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Vaccination, treatment, and saturated incidence in SEIQR-type epidemic models: A literature review

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Abstract

Compartmental epidemic models built on the Kermack-McKendrick susceptible-infected-recovered framework have been extended in many directions to capture how real interventions shape an outbreak. Three extensions matter most for the stability question addressed here: a quarantine or isolation compartment that removes exposed or infectious individuals from circulation, a vaccination term that moves susceptible individuals directly toward immunity, and a treatment function that returns infectious individuals to recovery at a rate that may saturate as caseloads grow. This review traces how these three control mechanisms have been added to SEIR-type models, generally alongside a saturated rather than bilinear incidence rate, and how the resulting systems are analysed for positivity, boundedness, the basic reproduction number, and local and global stability. Particular attention is given to the two dominant global-stability toolkits in this literature—the Lyapunov-function approach formalised by Korobeinikov and Maini and the next-generation-matrix method of van den Driessche and Watmough—and to how each has been adapted once a quarantine, vaccination, or treatment term is added. The review closes by noting that models combining all three control mechanisms together with an explicitly saturated incidence rate remain rare, with most studies isolating one or two mechanisms at a time.

Keywords: SEIQR model, basic reproduction number, saturated incidence rate, vaccination, quarantine, global stability, Lyapunov function, epidemic model, treatment function, next-generation matrix

Introduction

The Kermack-McKendrick model, first published in 1927, established the basic logic that still underlies most compartmental epidemic models: divide a population into classes according to disease status, write down the flow between classes as a system of ordinary differential equations, and study the long-run behaviour of that system ^[1]. The original model used a bilinear incidence term, new infections proportional to the product of susceptible and infectious numbers, which is simple but does not capture behavioural change, since people alter their contact patterns once an outbreak is visible. Capasso and Serio addressed this in 1978 by proposing what is now called the saturated incidence rate, motivated by a cholera outbreak in Bari, where new infections grow roughly linearly with the infectious population at low prevalence but level off as prevalence rises ^[2]. This single change has shaped a large share of the subsequent literature, including every study reviewed here.

A second line of development added structure to how the model responds to intervention. Hethcote, Zhen, and Shengbing formalised the effect of quarantine within six classical epidemic frameworks in 2002, showing how removing individuals from the infectious pool changes the threshold behaviour of the system ^[3]. Around the same time, van den Driessche and Watmough gave a general method, the next-generation matrix, for computing the basic reproduction number of compartmental models with many interacting classes, which became the standard tool for every model discussed below, however many compartments it contains ^[4]. A few years later, Korobeinikov and Maini constructed explicit Lyapunov functions for SIR- and SEIR-type models with nonlinear incidence, giving a general route to proving global, rather than merely local, stability ^[5]. With these tools available, the literature diversified along three largely separate tracks: models that add a quarantine or isolation compartment, models

That add a vaccination term acting on the susceptible class, and models that replace a constant-rate recovery with a treatment function whose effectiveness saturates once the infectious population is large enough to strain available medical resources. This review follows those three tracks and

the smaller number of studies that combine more than one of them, with particular attention to how each combination is analysed for positivity, boundedness, the basic reproduction number, and local and global stability of the disease-free and endemic equilibria.

