

To mix or not to mix?

- *Desirable and undesirable levels of segregation between groups*

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<https://luis-r-izquierdo.github.io/micopro/>



Outline

- The question
- Related literature
- The approach and the model
- A mean-dynamics (MD) approximation
- Analysis of the MD
- Robustness
- Conclusions



The question

How does **mixing** affect **contagion** processes?

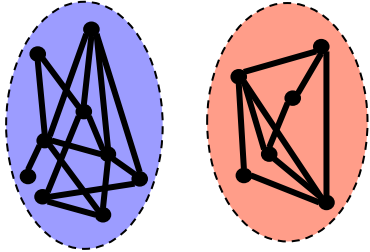
homophily

diffusion

assortativity

segregation

The question



Homophily

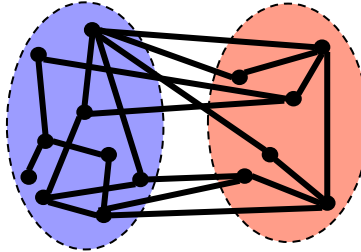
Assortativity

Segregation

100% intragroup

0% intergroup

No mixing



Random

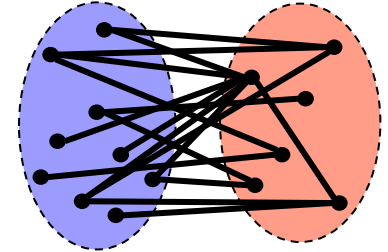
Random

Random

50% intragroup

50% intergroup

Some mixing



Heterophily

Disassortativity

No segregation

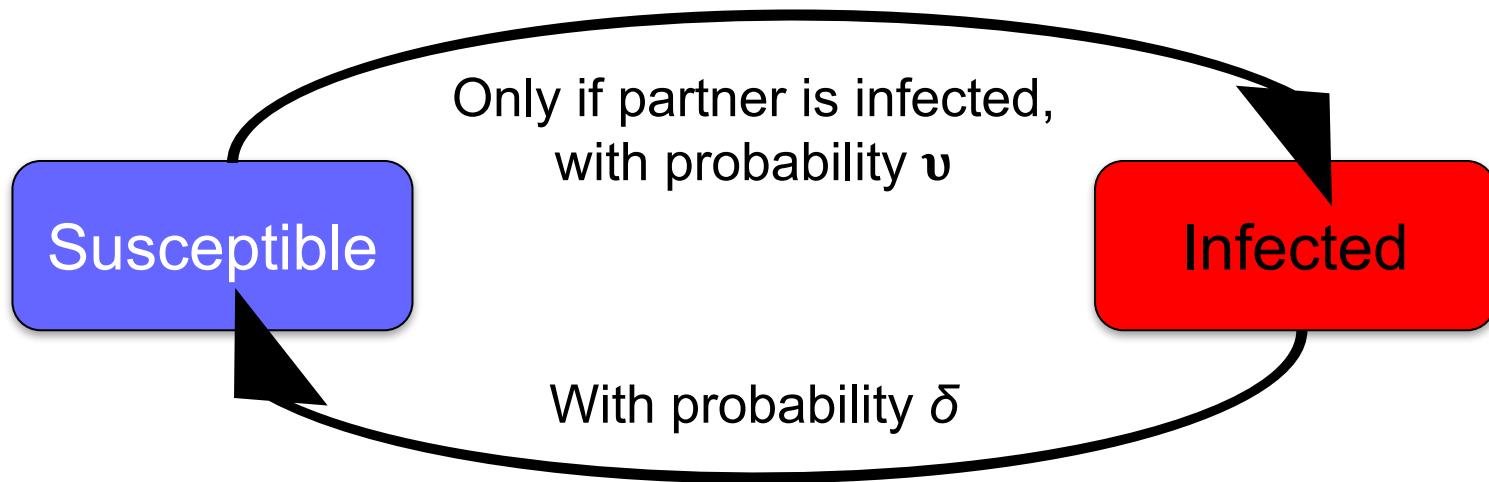
0% intragroup

100% intergroup

Full mixing

The question

How does **mixing** affect **contagion** processes?
diffusion

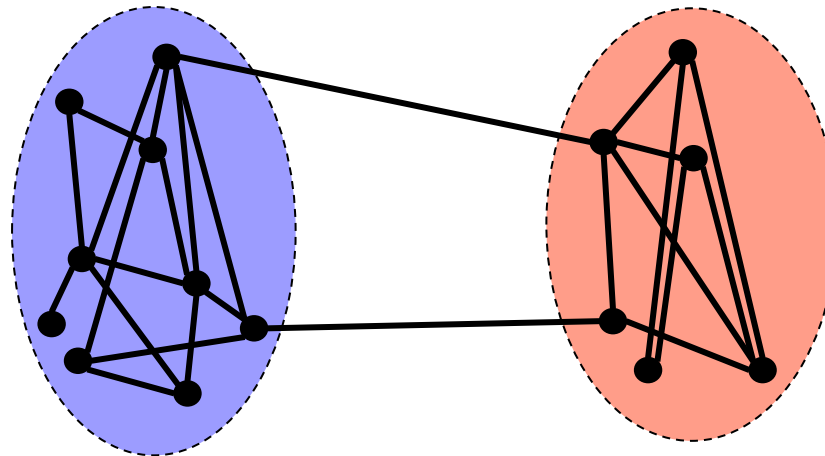


Some examples:

- Biological infections (e.g. common cold and influenza)
- Adoption of the latest technology
- Motivation in the classroom or at work

The question

How does mixing affect contagion processes?



