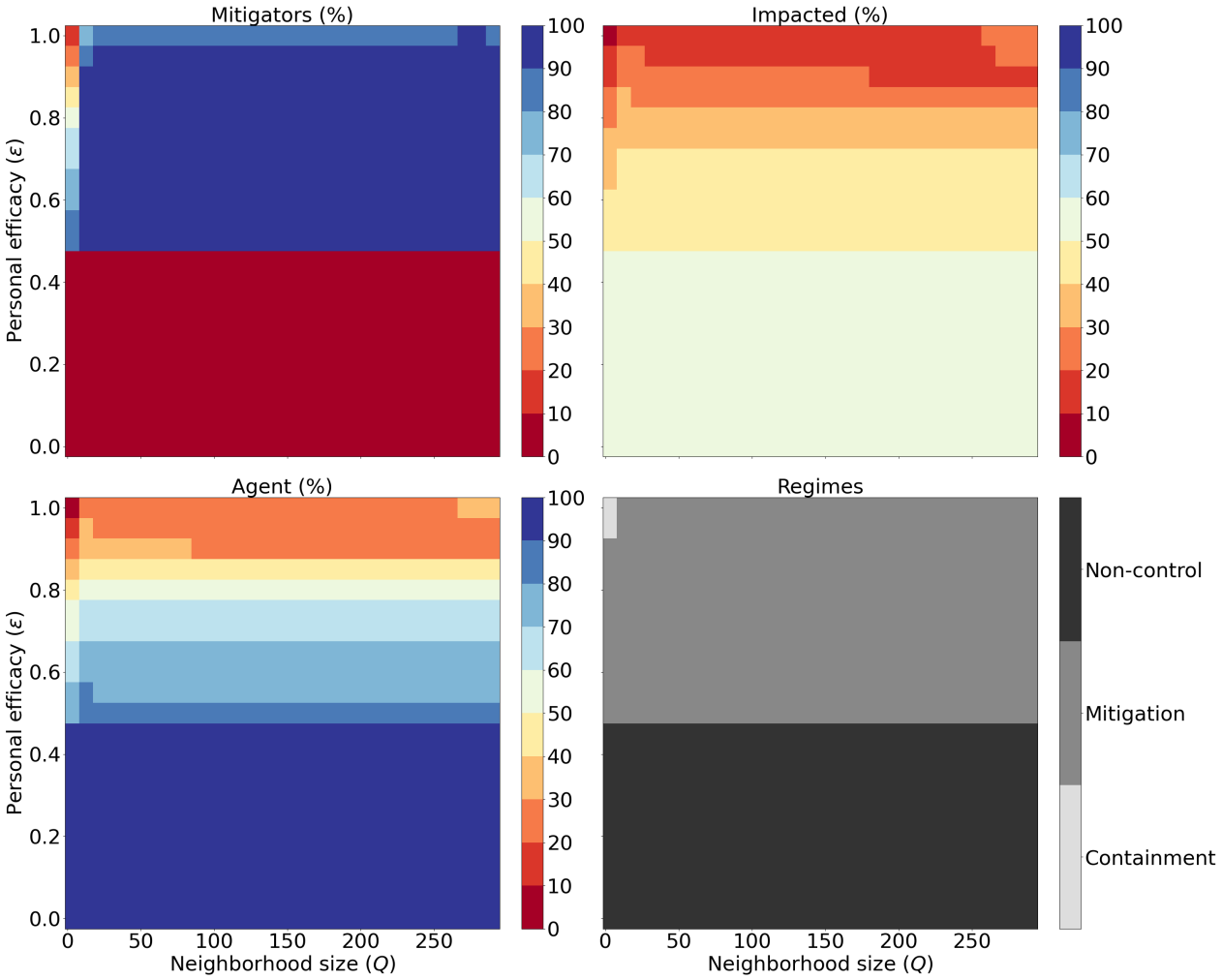
Supplementary Figure 7: Univariate analysis of model outcomes against personal efficacy ϵ (31 values from 0 to 1) on a scale-free (Barabási-Albert) network [3], in which each new node attaches to $\lfloor Q/2 \rfloor$ existing nodes. The varied parameters (a)–(d), their values, all other parameter values (including $c_M = 50$, $\delta = 0.2$ and $Q = 5$), the statistics shown and the regime definitions are as in Supplementary Figure 1, which uses a small-world network.