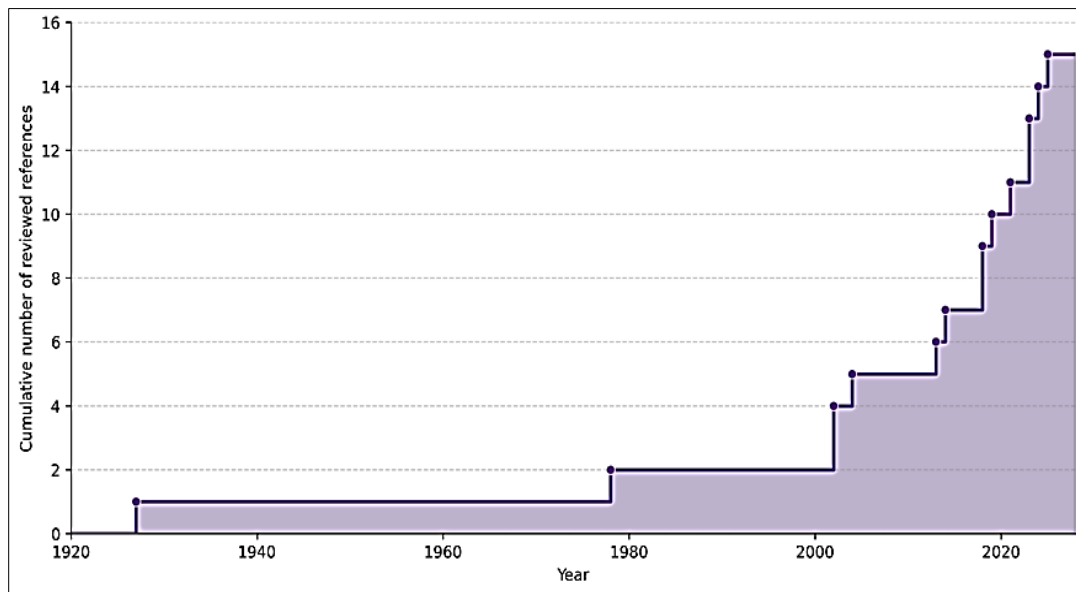


Fig 1: Cumulative growth of the fifteen reviewed studies on SEIQR-type models, 1927-2025

The curve is essentially flat for nearly eighty years, reaching only five references by 2013, then climbs steadily through two roughly decade-long growth phases to reach fifteen by 2025. Half of the entire reviewed literature was published within the last seven years covered here, which is consistent with the concentration of model-specific work noted throughout this review.

Foundations: Incidence functions and the basic reproduction number

Three results do most of the technical work in this literature. The first is the saturated incidence rate itself. Capasso and Serio's form, new infections proportional to the infectious population divided by one plus a multiple of that same population, tends to a ceiling as the infectious population grows, capturing both the crowding effect among infectives and the tendency of susceptible individuals to reduce contact once an outbreak is visible^[2]. Because this function is neither linear nor separable in the way the bilinear rate is, it changes the algebra of every stability proof that follows, which is why so many of the papers reviewed here spend a substantial part of their analysis simply establishing positivity and boundedness of solutions before turning to equilibria.

The second is the next-generation-matrix method. Rather than linearising the full system directly, van den Driessche and Watmough's approach isolates the new-infection terms from the transition terms among the infected compartments, builds two matrices from these, and defines the basic reproduction number as the largest eigenvalue of their product^[4]. This method scales cleanly as compartments are added, since quarantine, vaccination, and treatment terms all enter through one matrix or the other in a fairly mechanical way, which is a major reason it, rather than the classical Jacobian approach on its own, is the method of choice in nearly every SEIQR-type paper reviewed here. The third is the Lyapunov-function approach to global stability. Korobeinikov and Maini's construction, a composite quadratic-and-logarithmic function tailored to nonlinear incidence, gives conditions under which the disease-free equilibrium is globally, not just locally, stable whenever the basic reproduction number is at or below one, and under which a unique endemic equilibrium is globally stable above that threshold^[5]. Later authors adapt this same functional form when a quarantine, vaccination, or treatment compartment is added, which is why the Lyapunov functions appearing across this literature look structurally similar to one another even as the underlying models differ.

Table 1: Chronological summary of reviewed studies

Study (Year)	Ref.	Control Feature(s)	Incidence Type	Stability Method
Kermack & McKendrick (1927)	[1]	None (foundational)	Bilinear	Threshold analysis
Capasso & Serio (1978)	[2]	None (foundational)	Saturated (introduced)	N/A (incidence paper)
Hethcote <i>et al.</i> (2002)	[3]	Quarantine	Varies by variant	Equilibrium/threshold analysis
van den Driessche & Watmough (2002)	[4]	None (method)	General	Next-generation matrix (method)
Korobeinikov & Maini (2004)	[5]	None (method)	Nonlinear (general)	Lyapunov function (method)
Safi & Gumel (2013)	[6]	Quarantine	Quarantine-adjusted	Stability analysis
Zhang, Jia & Song (2014)	[7]	Treatment	Saturated	Routh-Hurwitz + Lyapunov
Mathur & Narayan (2018)	[8]	Vaccination	Saturated	Next-gen matrix + Lyapunov
Gao <i>et al.</i> (2018)	[9]	Vaccination	General	Lyapunov + geometric approach
Elazzouzi <i>et al.</i> (2019)	[10]	Vaccination + Treatment	Generalized nonlinear	Lyapunov function
Bhadoria <i>et al.</i> (2021)	[11]	Quarantine	Not saturation-specific	Lyapunov + Hopf bifurcation
Wang, Fan & Zhu (2023)	[12]	Quarantine + Vaccination + Treatment	Generalized	Stability + stochastic extension
Shen (2023)	[13]	Quarantine	Not specified	Threshold/global stability
Muthu & Kumar (2024)	[14]	Vaccination	Not saturation-specific	Bifurcation + Lyapunov
Chen, Su, Wen & Tu (2025)	[15]	Vaccination	Not saturation-specific	Global stability

