

Supplementary Materials: Segregated mobility patterns amplify neighborhood disparities in the spread of COVID-19

April 14, 2023

Here we include details about our results in Chicago regarding (i) datasets; (ii) model dynamics and accuracy; (iii) source of exposures; (iv) structural effects; (v) eliminating case rate disparities; (vi) demographic trade-offs; together with (vii) replication results in Milwaukee. Unless otherwise indicated, in all figures the following color scheme is applied: Majority Black, Majority Latinx, Majority White, and Mixed groups are denoted by red, yellow, green, and blue, respectively.

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S1 Datasets

Mobility and population data ZIP Code and group level population size and mobility data are depicted in Figure S1, together with the ZIP Code specific scaling factors in Tables S1–S4, and mobility-based connectivity in Figure S2.

Case and test data The reported weekly ZIP Code level COVID-19 case data (41) is first distributed uniformly across the days of the given week to obtain daily case counts (Figure S1), which is then corrected by considering testing disparities (Figure S3) as well as the data from the *covidestim* project that provides daily estimates of the case count in Cook county (44, 45). Their reported ratio $\xi^{(t)}$ captures the estimated number of cases for each positive test at the county level. Assuming that a similar relationship exists at the city level as well (Cook County fully encompasses the city of Chicago, but also includes many areas beyond the municipal boundary), the reported city-level case count $\bar{C}^{(t)}$ can be used to estimate the number of actual cases as $C^{(t)} = \xi^{(t)} \bar{C}^{(t)}$. We apply a similar mapping at the ZIP Code level, given by $C_i^{(t)} = \xi_j^{(t)} \bar{C}_i^{(t)}$ for ZIP Code i belonging to group G_j with the scaling factor $\xi_j^{(t)}$. Given that testing shows significant variation among the major demographic groups (Figure S3), instead of applying the uniform scaling $\xi_j^{(t)} = \xi^{(t)}$ we assume that the group-specific scaling factor is inversely proportional to the group-level testing frequency $\chi_j^{(t)} = \sum_{i \in G_j} T_i^{(t)} / [\sum_{i \in G_j} N_i^{(t)}]$, where $T_i^{(t)}$ denotes the number of tests performed in ZIP Code i on day t . Thus choosing $\xi_j^{(t)} = \xi_0^{(t)} / \chi_j^{(t)}$ for some $\xi_0^{(t)} > 0$ ensures that reported case counts in different groups are scaled up according to testing disparities among groups. The constant $\xi_0^{(t)} > 0$ is selected to ensure that the ZIP Code level case estimates yield the city level estimate from the *covidestim* project considering $C^{(t)} = \sum_{j=1}^4 \sum_{i \in G_j} \xi_0^{(t)} / \chi_j^{(t)} \bar{C}_i^{(t)}$, yielding $\xi_0^{(t)} = C^{(t)} / [\sum_{j=1}^4 \sum_{i \in G_j} \bar{C}_i^{(t)} / \chi_j^{(t)}]$, where $\tilde{C}_i^{(t)} = \bar{C}_i^{(t)} / \chi_j^{(t)}$.

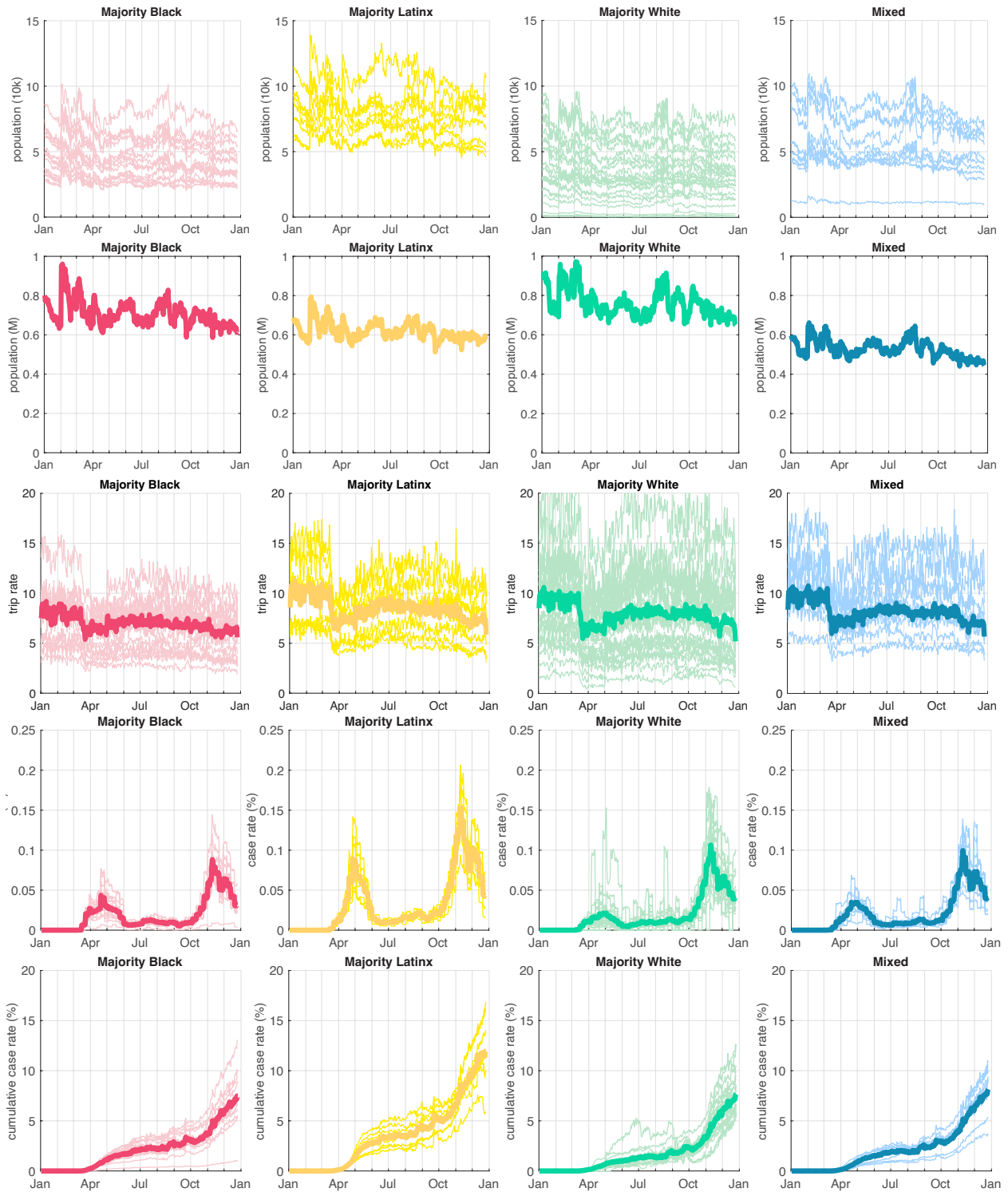


Figure S1: Population size, trip rate data, and reported case rate in each of the major major demographic groups in Chicago over 2020. ZIP Code level data is depicted with thin light curves, whereas group level aggregates are depicted with thick dark curves.

Table S1: Population size, device count, scaling factor, homophily, and estimated exposure statistics in the Majority Black group.

ZIP	pop. size	device count	scaling factor	self trip (%)	group trip (%)	exposure source original ZIPS		exposure source combined ZIPS	
						ZIP (%)	group (%)	ZIP (%)	group (%)
60612	34311	1672.12	20.52	67.01	78.73	82.45	88.60	83.75	89.95
60615	41563	1717.74	24.20	76.73	91.29	72.25	90.01	74.62	93.12
60617	82534	3587.23	23.01	87.95	94.75	84.70	92.54	86.68	94.61
60619	61258	3170.70	19.32	86.57	96.64	79.96	92.94	82.03	95.44
60620	68096	3614.08	18.84	86.32	93.83	81.33	90.27	82.68	91.78
60621	29042	1529.65	18.99	84.06	95.04	79.29	91.62	80.37	92.98
60624	36158	1846.08	19.59	74.65	87.71	75.26	87.23	76.34	88.58
60628	66724	3322.82	20.08	85.12	97.24	84.29	95.60	85.02	96.68
60636	32203	1685.52	19.11	65.96	75.09	76.74	81.53	77.16	82.08
60637	47454	2504.88	18.94	73.56	93.03	76.33	91.62	78.48	94.07
60643	49870	2273.65	21.93	86.96	95.24	86.97	94.49	88.24	95.84
60644	47712	2387.01	19.99	89.75	95.32	84.14	91.54	85.36	92.84
60649	46024	2360.27	19.50	79.85	95.56	77.04	91.93	80.34	95.79
60651	63218	2923.28	21.63	86.27	89.39	75.77	80.72	76.43	81.42
60653	31972	1540.72	20.75	71.42	86.19	83.94	91.23	86.22	93.68
60827	28577	976.35	29.27	88.12	97.50	32.16	79.30	33.85	84.90

Table S2: Population size, device count, scaling factor, homophily, and estimated exposure statistics in the Majority Latinx group.

ZIP	pop. size	device count	scaling factor	self trip (%)	group trip (%)	exposure source original ZIPS		exposure source combined ZIPS	
						ZIP (%)	group (%)	ZIP (%)	group (%)
60608	79205	2731.49	29.00	77.16	84.14	78.88	89.15	80.52	90.99
60609	61495	2676.95	22.97	81.53	89.69	88.08	94.52	89.15	95.72
60623	85979	3360.18	25.59	84.23	90.86	92.26	95.47	92.77	96.02
60629	111850	5057.31	22.12	87.26	93.96	84.89	92.56	85.53	93.36
60632	91039	3458.45	26.32	86.03	95.70	87.83	96.63	88.87	97.79
60638	58797	2878.10	20.43	94.86	97.48	90.56	95.91	91.80	97.21
60639	90517	4144.54	21.84	84.54	87.62	91.75	93.68	92.10	94.06
60641	71023	3130.71	22.69	76.37	79.20	81.15	86.23	81.82	86.93

Table S3: Population size, device count, scaling factor, homophily, and estimated exposure statistics in the Majority White group (ZIP Codes that are later combined are denote by an asterisk, exposure statistics for the combined structure are reported in the row of ZIP Code 60601).

ZIP	pop. size	device count	scaling factor	self trip (%)	group trip (%)	exposure source original ZIPS		exposure source combined ZIPS	
						ZIP (%)	group (%)	ZIP (%)	group (%)
*60601	14675	477.48	30.73	80.73	97.87	16.96	97.77	64.56	84.38
*60602	1244	37.25	33.40	6.96	97.98	36.43	97.53	-	-
*60603	1174	128.69	9.12	20.02	88.81	3.99	97.59	-	-
*60604	782	200.33	3.90	22.62	92.32	87.62	98.49	-	-
*60605	27519	1033.69	26.62	60.74	74.54	23.57	73.75	-	-
*60606	3101	145.11	21.37	15.66	94.22	7.68	98.54	-	-
60607	29591	1105.81	26.76	61.23	86.11	65.68	85.52	74.26	82.96
60610	39019	1468.60	26.57	85.86	97.83	77.55	95.20	85.34	95.28
60611	32426	1128.45	28.74	89.93	98.41	77.91	95.48	85.96	95.22
60613	50113	1900.35	26.37	80.08	96.90	78.11	95.21	79.86	95.22
60614	71308	2458.80	29.00	83.26	96.01	81.25	92.86	83.36	92.77
60622	52793	1948.60	27.09	79.61	88.68	82.76	87.83	83.81	87.70
60630	57344	2638.37	21.73	77.03	85.54	64.72	73.27	65.42	72.86
60631	29529	1582.03	18.67	92.35	98.96	84.06	95.51	84.94	95.44
60634	75995	3757.94	20.22	87.01	90.82	90.20	92.58	90.65	92.44
60640	69715	2508.13	27.80	83.69	94.46	78.21	90.69	79.90	90.65
60642	20201	670.71	30.12	66.08	91.98	69.91	90.90	74.94	90.75
60646	27987	1396.03	20.05	88.08	96.99	83.82	93.02	84.83	92.87
*60654	19135	572.75	33.41	69.30	97.16	76.34	96.88	-	-
60655	28804	1555.21	18.52	94.93	95.75	90.44	92.97	91.81	92.62
60656	27579	1672.62	16.49	88.34	98.34	86.38	95.53	87.76	95.47
60657	70052	2492.19	28.11	81.08	96.87	82.57	95.61	84.46	95.61
60660	43242	1739.92	24.85	84.62	92.98	81.16	89.79	83.60	89.66
*60661	9926	404.15	24.56	69.69	96.19	41.40	93.78	-	-

Table S4: Population size, device count, scaling factor, homophily, and estimated exposure statistics in the Mixed group.

