

SISMID 2021: Mathematical Models of Infectious Disease

Day 2: Breakout Session on Heterogeneity and Herd Immunity

Population heterogeneity influences the herd immunity threshold

Science

REPORTS

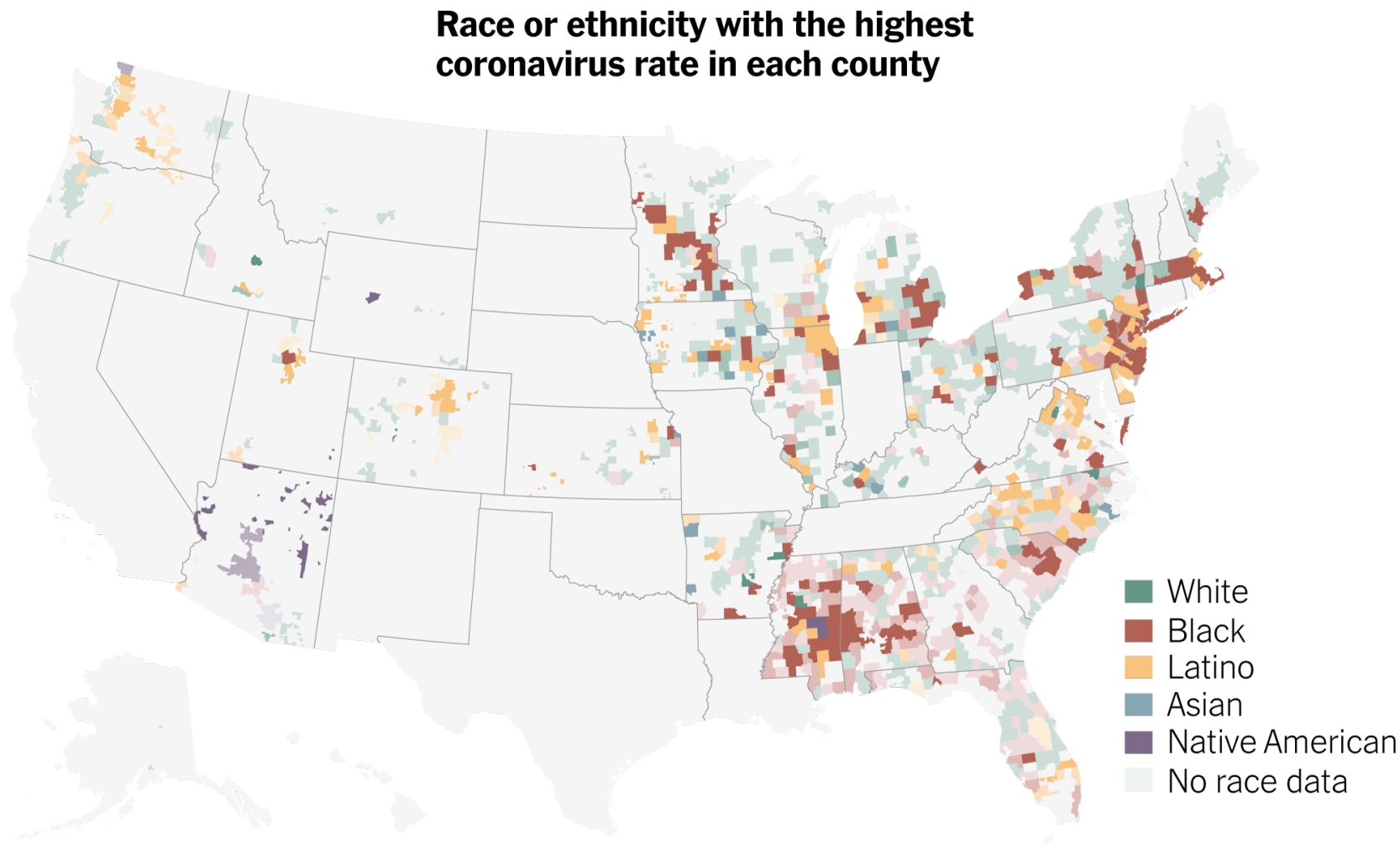
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10.1126/science.abc6810 (2020).

