

Understanding the Role of Mathematical Models in the Dynamics and Control of COVID-19 in California: A Scoping Review

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ABSTRACT

This scoping review examines how mathematical models helped explain and manage COVID-19 in California. Twelve studies published between 2020 and 2024 were identified through Web of Science and analyzed thematically. Overall, the models were powerful and useful tools for forecasting cases and hospitalizations, estimating the size of the epidemic, identifying thresholds for school reopening, and evaluating vaccination and decarceration strategies in state prisons. Models that represented interventions as discrete, named parameters produced the most policy-relevant findings, while models that folded policy effects into a changing transmission rate were less specific about why transmission changed. At the same time, common limitations included undercounted case data, limited attention to demographic differences, and reliance on retrospective validation. Future work should incorporate demographic and spatial stratification and use prospective validation to better support public health decision-making in California.

INTRODUCTION

COVID-19 is a contagious respiratory disease caused by the SARS-CoV-2 virus that can affect multiple body systems beyond the respiratory tract and can spread from individuals showing no symptoms [1].

The disease emerged in Wuhan, Hubei Province, China, when a cluster of unusual pneumonia cases was first reported in late December 2019 [2][3]. Public health officials identified a novel coronavirus as the causative agent within weeks, and escalating global spread prompted WHO to declare the outbreak a Public Health Emergency of International Concern on January 30, 2020 [2][3]. By March 11, 2020, with over 118,000 cases confirmed across 114 countries and 4,291 deaths, WHO declared COVID-19 a pandemic [4].

The United States confirmed its first case in Washington State in January 2020, with the CDC confirming the first instance of person-to-person community spread on January 30, 2020 [2]. The country's trajectory

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proved severe: over the course of 2020, the United States came to account for more COVID-19 cases and deaths than any other country [2]. In April 2020, the national unemployment rate rose to 14.7%, the highest monthly rate recorded since the U.S. Bureau of Labor Statistics began the series in 1948 [5]. In a nationally representative survey conducted June 24–30, 2020, 40.9% of U.S. adults reported at least one adverse mental or behavioral health condition, and 10.7% reported having seriously considered suicide in the previous 30 days [6].

By September 22, 2020, the recorded U.S. death toll from COVID-19 had surpassed 200,000 [1]. Together, this data illustrates how COVID-19 destabilized health, economic, and social systems in the United States at an unprecedented pace. The federal response included emergency declarations, travel restrictions, and Operation Warp Speed, which in July 2020 secured an initial order of 100 million Pfizer-BioNTech mRNA vaccine doses for the United States [7].

California had a key focus of public health officials, researchers, and policymakers. The state confirmed its first COVID-19 cases on January 26, 2020 [8]. A death on February 6, 2020, in Santa Clara County was later recognized as among the earliest known COVID-19 deaths in the United States [9][10]. By early 2021, California had become the first U.S. state to surpass 3 million confirmed infections and had recorded more than 40,000 deaths, more than any other state at that time [11][12]. California implemented interventions, including a statewide stay-at-home order issued on March 19, 2020, a Regional Stay At Home Order triggered when regional intensive care unit (ICU) capacity fell below 15%, and the "Blueprint for a Safer Economy" tiered framework to guide reopening decisions [8]. These responses utilized mathematical models to inform these decisions.

Understanding how those models functioned requires situating them within the longer history of mathematical epidemiology. The field's foundations date back to 1760, when Daniel Bernoulli developed the first documented disease transmission model to support smallpox inoculation, estimating that universal inoculation would increase life expectancy by approximately 3 years [13]. Modern epidemic modeling developed through W. H. Hamer's mass action principle (1906) and Ronald Ross's formalization of the basic reproduction number in 1911, which showed that diseases could be eliminated by reducing transmission below a critical threshold without completely eradicating infection sources [13]. Kermack and McKendrick further advanced the field between 1927 and 1933 by developing the compartmental models - susceptible–infectious–recovered (SIR), susceptible–infectious–susceptible (SIS), and susceptible–exposed–infectious–recovered (SEIR) - that remain central to epidemiological modeling today [14]. These models enable policymakers to predict disease spread, estimate transmission metrics, and evaluate the projected impact of interventions such as vaccination and social distancing [13].

California serves as a critical case study due to its large, diverse population of nearly 40 million residents, significant regional variation in disease burden, and innovative policy responses [14]. This unique context provides a valuable opportunity to examine how mathematical models contributed to understanding COVID-19 transmission dynamics and informing public health decision-making throughout the pandemic. The review was guided by the following questions:

1. What structural frameworks were deployed to model COVID-19 dynamics?
2. How did structural parameterization choices impact its policy relevance?
3. To what extent did California-focused models incorporate demographic stratification to capture disparities in disease burden?
4. What systematic data constraints and gaps persist within this area of epidemiological modeling?

