

# Validating and Modeling the Impact of High-Frequency Rapid Antigen Screening on Covid-19 Spread and Outcomes

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## SUPPLEMENTARY MATERIAL

**Table S1:** Summary of results of COVID-19 outcomes in 3 US Regions and Brazil as a result of Frequent Rapid Testing Protocol using SIDHRE-Q Model.

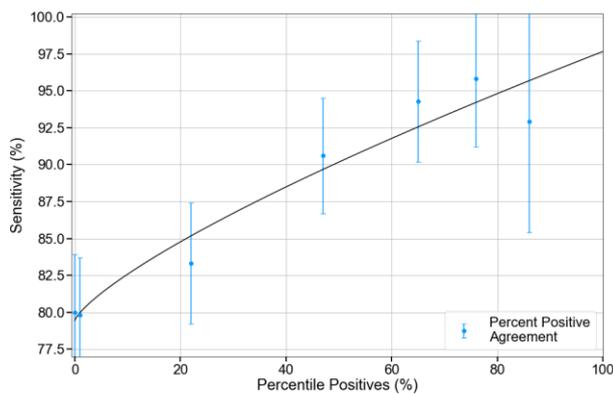
	Massachusetts		Los Angeles		New York City		São José do Rio Preto, Brazil	
	qRT-PCR	1 per 3 days	qRT-PCR	1 per 3 days	qRT-PCR	1 per 3 days	qRT-PCR	1 per 3 days
<b>Total Infected</b>	18.40%	1.60%	11.70%	1.42%	26.40%	9.45%	11.70%	0.186%
<b>Max Hospitalized</b>	0.056%	0.025%	0.028%	0.022%	0.144%	0.130%	0.054%	0.003%
<b>Total Deaths</b>	0.119%	0.029%	0.039%	0.009%	0.226%	0.157%	0.040%	0.003%

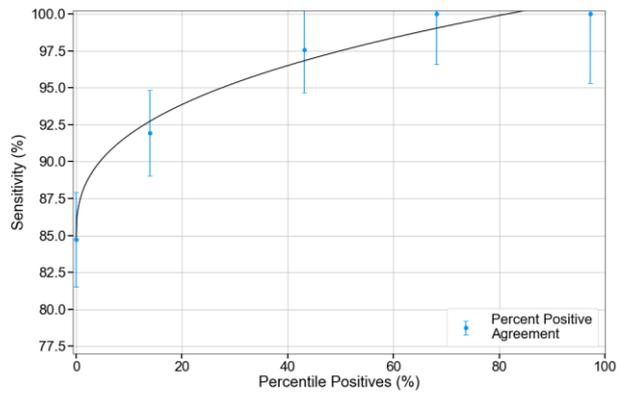
**Table S2:** Demographic and clinical summary of patients evaluated by the SARS-CoV-2 Direct Antigen Rapid Test (DART).

N response, N or mean of positive, and % or standard deviation for each group is presented. All samples (n=121) collected and tested in São José do Rio Preto, Brazil.

	TOTAL			COVID-19 positive			COVID-19 negative		
	N response	N or mean of positive	% or standard deviation	N response	N or mean of positive	% or standard deviation	N response	mean of positive	% or standard deviation
<b>Age</b>	121	40.43	17.17	72	43.37	12.58	49	36.12	15.3
0-14 yr	121	5	4.1%	72	2	2.8%	49	3	6.1%
15-29 yr	121	30	24.8%	72	17	23.6%	49	13	26.5%
30-59 yr	121	69	57.0%	72	39	54.2%	49	30	61.2%
≥60 yr	121	17	14.0%	72	14	19.4%	49	3	6.1%
<b>Gender</b>									
Female	121	75	62.0%	72	43	59.7%	49	32	65.3%
Male	121	46	38.0%	72	29	40.3%	49	17	34.7%
<b>Comorbidities</b>									
Cardiovascular disease	115	7	6.1%	71	6	8.5%	44	1	2.3%
Diabetes	115	9	7.8%	71	6	8.5%	44	3	6.8%
Asthma	115	1	0.9%	71	1	1.4%	44	0	0.0%
Pulmonary disease	115	4	3.5%	71	1	1.4%	44	3	6.8%
Chronic Kidney disease (Stage III, IV, V)	115	12	10.4%	71	1	1.4%	44	11	25.0%
Immunosuppression	115	3	2.6%	71	1	1.4%	44	0	0.0%
Post pregnant	115	2	1.7%	71	1	1.4%	44	1	2.3%
Neurologic Disease	115	0	0.0%	71	0	0.0%	44	0	0.0%
Chromosomal disease	115	0	0.0%	71	0	0.0%	44	0	0.0%
Hematological diseases	115	0	0.0%	71	0	0.0%	44	0	0.0%
Liver disease	115	0	0.0%	71	0	0.0%	44	0	0.0%
Obesity	115	0	0.0%	71	0	0.0%	44	0	0.0%
Hospitalization	116	5	4.3%	71	5	7.0%	45	0	0.0%
Asymptomatic	116	8	6.9%	71	6	8.5%	45	2	4.4%
<b>Initial symptoms</b>									
Fever	116	40	34.5%	71	32	45.1%	45	8	17.8%
Cough	116	66	56.9%	71	42	59.2%	45	24	53.3%
Sore throat	116	47	40.5%	71	22	31.0%	45	25	55.6%
Dyspnea	116	25	21.6%	71	17	23.9%	45	8	17.8%
Low Saturation	116	4	3.5%	71	4	5.7%	45	0	0.0%
Diarrhea	116	4	3.5%	71	4	5.7%	45	0	0.0%
Vomit	116	3	2.6%	71	2	2.9%	45	1	2.2%
Headache	116	43	37.4%	71	28	40.0%	45	15	33.3%
Days of fever/symptoms	120	3.23	2.64	71	3.29	2.46	49	3.14	2.9

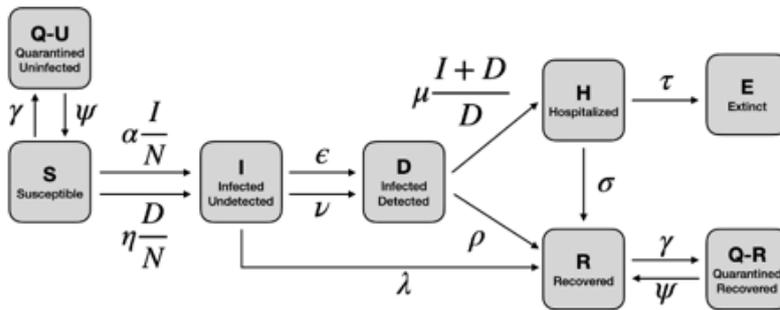
(A)





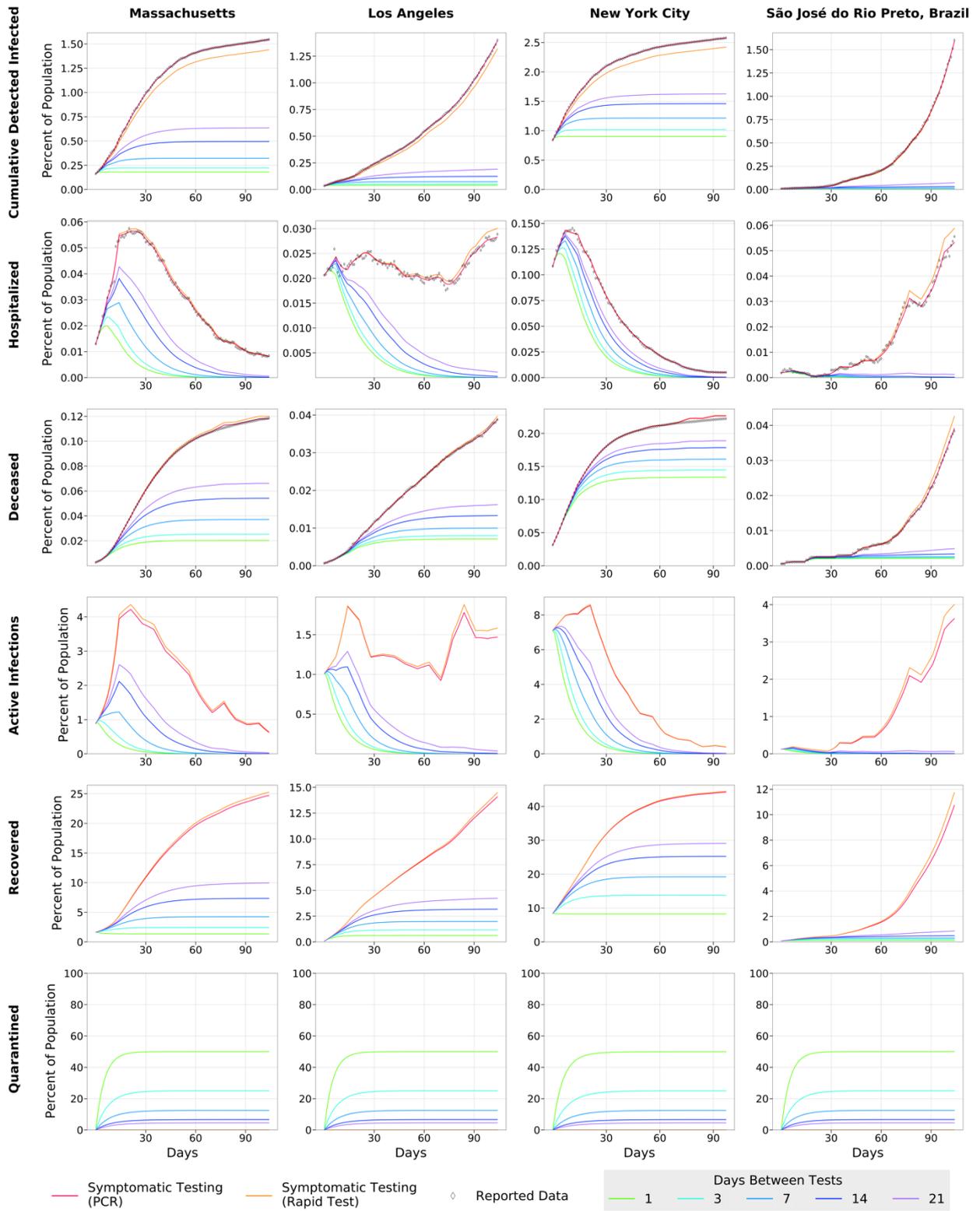
(B)

