

# SISMID 2021: Mathematical Models of Infectious Disease

Day 2: Breakout Session on Heterogeneity and Herd Immunity

# Population heterogeneity by age influences the herd immunity threshold

Science

REPORTS

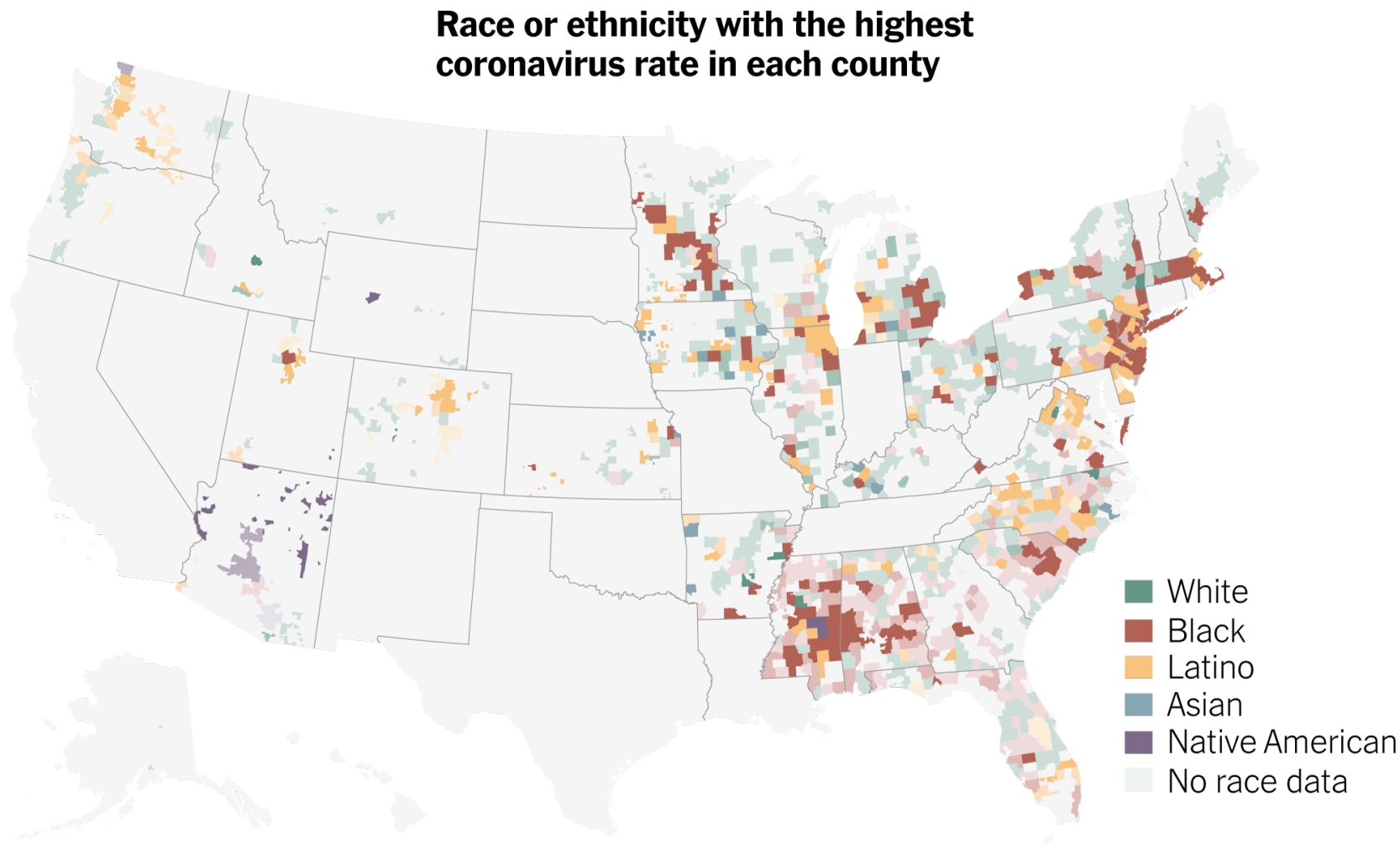
Cite as: T. Britton *et al.*, *Science* 10.1126/science.abc6810 (2020).