METHODS

Given this context, a scoping review methodology was used to identify, screen, and synthesize the mathematical modeling studies most relevant to COVID-19 in California. Figure 1 illustrates the framework used to guide this process.

Arksey and O'Malley Framework Stage	Description
1: Identifying the research question	Identifying the research question provides the roadmap for subsequent stages. Relevant aspects of the question must be clearly defined as they have ramifications for search strategies. Research questions are broad in nature as they seek to provide breadth of coverage.
2: Identifying relevant studies	This stage involves identifying the relevant studies and developing a decision plan for where to search, which terms to use, which sources are to be searched, time span, and language. Comprehensiveness and breadth is important in the search. Sources include electronic databases, reference lists, hand searching of key journals, and organizations and conferences. Breadth is important; however, practicalities of the search are as well. Time, budget and personnel resources are potential limiting factors and decisions need to be made upfront about how these will impact the search.
3: Study selection	Study selection involves <i>post hoc</i> inclusion and exclusion criteria. These criteria are based on the specifics of the research question and on new familiarity with the subject matter through reading the studies.
4: Charting the data	A data-charting form is developed and used to extract data from each study. A 'narrative review' or 'descriptive analytical' method is used to extract contextual or process oriented information from each study.
5: Collating, summarizing, and reporting results	An analytic framework or thematic construction is used to provide an overview of the breadth of the literature but not a synthesis. A numerical analysis of the extent and nature of studies using tables and charts is presented. A thematic analysis is then presented. Clarity and consistency are required when reporting results.
6: Consultation (optional)	Provides opportunities for consumer and stakeholder involvement to suggest additional references and provide insights beyond those in the literature.

Figure 1: Overview of the Arksey and O'Malley methodological framework for scoping study [15]

This study follows the scoping review framework developed by Arksey and O'Malley and refined by Levac et al. The framework is designed to map the breadth of existing literature, identify key concepts and evidence types, and highlight gaps in research. Scoping reviews are especially well suited for broad fields such as mathematical modeling, where methods, data sources, and policy applications vary widely across studies.

A literature search was conducted on the Web of Science Core Collection, combining three concept domains into this search query in February 2026:

TS=("COVID-19" OR "COVID" OR "SARS-CoV-2") AND TS=("California" OR "CA" OR "Los Angeles" OR "LA" OR "San Francisco" OR "SF" OR "Orange County") AND TS=("mathematical model" OR

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"compartmental model" OR "SEIR" OR "SIR" OR "SEIRS" OR "transmission model" OR "mathematical modelling")

This yielded 60 papers, which were screened sequentially by title, abstract, and full text against predefined inclusion and exclusion criteria. Studies were included if they focused on COVID-19 in California, used a quantitative mathematical or statistical modeling approach, and were published or posted as English-language papers from 2020 onward. Studies lacking a California focus or formal modeling were excluded. This process yielded 12 studies for final inclusion.

Study screening and data extraction were conducted independently which introduces potential selection and extraction biases which are evaluated as threats to validity in the limitations section.