ZIP	pop. size	device count	scaling factor	self trip (%)	group trip (%)	exposure source original ZIPS		exposure source combined ZIPS	
						ZIP (%)	group (%)	ZIP (%)	group (%)
60616	54464	1989.47	27.38	65.47	65.97	55.16	56.16	49.58	50.67
60618	94395	3717.73	25.39	84.28	90.51	80.95	89.88	81.77	90.82
60625	79243	3383.74	23.42	84.74	91.62	87.63	93.75	88.08	94.27
60626	49730	2251.52	22.09	84.02	93.60	83.26	95.87	83.88	96.59
60633	12871	627.56	20.51	87.13	87.33	81.66	81.95	82.44	82.72
60645	47732	2003.42	23.83	79.09	94.92	86.45	97.30	86.77	97.64
60647	87509	3195.58	27.38	76.72	82.55	85.41	87.96	86.17	88.74
60652	43907	2097.65	20.93	86.87	87.21	85.74	86.08	86.85	87.18
60659	41068	1840.23	22.32	82.82	92.88	82.09	94.89	82.23	95.12
60707	43019	2306.91	18.65	91.47	92.07	63.76	66.29	64.68	67.28

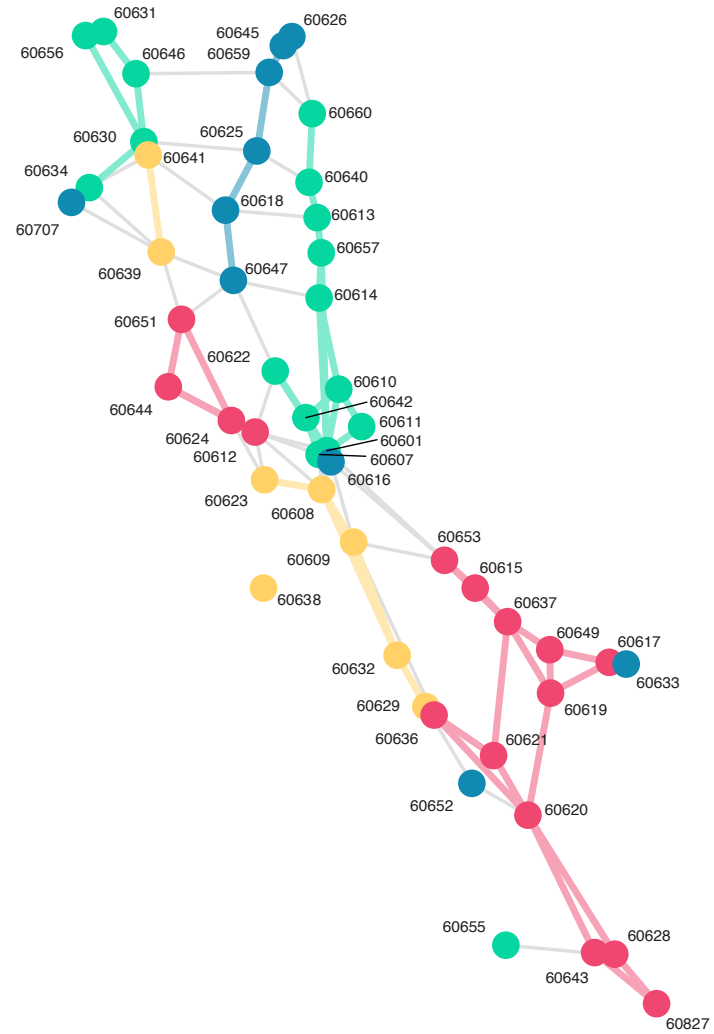
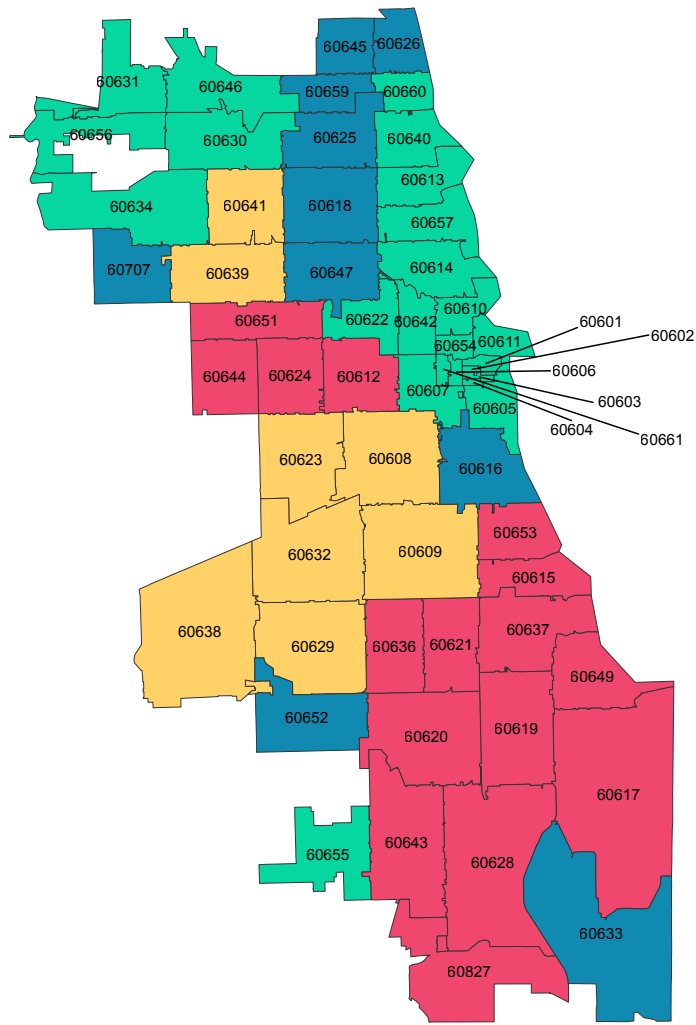


Figure S2: Left panel shows the map of Chicago, ZIP Codes are colored by the majority demographic group. Right panel depicts the network of ZIP Codes such that distance between nodes is inversely proportional to the probability of between ZIP Code trips. Trips (incoming and outgoing combined) are averaged over 2020 between ZIP Codes, normalized by the total average trip count for each ZIP Code; following this, within-ZIP trips and trips below 1% are removed before visualizing the network using the Fruchterman-Reingold method (53).

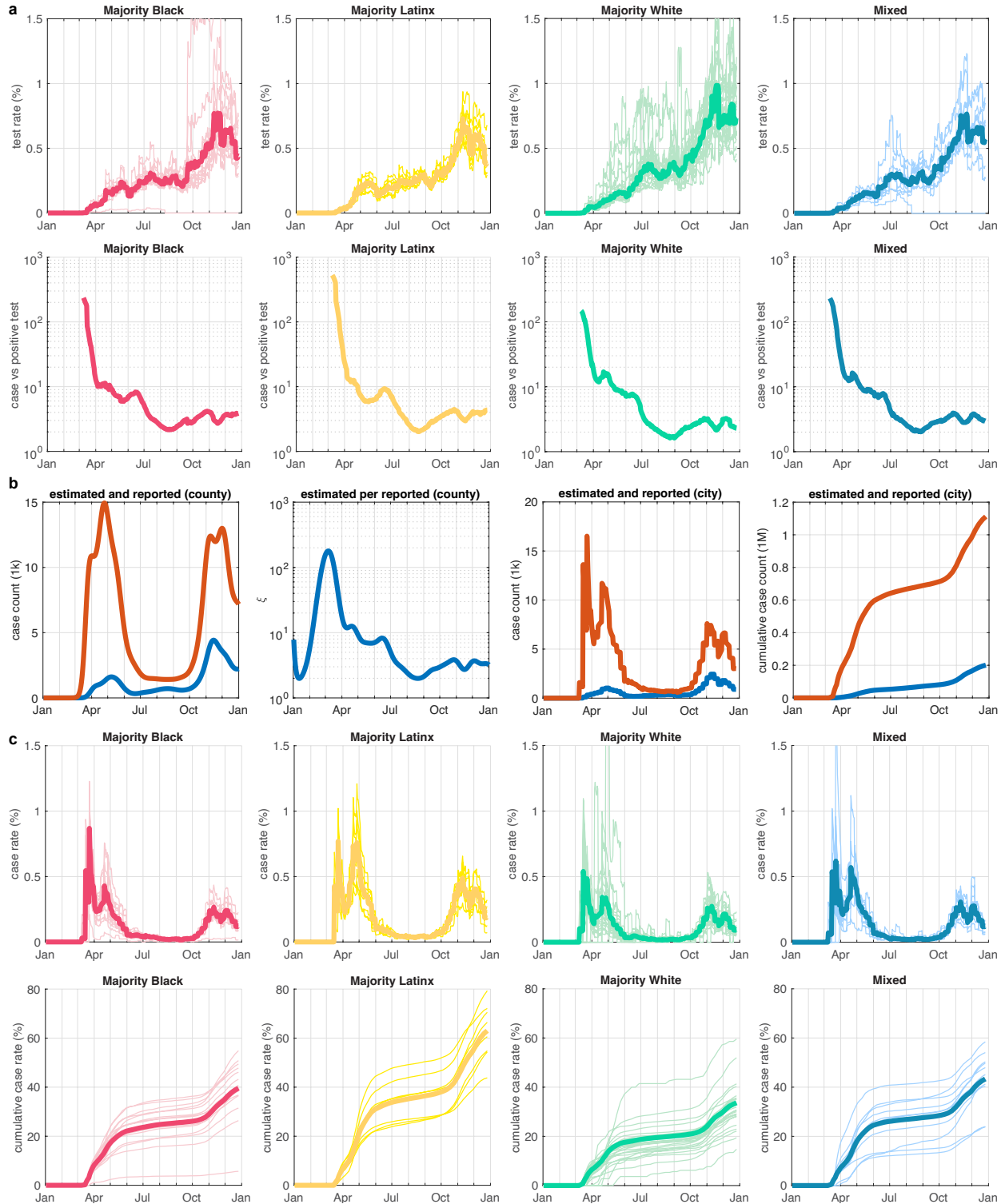


Figure S3: Case count estimation in each of the major major demographic groups in Chicago over 2020. (a) Test rate and group level correction term capturing the time-varying and group-dependent relationship between reported positive cases and estimated actual case counts (once testing begins). (b) Reported and estimated data are depicted in blue and red, respectively, using (45). (c) Estimated case rates, based on reported case rates and accounting for testing disparities and asymptomatic infections. ZIP Code level data is depicted with thin light curves, whereas group level aggregates are depicted with thick dark curves.

Mobility pattern data Tables S1–S4 show homophily as the percentage of trips occurring within the same ZIP Code and the same group in Chicago over 2020. Analyzing the mobility network also reveals that the declaration of national emergency further increased group level homophily from 90% to 92% (Majority Black: 92% → 94%, Majority Latinx: 89% → 91%, Majority White: 93% → 94%, Mixed: 85% → 90%). A similar pattern emerges when we consider 15 of the largest metropolitan areas: Chicago, IL (CHI); Columbus, OH (COLO); Dallas, TX (DAL); Detroit, MI (DET); Fort Worth, TX (FWTX); Houston, TX (HOU); Indianapolis, IND (IND); Los Angeles, CA (LA); Las Vegas, NV (LV); Miami, FL (MIA); New York, NY (NY); Philadelphia, PA (PHI); Phoenix, AZ (PHX); San Diego, CA (SD); Seattle, WA (SEA). For all major demographic groups (Majority Asian, Majority Black, Majority Latinx, Majority White, and Mixed), we calculated the percentage of trips leading outside the group over 2020 (Figures S4–S7), as well as before and after March 1, 2020 (Table S5).

Table S5: Percentage of trips within the same ZIP and group as the source ZIP Code before and after March 1, 2020.

