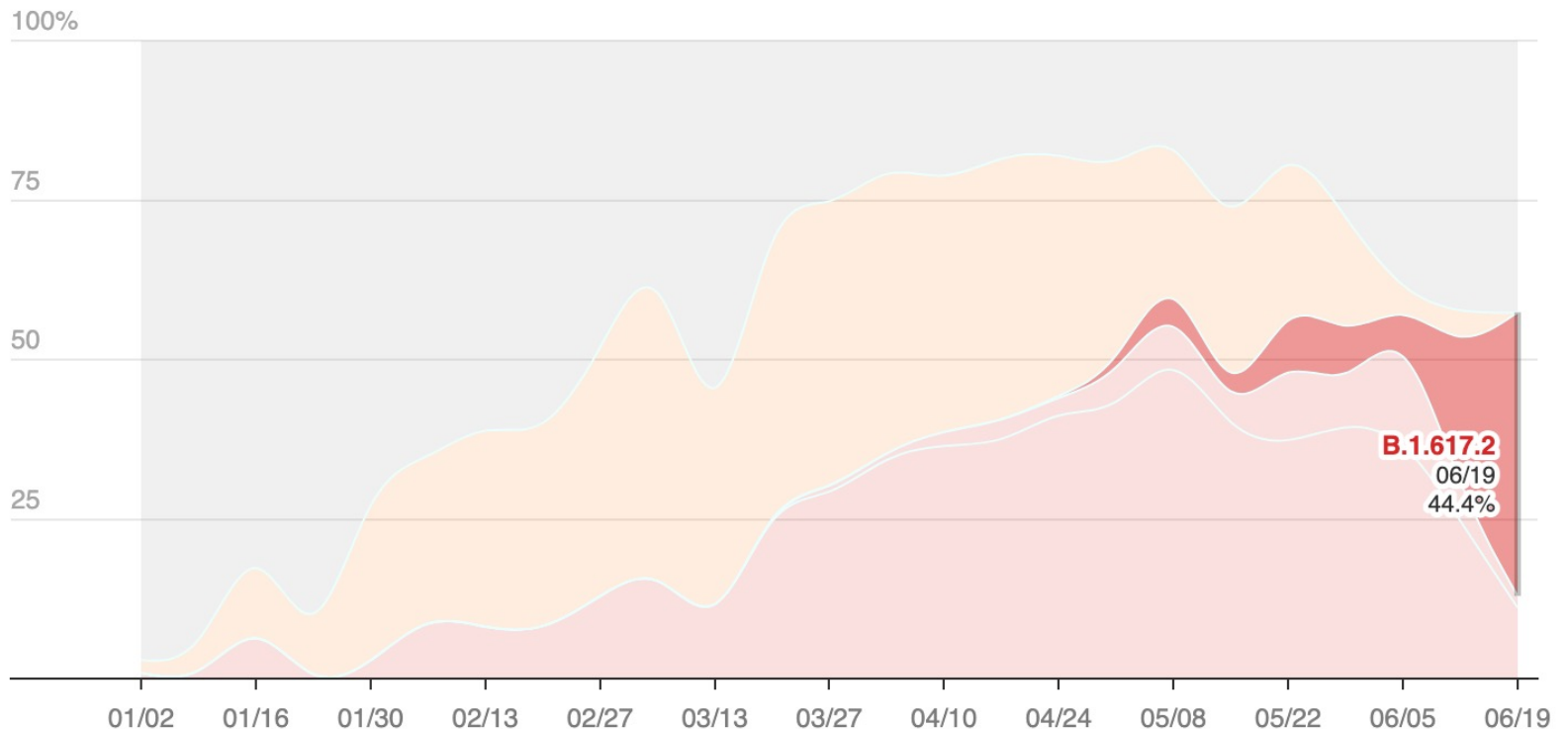


# Weakly coupled SIR models (840 groups of 10,000 people)



*NYC viral sequencing data showing a slow initial onset of the delta variant (B.1.617.2)*

# Implications of vaccine inhomogeneity

The goal of this simulation is to identify effects of vaccination inhomogeneity on the way a COVID-19 epidemic plays out. Rather than modeling a single population, I've split a population the size of New York City (8.4M) into chunks of 10,000, similar to a Manhattan zip code. These subpopulations have Gaussian-distributed  $R_0$  values and vaccination rates. Transmission is probabilistic (Poisson distributed).

## **What is in these slides?**

These slides show modeling results for three scenarios: (1) a conventional homogeneous scenario; (2) an inhomogeneous scenario with a modest inter-group infection rate; (3) an inhomogeneous scenario with weak inter-group infection. Model parameters are listed on the individual slides.