## A mathematical model reveals the influence of population heterogeneity on herd immunity to SARS-CoV-2

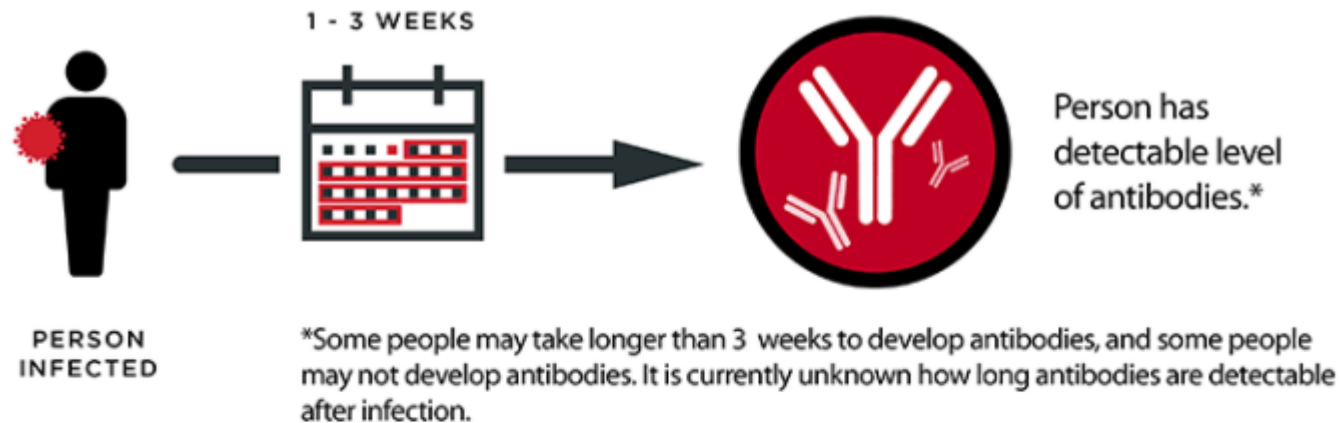
Tom Britton<sup>1\*</sup>, Frank Ball<sup>2</sup>, Pieter Trapman<sup>1</sup>

Population structure	$R_0 = 2.0$		$R_0 = 2.5$		$R_0 = 3.0$	
	$h_D$	$h_C$	$h_D$	$h_C$	$h_D$	$h_C$
Homogeneous	50.0	50.0	60.0	60.0	66.7	66.7
Age structure	46.0	50.0	55.8	60.0	62.5	66.7
Activity structure	37.7	50.0	46.3	60.0	52.5	66.7
Age and activity structure	34.6	50.0	43.0	60.0	49.1	66.7

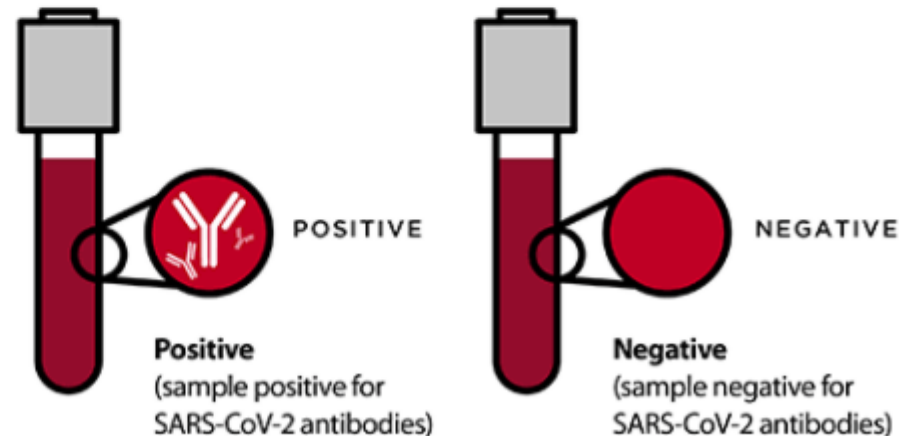
# Racial and ethnic disparities in COVID-19 incidence in the US