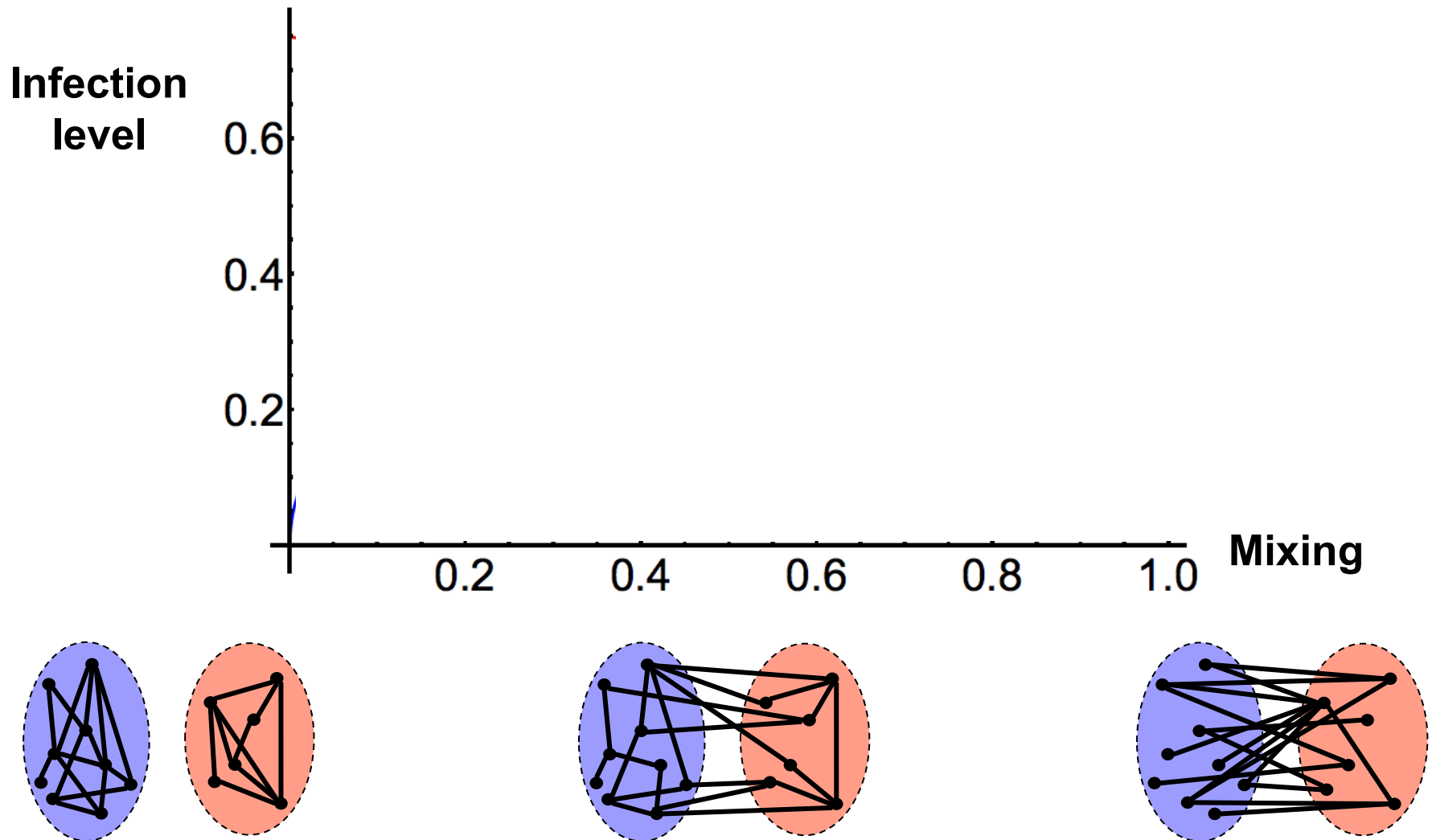
**Resistant
group**

Hard to infect /
motivate

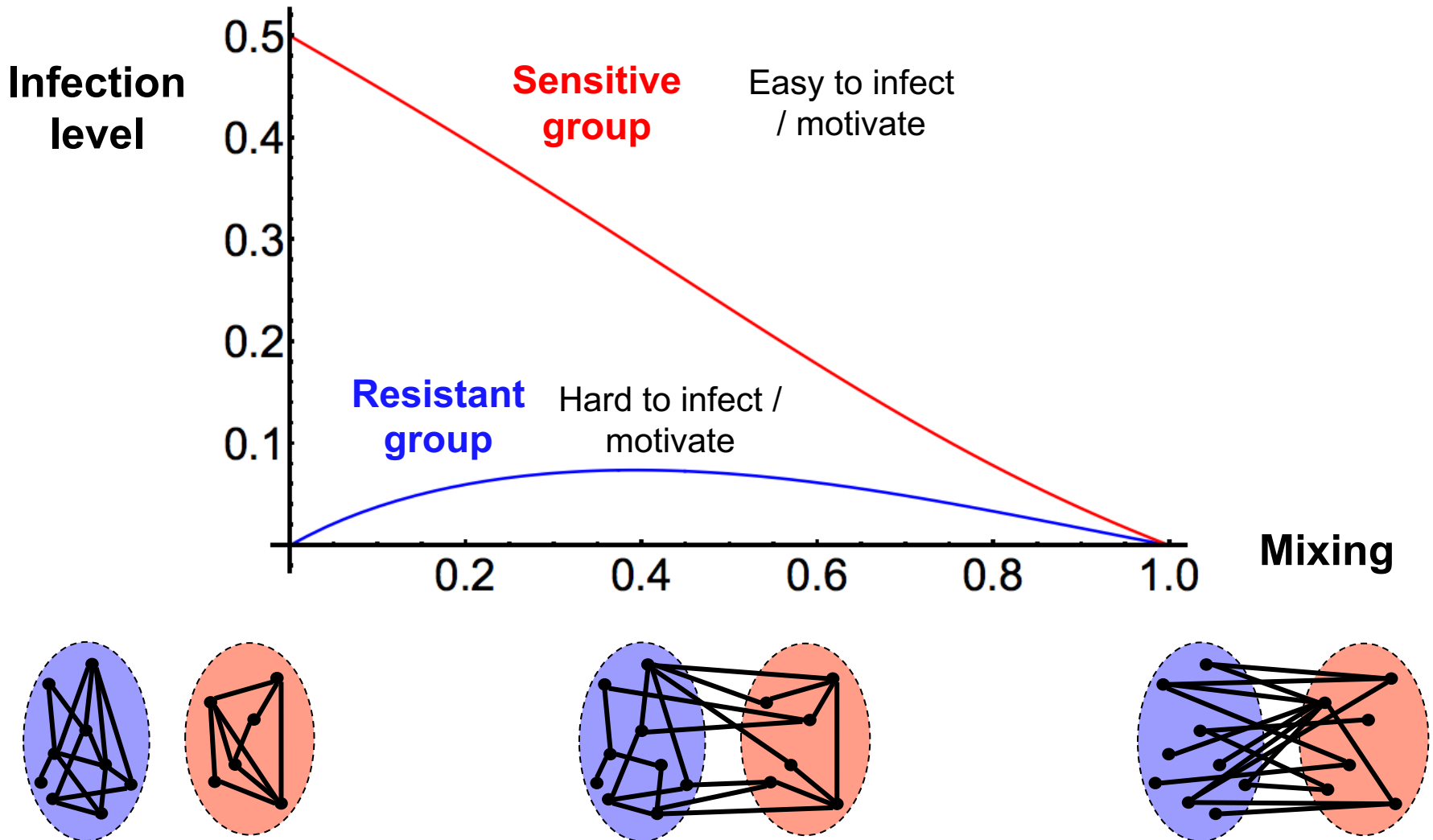
**Sensitive
group**

Easy to infect /
motivate

The question



The question





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Related literature

- Axelrod, R. (1997) The dissemination of culture - A model with local convergence and global polarization. *Journal of Conflict Resolution* 41(2), 203-226.
- McPherson, M., Smith-Lovin, L., & Cook, J. M. (2001). Birds of a feather: Homophily in social networks. *Annual Review of Sociology*, 27, 415–444.
- Jackson, M. O. & López-Pintado, D. (2013). Diffusion and contagion in networks with heterogeneous agents and homophily. *Network Science*, 1, 49-67.
- Yavaş, M., & Yücel, G. (2014). Impact of Homophily on Diffusion Dynamics over Social Networks. *Social Science Computer Review*, 32 (3), 354–372.



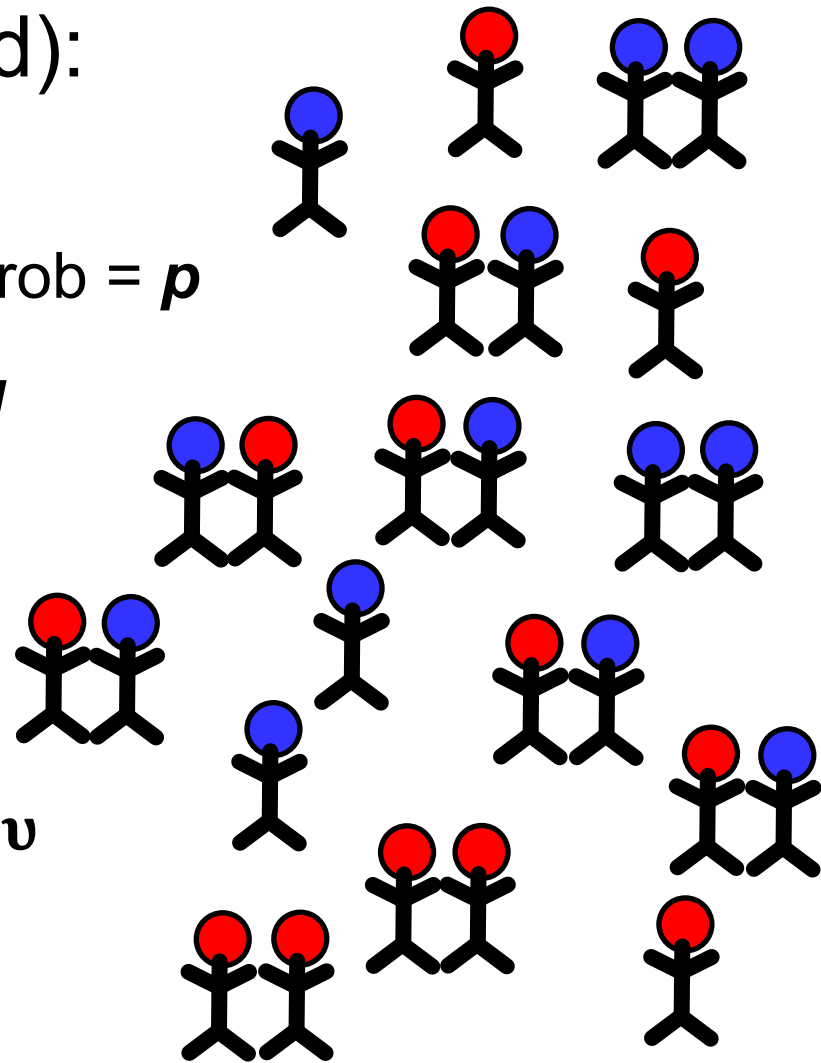
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The model

Matching model (undirected):

1. Two groups of equal size
2. Agents selected to interact with prob = p
3. Do matching according to *mixing*
4. For each agent:
 - If infected:
recover with prob = δ
 - Else: if mate infected,
become infected with prob = v





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A mean-dynamics (MD) approximation

When the population is very large, the law of large numbers enables us to:

- identify *expected* recoveries with *average* recoveries, and
- identify *expected* infections with *average* infections.

$$\frac{d\rho_1}{dt} = p(1 - \rho_1)v_1((1 - m)\rho_1 + m\rho_2) - \rho_1\delta_1$$

$$\frac{d\rho_2}{dt} = p(1 - \rho_2)v_2((1 - m)\rho_2 + m\rho_1) - \rho_2\delta_2$$

A mean-dynamics (MD) approximation

When the population is very large, the law of large numbers enables us to:

- identify *expected* recoveries with *average* recoveries, and
- identify *expected* infections with *average* infections.

