"Under What Conditions Can the SIR Model Approximate the SEIR Model?"

Anuar Shaimardan

Abstract

This study investigates the conditions under which the Susceptible–Infectious–Recovered (SIR) model can provide an acceptable approximation of the Susceptible-Exposed–Infectious–Recovered (SEIR) model. Although SIR is simpler and requires fewer compartments, it assumes that individuals become infectious immediately after infection, whereas SEIR accounts for a latent period through an exposed compartment. The study compares the two models across different combinations of the basic reproduction number (R_0), latent period, and infectious period. Their similarity is evaluated using infectious-population peak error and peak-time difference, with an approximation considered acceptable when the peak error is no greater than 10%, and the peak-time difference is no greater than 15 days. Across 20 tested parameter combinations, 3 were classified as acceptable. These cases occurred when the latent period was 1 day and the infectious period was 15 or 20 days, corresponding to latent-to-infectious ratios of approximately 0.050–0.067. As this ratio increased, the difference between the models became substantially larger, with the largest tested case producing a peak error of 302.98% and a peak-time difference of 90.85 days. The results indicate that SIR can serve as an approximation of SEIR when the latent period is very short relative to the infectious period, but SEIR becomes preferable when the latent stage has a substantial effect on epidemic dynamics. An interactive computational simulator was also developed to facilitate comparison of the two models and exploration of parameter effects.

Introduction

Mathematical models of infectious diseases play an important role in the understanding of infectious disease spread in populations. Epidemiological models can be used to mathematically describe a disease transmission process, to calculate potential outbreak development, and to compare the impact of various disease parameters (Weiss, 2013). The usefulness of a model depends not only on reliable parameters, but also on its simplicity and accuracy.

The SIR model is one of the more popular compartmental models. It categorizes people into three categories: Susceptible, who can be infected; Infectious, who can pass the disease; and Recovered, who can't spread the disease (Smith & Moore, 2004; Weiss, 2013). The SIR model assumes that a susceptible person becomes infectious as soon as they are infected. This assumption allows the model to be simplified and the number of estimated parameters to be reduced.

However, with many infectious diseases, there is a latent period between the time of infection and when the person becomes infectious. An individual is already infected, but not infectious

during this period. This process is captured in the SEIR model by adding an intermediate exposed compartment between the susceptible and infected compartments. The latent period, as used in this study, means the interval between infection and infectivity (Heng & Althaus, 2020).

The SEIR model provides a more detailed representation of disease progression, but in some cases, this additional complexity is not necessarily more helpful. To model the transition from the exposed compartment to the infectious compartment, another parameter is needed for the SEIR model. This parameter may be unknown or difficult to estimate, particularly in the early phase of an outbreak. A simpler SIR model might then be more appropriate if it gives results close enough to SEIR. If the latent period is long, however, the errors in estimating the height and timing of the peak of the epidemic, which are likely to result from ignoring the exposed stage, may be quite large (Heng & Althaus, 2020; Roda et al., 2020).

The central question in this work is not whether SEIR is more realistic than SIR, but under which epidemiological conditions the simpler SIR model can provide an acceptable approximation. Specifically, the difference in models might be related to the latent period to the infectious period relationship, and to the basic reproduction number (R_0).

Under controlled and identical initial conditions, this study compares the SIR and SEIR models through computer simulation in Python. A number of values for R_0 , latent period, and infectious period are tested. The maximum number of people who can be infectious at any one time, the time when the epidemic peak happens, and the overall difference between the infectious-population curves are compared for each setting of the parameters. The ratio of latent period to infectious period is identified as an important explanatory variable.

The research question for this investigation is:

Under what combinations of latent period, infectious period, and basic reproduction number can the SIR model provide an acceptable approximation of the SEIR model?

The goal of the study is to identify parameter combinations and trends under which the predictions of the two models are close and conditions under which the addition of an exposed compartment becomes important.