# Seroprevalence surveys allow us to estimate cumulative incidence of infection\*



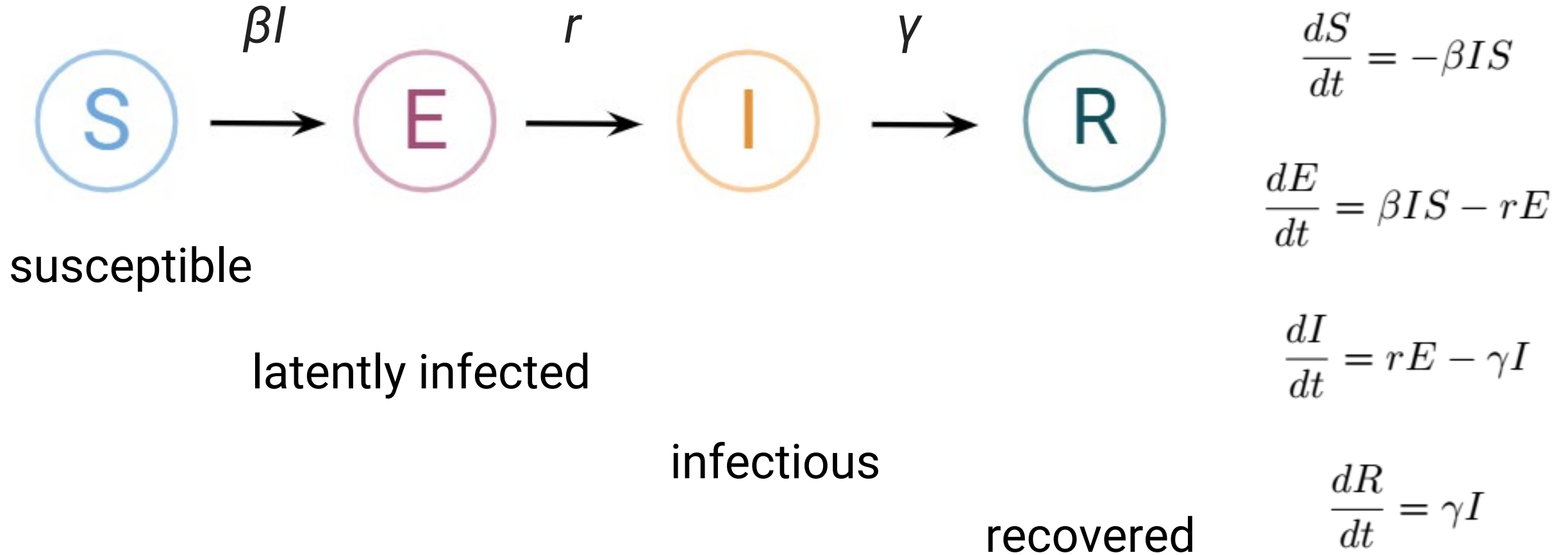
A **positive** result from this test may mean that a person was **previously infected** with the virus.



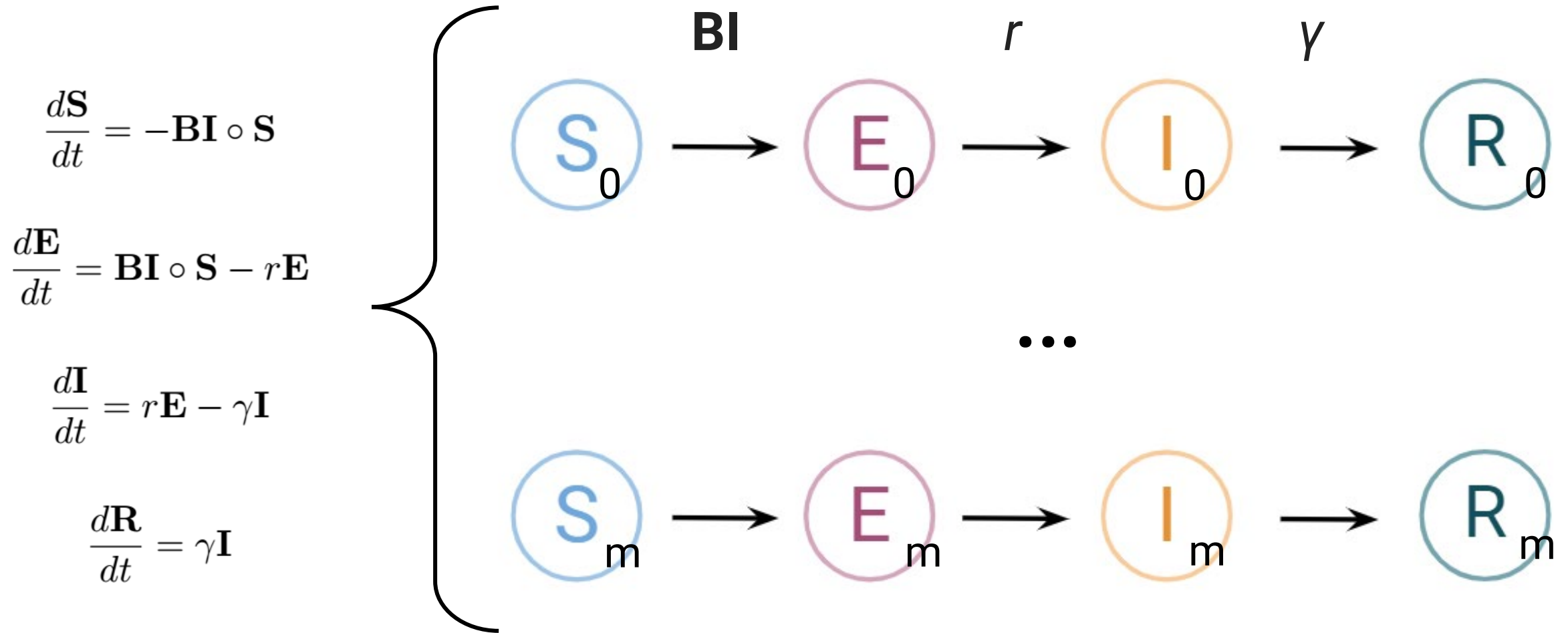
## NYC serosurvey by Rosenberg et al.