Adding control compartments: Quarantine, vaccination, and treatment

Quarantine was the first control mechanism to be formalised in this way. Hethcote, Zhien, and Shengbing examined six variants of SIR-type models with a quarantine class, showing that the way individuals enter quarantine, whether the transition depends on contact with an infectious or an exposed individual, materially changes the threshold conditions for disease persistence^[3]. Safi and Gumel extended this by making the incidence rate itself depend on the level of quarantine, arguing that quarantining susceptible individuals who may have been exposed, not only confirmed infectious individuals, changes the reproduction number in ways a simple quarantine-of-infectious model misses^[6].

Treatment was formalised somewhat differently. Rather than adding a compartment, most treatment-focused papers replace the constant-rate recovery term with a saturating function of the infectious population. Zhang, Jia, and Song combined this idea with Capasso and Serio's saturated incidence in a single SEIR model, showing that when treatment capacity is limited, the model can undergo a backward bifurcation, meaning the disease can persist even when the basic reproduction number is below one, because recovery cannot keep pace once the infectious population exceeds the available treatment capacity^[7]. This backward-bifurcation result recurs across several of the papers discussed later and is arguably the single most important qualitative finding to come out of pairing saturated incidence with saturated treatment.

Vaccination has been treated in two rather different ways across the reviewed literature: as a constant-rate flow that moves susceptible individuals directly into a vaccinated or recovered class, and as a strategy-dependent term evaluated under different coverage scenarios. Elazzouzi, Lamrani Alaoui, Tilioua, and Tridane combined a vaccination term with a treatment function and a distributed time delay in a single SIR-type model, extending the Lyapunov-function approach to handle both control mechanisms together and showing that global stability of the disease-free equilibrium survives the addition of delay provided the reproduction number stays below one^[10].

SEIQR and related multi-compartment models

Models that add an explicit exposed class alongside quarantine, vaccination, or both make up the part of the literature closest to the SEIQR structure. Mathur and Narayan proposed an SVEIRS model, susceptible-vaccinated-exposed-infected-recovered-susceptible, for measles and influenza, combining pre- and post-exposure vaccination with a saturated incidence rate and showing both local and global stability of the disease-free and endemic equilibria via the next-generation-matrix reproduction number^[8]. Gao, Huang,

Kang, and Zhang worked with a related SVEIR structure under a general, rather than specifically saturated, incidence function, and established global stability using a mix of Lyapunov functions and a geometric approach to the endemic equilibrium^[9].

Bhadauria, Devi, and Gupta added quarantine rather than vaccination to an SEIR base, building an SEIQR model with a delay between exposure and the onset of infectiousness, motivated directly by COVID-19. Their local and global stability analysis, again via Lyapunov's method, was paired with a Hopf bifurcation analysis showing that the delay itself can destabilise an otherwise stable equilibrium and produce periodic outbreaks^[11].

The closest match among the reviewed literature to a model combining quarantine, vaccination, and treatment together is Wang, Fan, and Zhu's 2023 SIQR model, which incorporates a generalised incidence rate function, a general treatment function, and a vaccination term in the same deterministic system, then extends the analysis to a stochastic version and validates the model against COVID-19 case data from Russia and Serbia^[12]. Their finding, that increasing either the quarantine rate of infectious individuals or the vaccination rate can eliminate the infection, is one of the few results in this literature that speaks directly to all three control mechanisms in a single model, though the incidence function used is left general rather than fixed to the specific saturated form of Capasso and Serio.