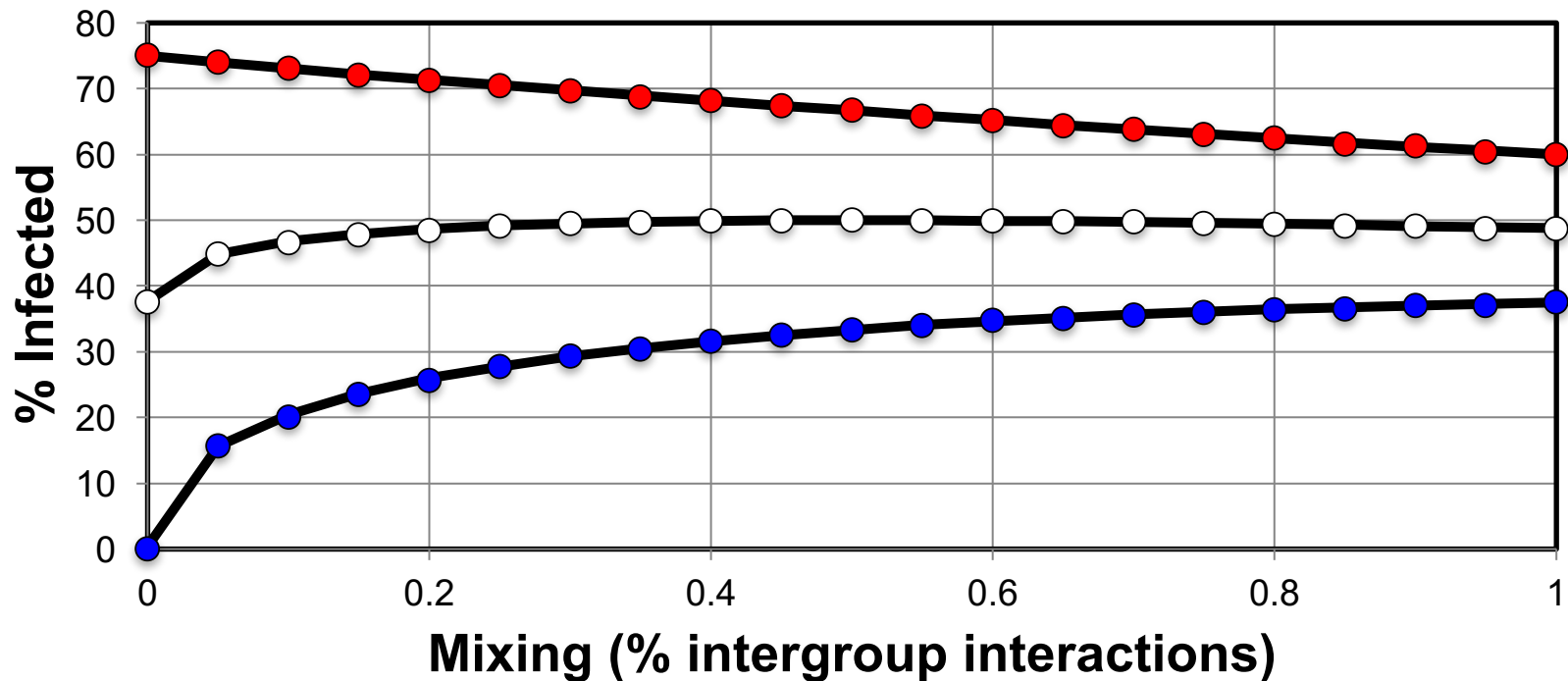
$$\frac{1}{\delta_1} \frac{d\rho_1}{dt} = \lambda_1 (1 - \rho_1) ((1 - m)\rho_1 + m\rho_2) - \rho_1$$

$$\frac{1}{\delta_2} \frac{d\rho_2}{dt} = \lambda_2 (1 - \rho_2) ((1 - m)\rho_2 + m\rho_1) - \rho_2$$

$$\lambda_i = p \frac{v_i}{\delta_i} \quad \text{Effective adoption rate}$$

A mean-dynamics (MD) approximation

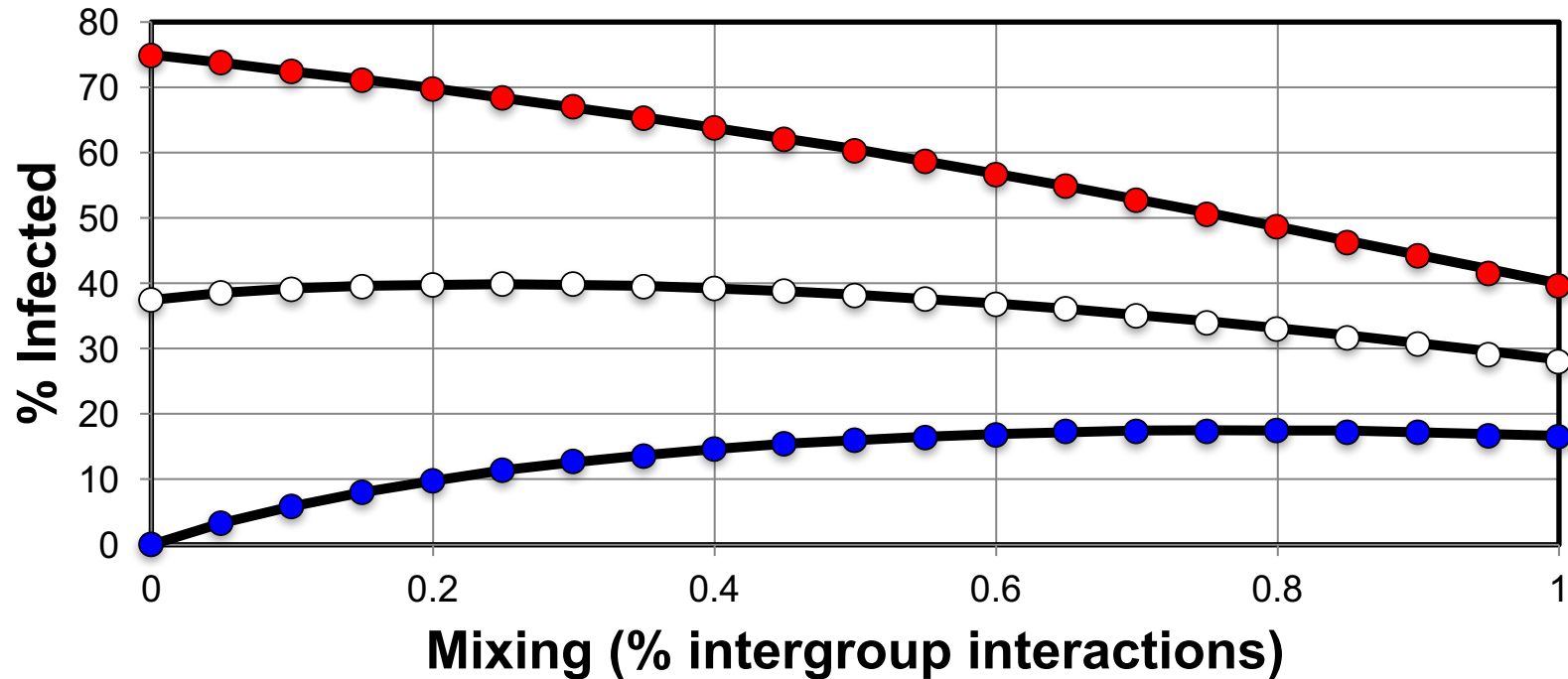
$$\lambda_1 = 4 ; \lambda_2 = 1$$



Circles are calculated using the ABM (1000 agents). Each circle is the average of 10 runs. For each run we have computed the average of the % infected from $t = 1001$ to $t = 2000$. Standard errors are below 1% in all cases. Black lines are computed using the MD.

A mean-dynamics (MD) approximation

$$\lambda_1 = 4 ; \lambda_2 = 0.5$$



Circles are calculated using the ABM (1000 agents). Each circle is the average of 10 runs. For each run we have computed the average of the % infected from $t = 1001$ to $t = 2000$. Standard errors are below 1% in all cases. Black lines are computed using the MD.



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Analysis of the MD

$$\frac{1}{\delta_1} \frac{d\rho_1}{dt} = \lambda_1(1 - \rho_1)((1 - m)\rho_1 + m\rho_2) - \rho_1 = 0$$

$$\frac{1}{\delta_2} \frac{d\rho_2}{dt} = \lambda_2(1 - \rho_2)((1 - m)\rho_2 + m\rho_1) - \rho_2 = 0$$

- Existence and uniqueness of a stable solution, for all parameter values, regardless of initial conditions.

Analysis of the MD

Result 1. Assume $\lambda_1 < \lambda_2$. A unique solution $(\rho_1^S, \rho_2^S) \neq (0,0)$ exists iff

$$\lambda_2(1 - m) \geq 1 \quad [a]$$

or
$$\frac{\lambda_1 m}{1 - \lambda_1(1 - m)} \frac{\lambda_2 m}{1 - \lambda_2(1 - m)} > 1 \quad [b]$$

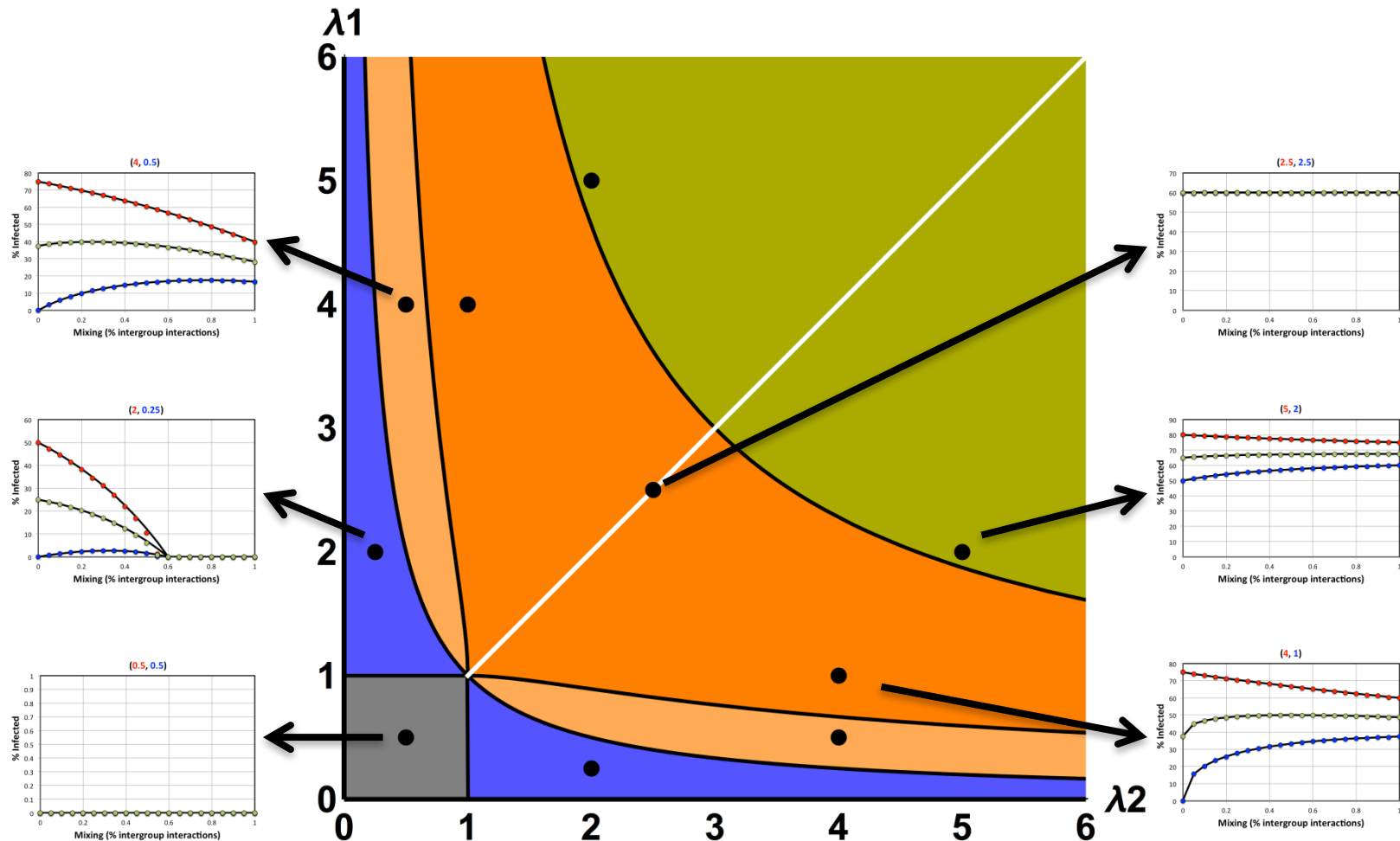
Corollary 1.1: If $\lambda_1 \lambda_2 > 1$ then there is a unique positive solution.