	Majority Asian		Majority Black		Majority Latinx		Majority White		Mixed		
	before	after	before	after	before	after	before	after	before	after	
ZIP-level homophily (%)	CHI	-	-	74.16	77.71	79.23	81.87	70.78	75.73	70.68	75.69
	COLO	-	-	66.95	69.66	-	-	67.33	72.73	72.53	76.24
	DAL	-	-	71.52	75.80	73.06	76.71	72.93	78.54	73.51	77.90
	DET	-	-	78.85	80.88	82.15	83.16	79.51	83.28	81.52	83.39
	FWTX	-	-	-	-	68.16	71.14	64.66	68.42	57.34	60.98
	HOU	-	-	69.73	73.52	68.11	72.12	66.53	71.75	68.38	73.29
	IND	-	-	65.41	69.48	-	-	61.28	64.68	68.60	73.75
	LA	74.36	81.42	67.94	74.60	70.71	75.52	69.11	76.09	69.22	75.42
	LV	-	-	-	-	72.12	76.14	65.33	71.46	61.31	66.99
	MIA	-	-	61.10	65.10	58.96	65.09	75.11	80.09	61.60	66.98
	NYC	72.79	77.99	80.62	84.06	80.32	83.44	73.92	78.39	77.28	82.06
	PHI	-	-	73.70	77.32	71.94	73.07	75.55	80.61	79.62	82.37
	PHX	-	-	-	-	67.37	70.38	66.30	70.66	69.79	73.98
	SD	-	-	-	-	67.07	71.74	68.76	74.46	64.59	71.29
	SEA	-	-	-	-	-	-	67.27	73.77	62.74	68.91
Group-level homophily (%)	CHI	-	-	86.96	89.02	85.93	87.87	93.72	94.66	78.61	82.43
	COLO	-	-	71.59	73.55	-	-	96.52	96.78	78.36	80.88
	DAL	-	-	85.26	87.80	83.16	86.02	88.03	89.97	86.78	88.99
	DET	-	-	92.72	94.11	85.68	86.18	98.10	98.55	83.45	84.81
	FWTX	-	-	-	-	77.97	80.96	90.13	91.10	67.92	70.44
	HOU	-	-	79.55	83.03	84.41	86.74	84.99	87.60	83.03	85.57
	IND	-	-	69.63	73.71	-	-	93.08	93.46	77.24	81.59
	LA	86.40	89.74	74.33	80.39	88.15	90.69	88.77	91.16	83.41	86.63
	LV	-	-	-	-	83.76	86.48	85.71	89.15	85.41	87.41
	MIA	-	-	79.80	83.45	96.25	96.92	75.36	80.27	67.61	71.35
	NYC	72.93	78.07	84.22	87.12	88.88	91.35	87.19	88.62	83.93	87.55
	PHI	-	-	90.97	93.72	71.94	73.07	90.54	92.39	89.83	92.33
	PHX	-	-	-	-	83.85	86.14	94.61	95.40	74.81	78.20
	SD	-	-	-	-	80.70	83.29	92.47	93.75	73.81	79.12
	SEA	-	-	-	-	-	-	92.69	94.37	84.38	87.29



Figure S4: Homophily of the major demographic groups in 15 of the largest cities of the US during 2020. Dot size is proportional to population size.

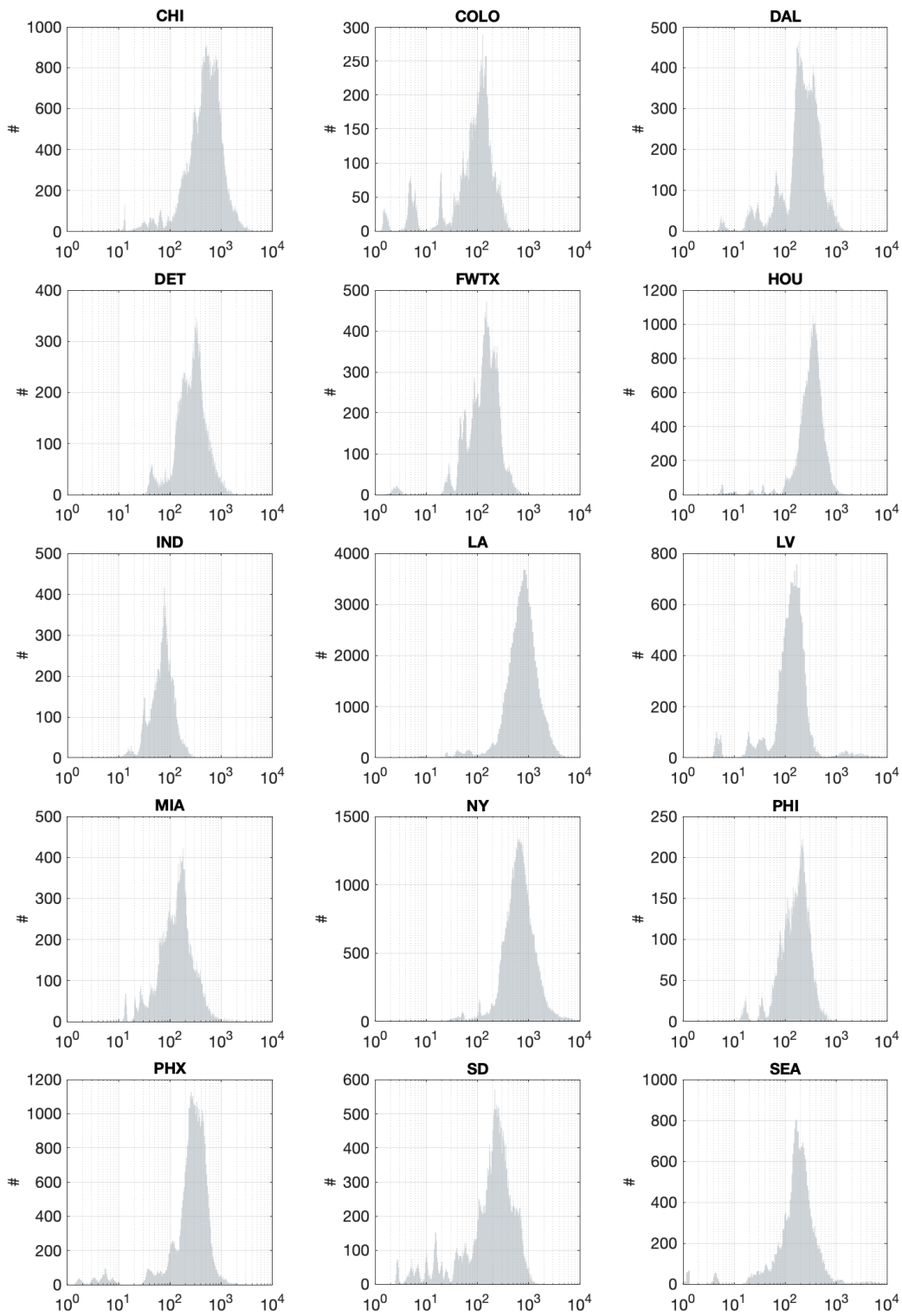


Figure S5: Histogram of the ratio of self-trip rate compared to average trips outside of the source ZIP Code in 15 of the largest cities of the US during 2020.

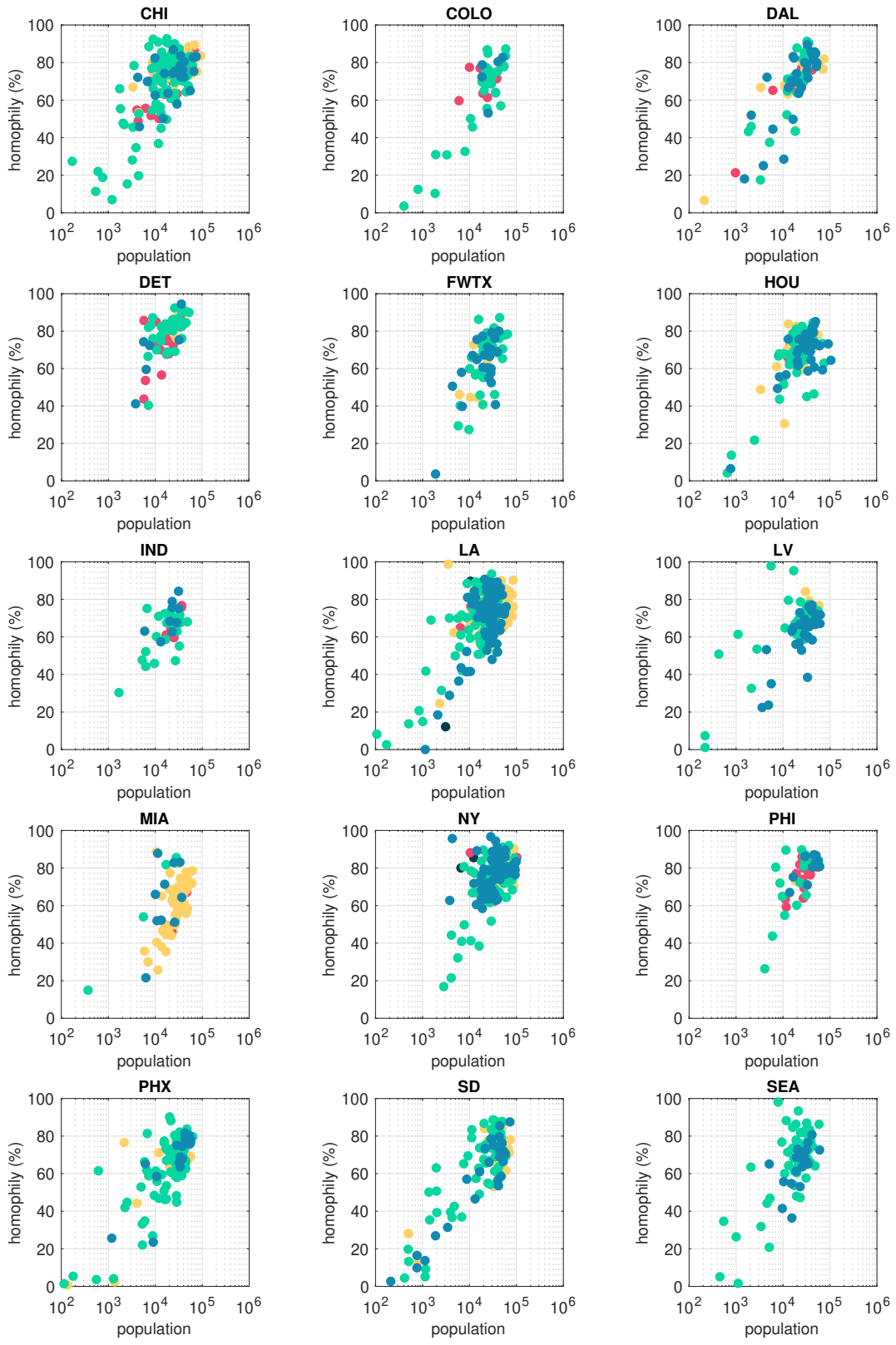


Figure S6: Scatter plot of annual mean population size and average ZIP Code level homophily in 15 of the largest cities of the US during 2020.

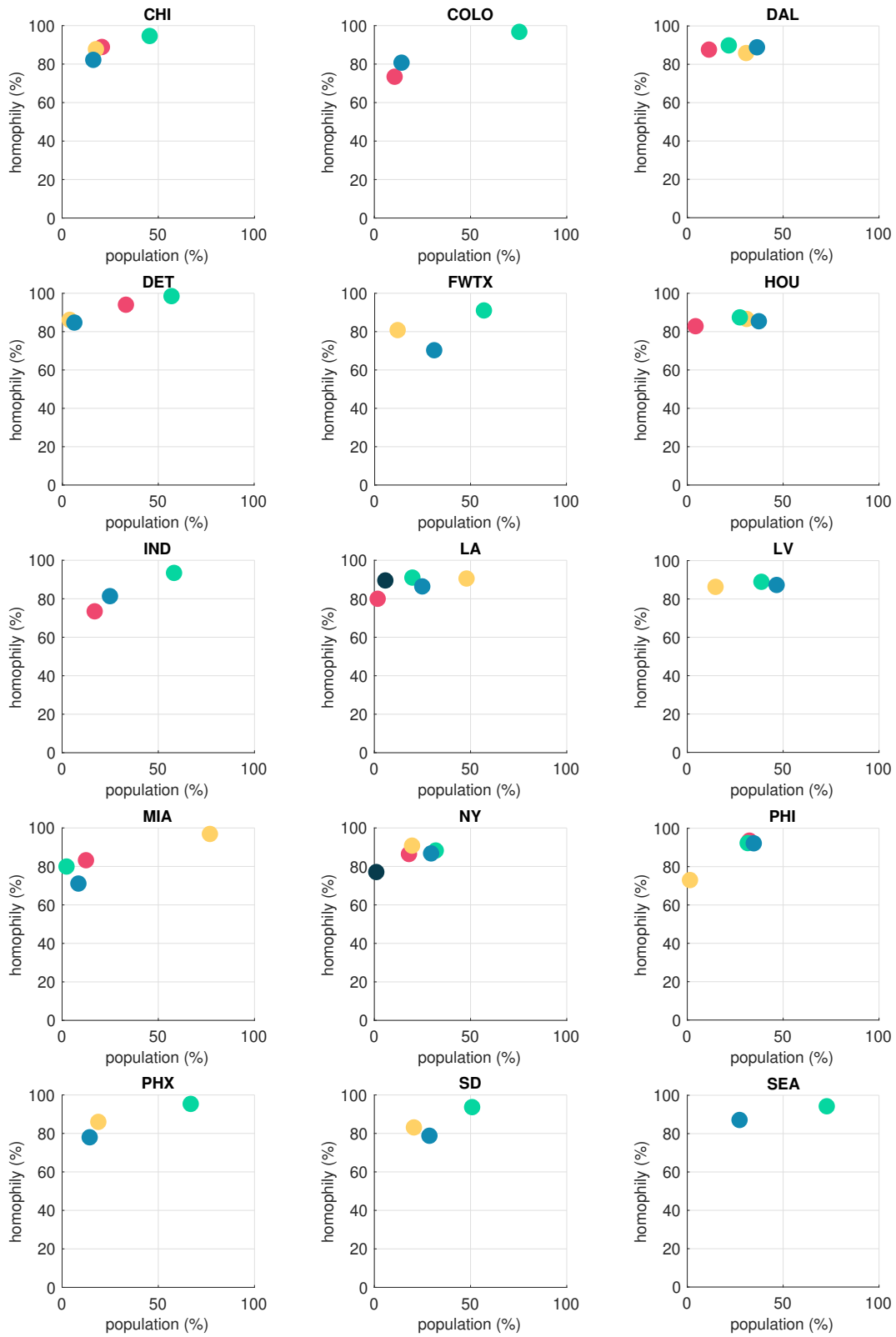


Figure S7: Scatter plot of annual mean population size and average group level homophily in 15 of the largest cities of the US during 2020.