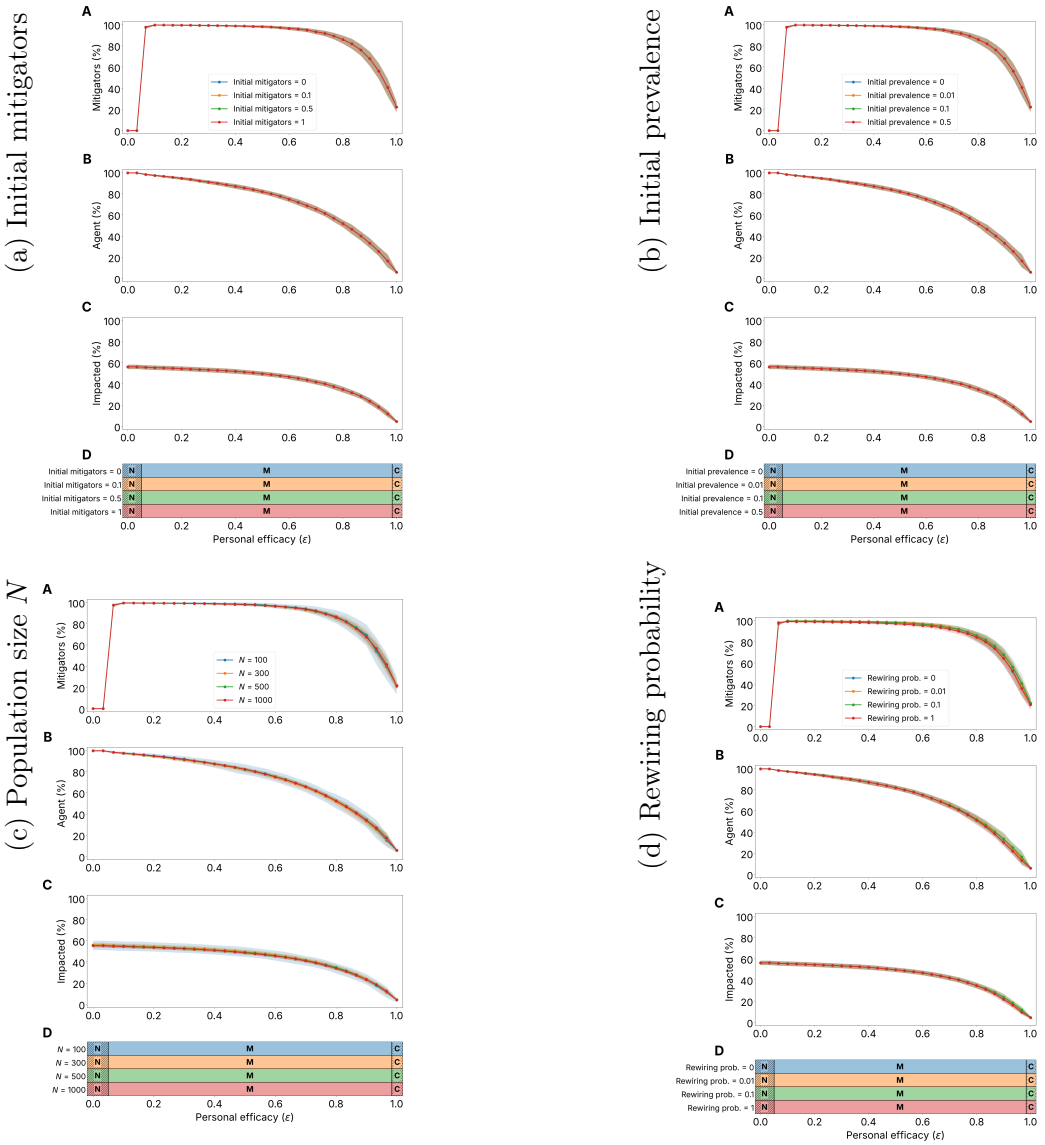
Supplementary Figure 8: Univariate analysis of model outcomes against Q (integers from 3 to 33) on a scale-free (Barabási-Albert) network [3], in which each new node attaches to $\lfloor Q/2 \rfloor$ existing nodes. Because each new node attaches to $\lfloor Q/2 \rfloor$ existing nodes, outcomes at $Q = 2k$ and $Q = 2k + 1$ coincide. The varied parameters (a)–(d), their values, all other parameter values (including $c_M = 450$, $\delta = 0.46$ and $\epsilon = 0.95$), the statistics shown and the regime definitions are as in Supplementary Figure 2, which uses a small-world network.