Recent developments

Three recent papers show where this literature has moved since 2023. Shen revisited the SEIQR structure with an isolation compartment and a threshold-dynamics framing, proving global stability of the disease-free equilibrium below the reproduction-number threshold and instability above it, in a model kept deliberately close to the classical SEIQR form rather than adding further compartments^[13]. Muthu and Kumar took a different approach, adding a hospitalised compartment alongside a vaccination strategy and a mask-efficiency parameter, and combined bifurcation analysis with global stability results to study how vaccination and non-pharmaceutical measures interact^[14]. Chen, Su, Wen, and Tu, publishing in late 2025, returned to a comparatively simple SEIR structure but added dynamic population births alongside vaccination, arguing that most vaccination-focused models hold the population constant and miss how ongoing births replenish the susceptible pool, which changes both the reproduction number and the long-run sensitivity of the system to vaccination coverage^[15]. None of these three papers combines quarantine, vaccination, treatment, and an explicitly saturated incidence rate in one system, consistent with the pattern running through the rest of this review.

Table 2: Key model components referenced in this review

Component	Ref.	Form (described)
Saturated incidence rate	[2]	New infections proportional to beta times S times I, divided by one plus alpha times I
Quarantine transition	[3]	A rate constant applied to the infectious or exposed compartment, diverting individuals into a quarantined class
Saturated treatment function	[7]	Recovery rate proportional to r times I, divided by one plus k times I, capturing limited treatment capacity
Basic reproduction number	[4]	The largest eigenvalue of the matrix product F times V-inverse, where F captures new-infection terms and V captures transition terms

Table 2 lists, in words rather than full notation, the four building blocks that recur most often across the studies discussed above;

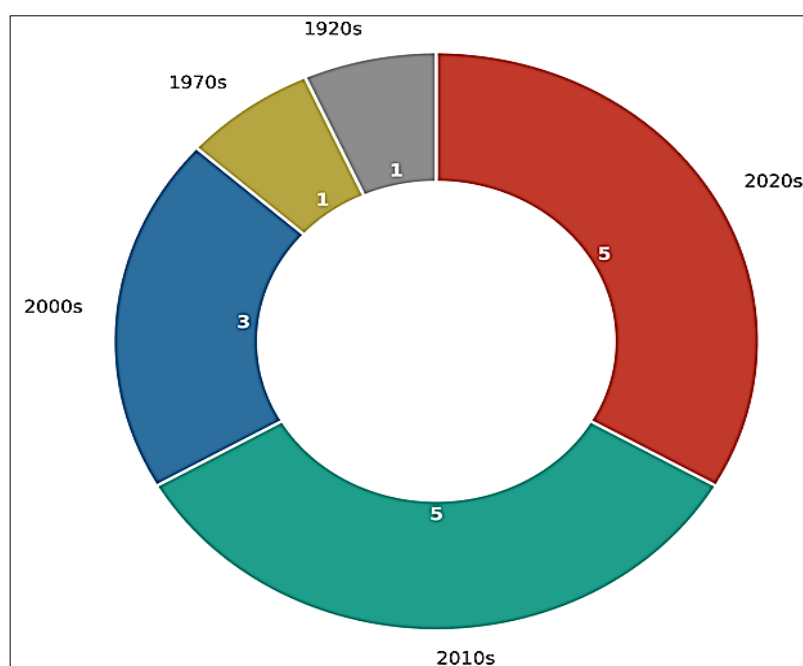
nearly every model reviewed here is some combination of these four components layered onto a base SEIR structure.

Table 3: Reference distribution by journal

Journal	Number of References
Mathematical Biosciences	3
Proceedings of the Royal Society of London Series A	1
Mathematical Biosciences and Engineering	1
Journal of Mathematical Analysis and Applications	1
Scientific World Journal	1
International Journal of Applied and Computational Mathematics	1
Boundary Value Problems	1
Advances in Difference Equations	1
Modeling Earth Systems and Environment	1
Applied Mathematical Modelling	1
International Journal of Mathematics Trends and Technology	1
Computational and Mathematical Biophysics	1
Electronic Research Archive	1

Mathematical Biosciences accounts for three of the fifteen references, including the two foundational papers on saturated incidence and quarantine; every other journal in the list contributes

exactly one reference, spreading the more recent, model-specific literature across a wide range of applied-mathematics and biology outlets.