## **What is a SIR model?**

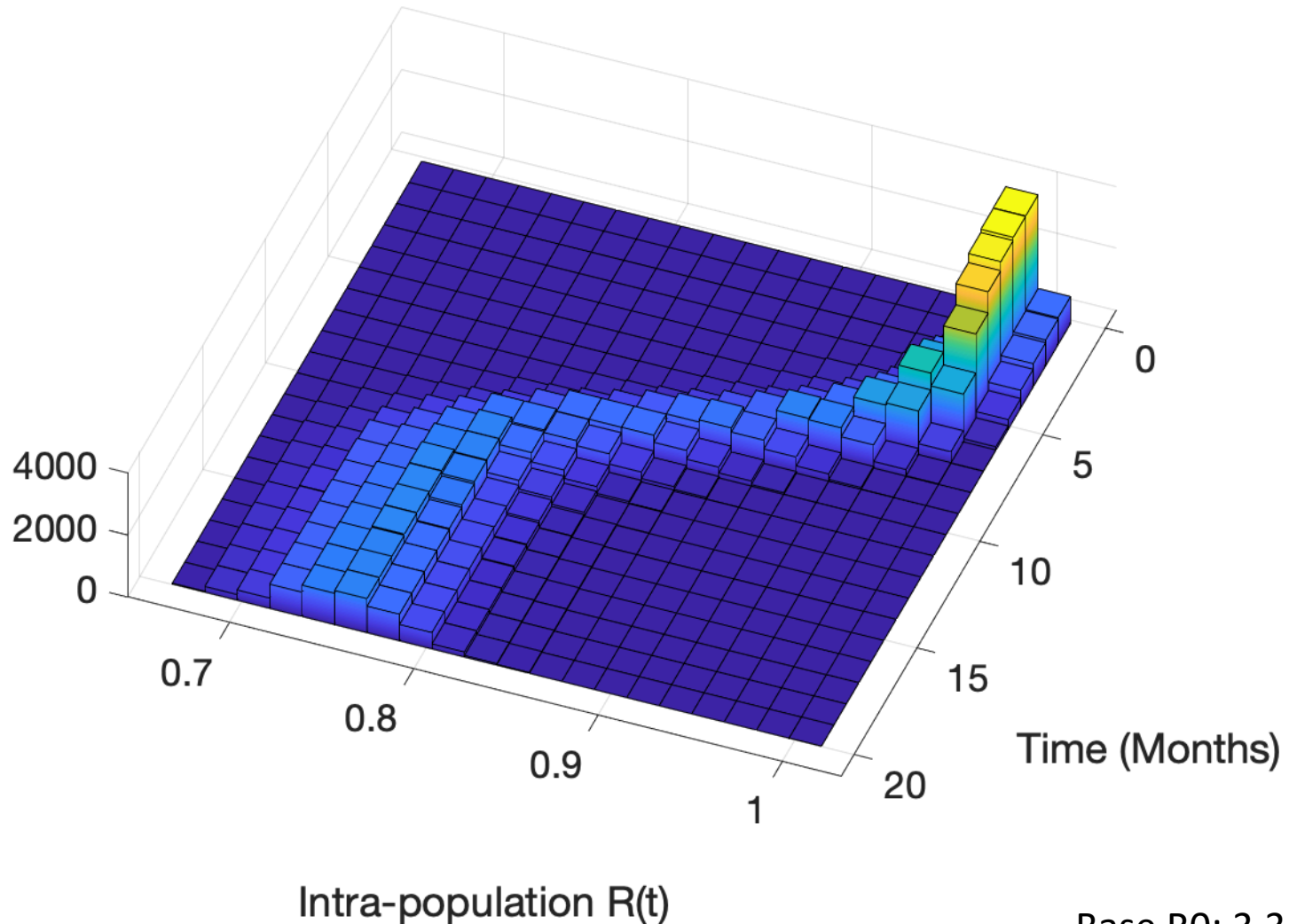
SIR models break the population into chunks that are susceptible, infected, and recovered (immune) to a disease. Plugging in the the basic reproductive number ( $R_0$ ) and generational time constants results in a simple system of coupled differential equations that can be solved numerically.

# Takeaways of the model (aka tl;dr)

1. Inhomogeneity yields an initially rising trend for the reproductive number ( $R(t)$ ), whereas  $R(t)$  goes down monotonically for a traditional SIR model. This represents the time it takes for the virus to find sensitive sub-populations and is roughly analogous to the phenomenon of superdiffusion in biophysics.
2. Inhomogeneity can boost the total number of cases by yielding higher peak case numbers. (a 'hotter burn')
3. When inhomogeneous groups are weakly coupled, one gets:
  - A longer, bumpy onset, containing preliminary epidemics that seed the disease into the broader population
  - A drawn-out recovery period, because weak inter-group coupling causes groups with  $R \sim 1$  to not fully 'burn out' with the primary outbreak).