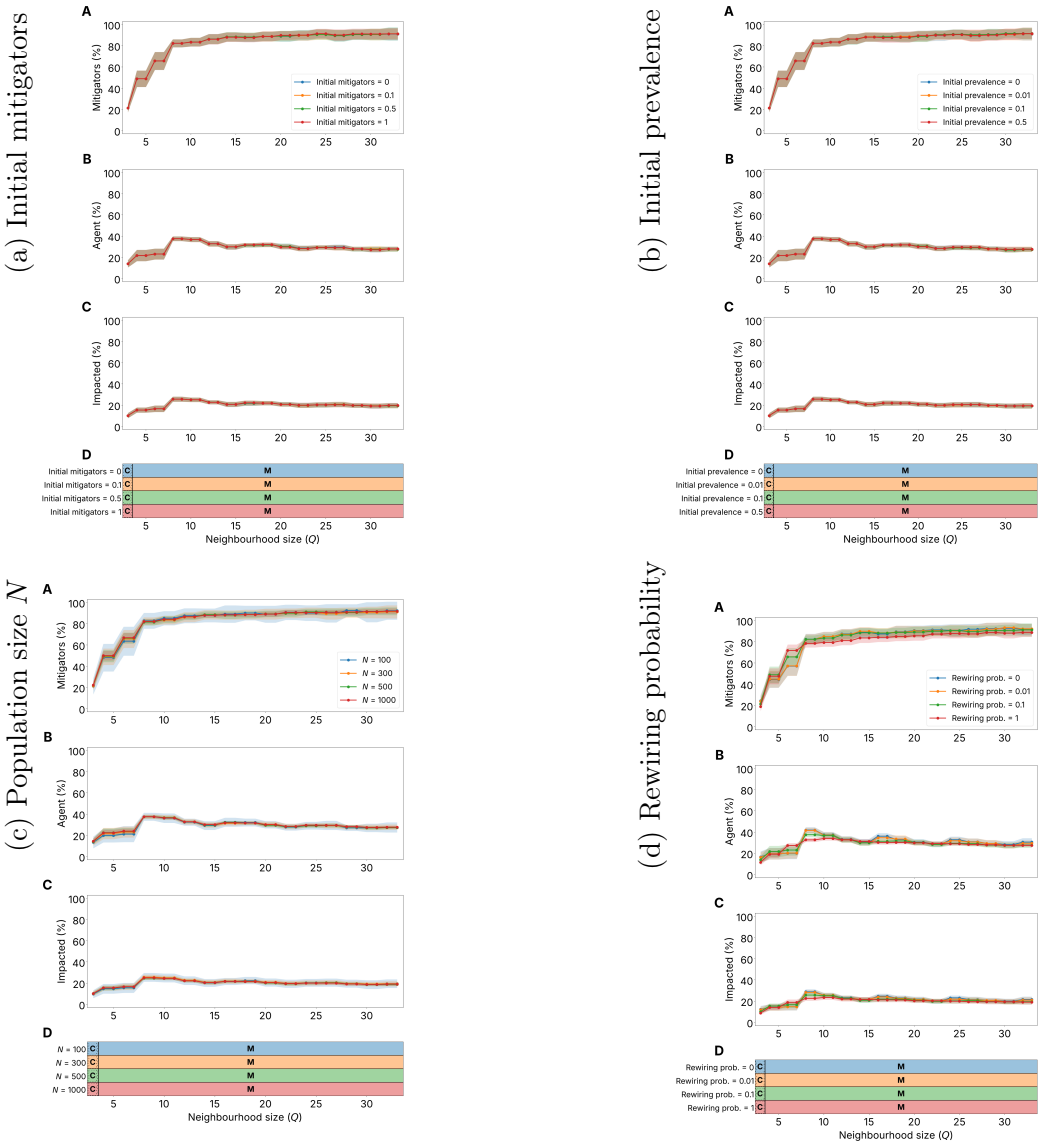
Supplementary Figure 9: Univariate analysis of model outcomes against decay rate δ (31 values from 0 to 0.5) on a scale-free (Barabási-Albert) network [3], in which each new node attaches to $\lfloor Q/2 \rfloor$ existing nodes. The varied parameters (a)–(d), their values, all other parameter values (including $c_M = 450$, $Q = 5$ and $\epsilon = 0.95$), the statistics shown and the regime definitions are as in Supplementary Figure 3, which uses a small-world network.