**Figure S1:** Performance of Direct Antigen Rapid Test (DART) for the detection of SARS-CoV-2 (A) nucleocapsid protein (n=158) and (B) spike glycoprotein (n=121). Shown are the percentile positive cases of the total positive population conditioned to qRT-PCR Cycle Threshold (Ct). Percentile Positive ranks the samples in order of high Ct to low Ct. DART sensitivity is determined by calculating true positive agreement to qRT-PCR; the plot uses an  $axb+c$  fit and 95% confidence intervals for the sensitivity.



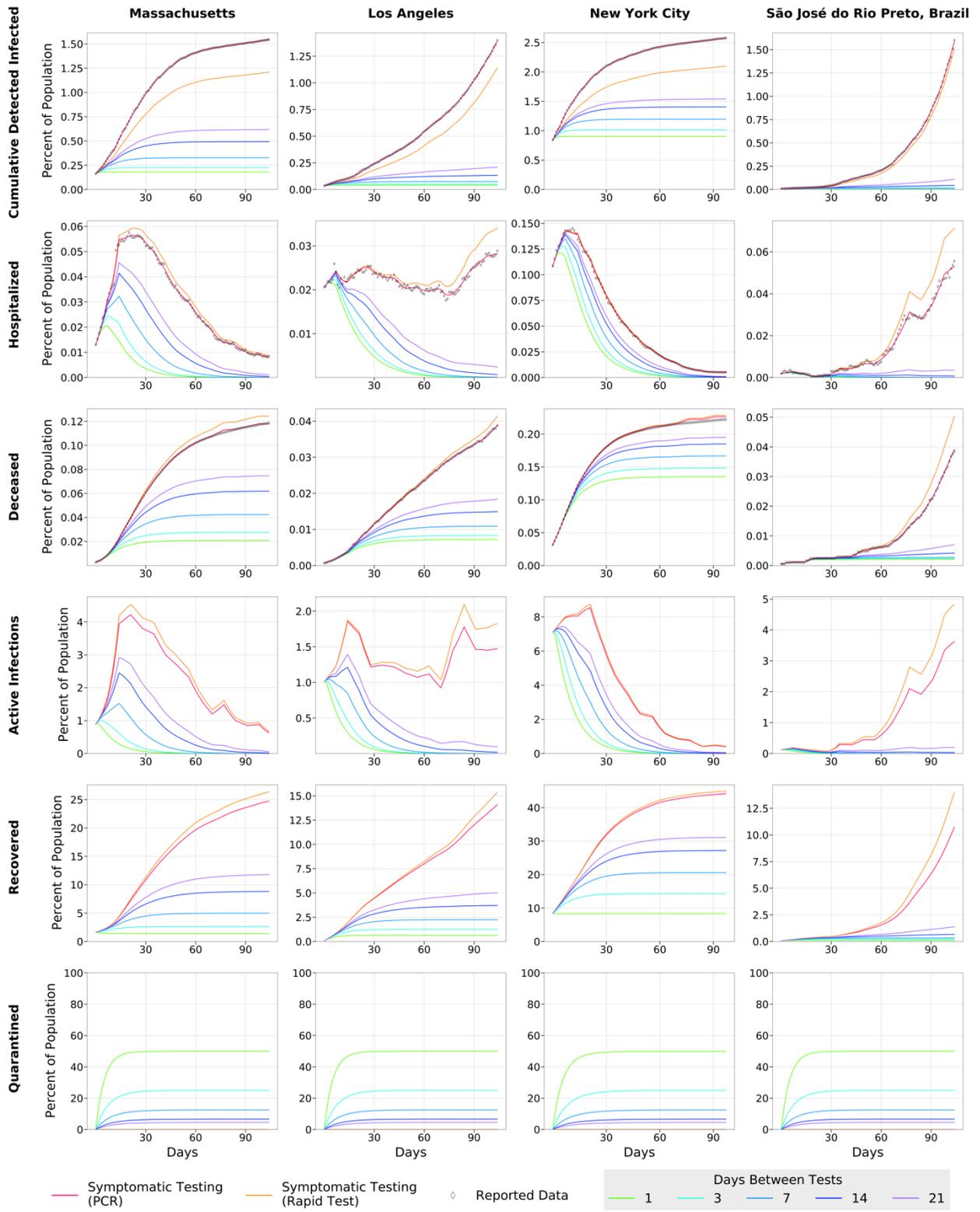
**Figure S2:** Graphical scheme displaying the relationships between the stages of quarantine and infection in SIDHRE-Q model: Q-U, quarantine uninfected; S, susceptible (uninfected); I, infected undetected (pre-testing and infected); D, infected detected (infection diagnosis through testing); H, hospitalized (infected with life threatening symptom progression); R, recovered (healed); E, extinct (dead); and Q-R, quarantine recovered (healed but in quarantine by false positive testing).

(A)



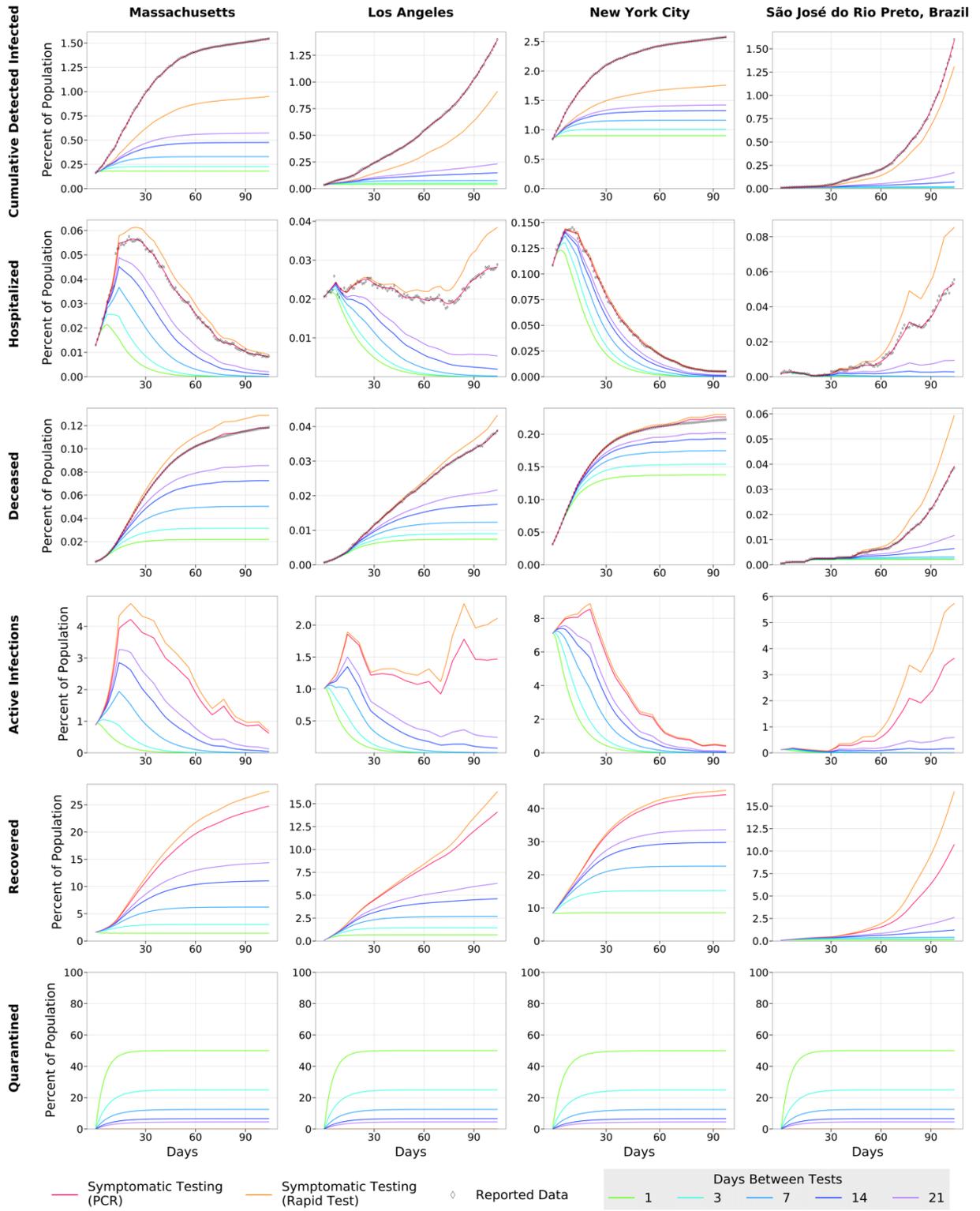
Sensitivity: 90.0% Specificity: 90.0%

(B)