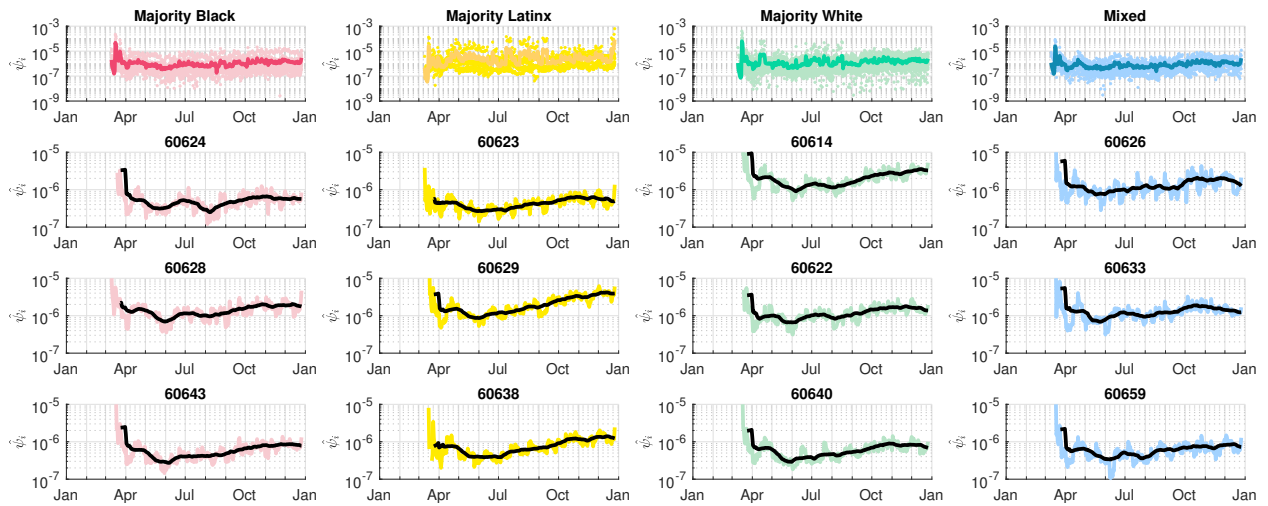


Figure S8: Temporal evolution of $\hat{\psi}_i(t)$ at the group level (light dots correspond to all $\hat{\psi}_i(t)$ within the group, dark curve denotes the group average) and for three randomly selected ZIP Code (indicated above each panel) in each group. Black curves denote 30-day moving averages.

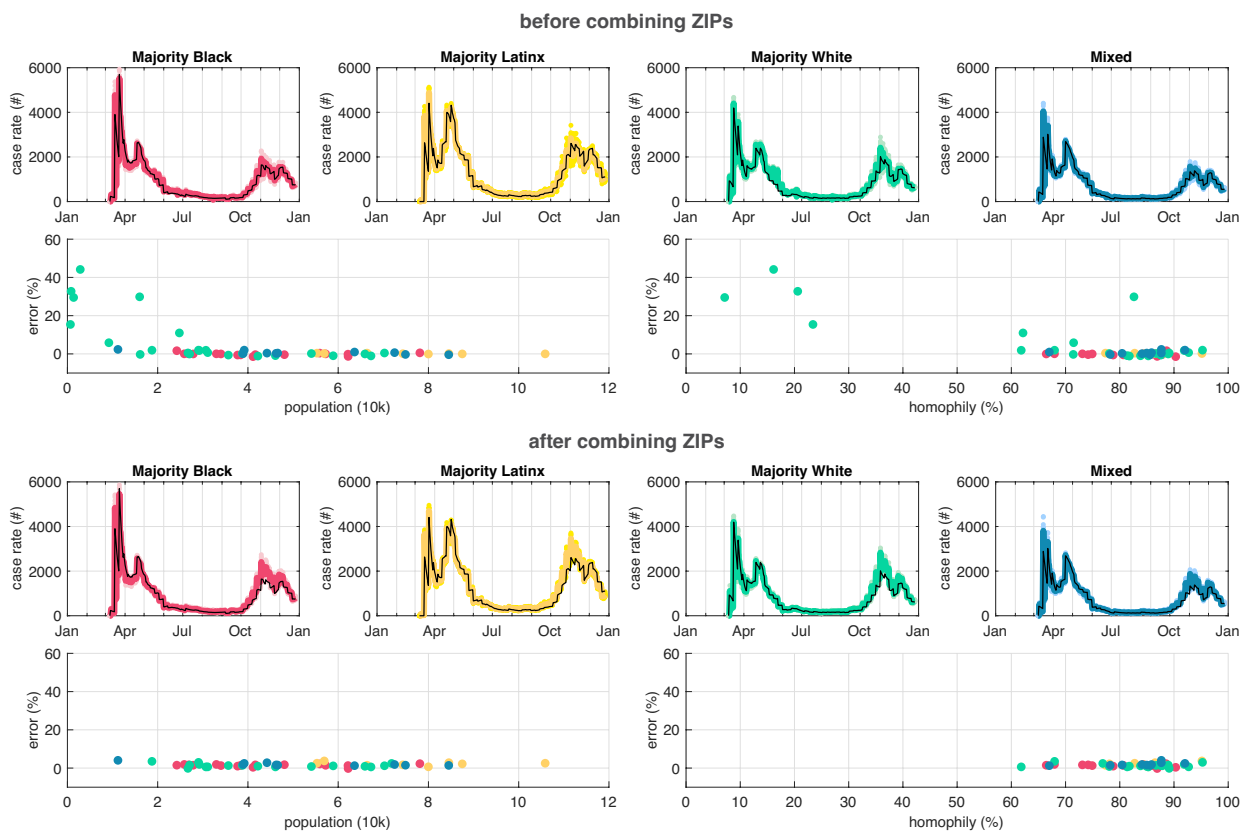


Figure S9: Model accuracy before and after combining ZIP Codes highlighted in Figure S10b. Group level estimated case rate is depicted in black, simulation data from 10 independent runs are depicted with dots, their average is displayed with thick curve of the same color. ZIP Code level accuracy (error between model output and reported case count) is depicted as a function of annual average population and ZIP Code level homophily.

S2 Model dynamics and accuracy

Calibration of the SEIR model is performed by estimating the value of the unknown parameter $\psi_i^{(t)}$ for each day t based on the new infections $C_i^{(t)}$ occurring on that specific day among the people residing in the ZIP Code. Group level data and sample trajectories of $\hat{\psi}_i(t)$ are presented in Figure S8 for three randomly selected ZIP Code in each group. After calibration, the resulting model fit is depicted in Figure S9 (top half). While the fit produces almost no error at the group level, performance in some of the ZIP Codes is considerably poorer. In particular, there are 8 ZIP Codes (60601, 60602, 60603, 60604, 60605, 60606, 60654, and 60661) where the error is significant. All these ZIP Codes belong to the Majority White group with relatively small population size and low homophily. To eliminate possible misattribution of trips, these ZIP Codes are combined in subsequent analysis into a composite node that has an area and population size similar to other ZIP Codes with movement pattern and epidemic progression closely aligned with the group level average (Figure S10a), and the model accuracy increases leading to virtually no error (Figure S9, bottom half). Furthermore, considering $\omega_i^{(t)} = w_{i,i}^{(t)}(n-1) / \sum_{j \neq i} w_{i,j}^{(t)}$ for all ZIP Code i and time t (measuring the frequency of within-ZIP trips compared to the average number of trips where the destination and origin ZIP Codes are different), its distribution contains a dominant peak between 100 and 1,000 with a few outliers that disappear once the above mentioned ZIP Codes are combined (Figure S10b). Therefore, in what follows, we consider the above ZIP Codes to be combined.

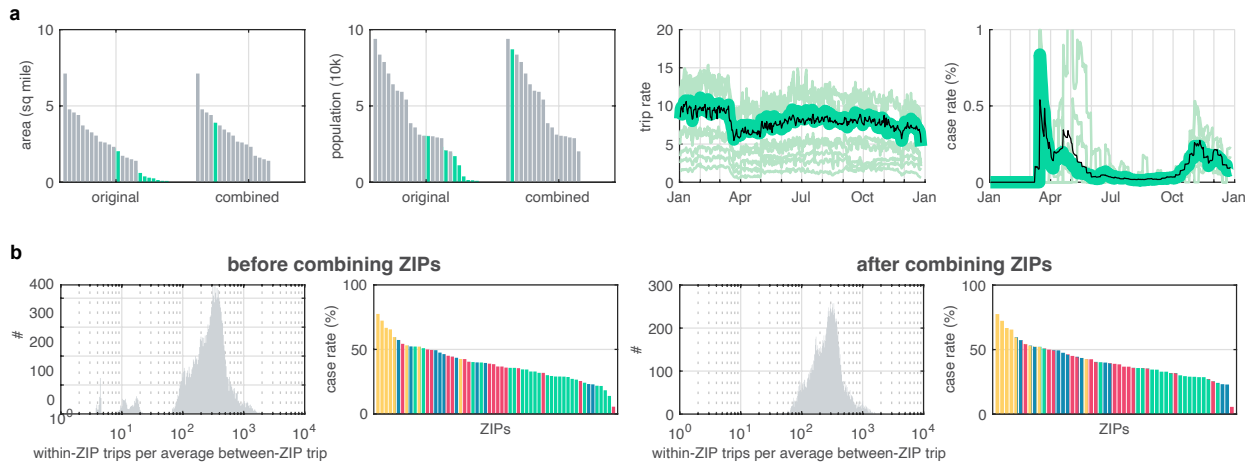


Figure S10: Combining ZIP Codes with significant model error yields a reasonable composite ZIP Code. (a) Distribution of area and population size of ZIP Codes within the same group (Majority White) before and after combining the following ZIP Codes: 60601, 60602, 60603, 60604, 60605, 60606, 60654, and 60661 (corresponding bars are depicted in green). Trip rate and case rate for the individual ZIP Codes are depicted with thin green lines, thick green lines correspond to the combined composite ZIP Code whereas the thin black line depicts the group averages. (b) Histogram of within-ZIP trips per average between-ZIP trips together with ZIP Code level case rate before and after combining the above ZIP Codes.

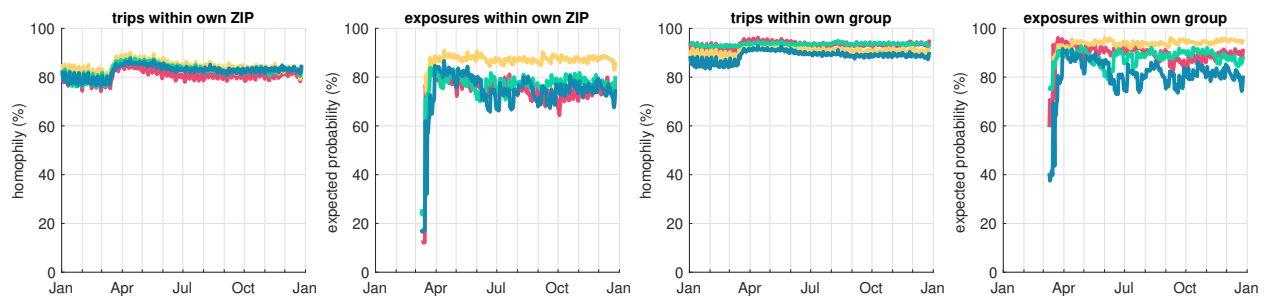


Figure S11: Group level average homophily and source of exposure within own ZIP Code and own group.