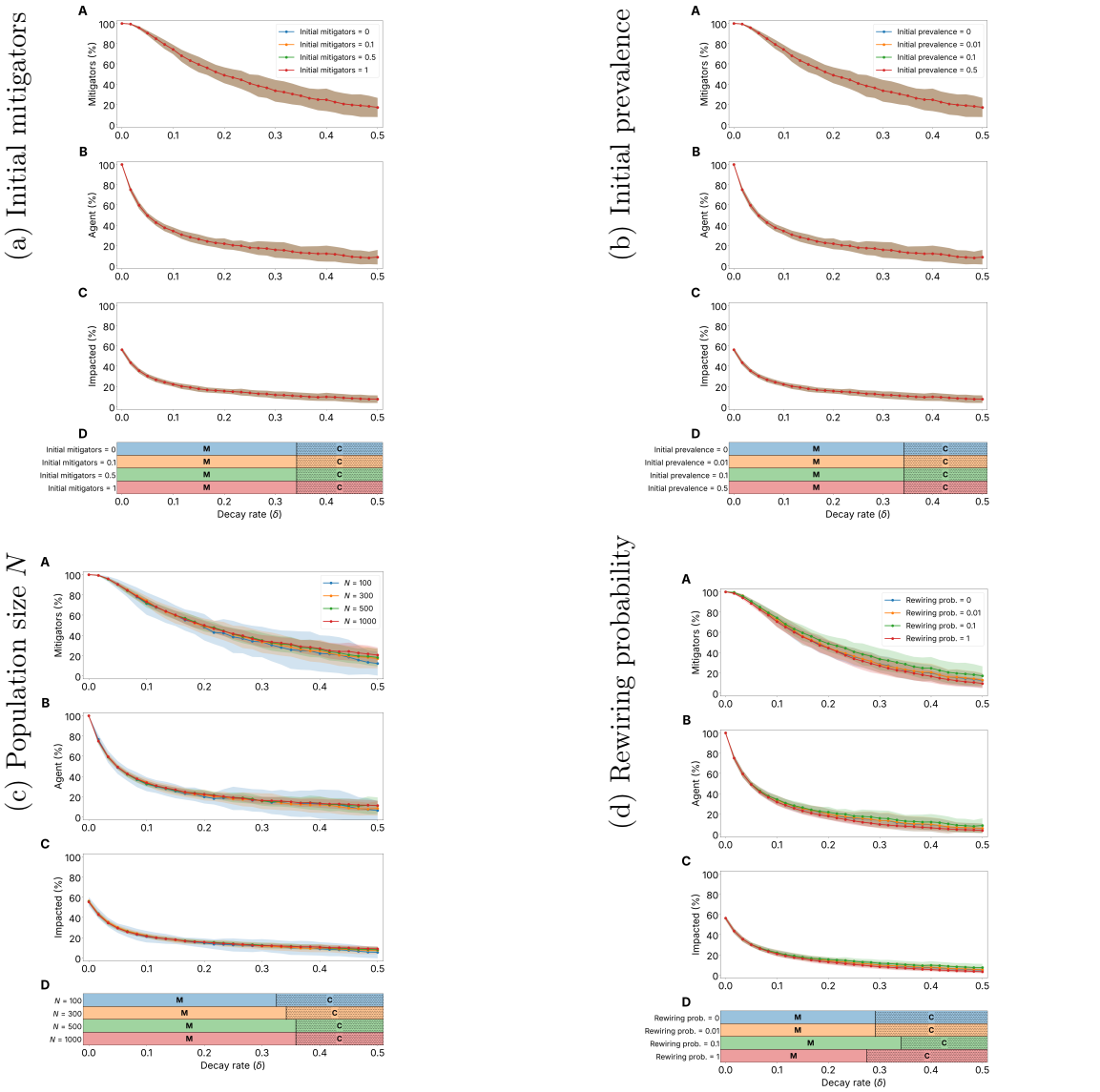
Supplementary Figure 10: Parameter plane of neighbourhood size Q (31 values from 3 to 290) against personal efficacy ϵ (21 values from 0 to 1) on a small-world network. Panels show the percentage of the population that are mitigators, are impacted and carry the natural agent, and the regime at each point, defined as in Supplementary Figure 1. Other parameters are as in Figure 4a of the main text: $c_M = 450$, $\delta = 0.2$, $R = 5$, $c_I = 1000$, $\beta = 0.2$, $D = 5$, agent generation probability 0.02, behavioural update probability $\sigma = 1$, $N = 300$ (rewiring probability 0.1), initial prevalence 1% of non-mitigators and initial mitigators 50%. Each point is a single simulation of 1000 time steps with a fixed random seed, averaged over the final 20% of time steps. The containment region at small Q and high ϵ corresponds to the COVID-like system, and the non-control region at low ϵ includes the climate-like corner of large Q and low ϵ.