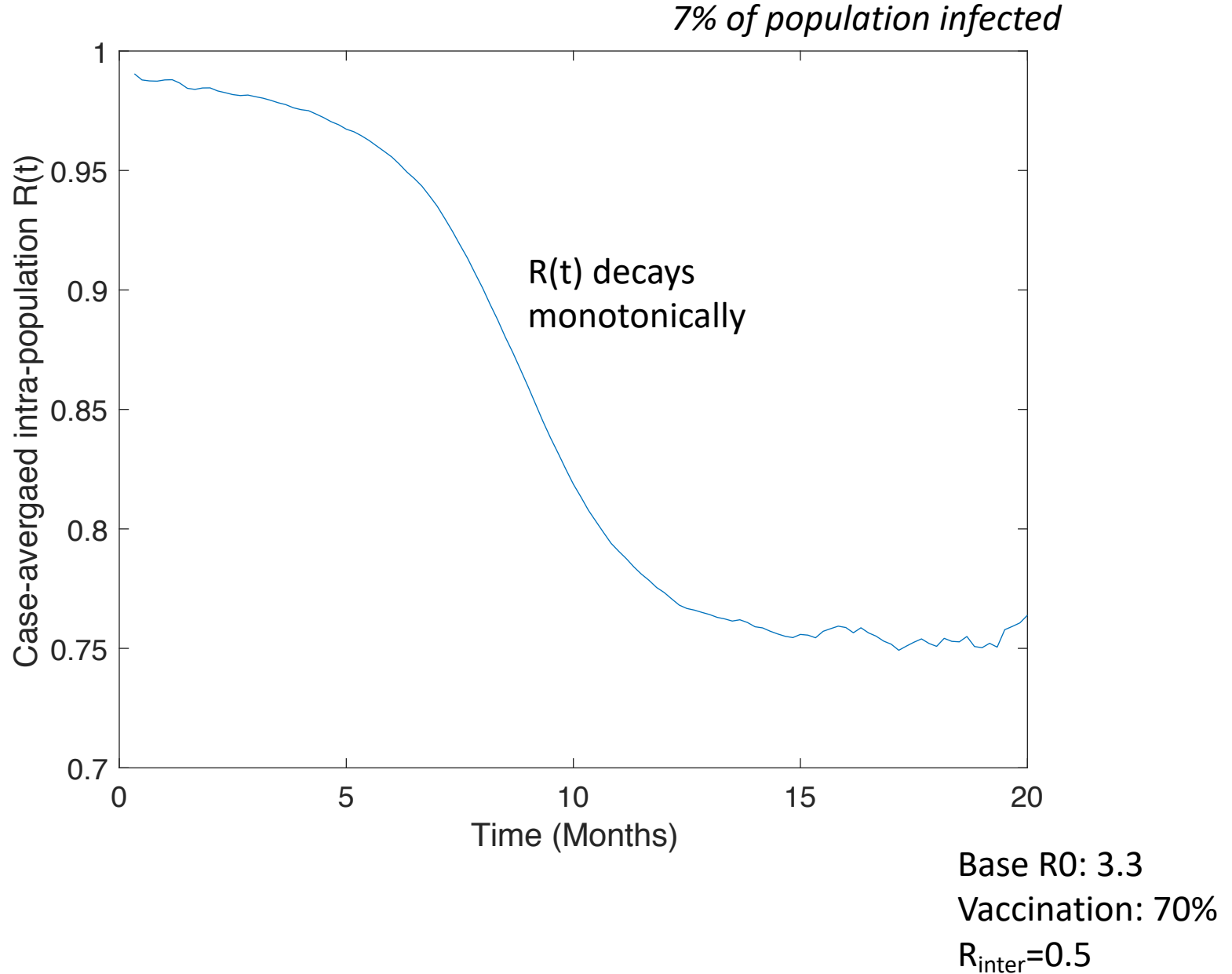
# Scenario 1: homogeneous vaccination and R (standard SIR model)