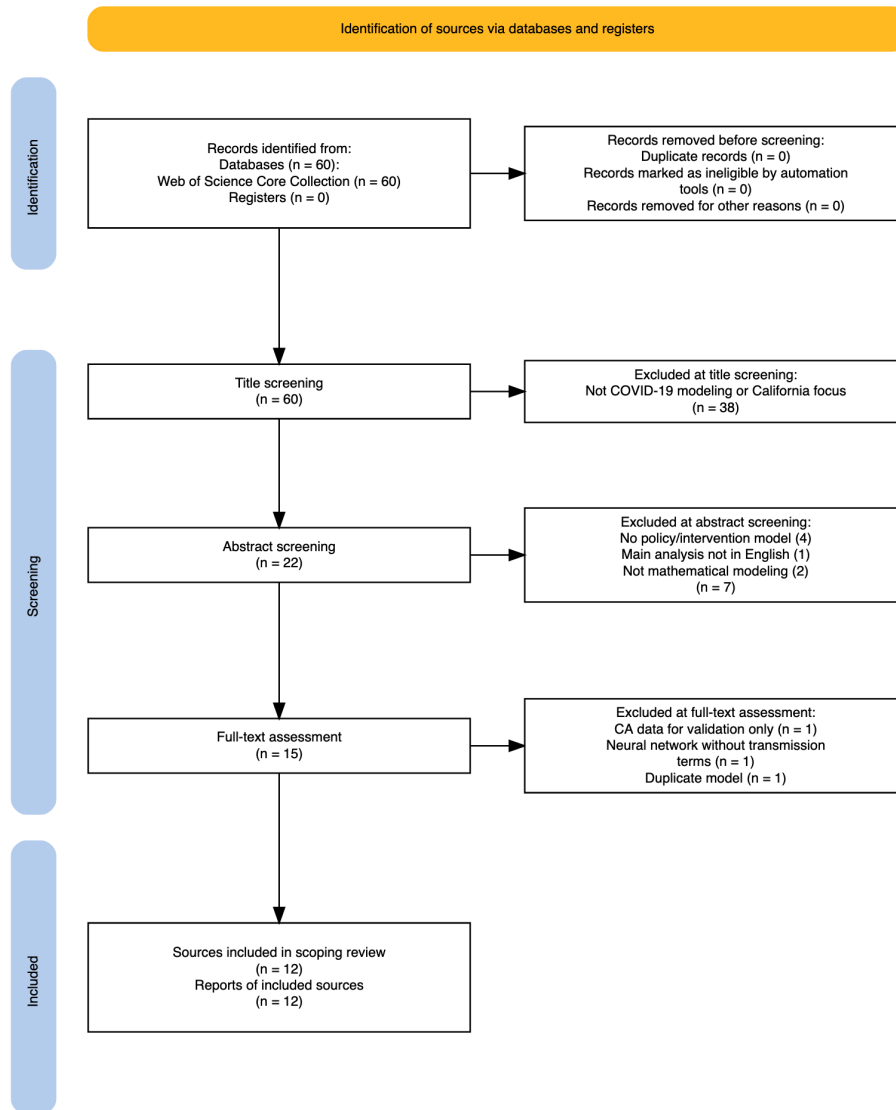


Figure 2: Prisma diagram of scoping review screening stages

Data was extracted from each included study using a standardized form capturing the following elements: study characteristics, model type, data sources and calibration methods, interventions modeled and outcomes reported, connections to policy decisions, equity considerations, and acknowledged limitations. Given the diversity of modeling approaches across included studies, findings are synthesized thematically through narrative analysis, with results organized around these variable categories to identify patterns, trends, and gaps across the literature.

RESULTS

Table 1 provides an overview of all the included papers for the study, summarizing their objectives, scope model type, target population and key findings.

Ref	Authors	Period	Scope	Model	Population	Key Finding
[16]	O'Dea and Drake	June 2020 to April 2021	Statewide CA	State-space SEIR with Kalman filter	General	Best hospital admission forecasts vs CDC ensemble
[17]	Deo and Grover	March 2020 to July 2020	CA and FL	Bayesian SI(Q/F)RD	General	97% of CA cases missed early; undetected spread 3x faster
[18]	Davarci et al.	March 2020 to August 2020	CA, NY, FL, TX, IL	Dynamic SEIRD	General	+2 weeks calibration cut CA forecast error 15-23%
[19]	Kain et al.	January 2020 to August 2020	LA and Santa Clara counties	Stochastic SEIR with superspreading	General	Targeting top 1% spread matched strictest lockdowns
[20]	Head et al.	Fall 2021 (128-day semester)	9-county Bay Area	Agent-based SEIR	K-12 students and staff	Masks + 70% vax kept schools under 50 excess cases per 1000
[21]	Ryckman et al.	January 2020 to May 2021 (200-day simulations)	5 CA prisons	Stochastic microsimulation	Incarcerated	Preemptive vax beat reactive control; dorms stayed high risk
[22]	Zhu et al.	March 2020 to December 2022	Statewide CA	Deterministic age-structured burden model	General (5 age groups)	59,514 QALYs lost; ages 18-49 bore 53%
[23]	Bayer et	March 2020 to	Orange	Bayesian	General	32-72%

	al.	February 2021	County	semiparametric ODE		infected; only 10-20% of cases reported
[24]	Mahmud et al.	December 2020 to April 2021 (forecasts to 2026-2028)	CA and US	Deterministic SEIR with vaccination	General	Vaccines under 90% efficacy had little effect
[25]	Childs et al.	March to June 2020 (fits April 1 to June 24)	Santa Clara County	Stochastic SEIR	General	Accurate until May; failed after SIP lifted
[26]	Blumberg et al.	April 2020 to February 2021	CA prisons (CDCR)	Hybrid 3-stage model	Incarcerated	20% depopulation cut expected cases 47%
[27]	Feng et al.	March to July 2020	SF Bay Area and NYC	Pairwise network SEIR	General	Household clustering drove SF vs NYC outbreak gap