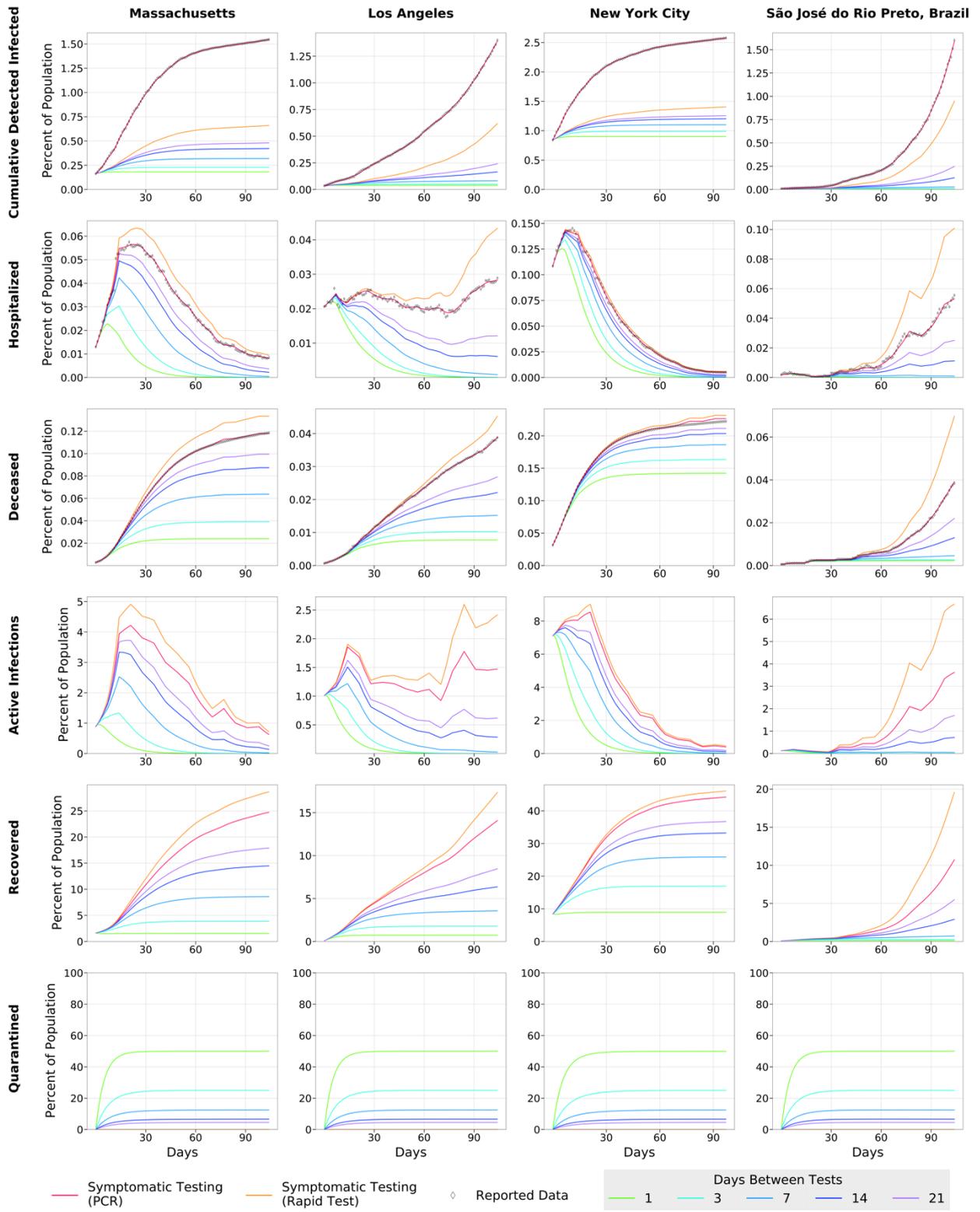
Sensitivity: 70.0% Specificity: 90.0%

(C)



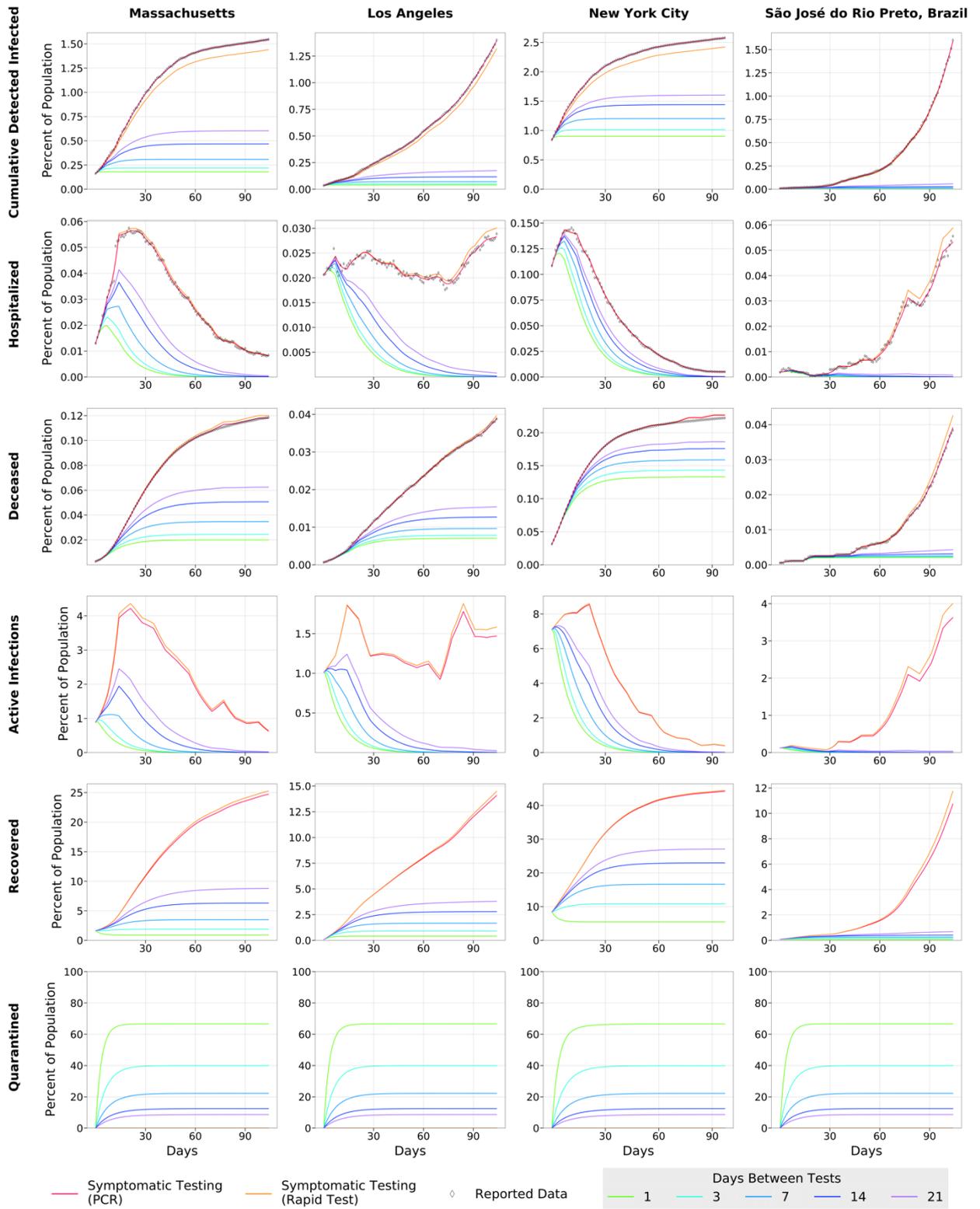
Sensitivity: 50.0% Specificity: 90.0%

(D)