- 100 grocery stores across New York state
- April 19-28, 2020
- 15,000 adults tested with information on race and ethnicity
- Overall cumulative incidence of 14%
- Limitation: single time point

# SEIR compartmental model for a homogeneous population



# Structured models address heterogeneity by explicitly modeling the demographic subgroups



Proportionate mixing assumes the contact rate between groups to be proportional to group activity levels

$$\begin{aligned}\frac{d\mathbf{S}}{dt} &= -\mathbf{B}\mathbf{I} \circ \mathbf{S} \\ \frac{d\mathbf{E}}{dt} &= \mathbf{B}\mathbf{I} \circ \mathbf{S} - r\mathbf{E} \\ \frac{d\mathbf{I}}{dt} &= r\mathbf{E} - \gamma\mathbf{I} \\ \frac{d\mathbf{R}}{dt} &= \gamma\mathbf{I}\end{aligned}$$

$$\mathbf{B} = q \begin{bmatrix} c_{0\leftarrow 0} & \dots & c_{0\leftarrow 2} & \dots & c_{0\leftarrow 4} \\ \vdots & & \vdots & & \vdots \\ c_{4\leftarrow 0} & \dots & c_{4\leftarrow 2} & \dots & c_{4\leftarrow 4} \end{bmatrix}$$

$$\beta_{i\leftarrow j} = q \frac{a_i a_j}{\sum_k a_k N_k}$$

Without contact survey data like POLYMOD, these assumptions are necessary



Assortative mixing partitions a fraction  $\epsilon$  of contacts to be exclusively within group (with the rest proportionately distributed)

$$\beta_{i \leftarrow j} = (1 - \epsilon) * q \frac{a_i a_j}{\sum_k a_k N_k} + \epsilon * q \frac{a_i}{N_i}$$

More complexity generally increases model realism, but also parameter count

$R_0$ ,  $R_{\text{eff}}$ , and the herd immunity threshold (HIT) for heterogeneous models

$R_0$  = dominant eigenvalue of  $N \mathbf{B} / \gamma$

$R_{\text{eff}}$  = dominant eigenvalue of  $S(t) \mathbf{B} / \gamma$

HIT = fraction of population that is non-susceptible when  $R_{\text{eff}} < 1$

# Overview of breakout session project

- Fit transmission models structured by race and ethnicity to Long Island and New York City seroprevalence data
- Evaluate the impact of 1) different model structures and 2) variability in seroprevalence across groups on herd immunity thresholds and epidemic final sizes
- Think carefully through model assumptions, accuracy versus transparency versus resolution, etc.

# Download code and overview

kevincma Update README.md		cc6a5eb 2 hours ago	🕒 12 commits
📄 README.md	Update README.md		2 hours ago
📄 SISNID_Day 2_Breakout_Slides.pdf	Create SISNID_Day 2_Breakout_Slides.pdf		3 days ago
📄 SISNID_Day_2_Breakout_Overview...	update group numbers		2 hours ago
📄 day-2-heterogeneity-breakout.R...	Add comments		2 hours ago

# Overview of the two main functions

- `fit.model()`
  - Input: **seroprevalence data**, demographics data, parameters (epsilon, latent period, infectious period)
  - Output: estimated activity level parameters
  - More on model fitting on Day 3
- `run.structured.model()`
  - Input: desired  $R_0$  value, demographics data, parameters (epsilon, latent period, infectious period, **activity levels**), initial conditions, timespan
  - Output: simulated epidemic trajectory

# Schedule

- Work in breakout groups from now until 2:10 PM Pacific / 5:10 PM Eastern (1.5 hours)
  - Read through PDF and code (~30 minutes)
  - Work on questions as a group (~50 minutes)
  - Finalize solutions and figures (if relevant) for your assigned question + be ready to present (~last 10 minutes)
- Discuss in big group for the last 20 minutes of class