Table 1: Overview of papers analyzed in scoping review

STUDY CHARACTERISTICS

The final sample included 12 modeling studies focused on COVID-19 in California, either as the primary setting or as one of several U.S. locations. Most examined statewide or county-level transmission in general populations, while a smaller subset targeted specific environments such as K–12 schools in the Bay Area, California state prisons, and other congregate settings. Publication years ranged from 2020 to 2024, with 10 of the 12 studies centered on the first 2020 waves and 2 more recent studies: Head et al. (2022) and Zhu et al. (2024), extending into 2022 to cover the Delta and Omicron periods and longer-term outcomes such as long COVID.

Several studies were designed as state or county-level models of community transmission, including O’Dea and Drake’s GISST state-space forecasting model for California [16], Deo and Grover’s SI(Q/F)RD model of underreporting in California and Florida [17], and Davarci et al.’s dynamic SEIRD approach applied to California and four other large states [18]. Others focused on specific high-stakes settings, such as Kain et al.’s superspreading model for Los Angeles and Santa Clara counties [19], Head et al.’s agent-based model of Bay Area school reopening in fall 2021 [20], and Ryckman et al.’s and Aug 2026

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Blumberg et al.'s models of outbreak control and reopening strategies in California prisons [21][26]. One study, by Zhu et al., did not model transmission but instead modeled the statewide burden of long COVID among confirmed California cases through December 2022 [22].

MODEL CHARACTERISTICS

The 12 included studies employed four broad structural frameworks: deterministic compartmental models, stochastic compartmental models, agent-based simulations, and hybrid or semiparametric models. Most studies built on SEIR or SEIRD foundations but introduced specific structural innovations to address a known limitation, such as fixed parameters, homogeneous mixing, or the inability to separate detected from undetected infections.

Among deterministic models, Davarci et al. used a modified SEIRD with all five key parameters allowed to evolve continuously over time [18], while Deo and Grover's SI(Q/F)RD split the infected population into detected and undetected groups with distinct transmission rates [17]. O'Dea and Drake extended this further with GISST, a state-space model that updated parameters daily via an extended Kalman filter [16], and Bayer et al. took a semiparametric approach that estimated the reproduction number and case detection rate week-by-week without pre-specifying when changes occurred [23]. Mahmud et al. used a deterministic SEIR extended with a vaccination compartment to evaluate six vaccine efficacy scenarios for California [24].

Stochastic models were used for chance scenarios. Childs et al. applied a stochastic SEIR retrospectively to Santa Clara County to evaluate early intervention timing [25]. Kain et al. assigned each individual a Gamma-distributed transmission rate to represent superspreading [19], and Blumberg et al. combined a stochastic branching process for outbreak initiation with a deterministic SEIR for growth, applying it to California prisons [26]. Feng et al. departed from compartmental structure entirely, modeling spread across a dynamic contact network that contracted into household clusters during shelter-in-place [27].

The most granular models were agent-based. Head et al. simulated 16,000 synthetic individuals across Bay Area schools [20], and Ryckman et al. took a similar approach for California state prisons, assigning each resident their own demographics, housing, and activity schedule [21]. Zhu et al. stood apart from all other studies, using a deterministic age-structured burden model that took confirmed case counts as inputs rather than modeling transmission, tracking long COVID severity progression through December 2022 [22].

DATA AND CALIBRATION

Across the 12 studies, confirmed case and death counts from Johns Hopkins CSSE were the most consistently used data source, appearing in nearly every community transmission model. Several studies

supplemented this core with additional sources: O'Dea and Drake incorporated HHS hospital admissions, Google mobility, and vaccination data [16], Davarci et al. added biweekly seroprevalence surveys to constrain the recovered compartment [18], and Deo and Grover used CDC excess death data and testing positivity to estimate true infections from deaths rather than reported cases [17]. Head et al. differed by grounding their model in a primary contact survey conducted across nine Bay Area counties rather than surveillance data [20].