Corollary 1.2: If $\lambda_2 \leq 1$ then $(\rho_1, \rho_2) = (0, 0)$ is the only solution.

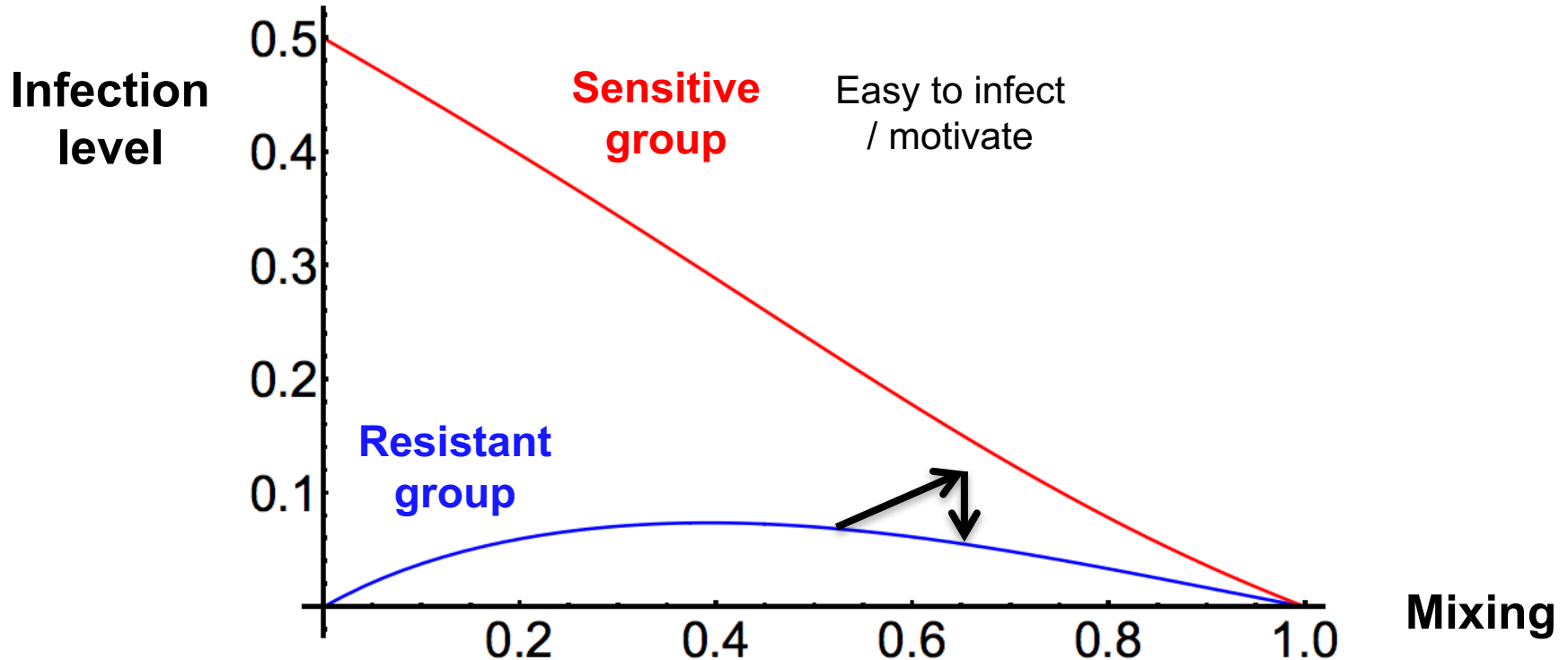
Corollary 1.3: If $\lambda_2 > 1$ but $\lambda_1 \lambda_2 \leq 1$ then there is a unique positive solution iff the mixing level m is lower than some critical level

$$m_{critical} = \frac{\lambda_1 + \lambda_2 - \lambda_1 \lambda_2 - 1}{\lambda_1 + \lambda_2 - 2\lambda_1 \lambda_2}$$

Analysis of the MD



Analysis of the MD



$$d\rho_1 = \frac{\partial \rho_1}{\partial m} dm + \frac{\partial \rho_1}{\partial \rho_2} d\rho_2$$



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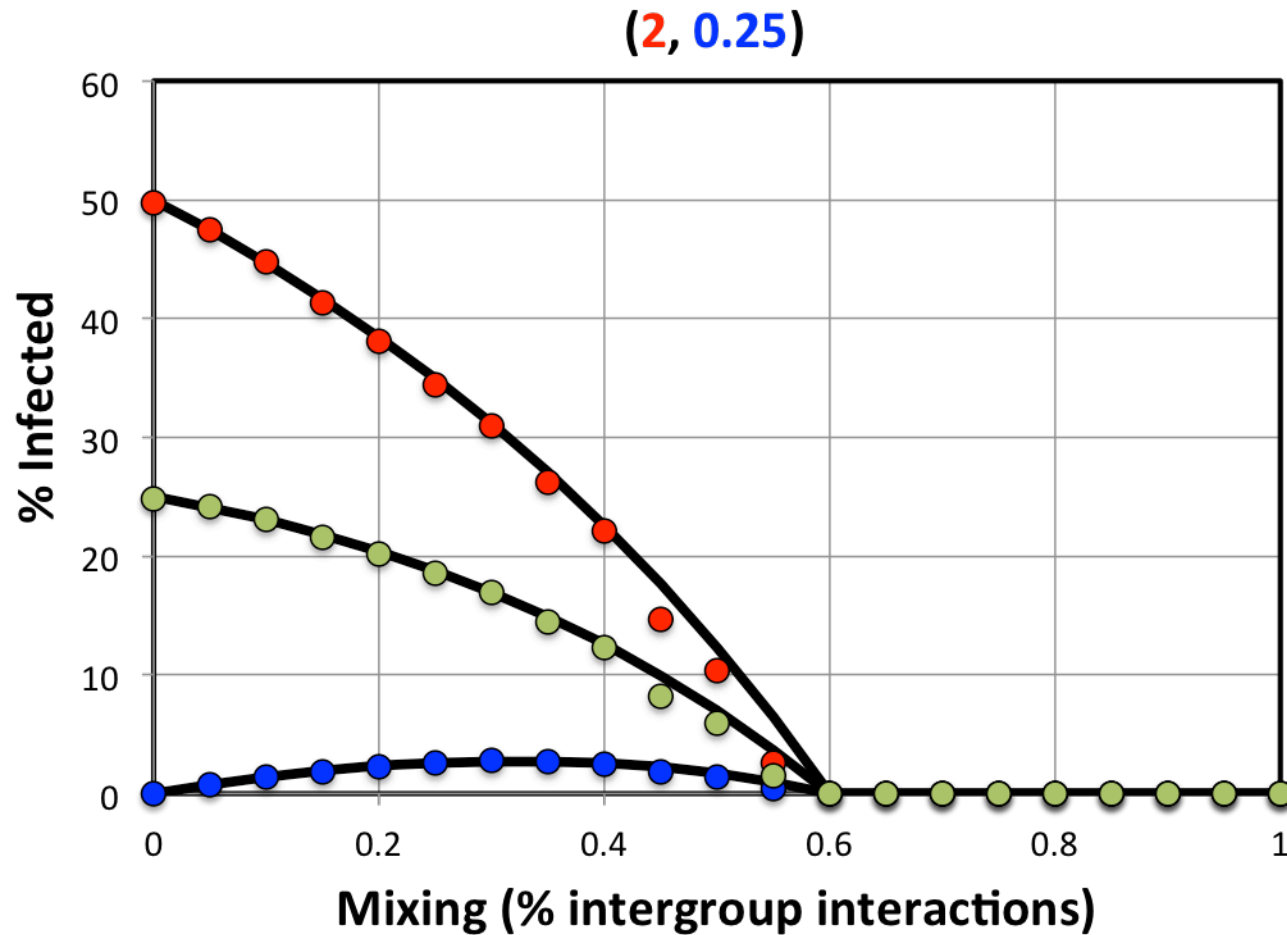
Robustness