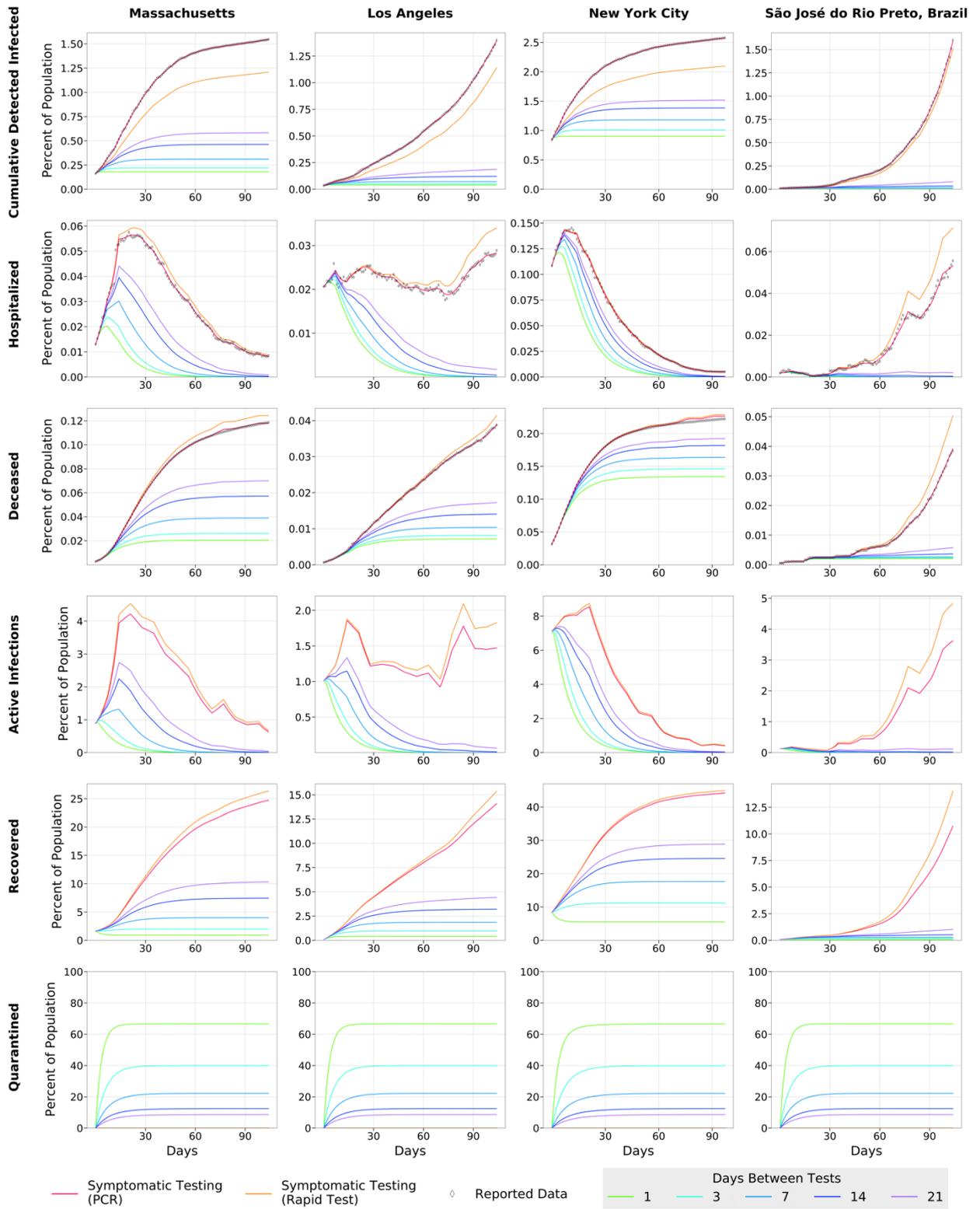
Sensitivity: 30.0% Specificity: 90.0%

(E)



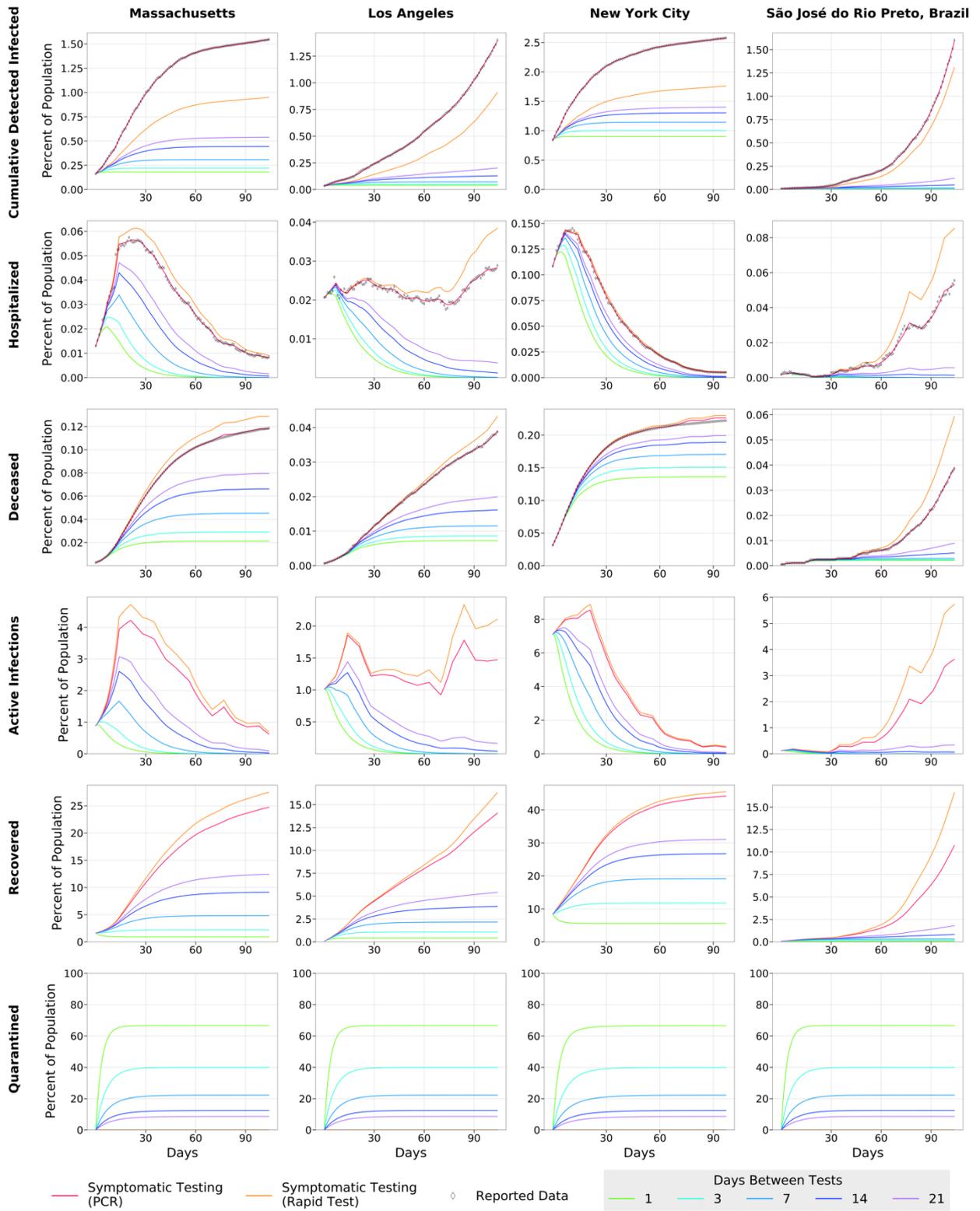
Sensitivity: 90.0% Specificity: 80.0%

(F)