Calibration strategies varied considerably. Dynamic approaches included O'Dea and Drake's extended Kalman filter, which updated state estimates daily [16], and Davarci et al.'s rolling one-week parameter re-estimation windows [18]. Bayesian methods appeared in Deo and Grover's MCMC fitting [17] and Bayer et al.'s Gaussian Markov Random Field priors [23]. Ryckman et al. and Blumberg et al. used CDCR prison case counts primarily for validation rather than calibration [21][26]. Underreporting posed a consistent data challenge: Deo and Grover estimated that roughly 96.6% of California cases went unreported early in the pandemic, specifically between March and April 2020, with the underreporting rate stabilizing around 43% by late 2021 [17]. Studies such as Davarci et al. and Kain et al. acknowledged that official case counts undercounted true infections, shaping how each study selected and weighted their input data [18][19]. Long-term required baseline assumptions regarding the post-acute effects: for example, the long COVID quality-adjusted life years (QALY) figures calculated by Zhu et al. relied on parameterizations from the version of their model updated through October 2022 [22].

INTERVENTIONS AND OUTCOMES

Most studies encoded interventions indirectly rather than as discrete policy events. In several models, the effects of California's March 19, 2020 shelter-in-place order and subsequent reopening phases appeared as shifts in time-varying transmission parameters or mobility data rather than as hard-coded policy changes [16][18]. Conversely, Feng et al. structurally parameterized San Francisco's shelter-in-place mandates by adjusting a pairwise network's clustering coefficient [27]. Kain et al. explicitly modeled three intervention types: broad social distancing via mobility, targeted superspreading prevention by truncating the highest individual transmission rates, and test-and-isolate [19]. Head et al. tested universal masking, masks plus weekly testing, and masks plus cohorts across three vaccination coverage levels for Bay Area schools [20], while Ryckman et al. and Blumberg et al. evaluated depopulation, vaccination, and transmission reduction strategies in California prisons [21][26].

Reported outcomes varied by study focus. The most common were short-term case and death forecasts over 1 to 4 week horizons [16, 18, 24, 25] and estimates of the effective reproduction number over time [16][19]. Other outcomes included hospital admissions [16], true epidemic size underreporting [17], congregate setting outbreak burden [21][26], and quality-adjusted life years lost to long COVID [22]. Additionally, Feng et al. modeled counterfactual outcomes evaluating the impact of varying policy durations across different urban density scenarios.

POLICY RELEVANCE

Several studies were explicitly designed for real-time decision support. O'Dea and Drake emphasized that GISST could produce weekly state-level forecasts in under four hours, with outputs including hospital admission projections and effective reproduction number estimates directly applicable to planning [16]. Head et al. directly informed CDC and CDPH guidance on fall 2021 school reopening, providing a risk framework that matched required interventions to acceptable case thresholds [20]. Blumberg et al., funded in part by the Office of the Federal Receiver overseeing California prison healthcare, directly informed vaccination decisions for California state prisons [26].

Other studies informed policy less directly but offered actionable insights. Davarci et al. argued against premature reopening by showing that extending the calibration window by just two weeks substantially improved forecast reliability for California [18]. Deo and Grover quantified the cost of insufficient testing, noting that California's official counts could not accurately reflect the true scope of the epidemic [17]. Kain et al. supported targeted intervention over blanket restriction, demonstrating that banning only the highest-risk gatherings could achieve control comparable to California's strictest April 2020 lockdowns [19].

DISCUSSION

This review identified and analyzed twelve mathematical models of COVID-19 transmission applied to California between 2020 and 2024, with the aim of evaluating how mathematical modeling contributed to pandemic policy decisions across the state. Studies were selected to span three distinct decision contexts: statewide epidemic forecasting, K-12 school reopening, and outbreak control in state prisons. For each study, I extracted the model structure, target population, intervention assumptions, and primary findings, then evaluated how directly the model's design enabled its policy conclusions. The findings show that mathematical models played a meaningful role in shaping California's pandemic response in several ways: by generating real-time forecasts that informed resource allocation, by identifying intervention thresholds for school reopening and prison management, and by quantifying the costs of inaction in congregate settings. At the same time, this comparative analysis revealed that structural choices, specifically whether interventions were encoded as discrete parameters or absorbed into a transmission term, were the primary determinant of a model's policy utility.

EVOLUTION OF MODELING APPROACHES

The progression of modeling approaches in this review tracks closely with the availability of new data streams and computational methods. Time-varying parameter frameworks became viable when daily surveillance feeds made continuous re-estimation feasible [16][18]. Agent-based models became practical

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when contact survey data existed and computing power allowed thousands of simulation runs [20][21]. Each innovation addressed a genuine limitation of the models that preceded it, and the improvements in forecast accuracy and policy specificity were real.