■ More general model

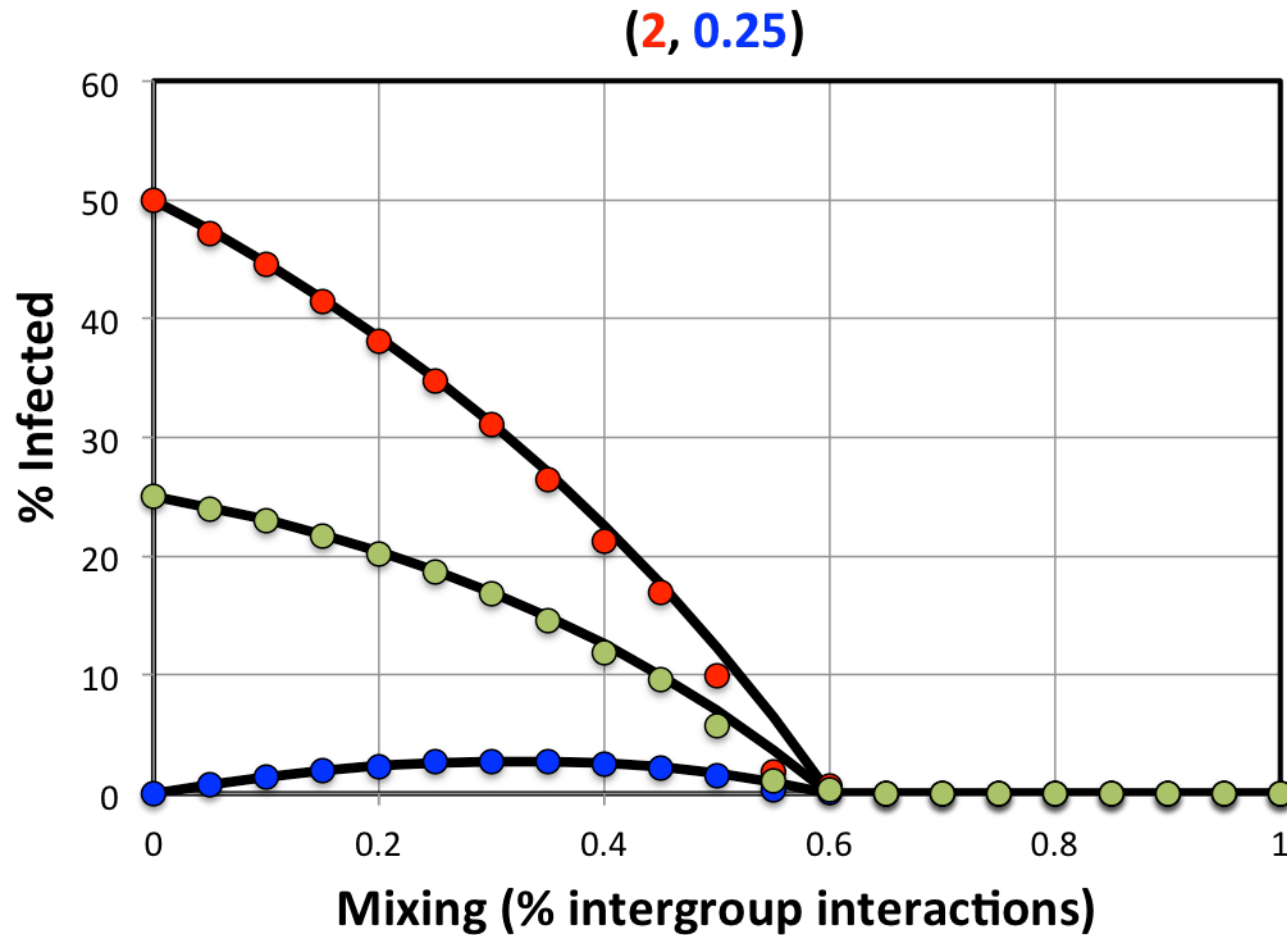
- $P(\text{Not Infected} \rightarrow \text{Infected} \mid \text{paired with infected})$ (v)
- $P(\text{Not Infected} \rightarrow \text{Infected} \mid \text{paired with Not infected})$ (0)
- $P(\text{Infected} \rightarrow \text{Not Infected} \mid \text{paired with infected})$ (δ)
- $P(\text{Infected} \rightarrow \text{Not Infected} \mid \text{paired with Not infected})$ (δ)