*7% of population infected*

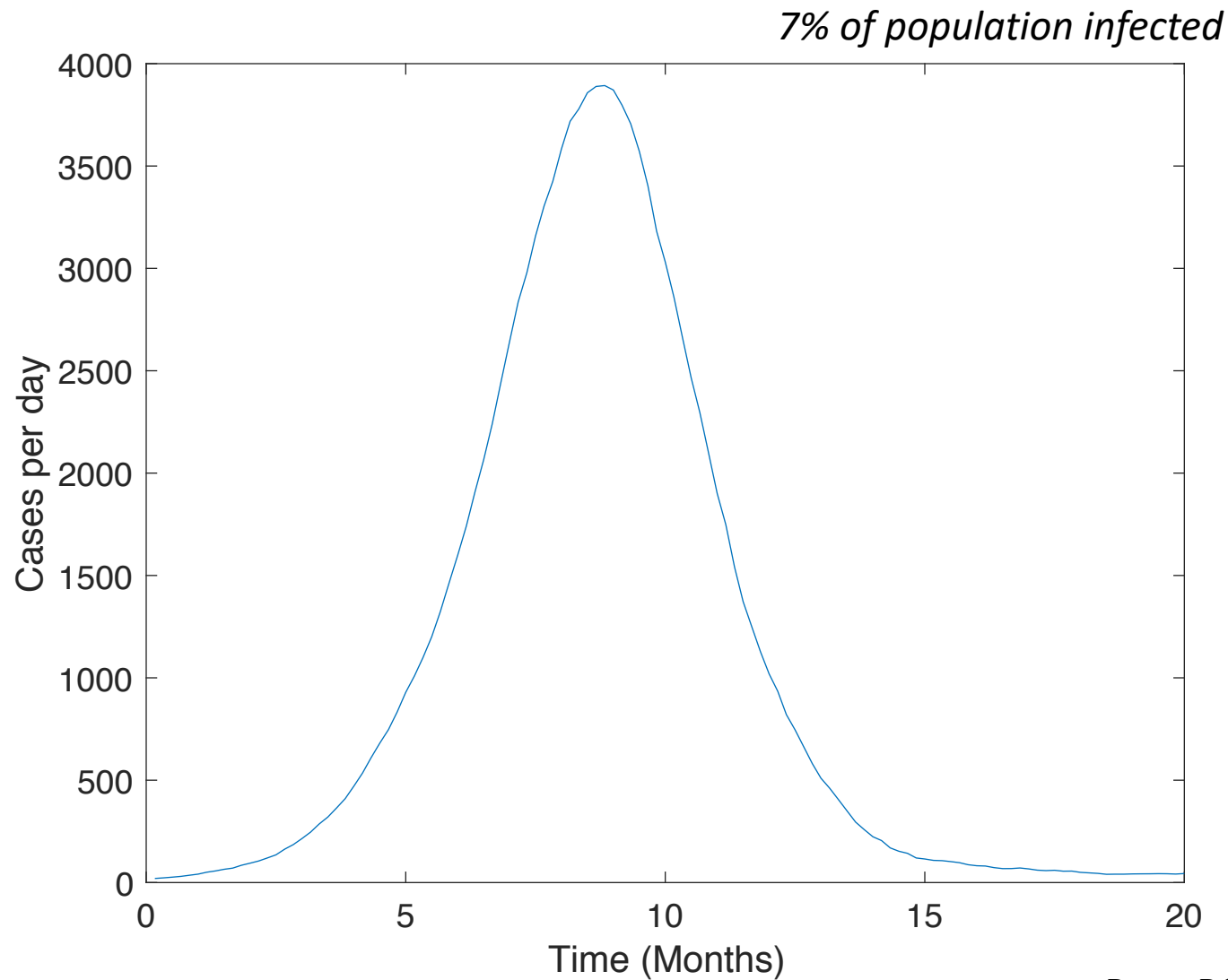


Base  $R_0$ : 3.3  
Vaccination: 70%  
 $R_{\text{inter}}=0.5$

# Scenario 1: homogeneous vaccination and R (standard SIR model)



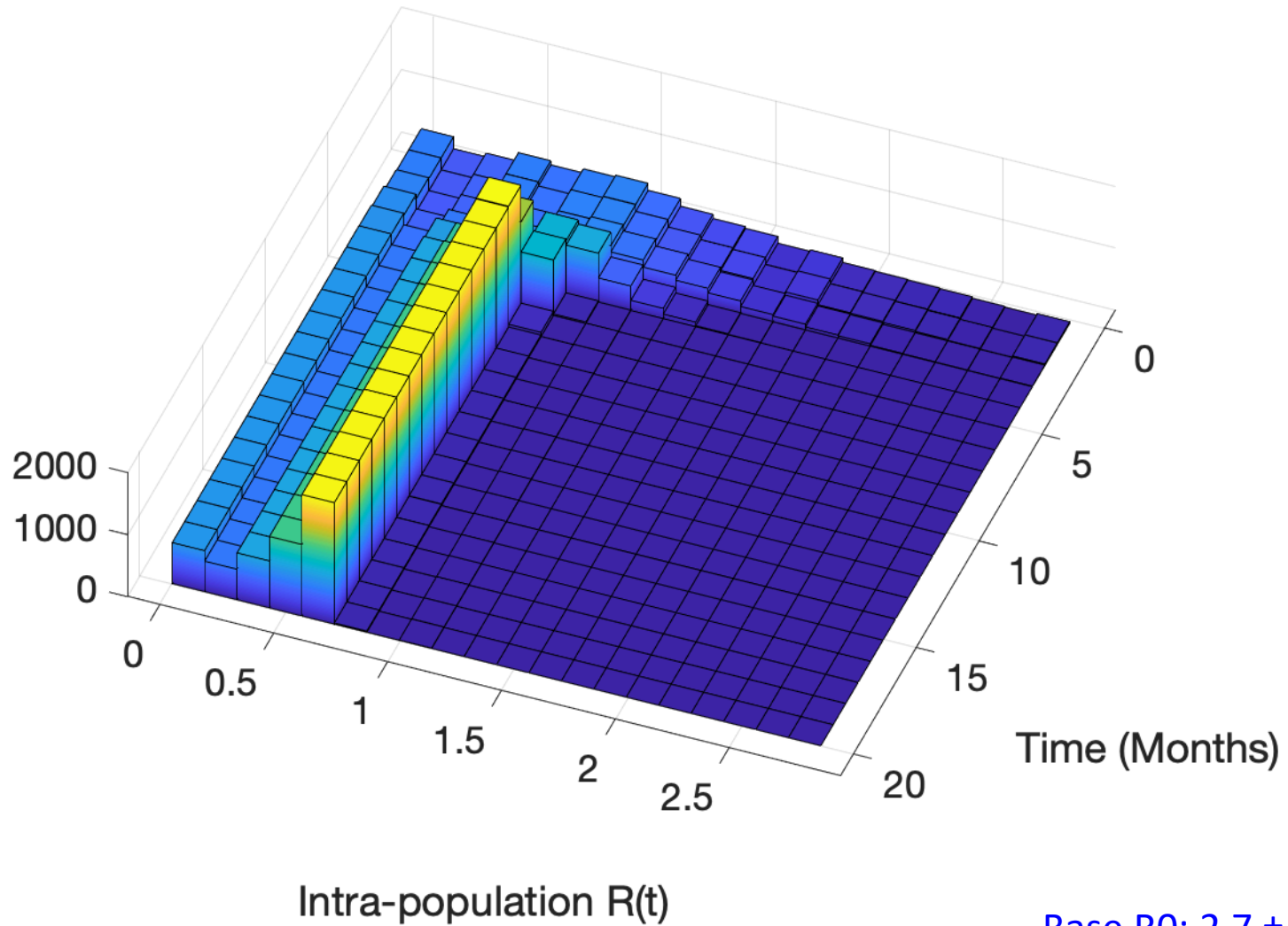
# Scenario 1: homogeneous vaccination and R (standard SIR model)