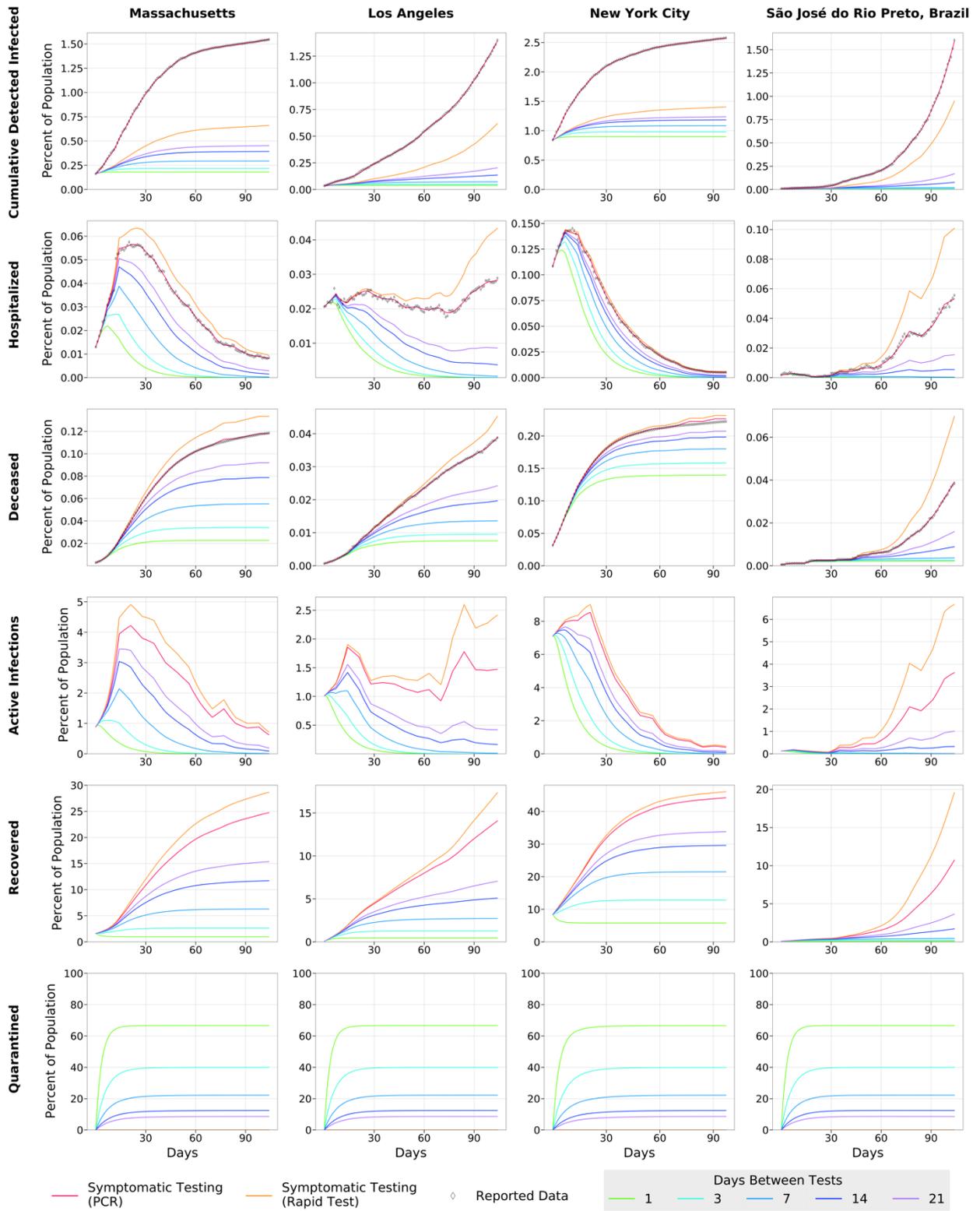
Sensitivity: 70.0% Specificity: 80.0%

(G)



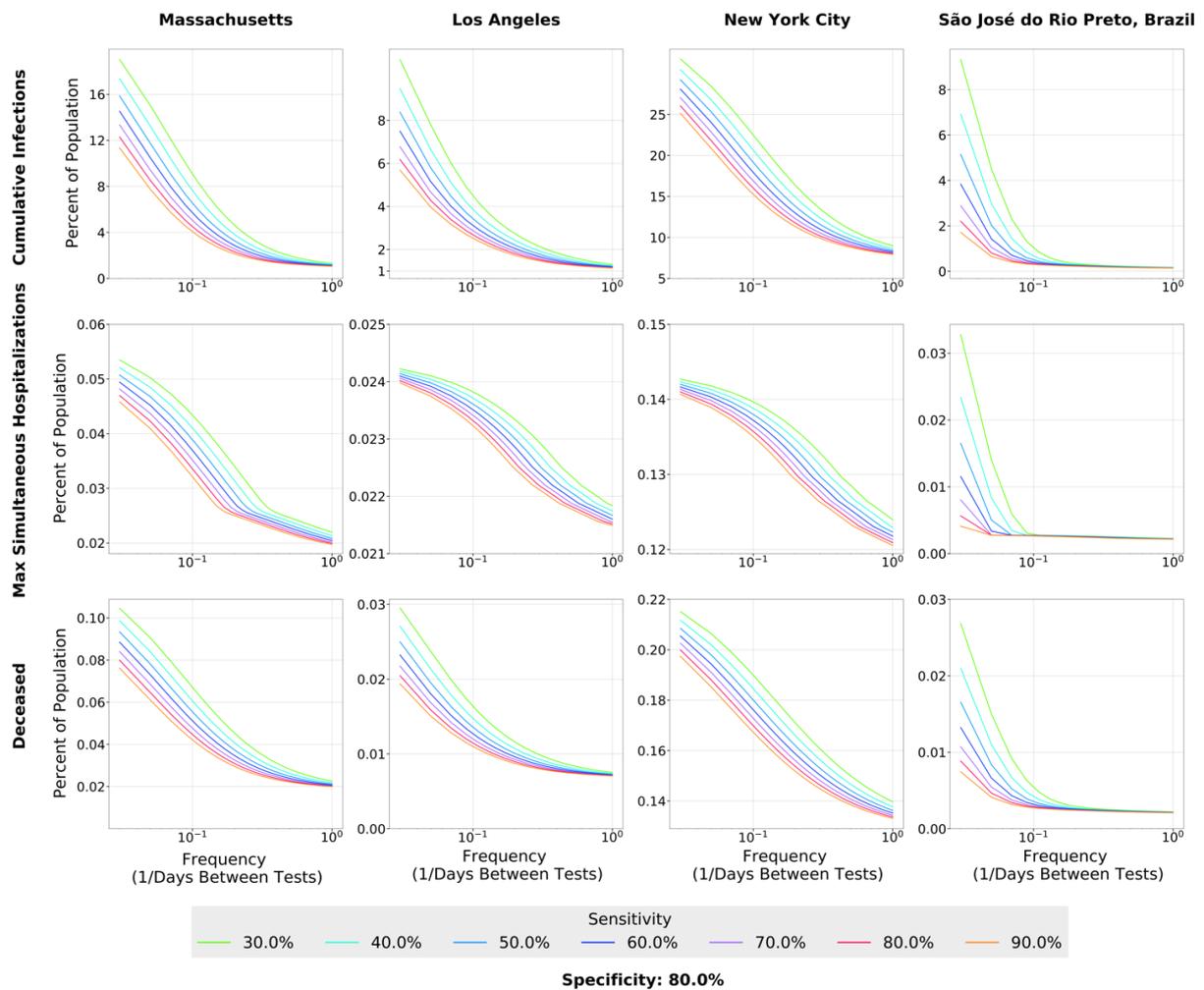
Sensitivity: 50.0% Specificity: 80.0%

(H)