■ Heterogeneity in agents' susceptibilities

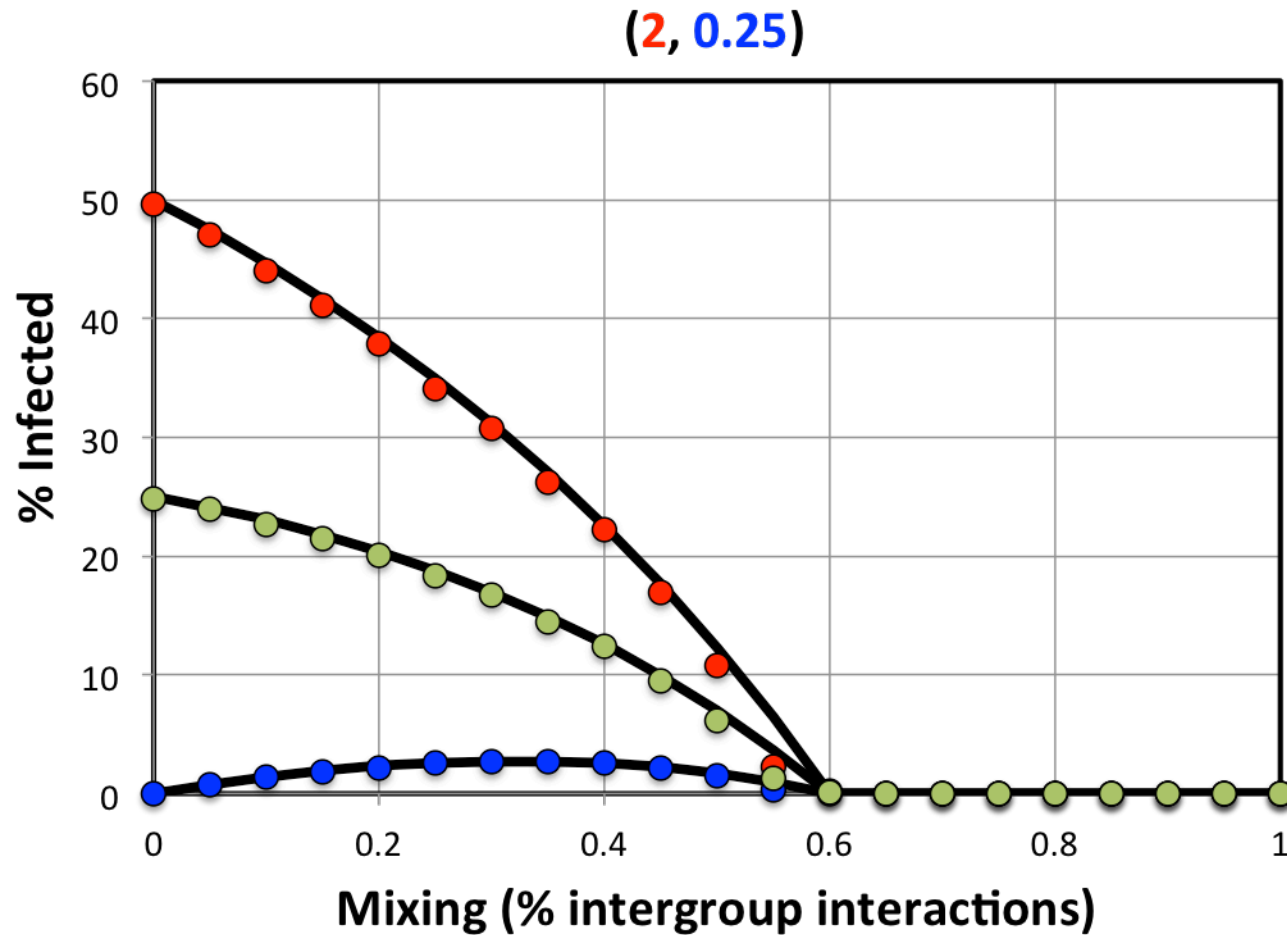
Robustness: variability = 0%



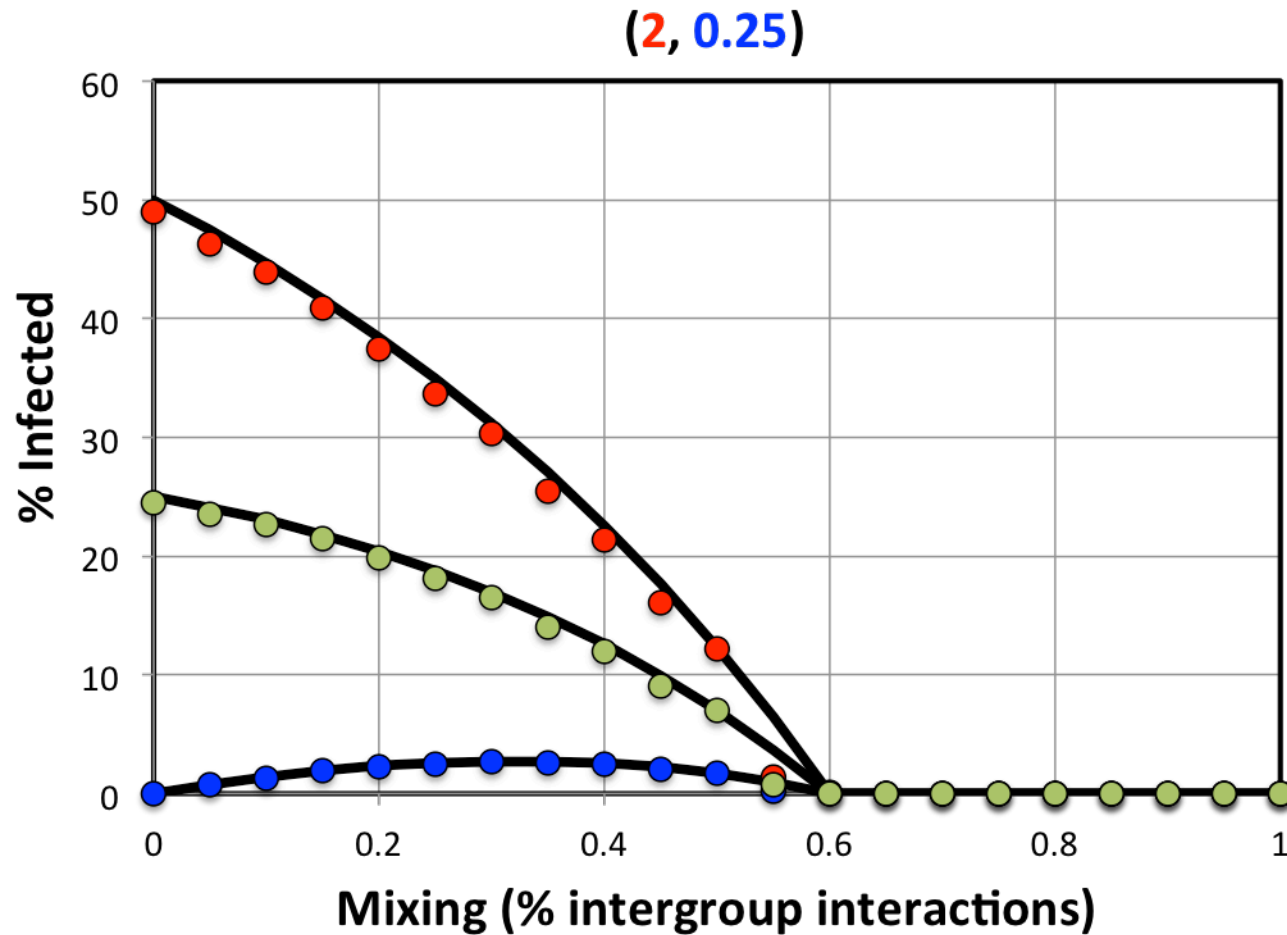
Robustness: variability = 10%



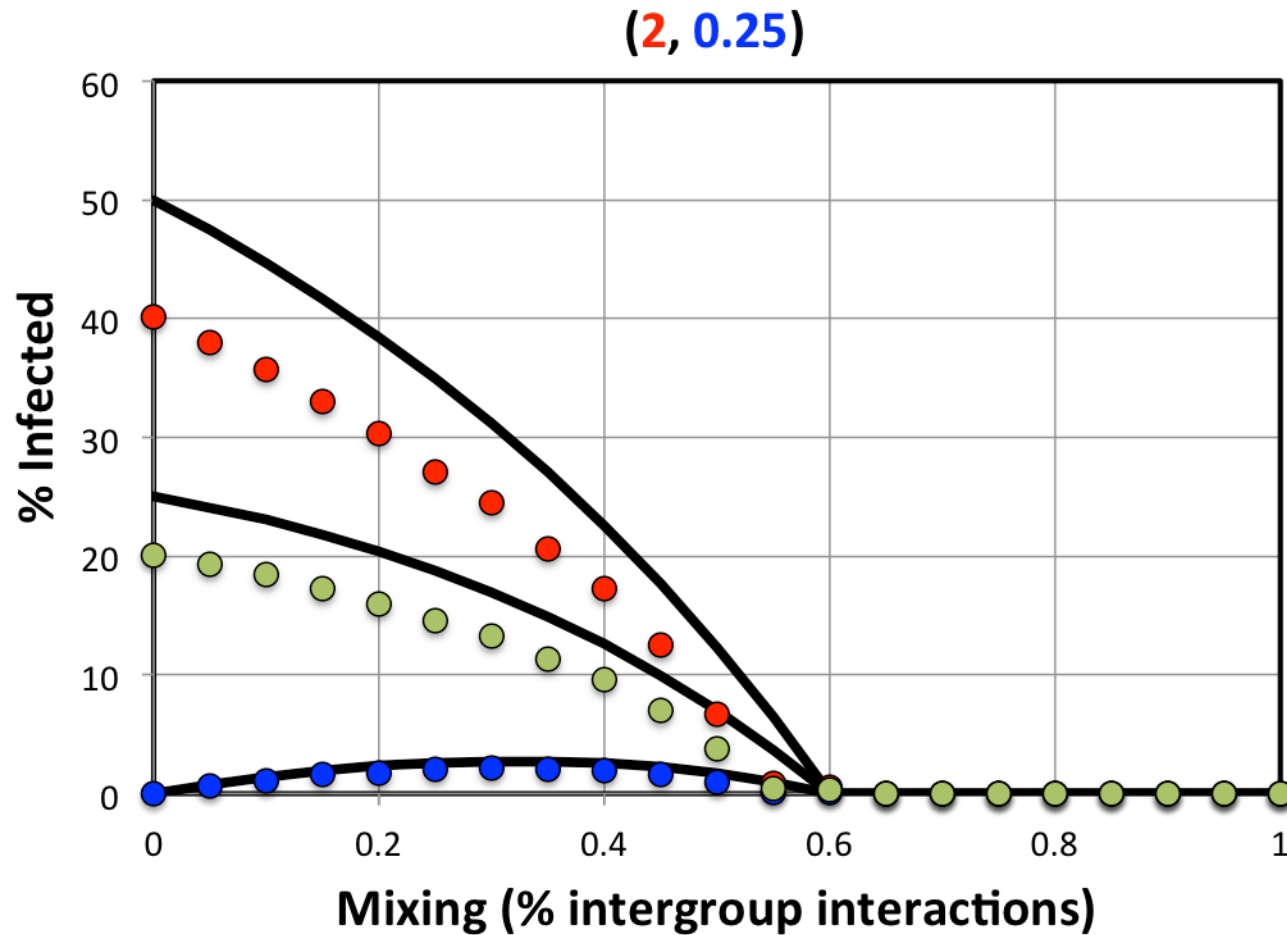
Robustness: variability = 20%



Robustness: variability = 30%



Robustness: variability = 100%



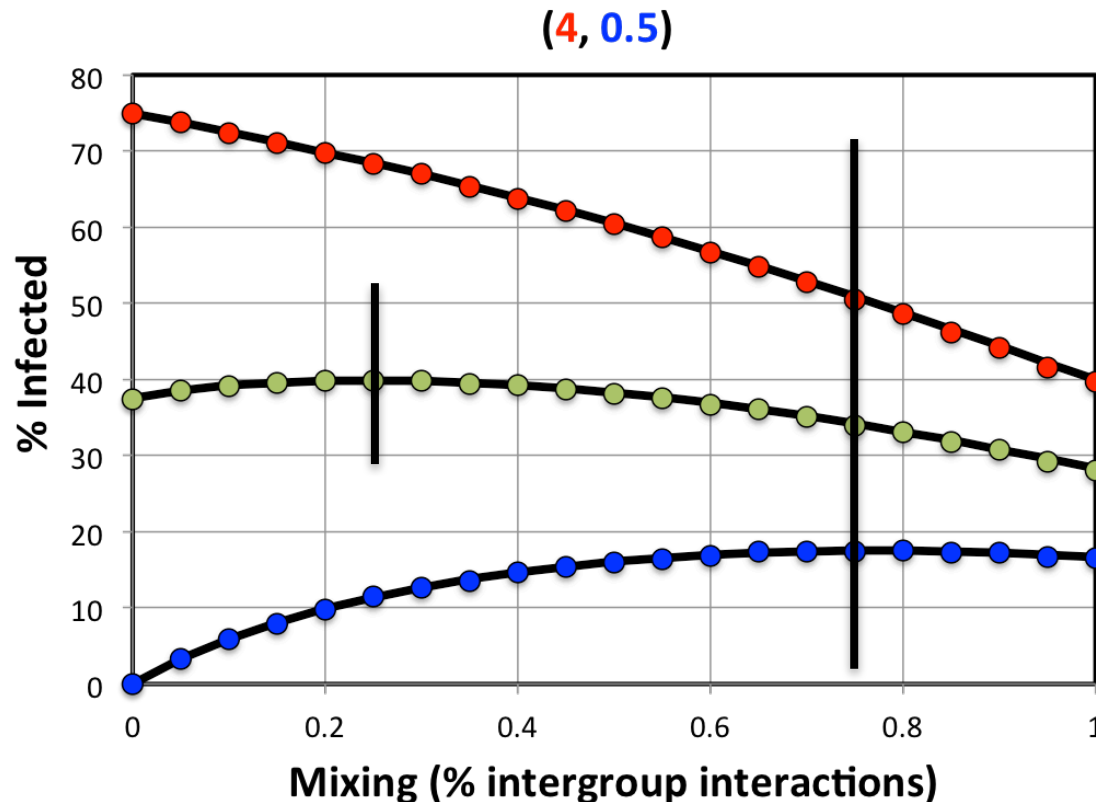


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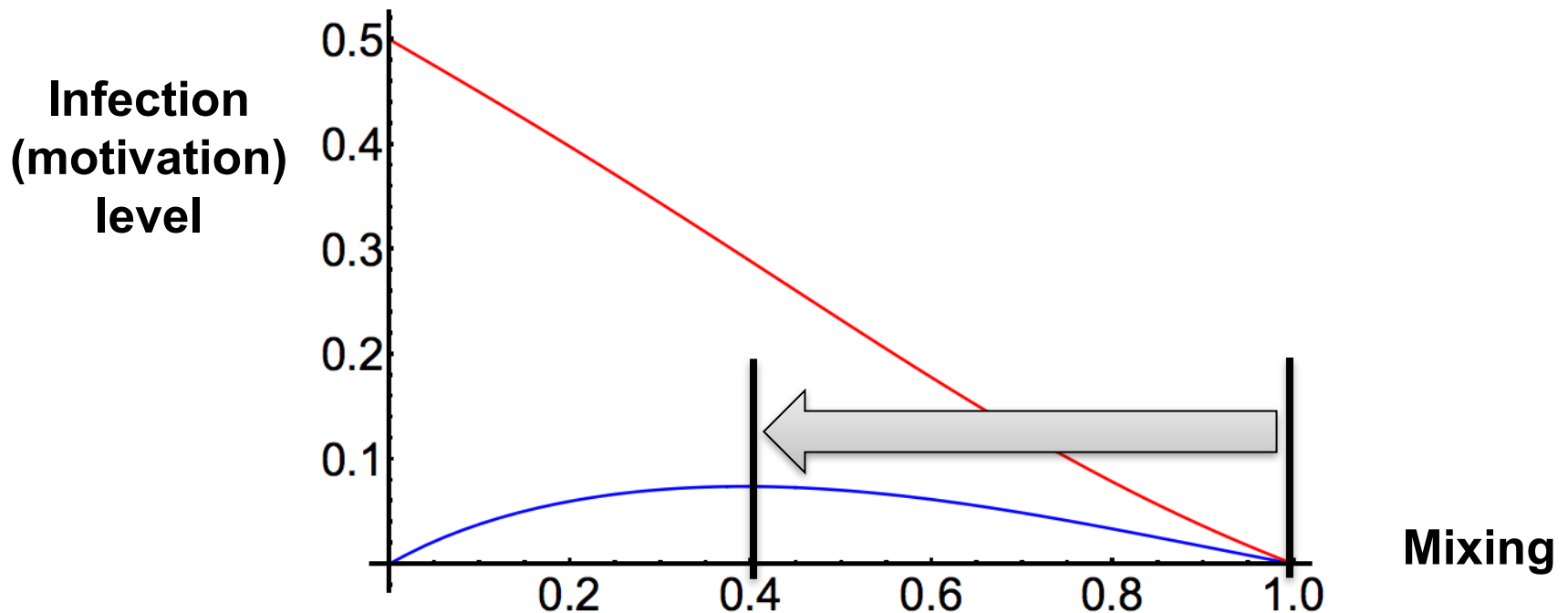
Conclusions

- Overall optimum levels of mixing (or segregation) may not be at the extremes (for the **resistant** group and for the **whole** group). Some levels of segregation are not Pareto optimal.



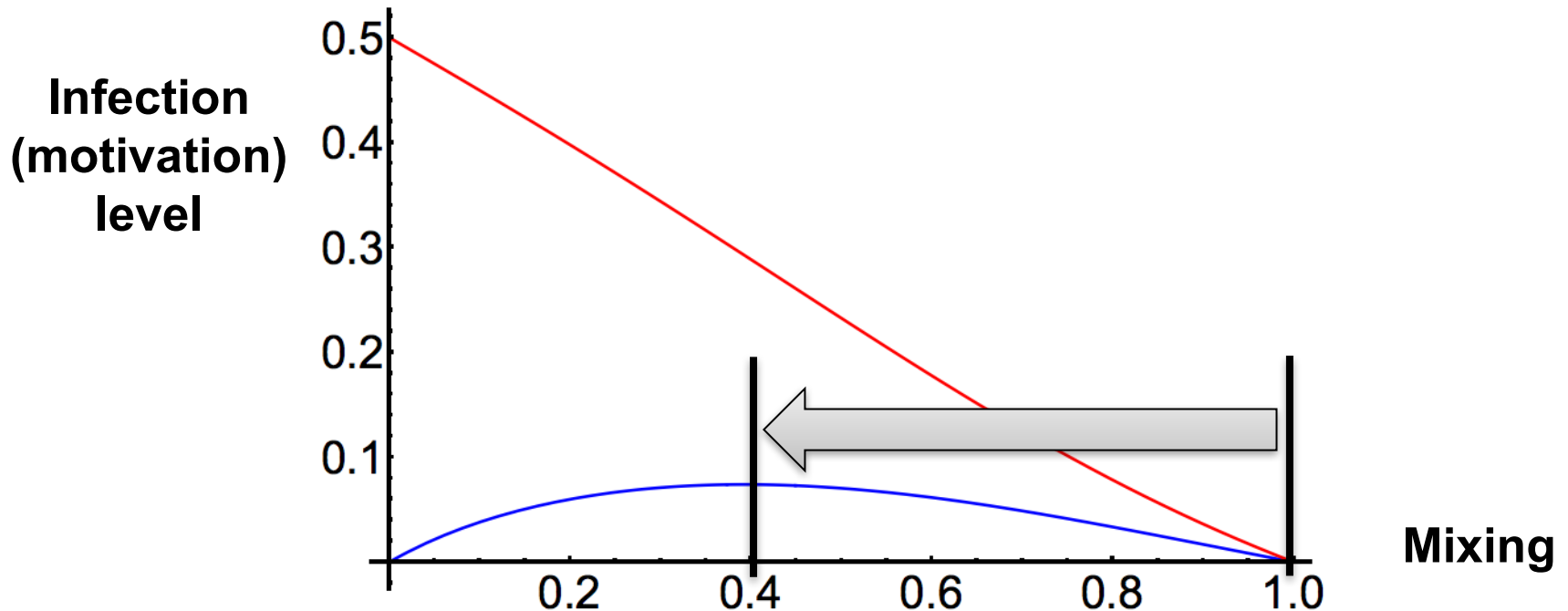
Conclusions