S3 Source of exposures

The group level average probabilities that exposure in group G_i happens due to trips within one's own ZIP Code and one's own group are displayed in Figure S11, together with the group level average fractions of trips within own ZIP Code (ω) and own group (ν) at time t in group i , computed as

$$\omega_i^{(t)} = \frac{1}{n_i} \sum_{j \in G_i} \frac{w_{j,j}^{(t)}}{\sum_{k=1}^n w_{j,k}^{(t)}}, \quad \text{and} \quad \nu_i^{(t)} = \frac{1}{n_i} \sum_{j \in G_i} \frac{\sum_{k \in G_i} w_{j,k}^{(t)}}{\sum_{k=1}^n w_{j,k}^{(t)}}.$$

Complementing this, Tables S1–S4 contain expected probabilities of exposures occurring within the same ZIP Code and group before and after combining the ZIP Codes highlighted in Figure S10b.

S4 Eliminating case rate disparities

Considering the expected number of new exposures, it follows that the transmission rate $\bar{\beta}_i^{(t)}$ can be estimated as $\beta_i^{(t)} = N_i^{(t)} C_i^{(t)} / [S_i^{(t)} I_i^{(t)}]$, where $C_i^{(t)}$ is the estimated number of new exposures in ZIP Code i on day t . Compared with $\bar{\beta}_i^{(t)}$, the approximate transmission rate $\beta_i^{(t)}$ neglects the effects of between-ZIP trips in two ways. First, by omitting trips leading to other ZIP Codes, the corresponding exposures are not taken into account. Second, by discarding incoming trips, thus the risk they carry, the infection rate $\lambda_i^{(t)}$ at ZIP Code i is also underestimated. The temporal averages of both the approximate transmission rate $\beta_i^{(t)}$ and $\bar{\beta}_i^{(t)}$ are plotted for each ZIP Code in Figure S12b. Although the approximate transmission rate $\beta_i^{(t)}$ neglects the effects of inter-ZIP travels, it encompasses three major factors: the parameter $\psi_i^{(t)}$, population density $N_i^{(t)} / a_i$ and self-trip rate $w_{i,i}^{(t)}$. While separately none of these factors displays strong correlation with the case count, their combination in $\beta_i^{(t)}$ has significant predictive power regarding the case count (Figure S13a).

With this, we can next explore differences at the group level and their source. To this end, we define vulnerability as $\psi_i^{(t)} N_i^{(t)} / a_i$, that is, the part of $\beta_i^{(t)}$ other than within-ZIP trip rate. The results presented in Figure S13b reveal, for instance, that while the outcomes in the Majority Black and Majority White groups are almost identical, focusing solely on these outcomes masks considerable differences between the two groups: while mobility in the former group is significantly lower, vulnerability is almost 40% higher. This together with the relationship in Figure S12c between group level mean β and case rate considering the counterfactuals described in the Materials and Methods section

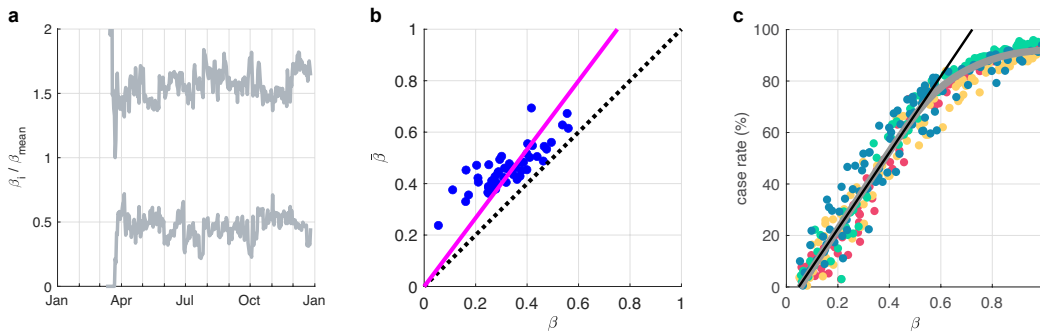


Figure S12: Relationship among β_i , β_{mean} , $\bar{\beta}$, β and case rate. (a) Range of β_i compared to the average $\beta_{\text{mean}}^{(t)} = \sum_{i=1}^n \beta_i^{(t)} / n$. The curves denote the 80% “confidence interval” as there is 10% of the ZIP Codes above and below them. (b) Blue dots correspond to $(\beta, \bar{\beta})$ pairs for all ZIP Codes, black dotted line denotes the case when $\bar{\beta} = \beta$, magenta line corresponds to the best fit (minimizing mean square error) of the form $\bar{\beta} = \beta(1 + \delta_\beta)$ with $\delta_\beta = 0.31$. The correlation coefficient between time-averaged β and $\bar{\beta}$ is 0.80, obtained by considering 10 independent computations of $\psi_i^{(t)}$. (c) Dots represent group level averages (obtained by randomly modifying trip rate via mobility and vulnerability via $\psi_i^{(t)}$, as detailed in the Materials and Methods section of the manuscript), the grey curve denotes the trend, and the black line corresponds to the linear fit with slope 148.33 and intercept -7.11 for $0 < \beta < 0.60$.

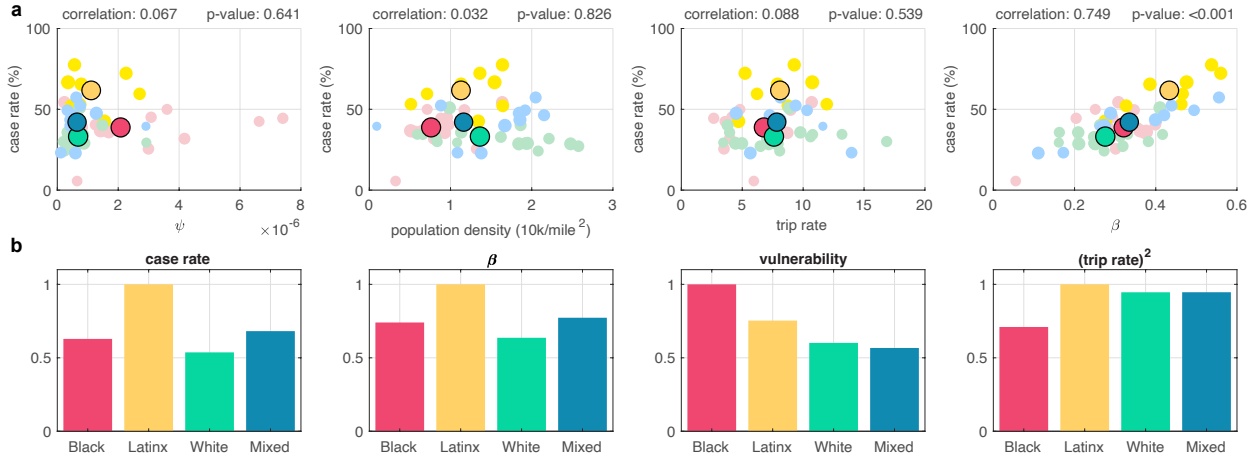


Figure S13: Relationship between case rate and ψ , population density, trip rate and β . (a) Circles without borders display ZIP Code level data, whereas those with borders correspond to group level averages (weighted by population size). Circle size represents population size. (b) Bars represent group level averages (weighted by population size), normalized to the maximum.

suggest that eliminating group level differences in ψ , population density, or trip rate alone does not mean comparable case count outcomes. Conversely, matching the average approximate transmission rate β of one group with that of another almost completely eliminates any difference in case rate (Figure S14–S25). To illustrate this, consider Figure S14 where characteristics of the Majority Black group are changed so that it matches those of the Majority Latinx.

In the top row we change the trip rate of each node in the Majority Black group (i) first by modifying their temporal evolution (while maintaining their mean) such that it matches the group level (population weighted) temporal evolution of the trip rate in the Majority Latinx group (but not the mean); (ii) second by modifying their mean (while maintaining their temporal evolution) such that it matches the group level mean of the trip rate in the Majority Latinx group (but not the temporal evolution); and (iii) third by modifying both their mean and temporal evolution such that they match the group level mean and temporal evolution of the trip rate in the Majority Latinx group. In the second row that same is performed for vulnerability by modifying $\psi_i^{(t)}$ for each node in the Majority Black group to match the behavior of the Majority Latinx group.

Finally, in the third row the approximate transmission rate $\beta_i^{(t)}$ is adjusted for nodes in the Majority Black group so that the group level average matches that of the Majority Latinx group. In particular, we (i) first modified it by adopting the temporal evolution of the group level (population weighted) average in the Majority Latinx group (while maintaining the original means in the Majority Black group); (ii) second we also modified the group level average in the Majority Black group by adjusting the vulnerability of all nodes in the Majority Black group by the same factor until it reached the group level mean in the Majority Latinx group; and (iii) third we also modified the group level average in the Majority Black group by adjusting the trip rate of all nodes in the Majority Black group by the same factor until it reached the group level mean in the Majority Latinx group. Figures S15–S25 can be interpreted similarly.

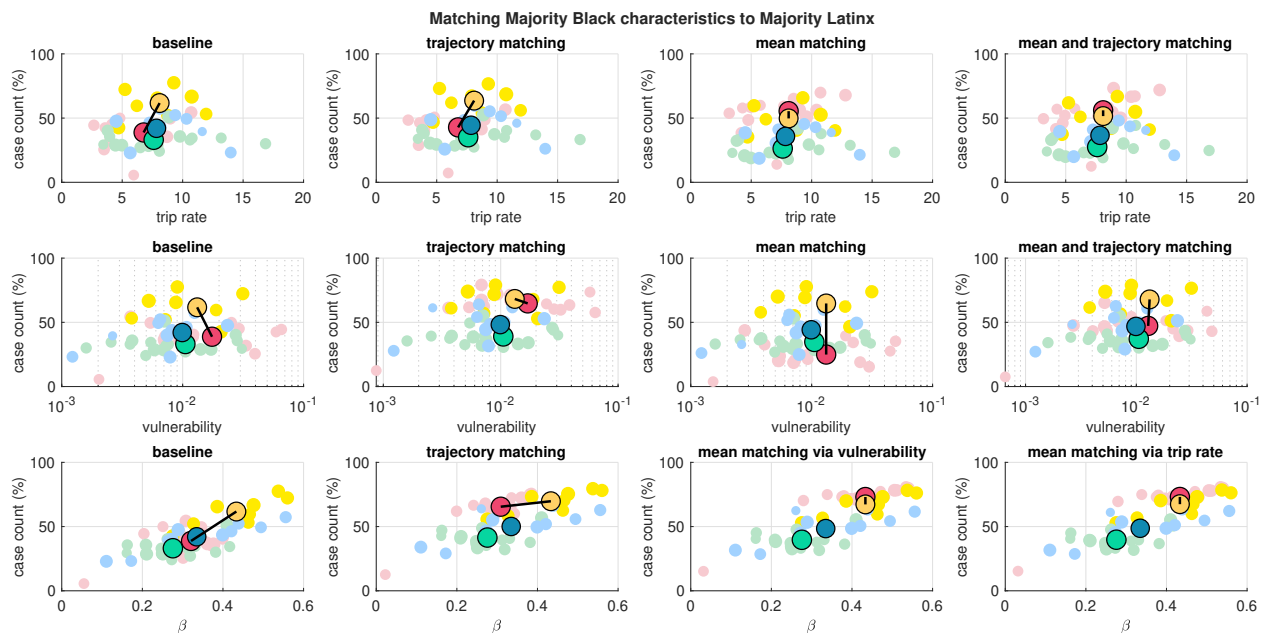


Figure S14: Matching group level characteristics of Majority Black group (modified) to Majority Latinx group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