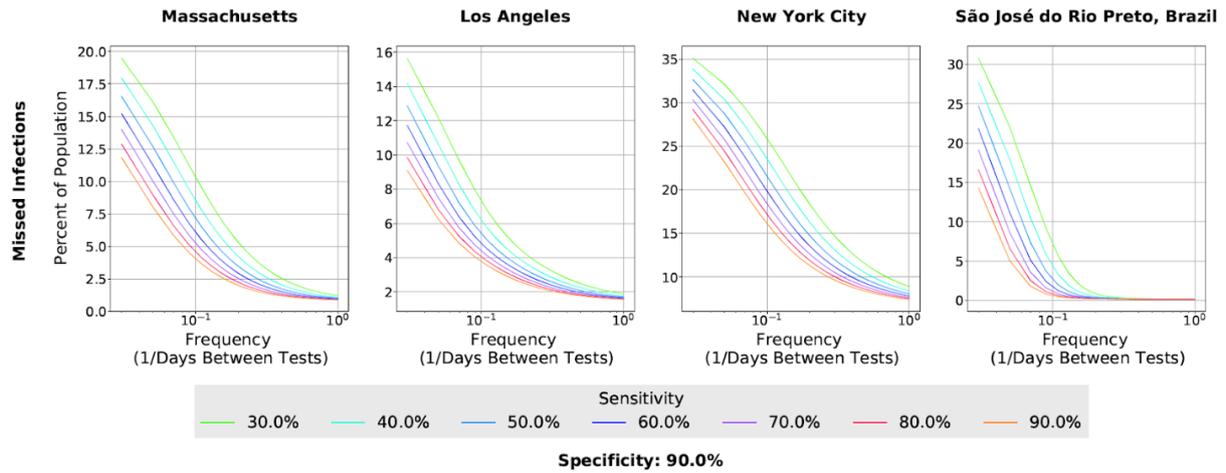


Sensitivity: 30.0% Specificity: 80.0%

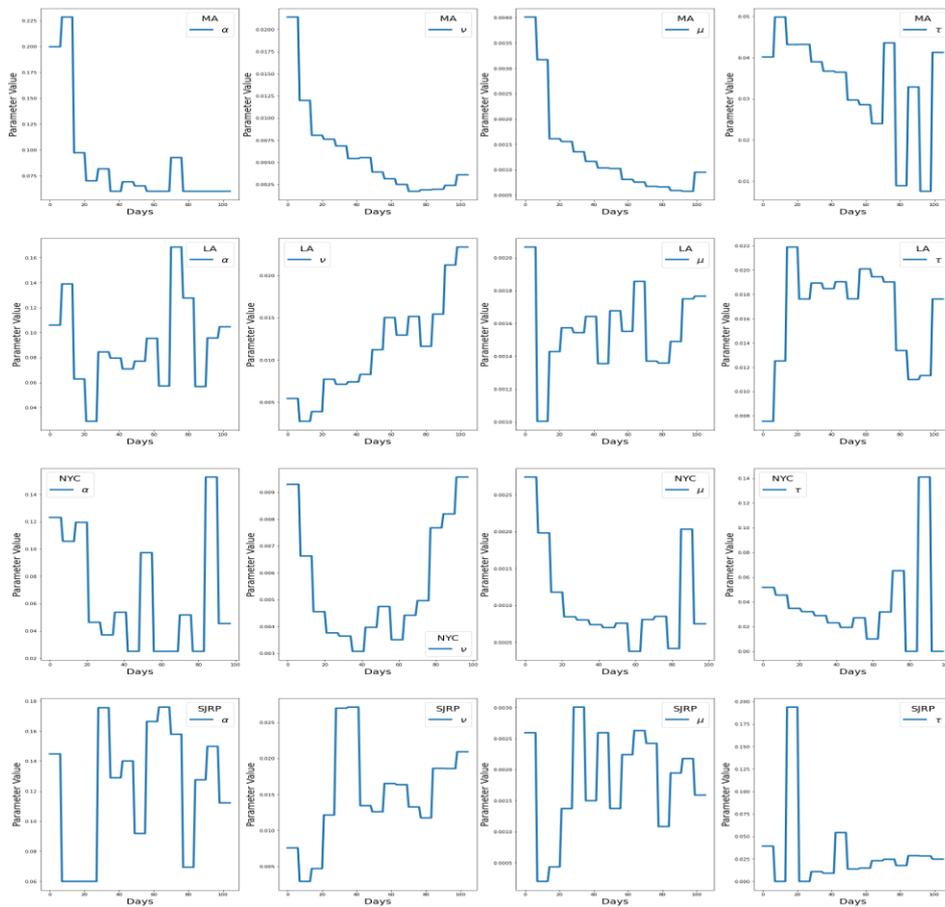
**Figure S3:** COVID-19 Outcomes as a result of Frequent Rapid Testing Protocol with variable test performances using SIDHRE-Q Model. The Cumulative Detected Infected, Hospitalized, Deceased, Active Infections, Recovered, and Quarantined are modeled over 105 days (top to bottom) using reported data from 4 global regions: Massachusetts, Los Angeles, New York City, and São José do Rio Preto in Brazil (left to right). The COVID-19 population spread and outcomes are modeled under a Rapid Testing Protocol with variable testing frequencies ranging from 1-21 days between tests, and variable test performances: 90% specificity with 90% sensitivity (A), 70% sensitivity (B), 50% sensitivity (C), and 30% sensitivity (D); and 80% specificity with 90% sensitivity (E), 70% sensitivity (F), 50% sensitivity (G), and 30% sensitivity (H). This protocol is compared to a symptom-based Rapid Testing protocol and a symptom-based qRT-PCR protocol.



**Figure S4:** Effect of Rapid Testing Protocol under variable testing sensitivities and increasing frequency under the SIDHRE-Q Model. The Cumulative Infections, Maximum Simultaneously Hospitalized, and Deceased populations are modeled for Massachusetts, Los Angeles, New York City, and São José do Rio Preto in Brazil. The effect of increasing frequency of testing is modeled for various testing sensitivities (30%-90%) with an 80% specificity.

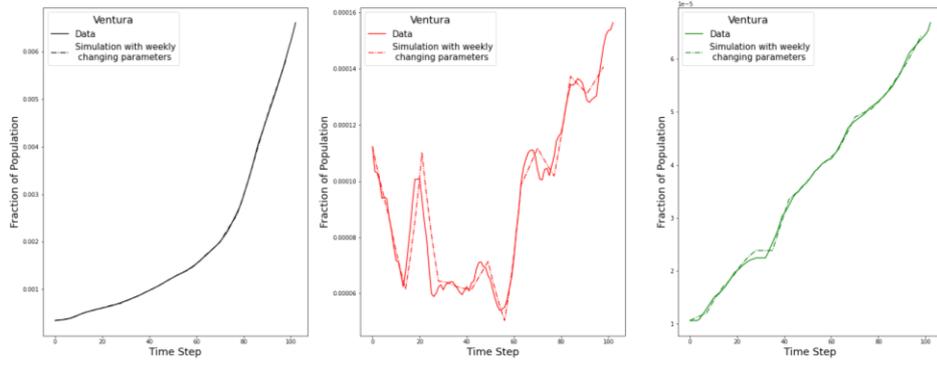


**Figure S5:** Missed infections-number of infections that were never diagnosed by the rapid test as a function of  $\log(\text{frequency})$  for a range of sensitivities with a 90% specificity. Models are shown for MA, LA, NYC, and SJRP.

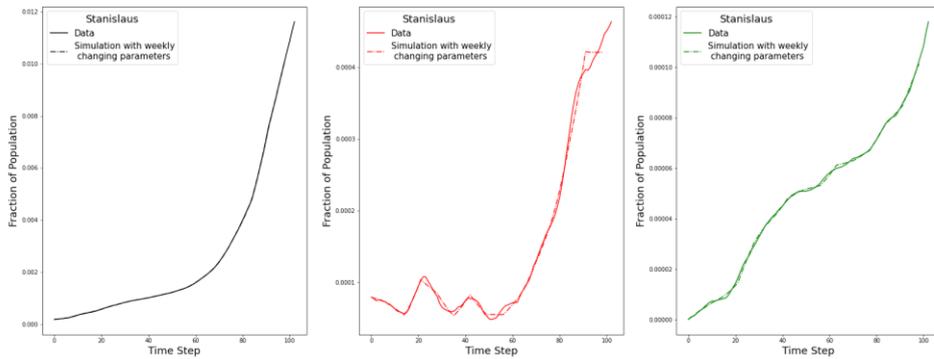


**Figure S6:** Time series of the four fitted parameters  $\alpha$ ,  $\nu$ ,  $\mu$ , and  $\tau$  (left to right) for MA, LA, NYC, and SJRP (top to bottom). See Table 3 in the Methods section for an explanation of the parameters. The values are extracted every seven days from data provided by the respective regions. The parameters vary significantly over time and location. Flat points occur during the seven day windows where the parameters are held constant. The fitting procedure is also outlined in the Methods section.

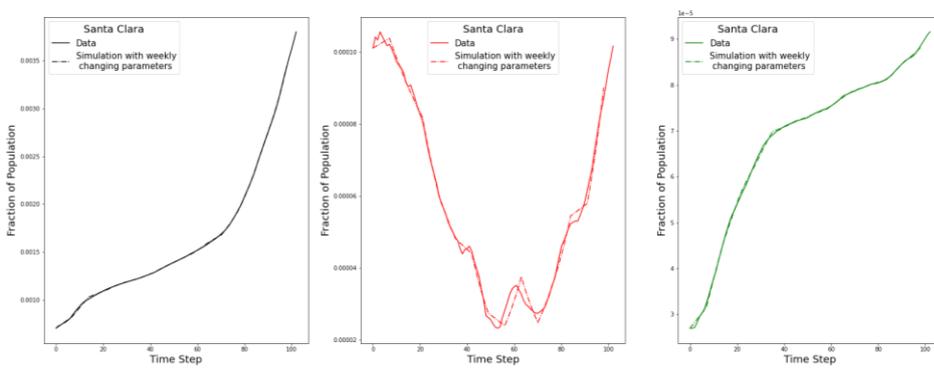
(A)



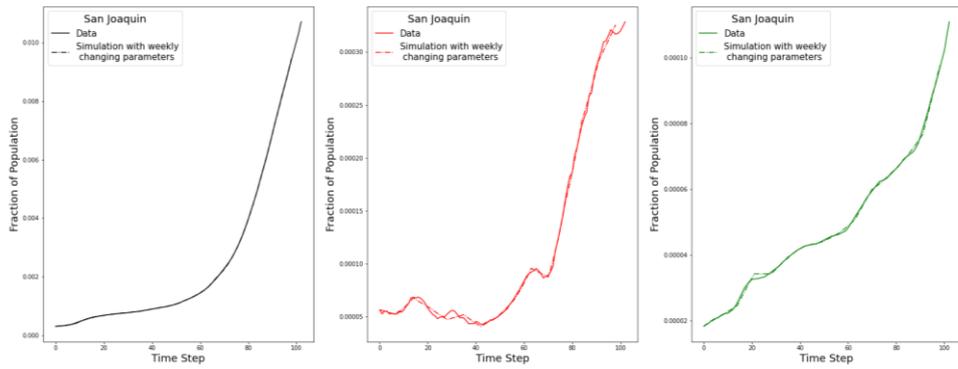
(B)