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

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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

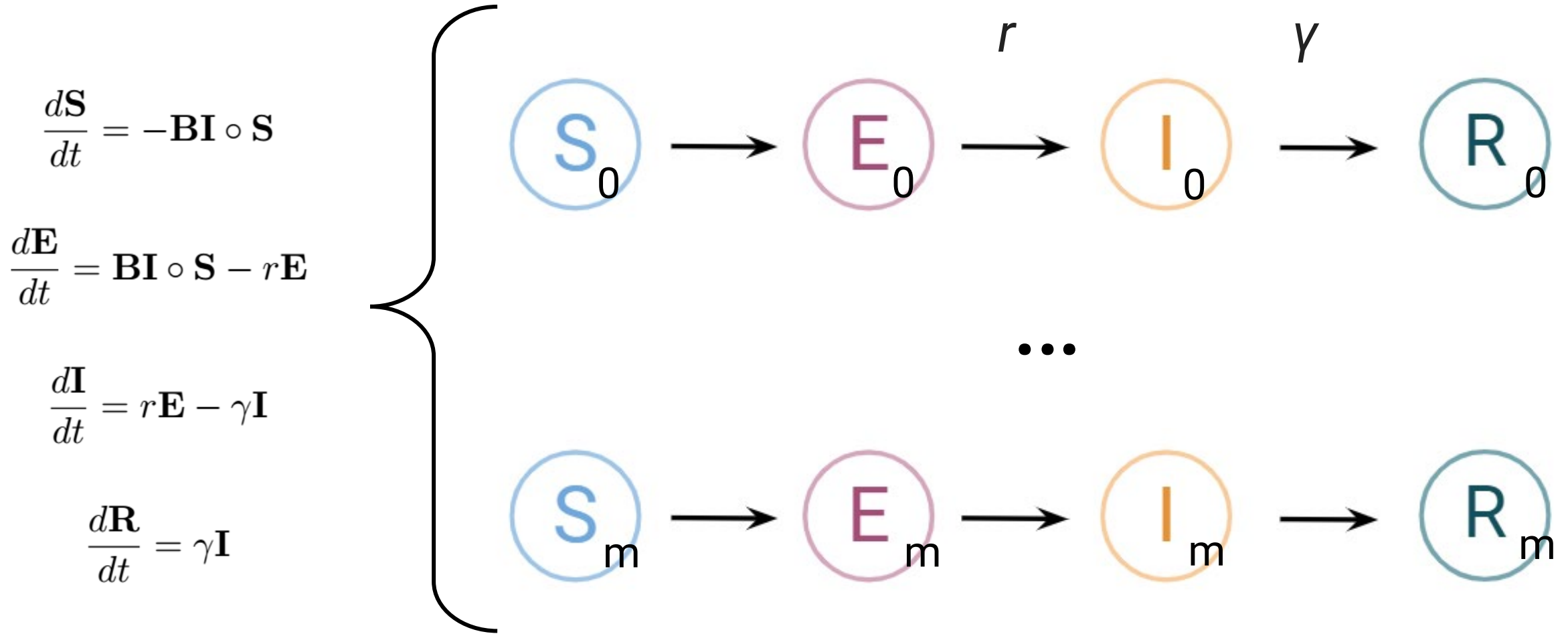
Racial and ethnic disparities in COVID-19 incidence in the US



Overview of breakout session project

- Fit transmission models structured by race and ethnicity to New York seroprevalence data under different assumptions of what the transmission matrix could be
- Evaluate the impact of different model structures on herd immunity thresholds, epidemic final sizes, and optimal vaccination strategies

Structured models incorporate heterogeneity by explicitly modeling demographic subgroups



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

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

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

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

NYC seroprevalence data

- Seropositivity: a (less biased) marker of who's been infected
- 100 grocery stores across New York state
- April 19-28, 2020
- 15,000 adults tested in total
- Overall cumulative incidence of 14%

Modeling heterogeneity in exposure using proportionate mixing: the contact rate between each group is proportional to the activity levels of the two groups

$$\frac{d\mathbf{S}}{dt} = -\mathbf{B}\mathbf{I} \circ \mathbf{S}$$

$$\frac{d\mathbf{E}}{dt} = \mathbf{B}\mathbf{I} \circ \mathbf{S} - r\mathbf{E}$$

$$\frac{d\mathbf{I}}{dt} = r\mathbf{E} - \gamma\mathbf{I}$$

$$\frac{d\mathbf{R}}{dt} = \gamma\mathbf{I}$$

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

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

Fit activity level for each group

Model assortative mixing by partitioning a fraction ϵ of contacts to be exclusively within group

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