**Fig 3:** Reviewed references by decade of publication (n = 15)

A third of the reviewed literature, five of fifteen references, comes from the 2010s and another five from the 2020s so far, against a combined total of five references spanning the preceding nine decades. The model-specific literature

reviewed here is therefore heavily concentrated in the last fifteen years, even though the underlying mathematical tools date back to 1927.

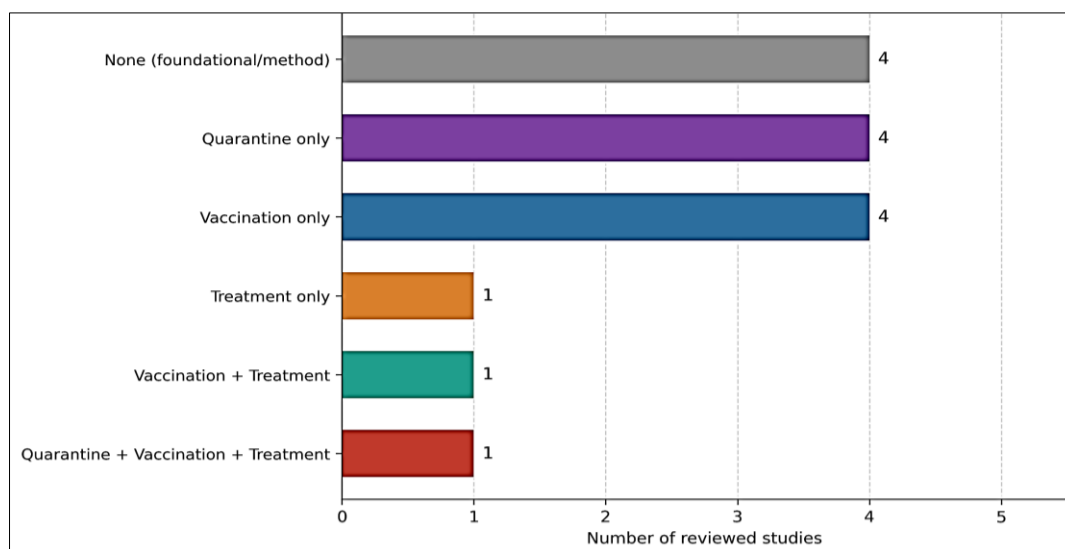
**Fig 2:** Number of reviewed studies by control-mechanism combination (n = 15)

Figure 2 counts the same fifteen studies by which control mechanisms they feature. Quarantine-only and vaccination-only studies are the two largest groups, with four studies each, and a further four studies are foundational or purely methodological rather than tied to a specific mechanism. Only one study pairs vaccination with treatment, and only one,

Wang, Fan, and Zhu, combines all three mechanisms in a single model. None of the reviewed studies combines all three mechanisms with the specific saturated incidence rate of Capasso and Serio, which is the empirical basis for the gap discussed below.