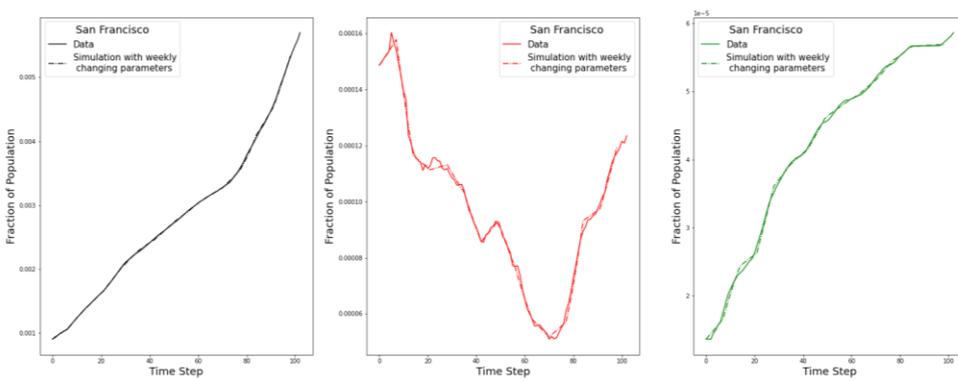
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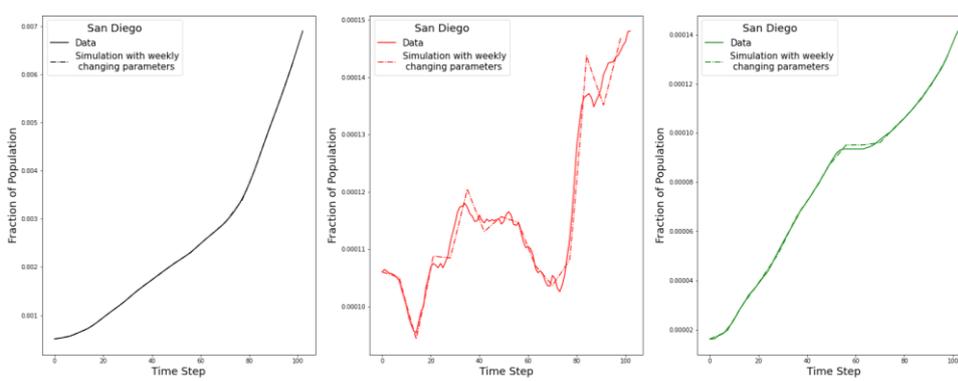
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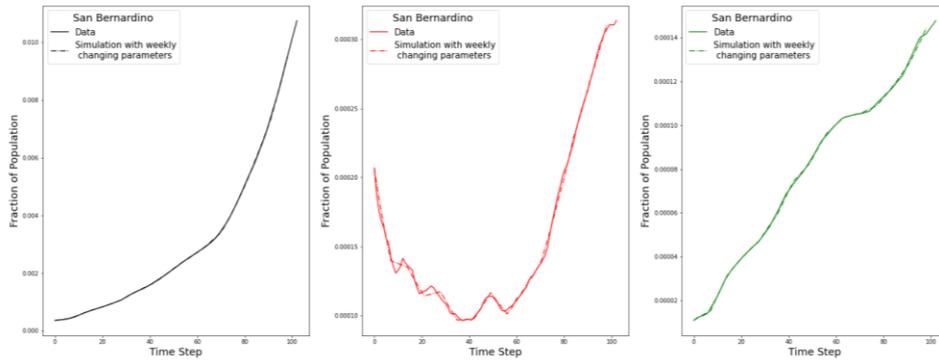
(E)



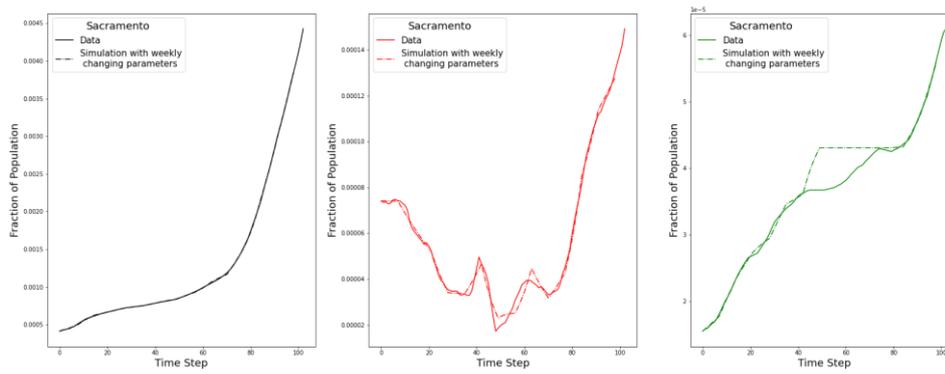
(F)



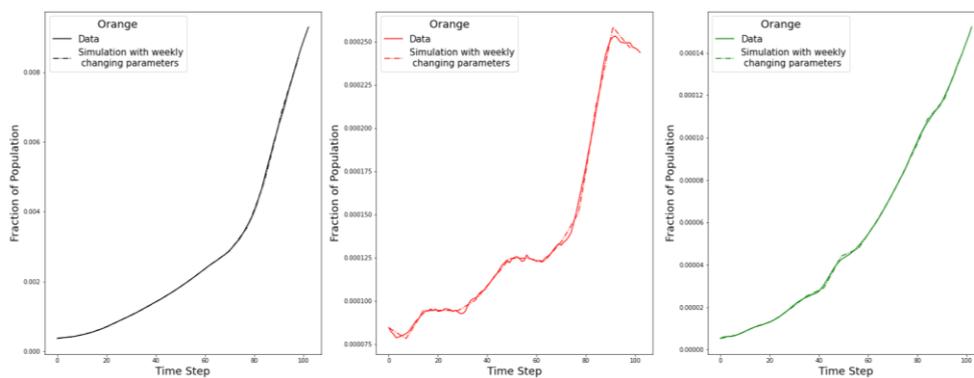
(G)



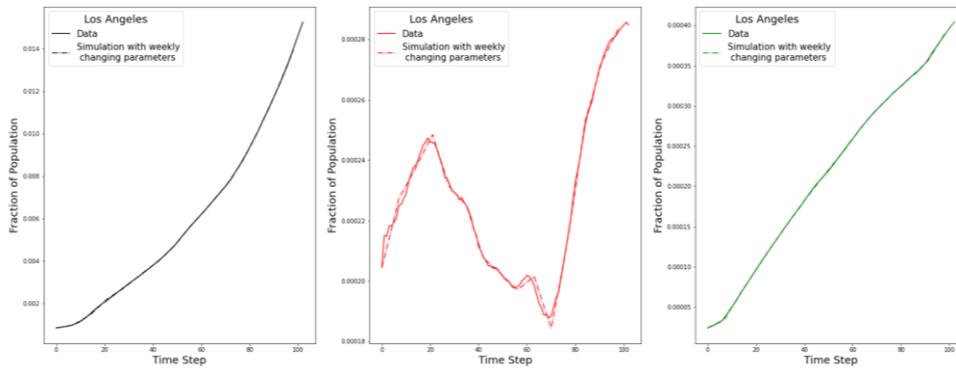
(H)



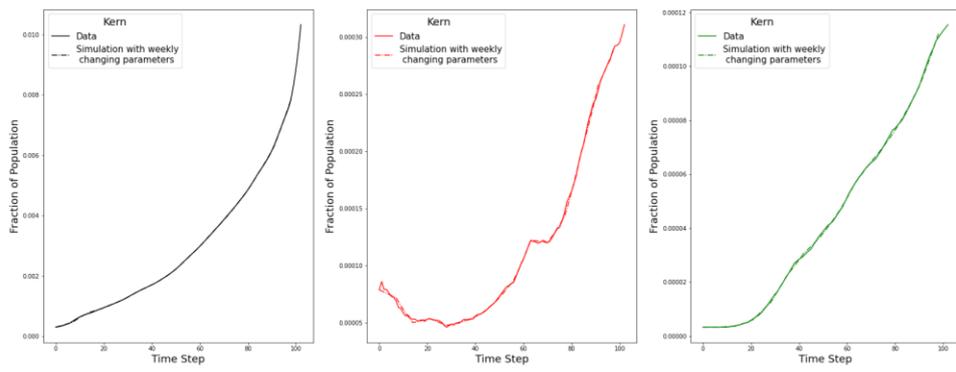
(I)



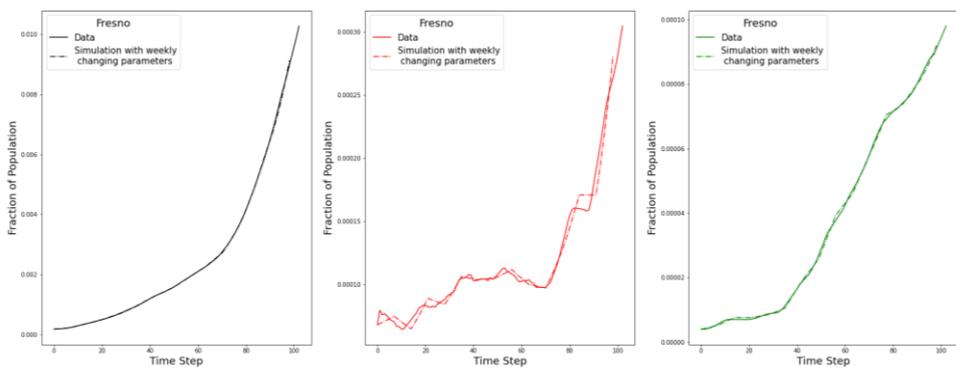
(J)