Base  $R_0$ : 3.3  
Vaccination: 70%  
 $R_{\text{inter}}=0.5$

## Scenario 2: inhomogeneous vaccination and R, modest inter-group R

*13% of population infected*

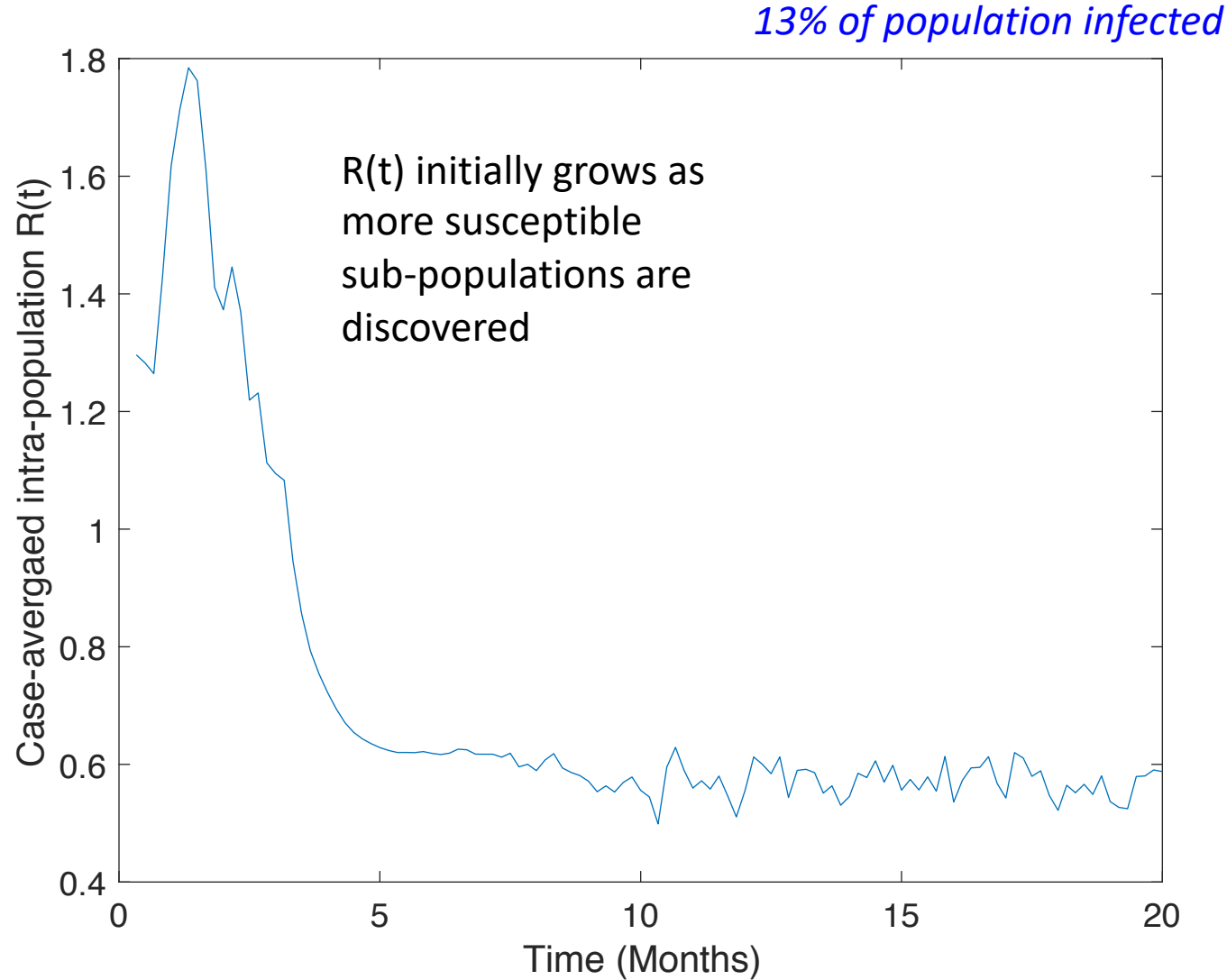


Base  $R_0$ :  $2.7 \pm 0.7$

Vaccination:  $70\% \pm 20\%$

$R_{\text{inter}}=0.5$

## Scenario 2: inhomogeneous vaccination and $R$ , modest inter-group $R$



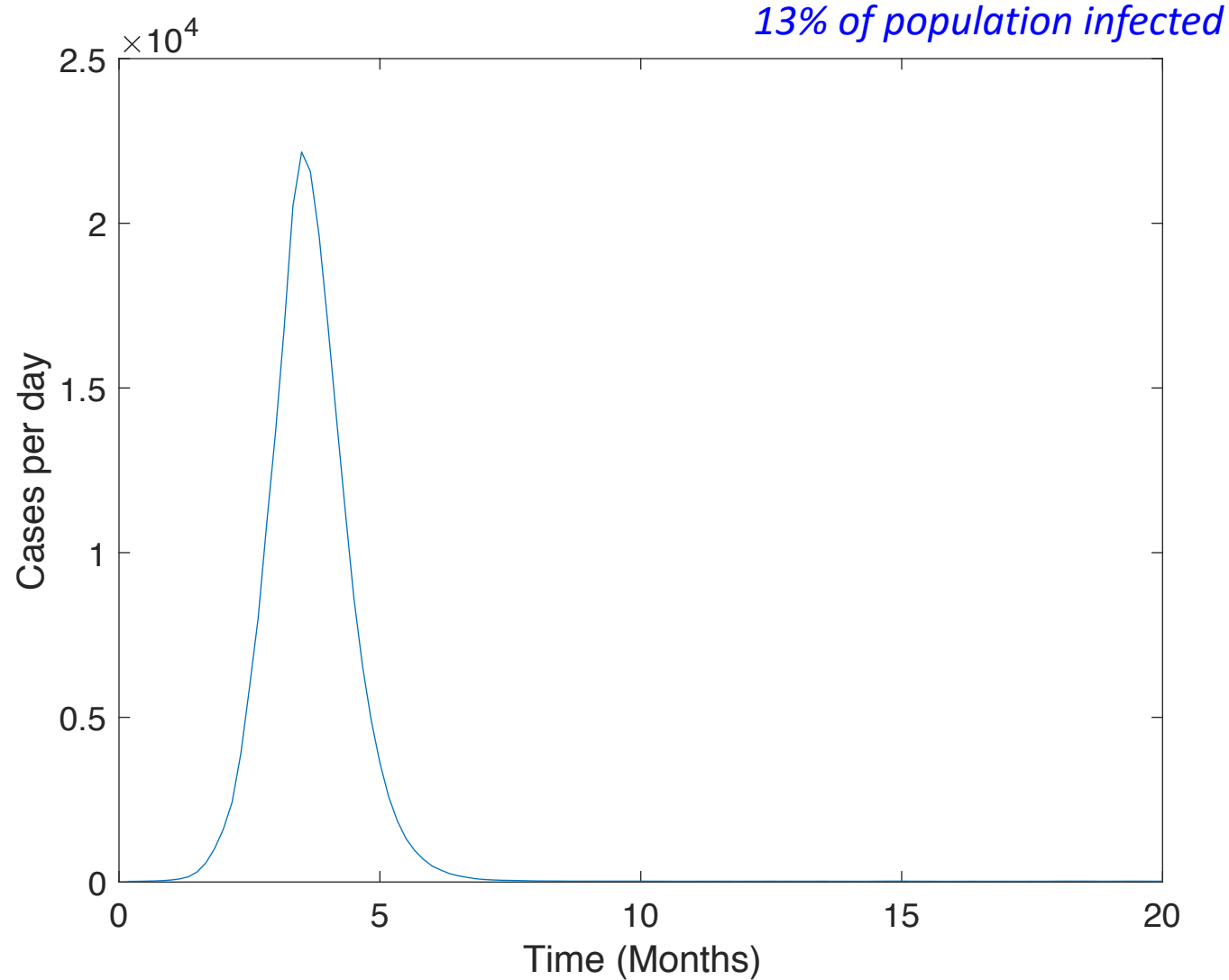
Base  $R_0$ :  $2.7 \pm 0.7$

Vaccination:  $70\% \pm 20\%$

$R_{\text{inter}}=0.5$



## Scenario 2: inhomogeneous vaccination and R, modest inter-group R



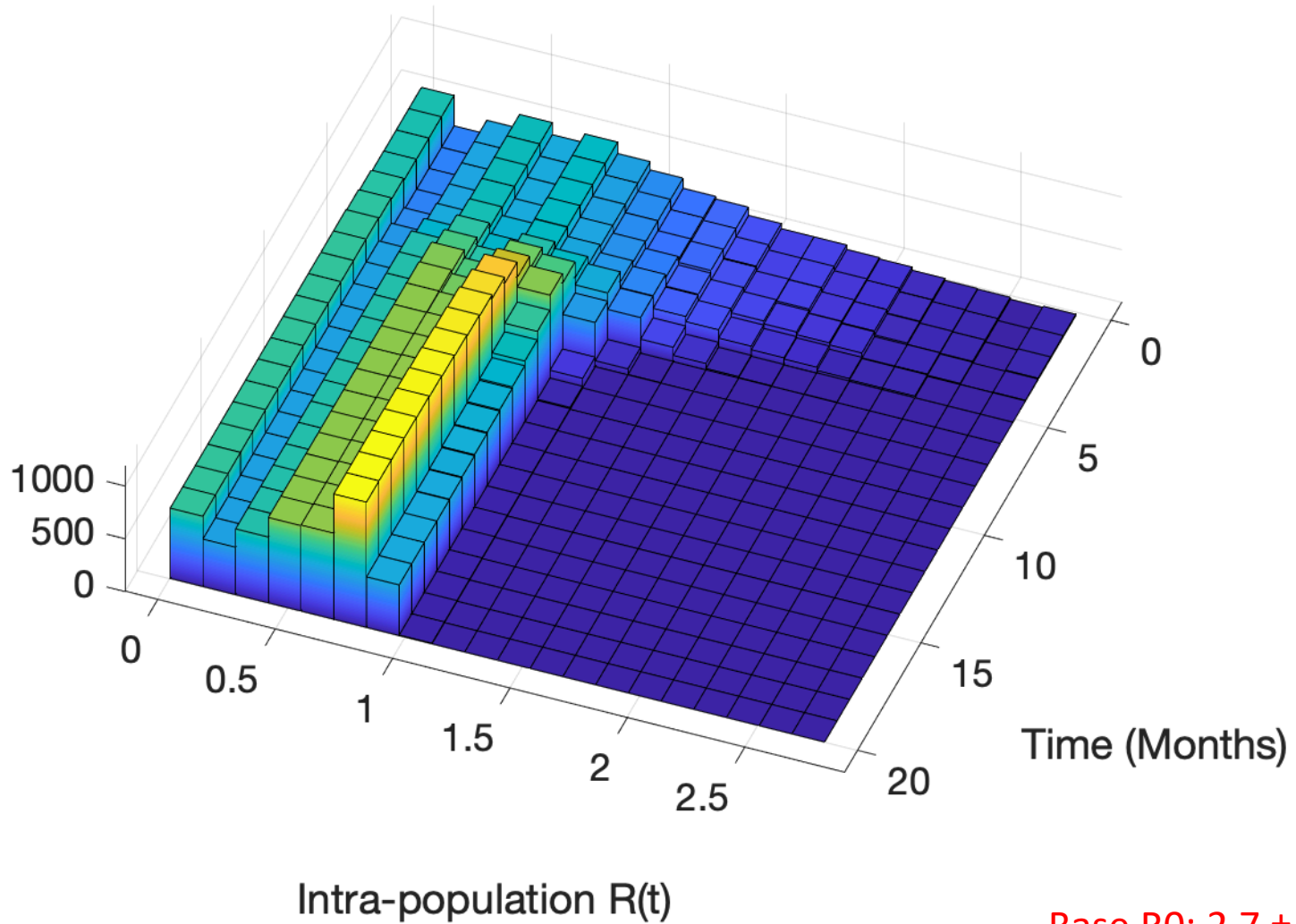
Base  $R_0$ :  $2.7 \pm 0.7$

Vaccination:  $70\% \pm 20\%$

$R_{\text{inter}}=0.5$