Supplementary Figure 11: Robustness of the sweep of personal efficacy ϵ (31 values from 0 to 1) in Figure 4b of the main text to (a) the initial fraction of mitigators (0, 0.1, 0.5, 1), (b) the probability that a non-mitigator initially carries the natural agent (0, 0.01, 0.1, 0.5), (c) the population size N (100, 300, 500, 1000) and (d) the rewiring probability of the small-world network (0, 0.01, 0.1, 1). A rewiring probability of 0 gives a ring lattice with high clustering, and a rewiring probability of 1 gives a network close to a random graph. All other parameter values are as in Figure 4b ($c_M = 50$, $\delta = 0.2$, $Q = 5$, $R = 5$, $c_I = 1000$, $\beta = 0.2$, $D = 5$, $\sigma = 1$, agent generation probability 0.02, $N = 300$, rewiring probability 0.1, initial prevalence 1% of non-mitigators and initial mitigators 50%). The statistics shown and the regime definitions are as in Supplementary Figure 1 (50 independent runs per point, 500 time steps).



Supplementary Figure 12: Robustness of the sweep of Q (integers from 3 to 33) in Figure 4a of the main text to (a) the initial fraction of mitigators (0, 0.1, 0.5, 1), (b) the probability that a non-mitigator initially carries the natural agent (0, 0.01, 0.1, 0.5), (c) the population size N (100, 300, 500, 1000) and (d) the rewiring probability of the small-world network (0, 0.01, 0.1, 1). A rewiring probability of 0 gives a ring lattice with high clustering, and a rewiring probability of 1 gives a network close to a random graph. All other parameter values are as in Figure 4a ($c_M = 450$, $\delta = 0.2$, $\epsilon = 0.95$, $R = 5$, $c_I = 1000$, $\beta = 0.2$, $D = 5$, $\sigma = 1$, agent generation probability 0.02, $N = 300$, rewiring probability 0.1, initial prevalence 1% of non-mitigators and initial mitigators 50%). The statistics shown and the regime definitions are as in Supplementary Figure 1 (50 independent runs per point, 500 time steps).



Supplementary Figure 13: Robustness of the sweep of decay rate δ (31 values from 0 to 0.5) in Figure 4c of the main text to (a) the initial fraction of mitigators (0, 0.1, 0.5, 1), (b) the probability that a non-mitigator initially carries the natural agent (0, 0.01, 0.1, 0.5), (c) the population size N (100, 300, 500, 1000) and (d) the rewiring probability of the small-world network (0, 0.01, 0.1, 1). A rewiring probability of 0 gives a ring lattice with high clustering, and a rewiring probability of 1 gives a network close to a random graph. All other parameter values are as in Figure 4c ($c_M = 50$, $Q = 5$, $\epsilon = 0.95$, $R = 5$, $c_I = 1000$, $\beta = 0.2$, $D = 5$, $\sigma = 1$, agent generation probability 0.02, $N = 300$, rewiring probability 0.1, initial prevalence 1% of non-mitigators and initial mitigators 50%). The statistics shown and the regime definitions are as in Supplementary Figure 1 (50 independent runs per point, 500 time steps).

References

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