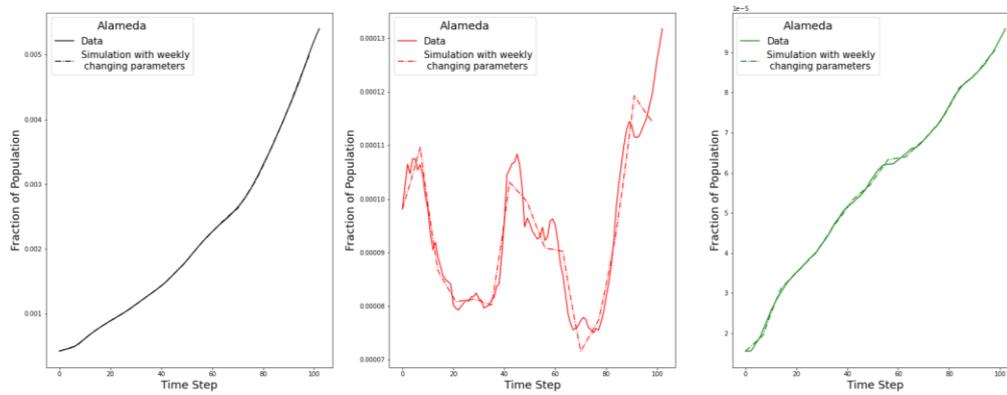
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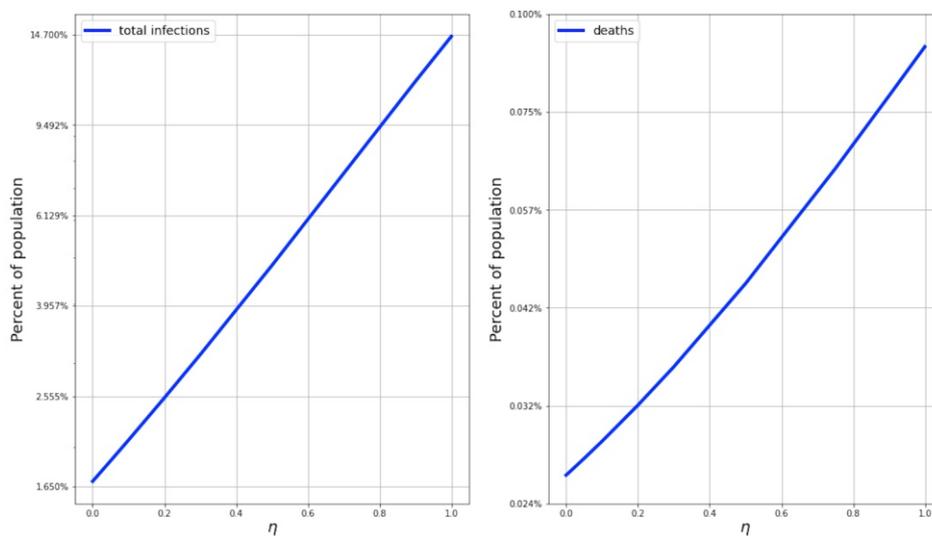
(L)



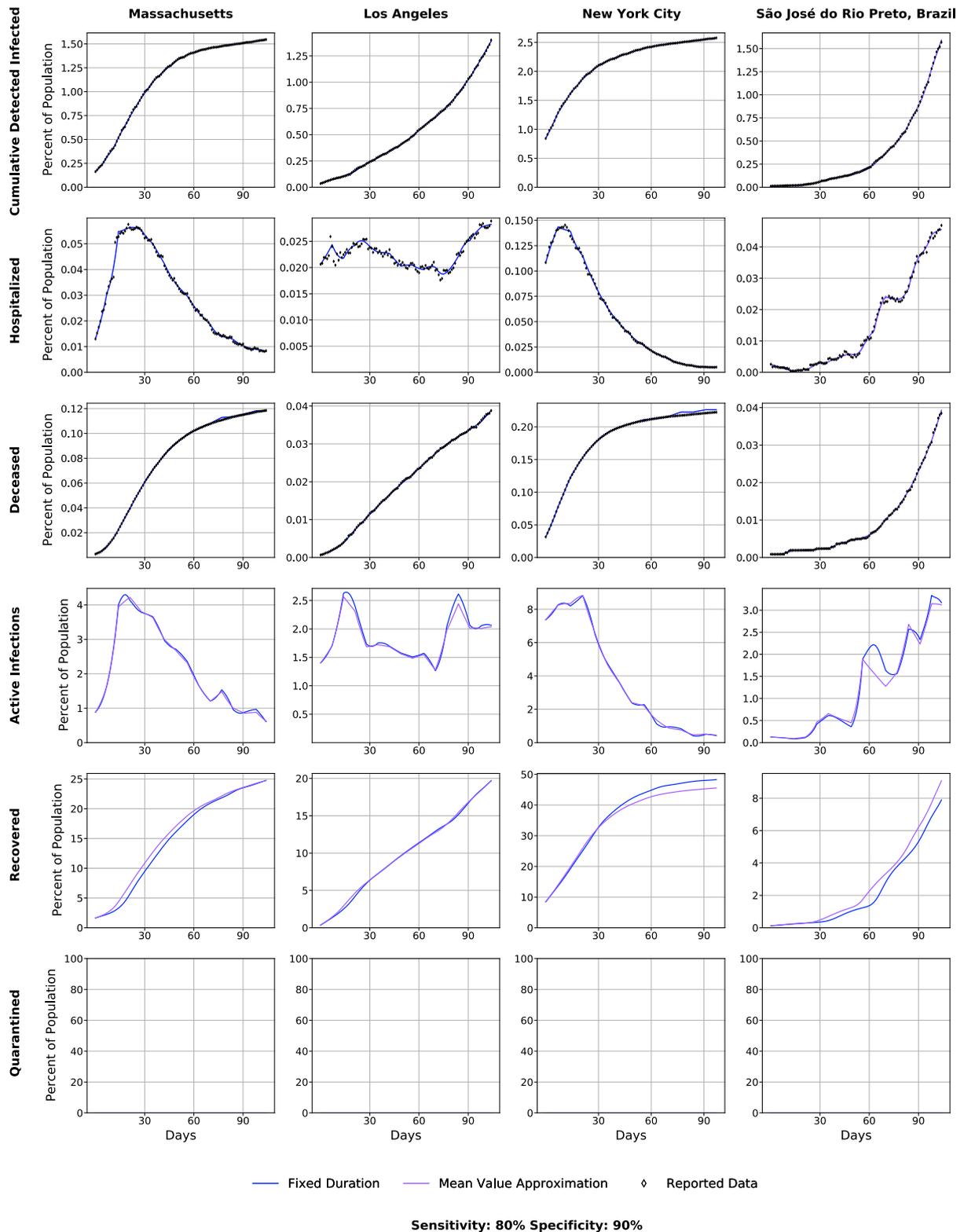
(M)



**Figure S7:** Time series of the three fitted pieces of data Cumulative Cases, Daily Hospitalized, and Cumulative Deaths (left to right) for each county receiving testing in CA; Ventura (A), Stanislaus (B), Santa Clara (C), San Joaquin (D), San Francisco (E), San Diego (F), San Bernardino (2G), Sacramento (H), Orange (I), Los Angeles (J), Kern (K), Fresno (L), Alameda (M). The counties included satisfy two requirements: population greater than 1.5% of the total CA population and nonzero total number of deaths at each point in time. The fitting procedure is outlined in the Methods section.



**Figure S8:** Dependence of total infections and deaths over the 105 day period in Massachusetts shown as a function of  $\eta$ , the value of which indicates quarantine effectiveness, with  $\eta=0$  reflecting full compliance (no transmission due to quarantined individuals) and  $\eta=1$  reflecting no compliance (same transmission due to quarantined individuals as those not quarantined).



**Figure S9:** Comparison of using a mean value approximation as opposed to fixed duration quarantine and infection periods. To test the validity of the mean value approximation, we repeat the simulations of the model but replace the single I state with 10 substates, each of which corresponds to a different day of infectivity, D with  $10 \times 10$  sub-states, one for each (day infected, day diagnosed) combination, as well as the Q state with 10 sub-states corresponding to each day of quarantine. From sub-state

$n < 10$  of I, there is a flow of value 1 to sub-state  $n+1$  of I as well as a flow into sub-state  $n$  of D, corresponding to rate of diagnosis. The fixed duration model introduces produces only minimally different results from the mean value scheme when simulated using otherwise identical models.