The variety of modeling approaches in this review is not a weakness of the literature but a reflection of how epidemiological modeling works. The question determines the model. Statewide forecasting calls for a framework that can update daily from routine surveillance data. Evaluating school reopening requires representing individual contacts and testing specific intervention combinations. Modeling outbreaks in prisons means accounting for stochastic introductions and superspreading in a way that compartmental models are not built to capture. Each study made structural choices suited to its question and the data available, and that alignment is where the policy value came from. What the literature did not do as well was build on itself. Recurring problems around data quality, demographic heterogeneity, and real-world validation were acknowledged study by study and then largely left for the next paper to rediscover.

UNDERREPORTING

A central constraint across the included studies was the quality of the surveillance data on which most models depended. Confirmed case counts from Johns Hopkins CSSE served as the primary calibration input for nearly every community transmission model, yet Deo and Grover showed that these counts captured only a fraction of true infections [17]. Their SI(Q/F)RD model, which inferred infections from deaths using a fixed case fatality rate and an 18-day infection-to-death lag, estimated that approximately 96.6% of California COVID-19 cases went unreported early in the pandemic, specifically between March and April 2020, with the underreporting rate stabilizing around 43% by late 2021 as testing expanded [17].

This degree of underdetection has implications that extend far beyond a single study. Models such as those by Davarci et al. and Kain et al. acknowledged that their calibration data undercounted true infections, yet continued to rely on official case counts as primary inputs because no reliable statewide alternative existed [18][19]. In this context, transmission rates, reproduction numbers, and forecast trajectories are calibrated to the observed epidemic rather than the true one. Two studies in this review tried to reduce that bias by fitting primarily to deaths rather than cases, arguing that mortality data, while lagged, were less sensitive to fluctuations in testing volume than reported infections [23][25]. These decisions demonstrate that when empirical testing data is incomplete, the choice of a model's internal mechanics becomes even more critical for capturing real dynamics.

Underreporting also had an equity dimension that none of the included models confronted directly. Deo and Grover treated missed infections as a statewide average that declined uniformly as testing expanded [17]. In practice, access to testing was strongly patterned by income, job flexibility, transportation, and local infrastructure, with lower income communities and those farther from testing sites less likely to appear in case data at all [28]. A global correction of 96.6 percent says little about how that gap was distributed across neighborhoods within Los Angeles County or across agricultural versus urban regions.

No study in this review attempted to estimate community-specific or demographic-specific underreporting rates, which means that structural bias from the input data was carried into the models without explicit adjustment.

Data limitations extended beyond case counts. Davarci et al. relied on biweekly seroprevalence surveys to constrain the recovered compartment because California did not consistently report recoveries, but those surveys had wide uncertainty intervals and were only available at sparse time points [18]. Kain et al. used SafeGraph smartphone mobility as a proxy for physical distancing, and noted that smartphone-based mobility likely underrepresents low-income communities, who have lower rates of smartphone ownership and are more likely to hold essential jobs that prevent them from staying home regardless of risk [19]. These issues indicate that the modeling literature documented here was built on a surveillance infrastructure with systematic gaps, and that those gaps were not randomly distributed.

INTERVENTION MODELING

Most studies in this review represented California's interventions indirectly, as changes in parameters or mobility rather than as explicit policy events. In Davarci et al., the March 19 shelter in place order appears as a sharp decline in the estimated transmission rate β ; in O'Dea and Drake, it appears as a shift in the relationship between mobility and transmission [16][18]. In both cases, the models detect that a change occurred but treat the full bundle of policy actions and voluntary behavior changes as a single composite signal. Reductions in workplace contacts, school closures, masking, and risk avoidance are compressed into one parameter path.

Only a few studies analyzed clearly defined interventions. Kain et al. compared targeted superspreading control with broader social distancing [19]. Head et al. evaluated specific combinations of masking, testing, and cohorting across vaccination scenarios in Bay Area schools [20]. Ryckman et al. and Blumberg et al. modeled depopulation, vaccination, and reopening strategies in California prisons [21][26]. These studies address named policies and produce outputs that map directly to decisions, such as masking thresholds or tradeoffs between preemptive and reactive measures.

When a model absorbs all of California's March 2020 interventions into a single shifting transmission rate, it can show that transmission fell but cannot show why. School closures, workplace restrictions, and voluntary behavior change all enter through the same parameter, so their individual effects cannot be separated after the fact. Based on the sample analyzed in this review, an interpretive conclusion emerges that models encoding interventions as distinct parameters often generated highly specific and actionable findings. Kain et al. showed that targeting only the top one percent of transmission events could match California's strictest lockdowns [19]. Head et al. gave CDPH a direct threshold framework for school reopening by testing masking, cohorting, and weekly testing independently [20]. That specificity came from structure, not from better data. While this specificity is associated with model structure, this correlation doesn't entail causation. Structural choices remain inherently entangled with the specific type of policy question each model was originally engineered to answer. Thus, highly granular policy

questions naturally demanded granular structural parameterizations, making policy utility a reflection of aligned study design rather than structure alone.