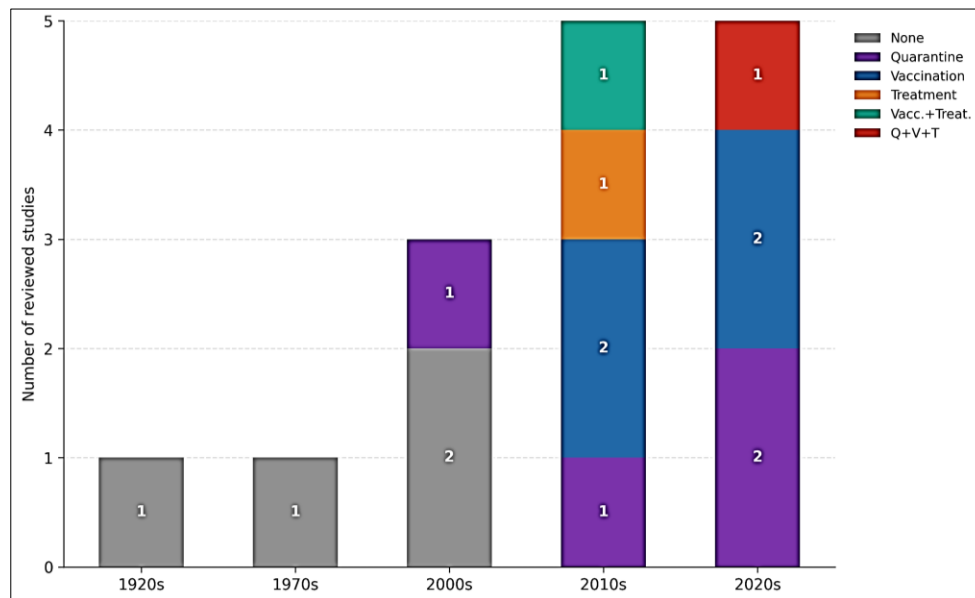


Fig 4: Control mechanism composition by decade of publication ($n = 15$)

Figure 4 breaks each decade's bar down by control mechanism. Both the vaccination and quarantine segments reach two studies in the 2020s bar, showing that single-mechanism work has continued well after each mechanism was first introduced, while the treatment, vaccination-plus-treatment, and all-three-mechanism segments each appear exactly once, concentrated in the 2010s and 2023 respectively. No bar outside the 2010s and 2020s contains more than a single foundational or methodological segment, confirming that model-specific work is a comparatively recent and still narrowly distributed phenomenon in this literature.

Synthesis and research gaps

Read as a whole, this literature shows a field that has been thorough about extending the classical SEIR model one mechanism at a time but has combined mechanisms only occasionally. Quarantine, vaccination, and treatment have each been studied in reasonable depth on their own, generally paired with either the saturated incidence rate of Capasso and Serio or a general nonlinear incidence function, and generally analysed using either the next-generation-matrix method of van den Driessche and Watmough or a Lyapunov function in the style of Korobeinikov and Maini [2, 4, 5]. What is comparatively rare, as Figure 2 shows directly, is a model that puts all three mechanisms together in one system.

Wang, Fan, and Zhu come closest, and their result that both quarantine and vaccination rates can independently drive the infection to elimination is a useful one, but their incidence function is left general rather than fixed to the specific saturated form used throughout most of the rest of this literature, and their model does not include the delay structures that Bhadauria, Devi, and Gupta and Elazzouzi and colleagues show can materially change stability conclusions [10, 12]. A model that combined a genuinely saturated incidence rate, an explicit quarantine compartment, a vaccination term, and a saturating treatment function in one system, then examined both local and global stability with the tools already

well established in this literature, would fill a gap that the chronology and the count in Figures 1 and 2 both point to rather clearly. A second observation is more practical. Several of the papers reviewed here, particularly the more recent ones, validate their models against real epidemic data, generally COVID-19 case counts from a specific country or region, while the earlier foundational papers rely entirely on illustrative parameter sets. This shift toward data validation is a genuine improvement, but it also means that comparing reported parameter values or reproduction numbers across studies is not always meaningful, since the underlying disease, population, and time period differ from paper to paper.

Conclusion

This review has traced how the classical Kermack-McKendrick model has been extended along three largely separate tracks, quarantine, vaccination, and treatment, generally alongside a saturated incidence rate, and analysed using the next-generation-matrix and Lyapunov-function tools that became standard in the early 2000s. Each track is individually well developed, and the four studies reviewed here that combine two or more mechanisms show that the underlying mathematics extends without fundamental difficulty when mechanisms are combined. The clearest gap identified here is the near-absence of a model that combines quarantine, vaccination, and a saturating treatment function together with an explicitly saturated incidence rate, then works through positivity, boundedness, the basic reproduction number, and both local and global stability in the way the individual-mechanism papers already do. Given how directly the existing Lyapunov-function and next-generation-matrix machinery appears to extend from one mechanism to two, building and analysing such a four-feature model looks like a tractable next step, alongside more consistent use of real epidemic data so that results across studies can be compared on similar footing.

Declarations

Conflict of interest: The author(s) declare no conflict of interest.

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