# Scenario 3: inhomogeneous vaccination and R, weak inter-group R

*9% of population infected*

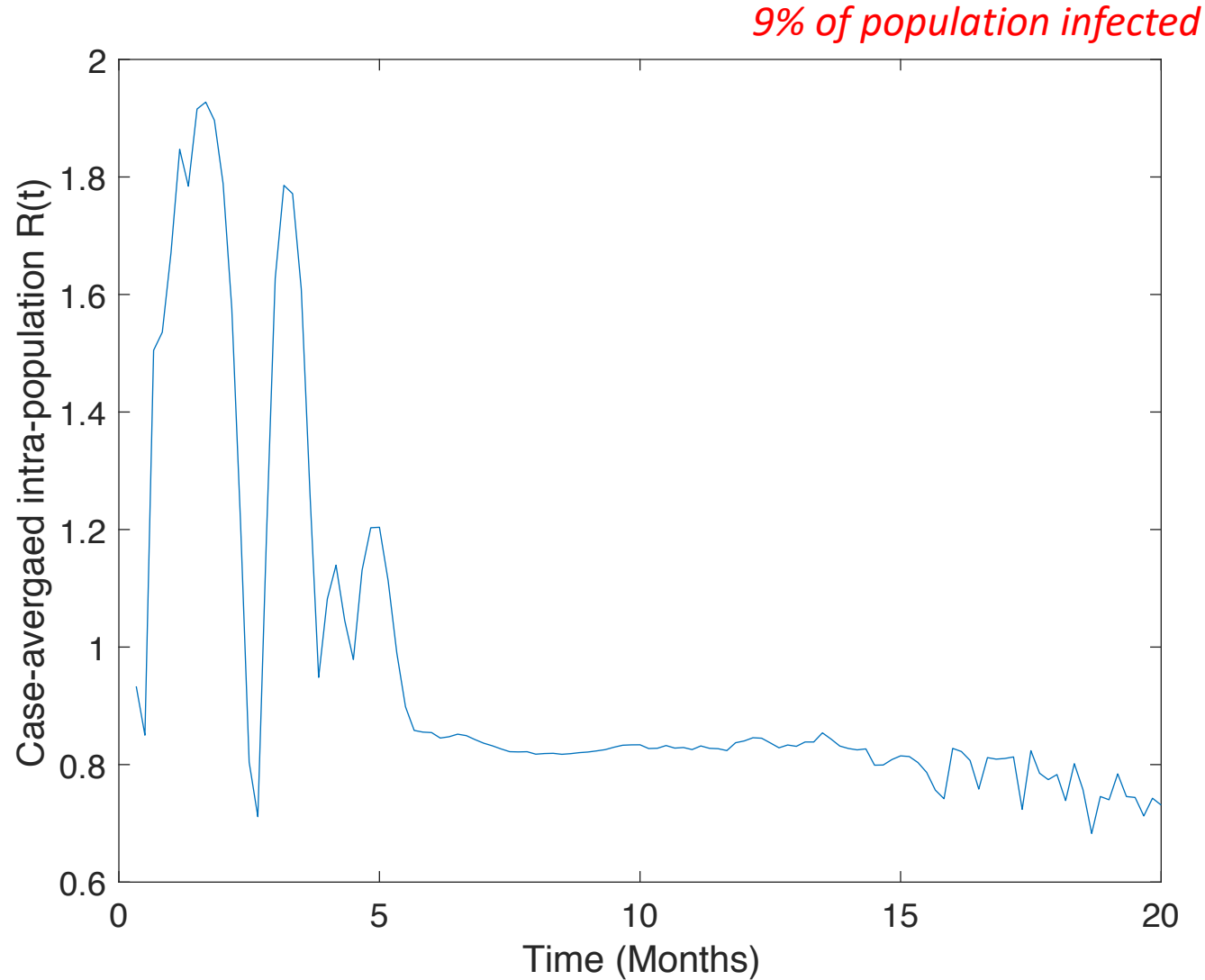


Base  $R_0$ :  $2.7 \pm 0.7$

Vaccination:  $70\% \pm 20\%$

$R_{\text{inter}}=0.1$

## Scenario 3: inhomogeneous vaccination and R, weak inter-group R

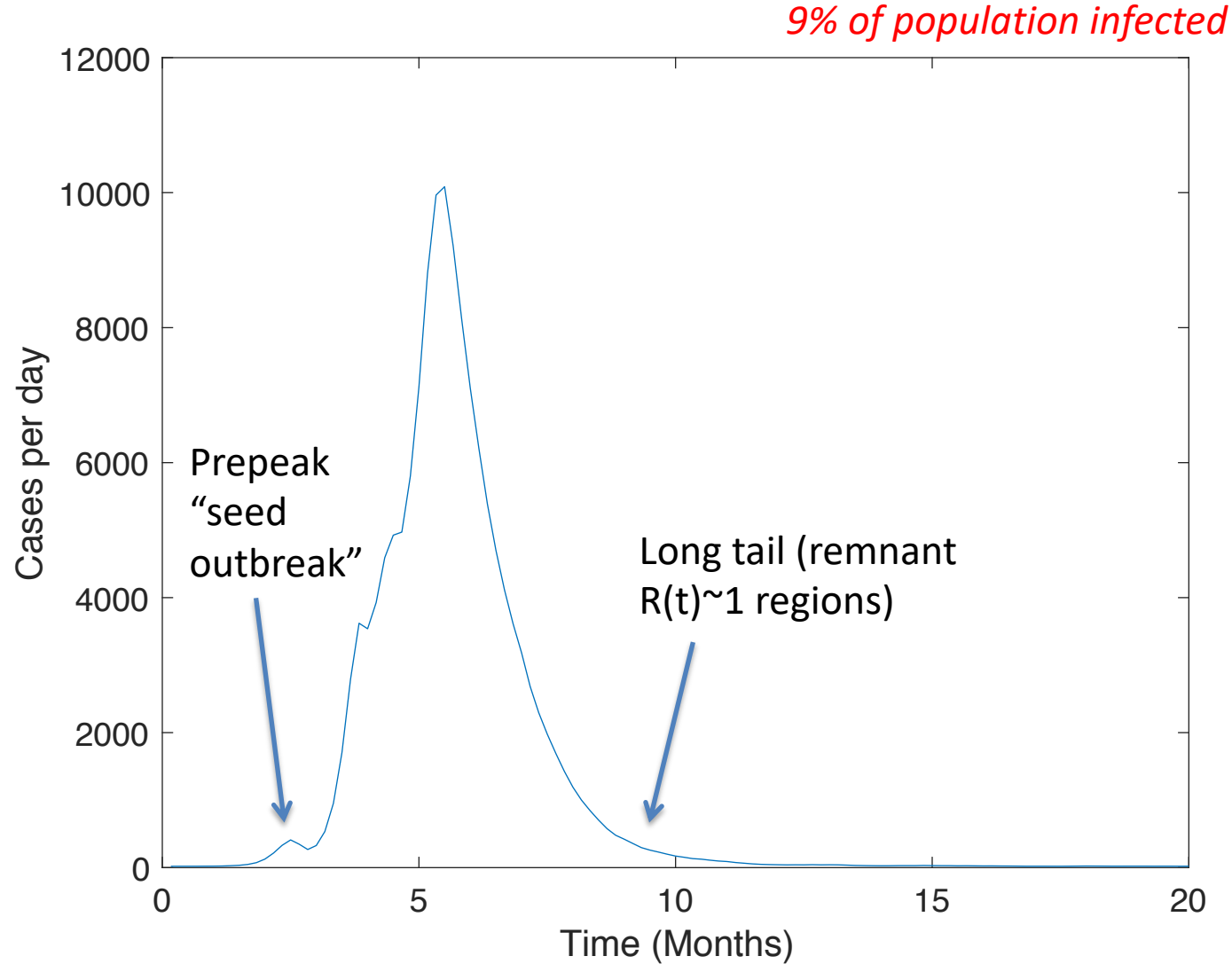


Base  $R_0$ :  $2.7 \pm 0.7$

Vaccination:  $70\% \pm 20\%$

$R_{\text{inter}}=0.1$

## Scenario 3: inhomogeneous vaccination and $R$ , weak inter-group $R$



Base  $R_0$ :  $2.7 \pm 0.7$

Vaccination:  $70\% \pm 20\%$

$R_{\text{inter}}=0.1$

# Takeaways (again)

1. Inhomogeneity yields an initially rising trend for the reproductive number ( $R(t)$ ), whereas  $R(t)$  goes down monotonically for a traditional SIR model. This represents the time it takes for the virus to find sensitive sub-populations and is roughly analogous to the phenomenon of superdiffusion in biophysics.
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3. When inhomogeneous groups are weakly coupled, one gets:
  - A longer, bumpy onset, containing preliminary epidemics that seed the disease into the broader population
  - A drawn-out recovery period, because weak inter-group coupling causes groups with  $R \sim 1$  to not fully 'burn out' with the primary outbreak).

# Caveats

1. The size of the subpopulation bins is inspired by the size of nearby NYC zip codes but is fundamentally arbitrary. The model should be sensitive to the log of this parameter.
2. The length of a viral generation is set to 5 days in this model, based on papers early in the pandemic, but may be around 3 days for the delta variant. For COVID, the effective  $R_0$  value and generation time are both significantly influenced by public policy.
3. The upper Gaussian tail of the vaccination rate is cut off at 100%, leading to a 7% reduction in the mean vaccination rate for Scenarios #2-3. This is more than compensated for by the 16% lower mean  $R$  value in Scenarios 2-3 relative to Scenario #1.
4. These results were generated over a couple of days in June, 2021. This is an extremely quick dip into a large parameter space.