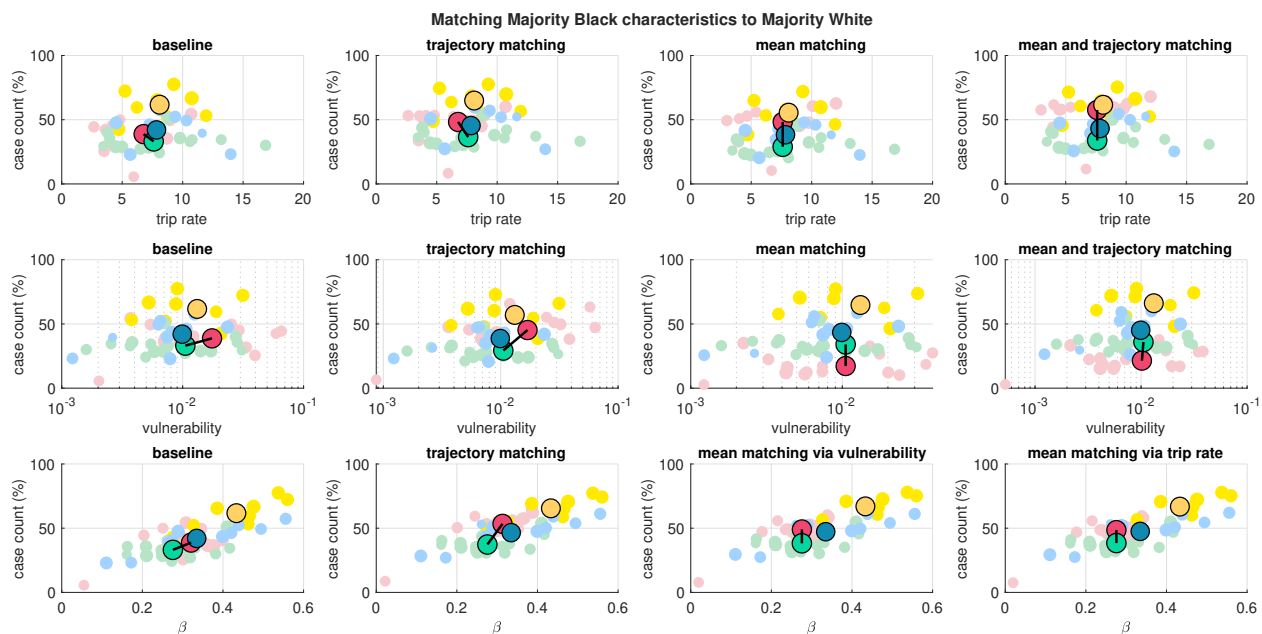


Figure S15: Matching group level characteristics of Majority Black group (modified) to Majority White group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.



Figure S16: Matching group level characteristics of Majority Black group (modified) to Mixed group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

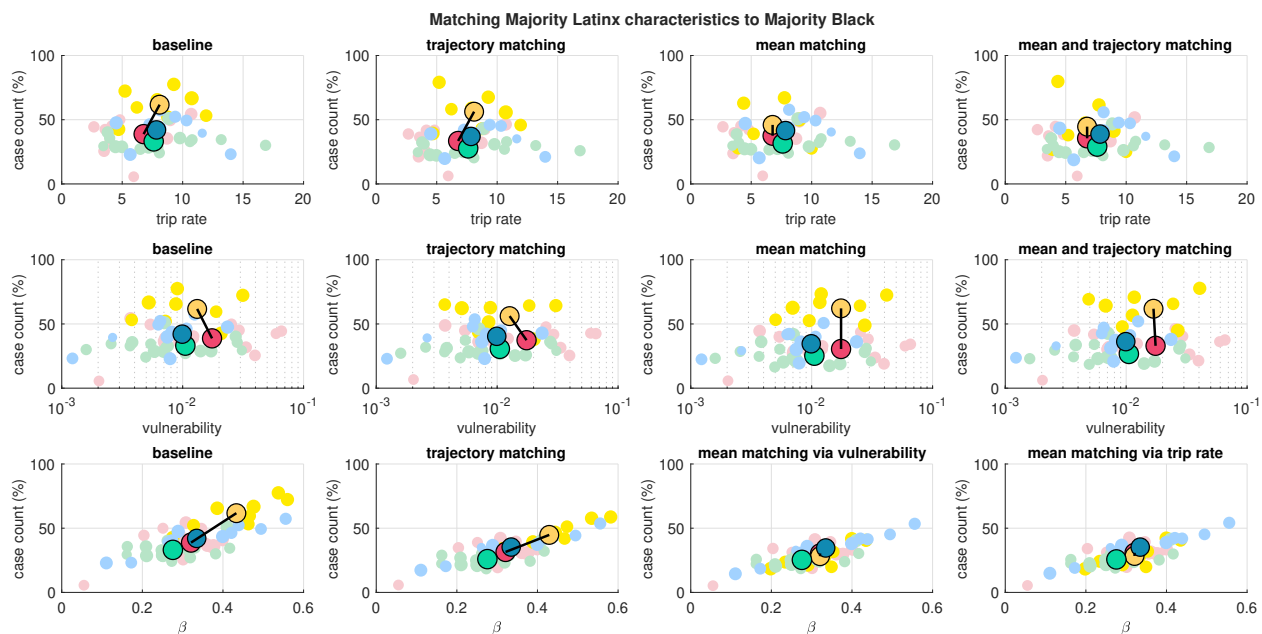


Figure S17: Matching group level characteristics of Majority Latinx group (modified) to Majority Black group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

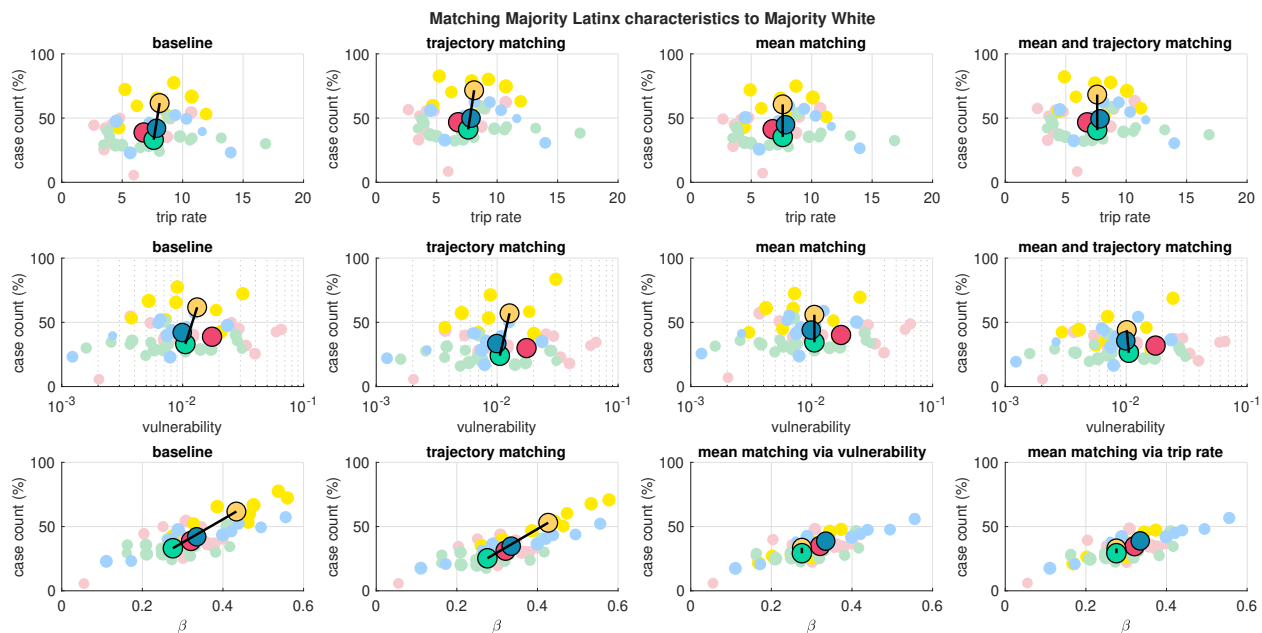


Figure S18: Matching group level characteristics of Majority Latinx group (modified) to Majority White group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

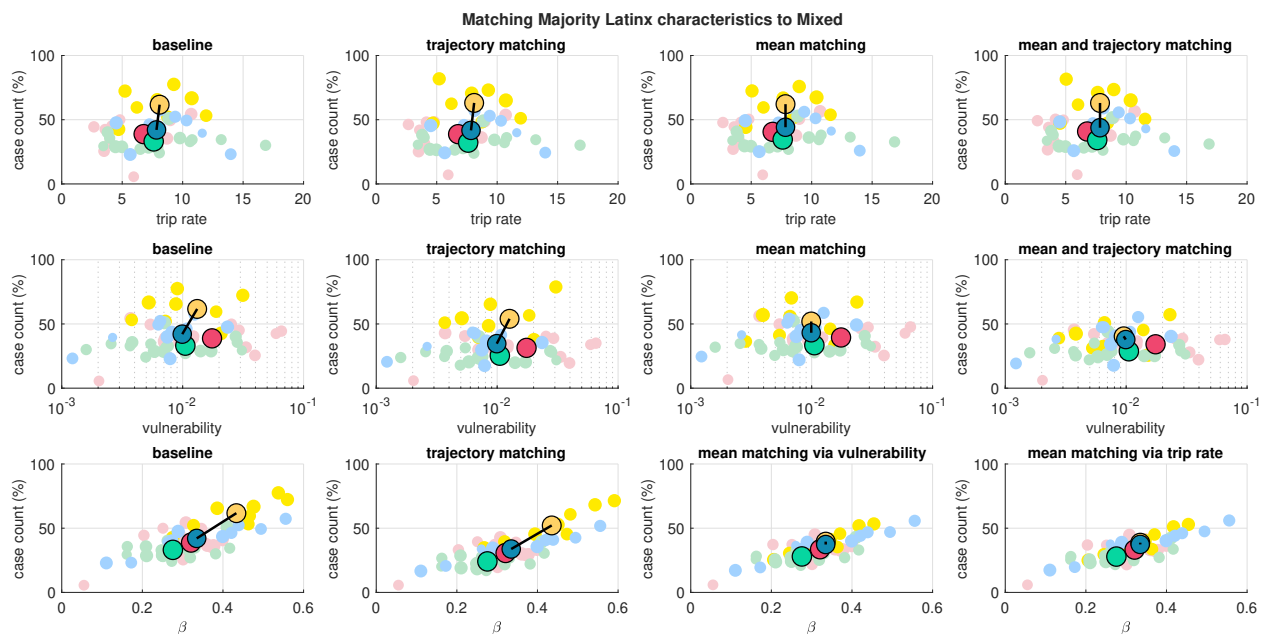


Figure S19: Matching group level characteristics of Majority Latinx group (modified) to Mixed group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

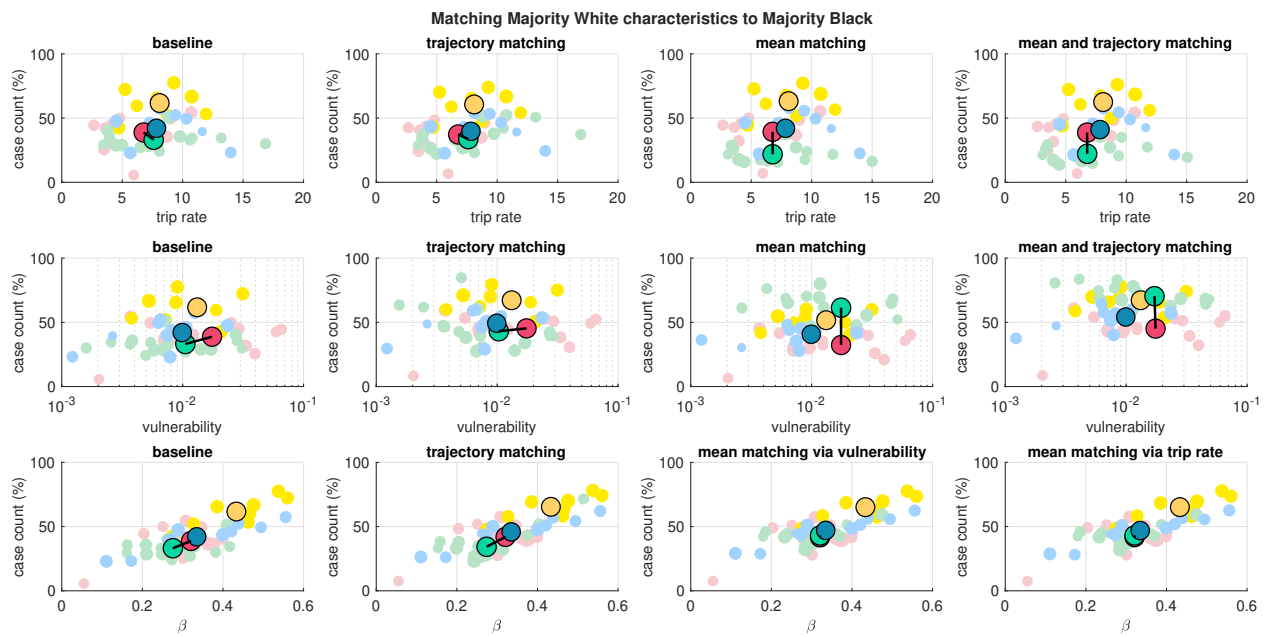


Figure S20: Matching group level characteristics of Majority White group (modified) to Majority Black group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