- School case: It may well be in the **harder-to-motivate** group's interest to protect the **easier-to-motivate** group from interacting too much with them.



Conclusions

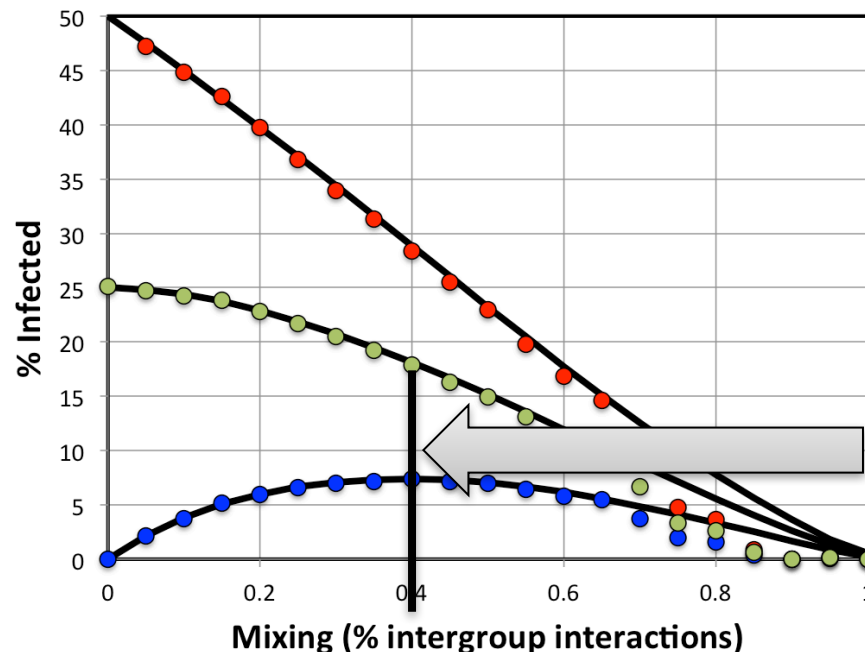
- School case: Policies which assume that, in order to improve the performance of **lower-performance** students, it will always be good to increase their mixing with **higher-performance** students, can be misguided.
Increasing segregation may benefit everyone.



Conclusions

- School case: Policies which assume that, in order to improve the performance of **lower-performance** students, it will always be good to increase their mixing with **higher-performance** students, can be misguided.
Increasing segregation may benefit everyone.