EQUITY GAP

California's COVID-19 epidemic was marked by clear disparities in infection, hospitalization, and death by race, income, occupation, and neighborhood. Despite this, equity was largely invisible in the modeling literature covered by this review. With rare exceptions, studies treated California or its counties as homogeneous units. In those models, a resident of an overcrowded multigenerational household and a resident working remotely in a single-family home contribute to the transmission process in the same way.

The few studies that did foreground high-burden communities show what becomes possible when equity is treated as an analytic priority. Head et al. stratified by age and vaccination eligibility and found that nearly 90 percent of child infections fell among unvaccinated children under 12 who lacked access to vaccines at the time [20]. Blumberg et al. focused on incarcerated people in California state prisons, a group with higher comorbidity burdens and very limited ability to reduce exposure, and quantified how modest depopulation produced disproportionately large reductions in expected cases [26]. These designs demonstrate that incorporating structural vulnerability into model structure is feasible and yields results that directly inform protection of high-risk groups.

The broader literature, however, left these patterns largely unmodeled. Kain et al.'s use of smartphone mobility likely underweighted movement in low-income communities. Deo and Grover's statewide underreporting adjustments did not distinguish between neighborhoods with ready access to testing and those dependent on overstretched safety net clinics. When such outputs are presented as statewide effects, they effectively describe the experience of populations with average exposure risk and average access to care rather than the communities that carried the greatest burden. The result is a body of work that is technically sophisticated in its representation of transmission but structurally blind to the populations where its findings mattered most.

SCALABILITY V. ACCURACY

The studies in this review also highlight a consistent tension between structural accuracy and operational scalability. At one end of the spectrum, agent-based models such as those by Head et al. and Ryckman et al. achieved detailed representations of individuals, contacts, and settings [20][21]. Their ability to evaluate specific school or prison policies depended on fine-grained inputs, including primary contact surveys and individual-level institutional records. These data requirements make such models powerful in the settings they cover, but difficult to apply quickly in new contexts.

At the other end, statewide compartmental models prioritized speed and portability. GISST produced forecasts for California in under four hours per week using routinely available surveillance data [16].

Davarci et al.'s dynamic SEIRD framework was explicitly designed to be applied across multiple states with the same pipeline [18]. These properties are important for real-time decision support, but they rest on stronger assumptions about population homogeneity and data quality.

No study in this review treated this tradeoff as a central design question. Authors described their own approach and noted limitations, but none articulated criteria for when a highly granular model is warranted, when a faster aggregate model is preferable, or how to link the two in a coherent modeling strategy for California. For a state that combines dense urban centers, rural agricultural regions, and large congregate facilities, the absence of an explicit framework for matching model type to decision context is itself an important gap. In effect, the models best equipped to describe how specific interventions worked in high-risk settings and the models best positioned to run every week for the whole state operated on parallel tracks, with little mechanism for transferring information between them. This ties into the data problem that runs across all included studies. Each team built its own pipeline from the same raw surveillance sources, applying different cleaning decisions, underreporting assumptions, and calibration windows independently. Without shared standards or a common data infrastructure, parameter estimates and model outputs that appear comparable across studies may reflect different underlying representations of the same epidemic.

POLICY TRANSLATION

The connection between modeling and policy across these studies was uneven. A small subset had a clear, documented influence. Head et al. reported that their model directly informed CDC and CDPH guidance on fall 2021 school reopening by specifying intervention combinations needed to keep school-attributable risk below defined thresholds [20]. Blumberg et al. worked with the Office of the Federal Receiver for California prison health care and produced an interactive tool that allowed officials to explore decarceration and vaccination options [26]. In both examples, there was a defined policy partner and a model built around that partner's decision space. This reflects what Metcalf et al. identify as the most productive arrangement for modeling to influence policy: not a one-off academic contribution, but an ongoing relationship where modelers understand the decision context and decision-makers understand what the model can and cannot provide [29].