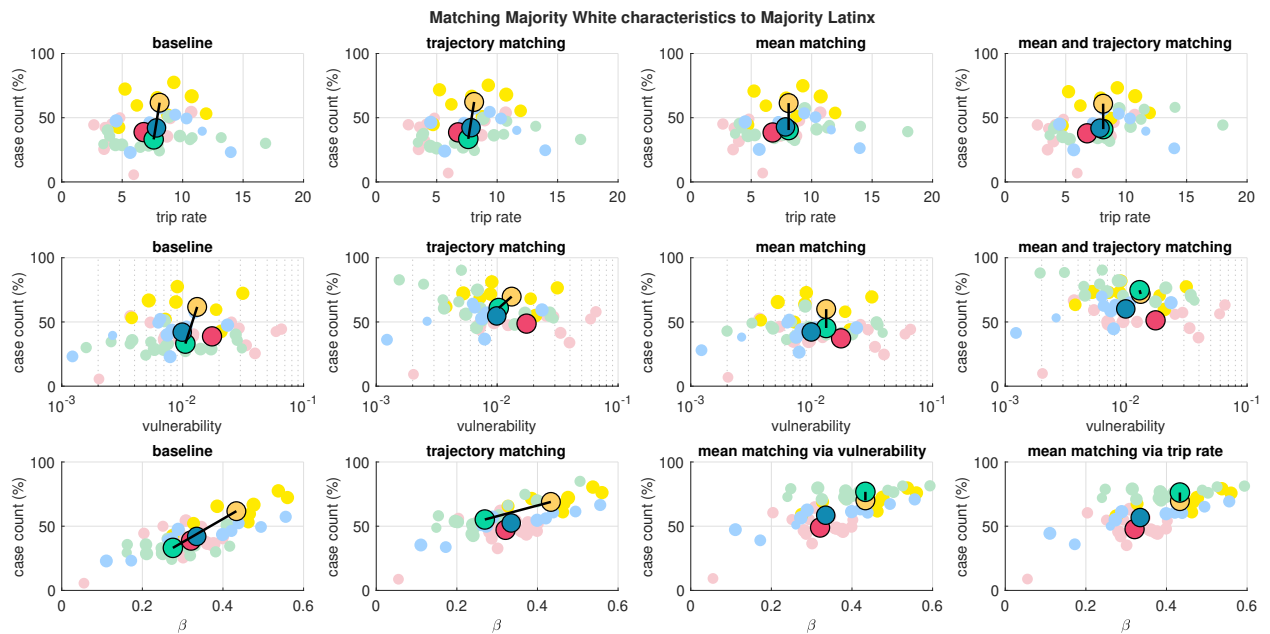


Figure S21: Matching group level characteristics of Majority White group (modified) to Majority Latinx group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

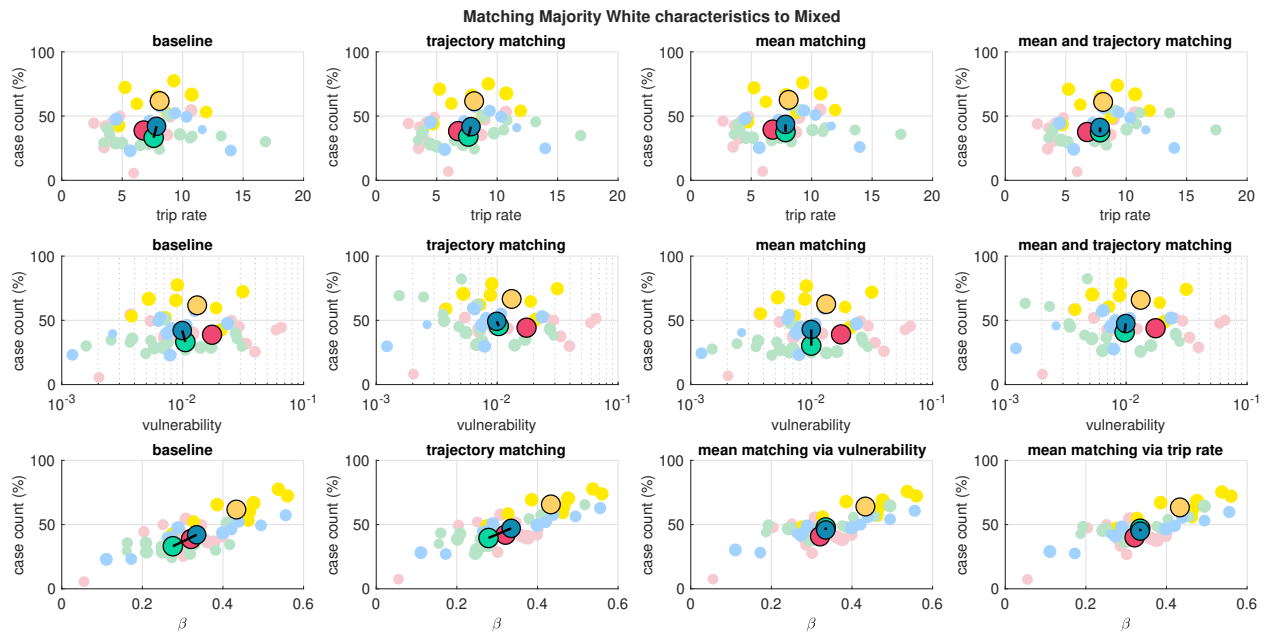


Figure S22: Matching group level characteristics of Majority White group (modified) to Mixed group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

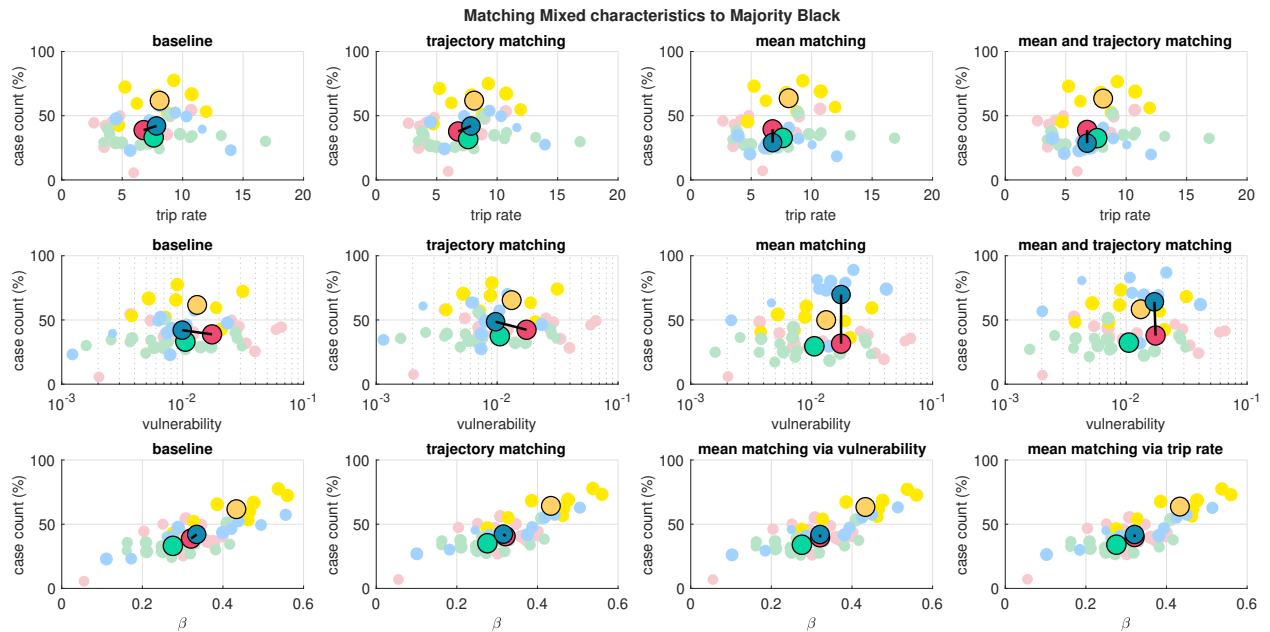


Figure S23: Matching group level characteristics of Mixed group (modified) to Majority Black group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

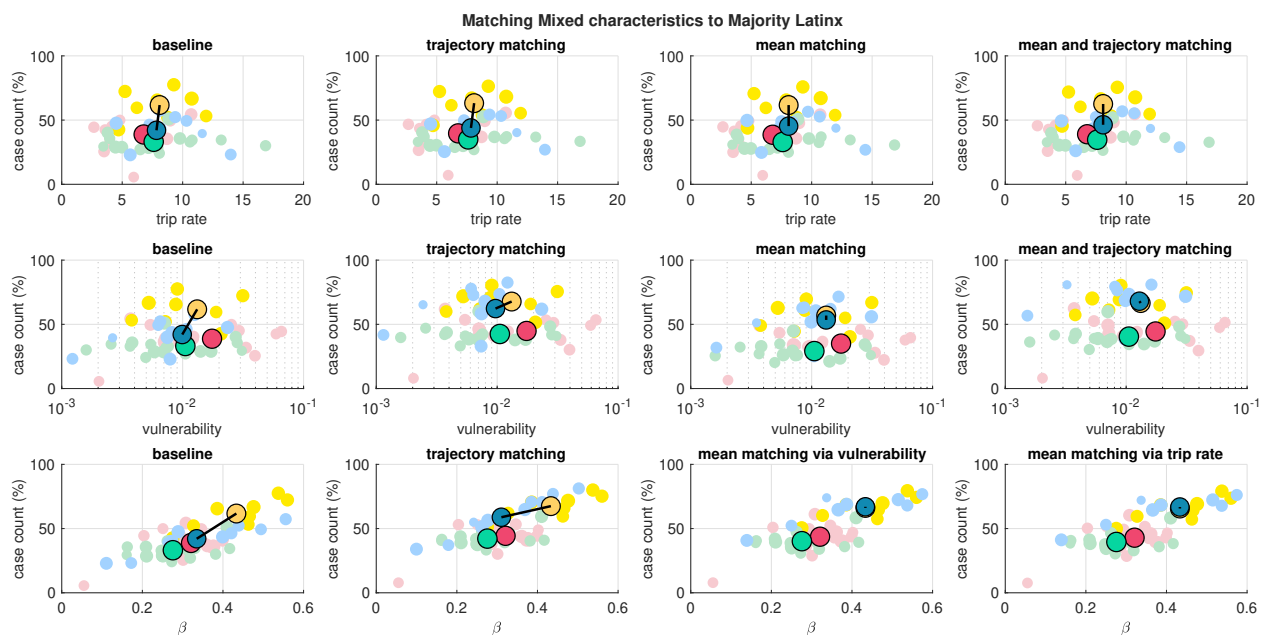


Figure S24: Matching group level characteristics of Mixed group (modified) to Majority Latinx group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.



Figure S25: Matching group level characteristics of Mixed group (modified) to Majority White group (remains unaffected). Majority Black: red; Majority Latinx: yellow; Majority White: green; Mixed: blue.

S5 Structural effects

To reveal how reduced group homophily would have affected the spread of COVID-19, we transform the movement matrices via Laplace smoothing, and conversely, the effects of increased homophily are investigated via isolation of groups and nodes via the transformations outlined in the Materials and Methods. The corresponding simulation results are presented in Figure S26 for both decreasing and increasing homophily. Complementing these, in Table S6 we present changes in group level case rate data and inequality (percentage difference between most and least affected groups) by modifying group level homophily to match their pre-COVID levels (Majority Black: 94% \rightarrow 92%, Majority Latinx: 91% \rightarrow 89%, Majority White: 94% \rightarrow 93%, Mixed: 90% \rightarrow 85%).