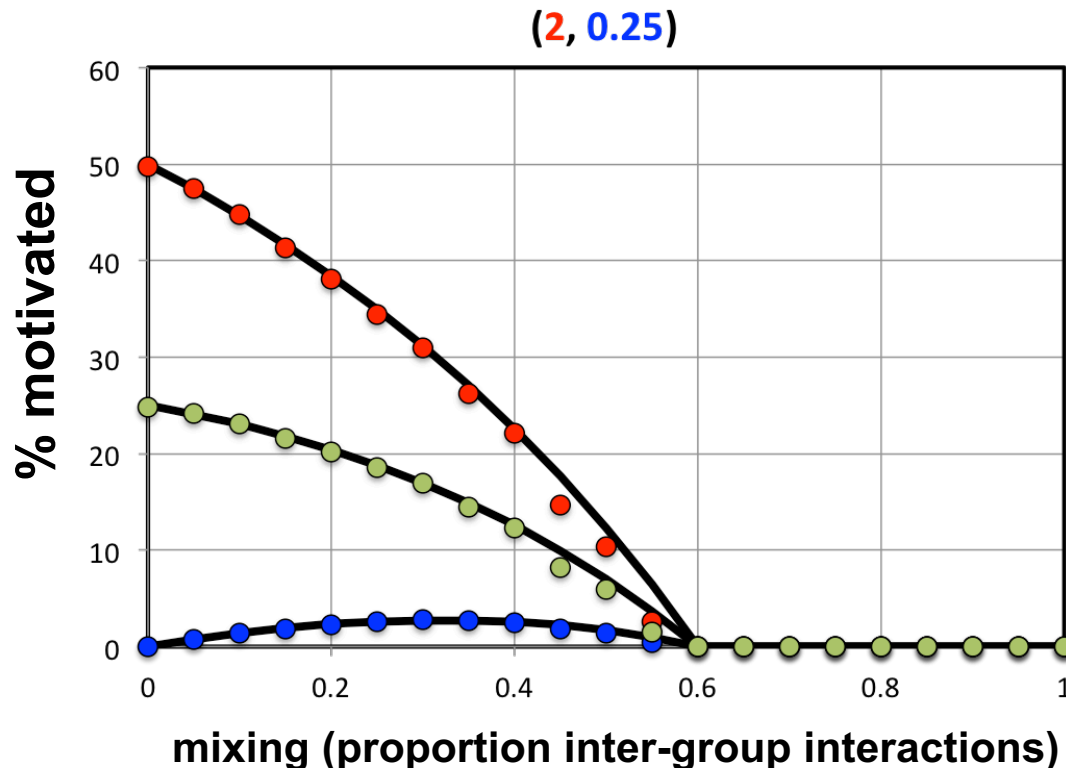
Infection
(motivation)
level



Mixing

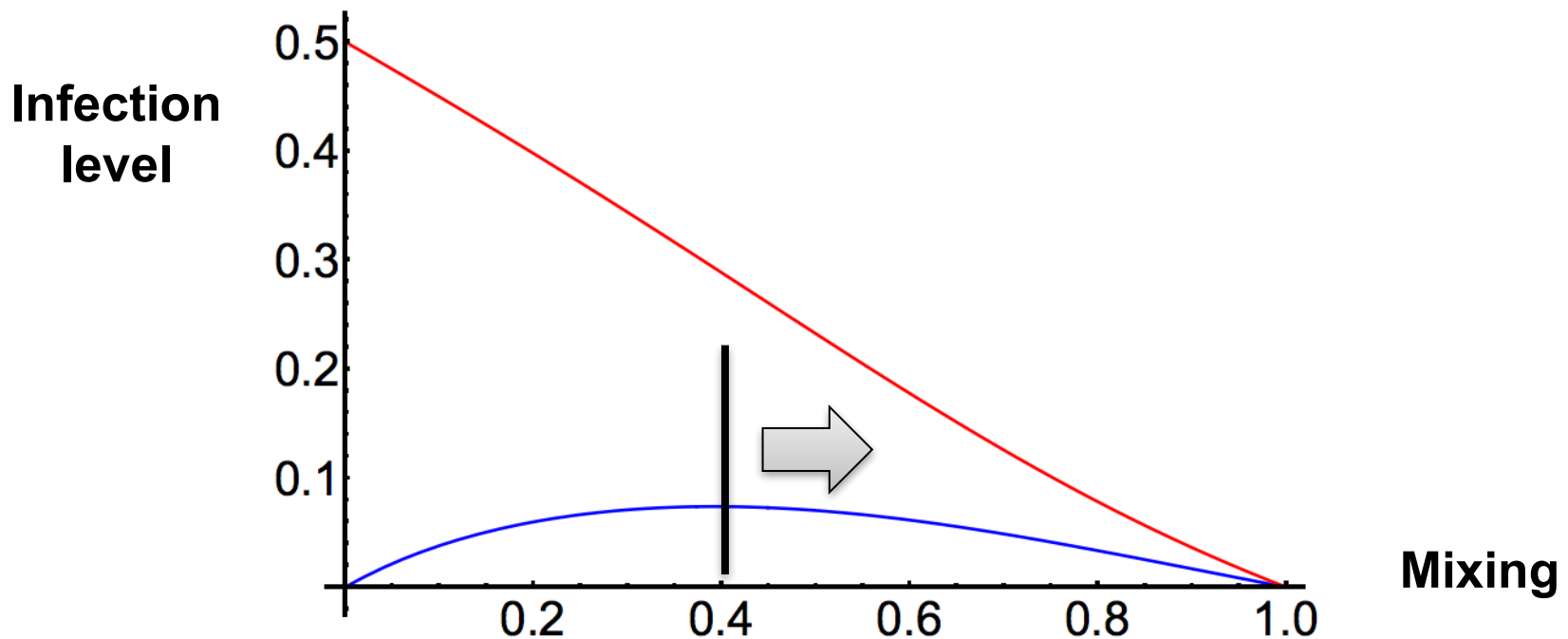
Conclusions

- School case: In extreme cases, the **harder-to-motivate** group may “kill” everyone’s motivation if they interact too much with the **easier-to-motivate** group.



Conclusions

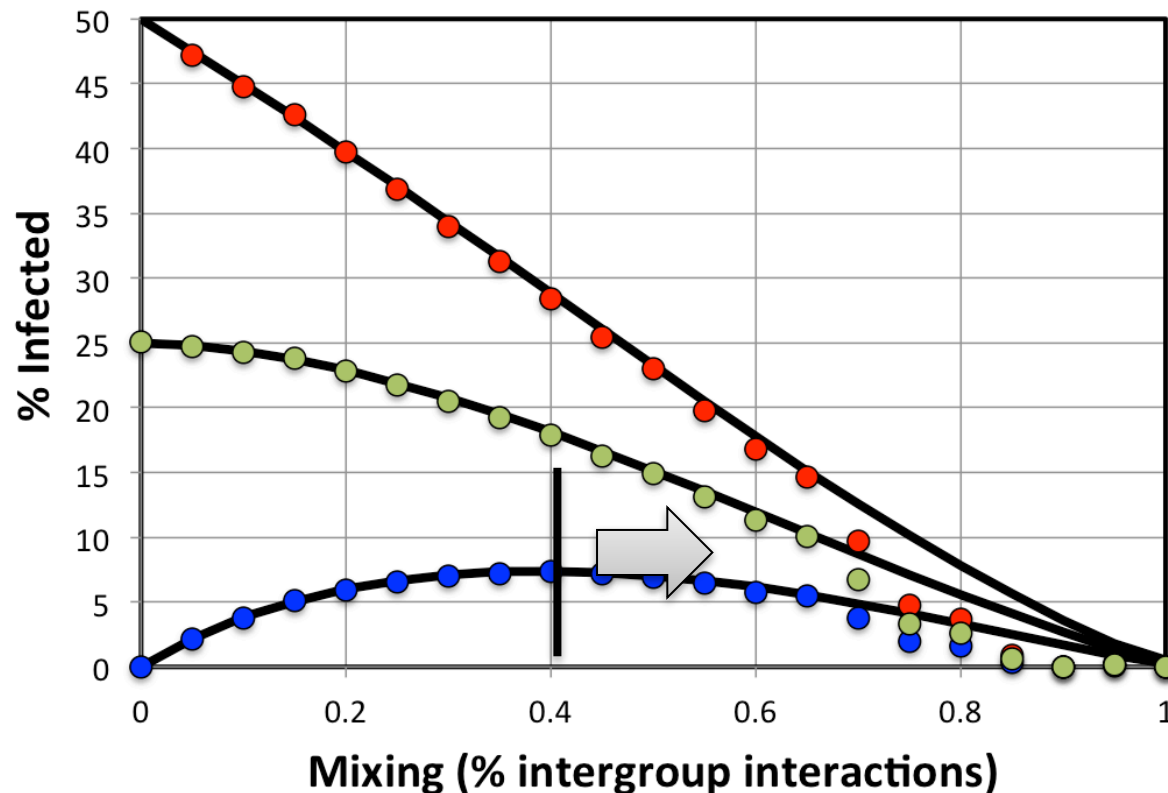
- Disease case: Increasing your mixing with a **group that has a greater level of infection** than you can be beneficial for **you** (and, naturally, for them).

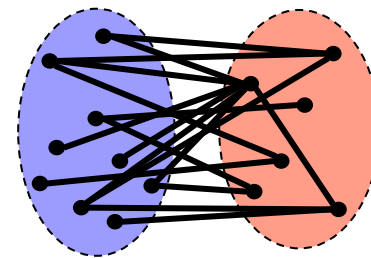
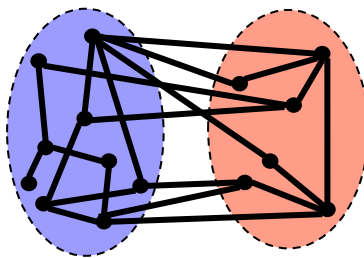
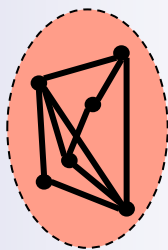
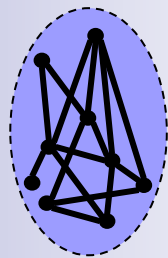


Conclusions

- Disease case: Increasing your mixing with a group that has a greater level of infection than you can be beneficial for you (and, naturally, for them).

(2, 0.5)





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- *Desirable and undesirable levels of segregation between groups*

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