Most other studies in this review lacked both a defined policy partner and a publication timeline aligned with active decision-making. Many were published after the time periods they analyzed, and none laid out a systematic pathway for communicating results to California public health agencies. For instance, while Feng et al. offered a sophisticated structural approach to mapping human contact networks, its retrospective nature meant it functioned more as a proof-of-concept rather than an active tool for real-time local policy [27]. In practice, even technically strong models may therefore have had limited influence on actual decisions. Preprints and open source code, as in the cases of GISST and Blumberg et al., improve access, but as Metcalf et al. note, availability is not the same as integration — the full potential of modeling can only be realized when it is embedded in the policy process rather than delivered to it from outside [29].

California's institutional context may have made this integration more feasible than in many other settings. The state had established public health infrastructure, direct relationships between academic modeling groups and agencies like CDPH and UCSF, and the organizational capacity to commission, receive, and act on model outputs in near real time. The Lancet Commission on Strengthening the Use of Epidemiological Modelling explicitly identifies this kind of institutional capacity as unevenly distributed globally, and argues that strengthening equitable partnerships between high- and low-resource settings is essential for models to reach their policy potential [30]. Viewed from that perspective, the cases where California modeling did influence policy — school reopening, prison management — were not simply the product of good science. They reflected a pre-existing infrastructure that allowed good science to be heard.

The literature as a whole, however, provides little detail on how models were received, interpreted, or balanced against other forms of evidence by policymakers. This is itself a gap. Metcalf et al. argue that the modeler-policy relationship should function as a feedback cycle, where models inform decisions, decisions generate new data, and new data refines the models [29]. None of the studies in this review described such a cycle. The disconnect between technical output and institutional uptake suggests that California, despite its relative advantages, still fell short of the kind of sustained, embedded modeling infrastructure that would be needed to realize that ideal in practice.

LIMITATIONS OF THE REVIEW

Several methodological constraints introduce distinct threats to validity that bound this review's findings. First, relying exclusively on a single legacy database and omitting preprint servers was a deliberate choice to prioritize peer-reviewed, parameter-stable literature and bypass the extreme volatility of unverified pandemic modeling. However, because preprints were explicitly within scope, this single-source approach introduces severe selection bias. Legacy databases frequently under-index preprint repositories and certain quantitative public health journals. Because many highly influential, real-time local models could be circulated as preprints to inform active governance, this review likely omitted critical active-phase tools, thereby over-representing retrospective academic models at the expense of nimble, real-time public health interventions.

Second, the single-reviewer screening and extraction process represents an additional threat to internal validity. Without secondary cross-checking, the workflow is inherently vulnerable to human error in study selection and subjective bias in parameter extraction. While resource constraints did not permit a multi-database or multi-reviewer design for this study, future scoping reviews mapping epidemiological infrastructure should utilize multi-reviewer consensus protocols and integrate a wider array of database types to maximize reproducibility and mitigate these systemic biases.

FUTURE DIRECTIONS

The gaps identified across these studies suggest several priorities for future infectious disease modeling in California. First, models that operate simultaneously at state, county, and neighborhood levels would better reflect California's geographic and demographic heterogeneity than single scale approaches. Second, demographic and occupational stratification by race, income, and job type is essential if models are to illuminate, rather than obscure, the inequities that shaped COVID-19 outcomes. Several authors named such stratification as a necessary next step in their own future work sections [17][20][21].

Third, greater emphasis on prospective real-time validation would help close the timing gap between methodological innovation and policy relevance. Building and testing models during active outbreaks, rather than only in retrospect, would provide more realistic information about performance under uncertainty and about how forecasts behave while the underlying system is still changing [25]. It would also highlight points of growth for data collection, but also model structure. This approach requires institutional support for continuous model updating and evaluation rather than one-time analyses.

Finally, the literature has only begun to engage with post acute outcomes. Zhu et al. was the sole study in this review to model long COVID burden and associated quality adjusted life year loss for California [22]. As the state continues to manage the long term consequences of COVID-19, integrating health burden into modeling frameworks, rather than focusing exclusively on infections, hospitalizations, and deaths, will be an important extension of the work documented here.

CONCLUSION

Mathematical models proved powerful tools for California's COVID-19 response, delivering real-time forecasts, estimating true epidemic size, identifying school reopening thresholds, and evaluating vaccination and decarceration strategies in state prisons.

Despite this demonstrated capability, four key gaps limited broader impact. Surveillance data undercounted true infections unevenly across communities. Population heterogeneity by race, income, and occupation went largely unmodeled. Scalability and structural accuracy tensions lacked explicit decision frameworks. Policy pathways remained dependent on pre-existing relationships rather than systematic integration. With strategic guidance on these fronts, mathematical modeling can reliably deliver public health impact in future emergencies.

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