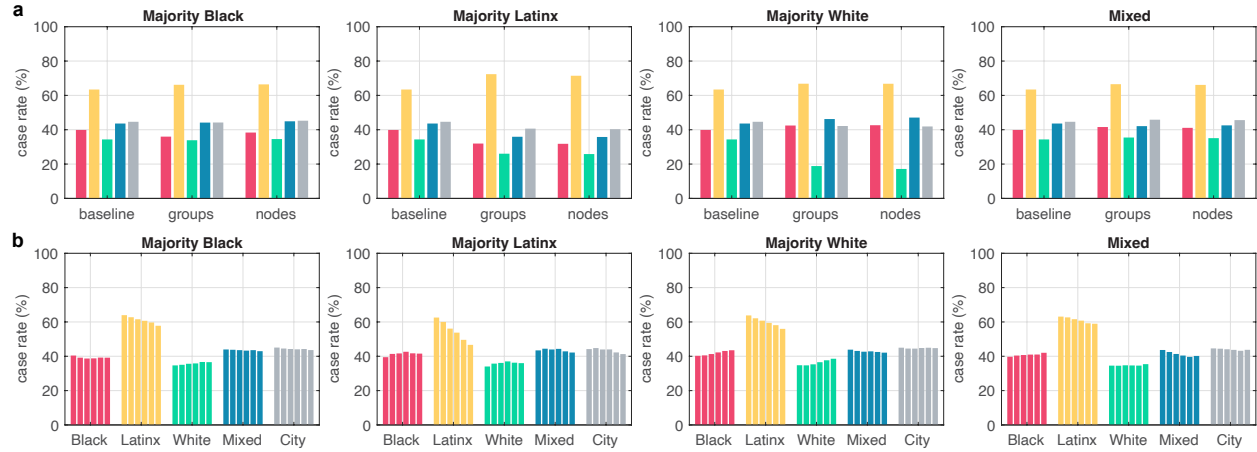


Figure S26: Effects of homophily (isolation) on disease progression. (a) Increasing isolation of groups. The group indicated above each panel is isolated from the rest of the network. No modifications to network structure is referred to as 'baseline,' whereas 'groups' and 'nodes' correspond to the cases where intragroup edges are modified as detailed in the Materials and Methods. (b) Decreasing isolation of groups via Laplace smoothing. Trips originating in the group indicated above each panel are undergoing Laplace smoothing. Bars within one group from left to right represent 0%, 5%, 10%, 15%, 20%, 25% reduction in group homophily.

Table S6: Percentage point change in case rate and inequality when modifying homophily during COVID (after March 15) to match pre-COVID levels (before March 15), considering 100 independent simulations and compared to the baseline scenario (Figure S9).

	Majority Black		Majority Latinx		Majority White		Mixed		City		Inequality	
	mean	std	mean	std	mean	std	mean	std	mean	std	mean	std
homophily changed to pre-COVID level												
Majority Black	-0.46	1.32	-0.30	1.32	0.19	1.45	-0.09	1.47	-0.16	1.32	-0.50	0.75
Majority Latinx	0.77	1.30	-1.44	1.38	0.81	1.46	0.52	1.42	0.21	1.32	-2.25	0.76
Majority White	0.36	1.44	-0.03	1.46	0.30	1.52	0.05	1.49	0.19	1.41	-0.34	0.78
Mixed	0.23	1.36	-0.72	1.42	0.37	1.43	-0.93	1.36	-0.19	1.33	-1.10	0.74
All groups	0.74	1.32	-2.95	1.46	1.21	1.57	-0.89	1.49	-0.33	1.40	-4.16	0.70

S6 Demographic trade-offs

Here, we reveal how changes in group level characteristics such as trip rate and vulnerability would have corresponded to case rate outcomes, as well as how these could be interpreted in terms of socio-economic differences. Correlation and linear regression analysis results between socio-economic factors, case rate, and β are presented in Figure S27.

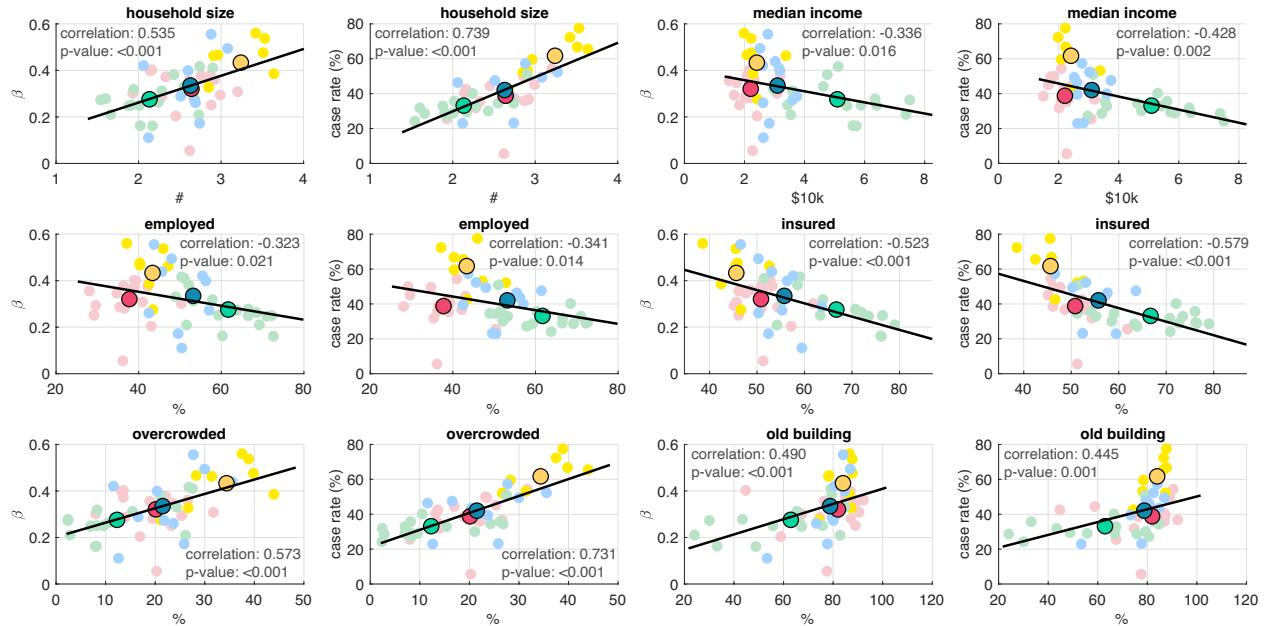


Figure S27: Linear regression between socio-economic factors, case rate, and β . Circles without borders denote ZIP Code level data, whereas those with borders correspond to population weighted group level averages. Black lines denote the result of linear regression.

S7 Milwaukee

Due to potential mis-attribution of trips (indicated by low levels of homophily), the following ZIPs were combined in Milwaukee: 53203 with 53233 (composite is Majority White), and 53205 with 53206 (composite is Majority Black). Note that similar steps were undertaken in Chicago, i.e., our approach in processing the data in Milwaukee is the same as in the Chicago case. The resulting analysis details are presented in Figure S28, depicting an overall picture that is qualitatively similar to the one revealed in Chicago: (i) the progression of the pandemic can be faithfully reconstructed, including multiple peaks; (ii) daily mobility is essentially concentrated within one's own ZIP Code and demographic group, a pattern closely mirrored by the distribution of exposures; (iii) group level differences in the volume of mobility (trip rate) and the average risk each trip represents (vulnerability) together govern epidemic progression as only when differences in both are simultaneously eliminated do group level case rate disparities disappear; and (iv) reduced homophily decreases inequality as the groups with case rates above the city level average (27%) experience a drop (Majority Latinx), while those below it show either no appreciable change (Majority Black, Mixed) or an increase (Majority White). Similarly to what was observed in Chicago (Table S6), inequality in case rates decreases by over 2% when modifying group level homophily to match pre-COVID levels (Majority Black: 91% \rightarrow 88%, Majority Latinx: 80% \rightarrow 78%, Majority White: 96% \rightarrow 95%, Mixed: 64% \rightarrow 59%).

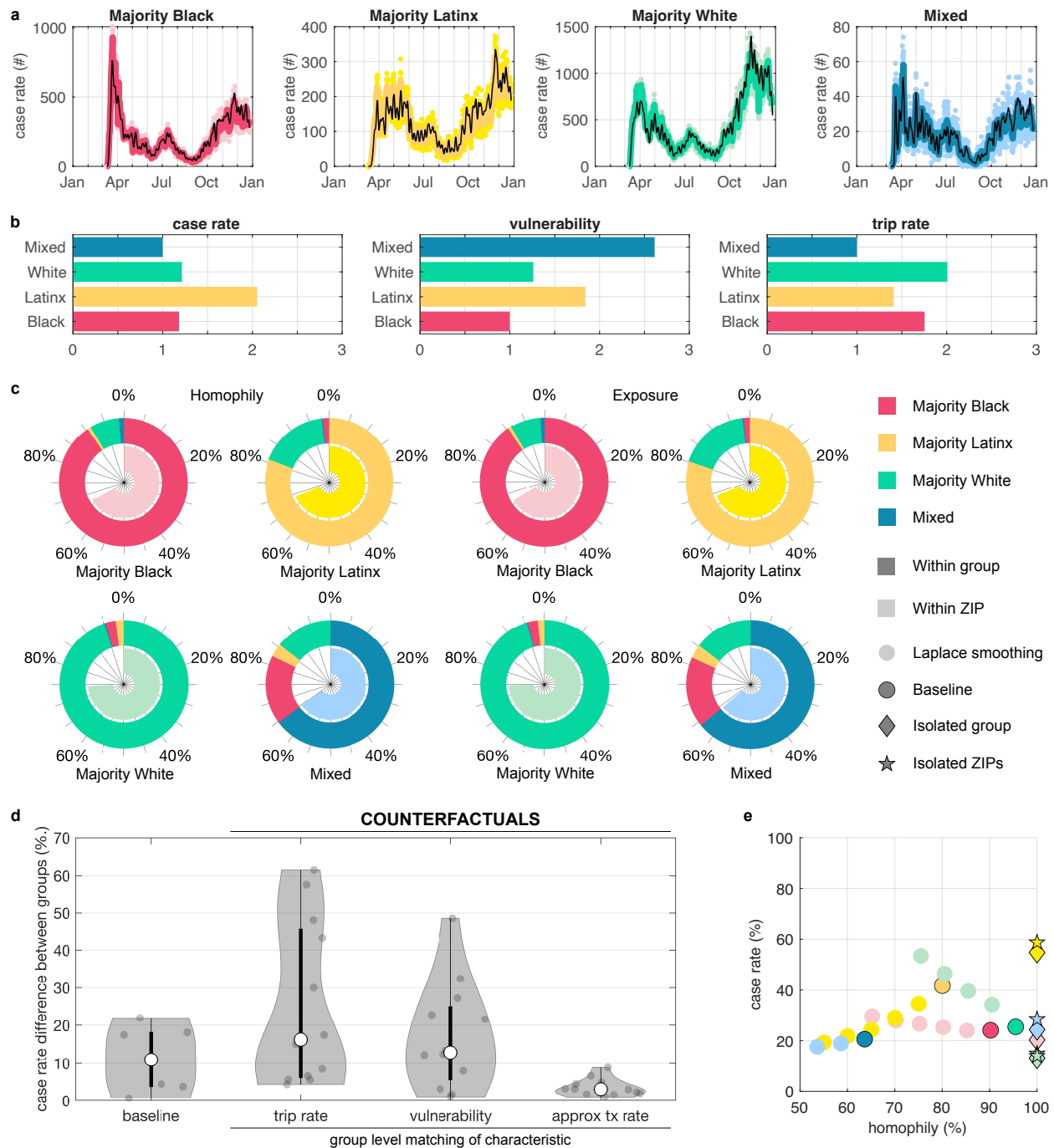


Figure S28: Analysis results in Milwaukee. **(a)** Model fit with combined ZIPs. Group level estimated case rate is depicted in black, simulation data from 10 independent runs are depicted with dots, their average is displayed with thick curve of the same color. **(b)** Group level averages of case rate, vulnerability and trip rate (all normalized to the smallest value across the groups). **(c)** Group level averages of outgoing trip distribution and estimated sources of exposure (inner rings represent trips to own ZIP and exposures within own ZIP). **(d)** Difference in case rate between groups (grey dots). The baseline scenario refers to the observed outcome in Milwaukee over 2020, the counterfactuals are obtained as in Figure 3b. **(e)** Baseline refers to the observed mobility data (dark circles). Homophily is increased either by isolating a select group from the rest of the network (diamonds) or by further isolating nodes (ZIPs) within the group (stars). Homophily is reduced by rescaling outgoing trips using Laplace smoothing for all nodes within a select group in 5% increments (light circles), keeping both the trip rate and the ordering of weights (i.e., importance of connections) unchanged, without affecting trips originating in other groups.