The hypothesis is that the SIR model would be a better approximation of SEIR dynamics if the latent period was short when compared to the infectious period. The longer the latent period relative to the infectious period, the further the difference between the models is likely to be, especially in terms of when and how large the epidemic peak will be. This ratio may also affect the impact depending on (R_0).

This investigation could help enrich our understanding of how to strike a balance between model simplicity and model detail, where a simpler epidemic model can yield adequate results under certain conditions. The results could also provide insights into why the selection of an epidemic model should vary according to the properties of the disease and the prediction being made.

Literature Review

Mathematical models are currently extensively used to model the spread of infectious diseases, and to explore the dynamics of epidemics as the biological situation changes. One of the well-established methods is the compartmental models that partition a population into compartments based on disease status. The two most common and widely-used compartmental models are Susceptible – Infectious – Recovered (SIR) and Susceptible – Exposed – Infectious – Recovered (SEIR). Such a detailed description of disease progression can be included in the SEIR model but may not be advantageous in all scenarios. So one of the key modelling questions is: is the simpler SIR model able to reproduce the key behaviours of the SEIR model for certain sets of epidemiological parameters?

The SIR model

The SIR model divides a closed population into susceptible, infectious and recovered compartments. Susceptible individuals become infectious through contact with infectious individuals, while infectious individuals move into the recovered compartment after losing their ability to transmit the disease. Smith and Moore explain that the model may be expressed either in terms of population counts or population proportions, since the two representations contain equivalent information about epidemic development. They also show that the total population remains constant when births, deaths and migration are ignored.

The standard SIR model is based on several simplifying assumptions. These include a closed population, homogeneous mixing, permanent immunity following recovery and the absence of a latent stage. In particular, newly infected individuals are assumed to become infectious immediately. Weiss (2013) identifies the zero-latency assumption as one of the important limitations of the SIR model. The assumption may be reasonable for an infection with a negligible latent period, but it becomes less realistic when a substantial delay exists between infection and infectiousness.

Despite these limitations, SIR remains useful because of its simplicity and interpretability. Its transmission dynamics are mainly determined by the transmission rate (β) and recovery rate (γ) . The mean infectious period is represented by:
$\gamma = 1 / infectious\ period,$

while, in the model without demographic change, the basic reproduction number can be written as

$$R_0 = \beta / \gamma$$

The value of (R_0) determines whether the number of infectious individuals initially increases. When $(R_0>1)$, an epidemic can grow, whereas an (R_0) below one leads to a decline in transmission. Weiss (2013) argues that simple models such as SIR can provide important qualitative conclusions even when their assumptions do not reproduce every feature of a real

population. Weiss also recommends beginning with the simplest model and introducing additional complexity only when it is necessary.

The SEIR extension

The SEIR model extends SIR by including an exposed compartment. Individuals in this compartment have been infected but are not yet infectious. They leave the exposed compartment and enter the infectious compartment at rate:

$$\sigma = 1 / L$$

where (L) is the mean latent period. The term *latent period* is used in the present study rather than *incubation period*, because the exposed compartment specifically represents the time from infection to the beginning of infectiousness. The incubation period, in contrast, normally refers to the time from infection to the appearance of symptoms, and the two periods are not always identical.

Maassen (2020) describes SEIR as a natural extension of SIR that requires one additional differential equation and one additional parameter. This additional compartment can delay the growth and peak of the infectious population because newly infected individuals do not immediately contribute to further transmission. Under the closed-population formulation used in the present investigation, both models may use the same values of (β), (γ) and (R_0), while SEIR additionally includes (σ).

The practical value of SEIR has been demonstrated in disease-specific studies. Kamrujjaman et al. (2022), for example, applied a deterministic SEIR model to COVID-19 data from Italy. Their work included stability analysis, parameter sensitivity analysis and estimation of reproduction numbers. This study demonstrates that the exposed stage and the parameters governing transitions between compartments can be important when representing an infection with a non-negligible delay before infectiousness. However, their purpose was to fit and analyse a particular epidemic rather than to determine whether a simpler SIR model could produce comparable results.

Model complexity and approximation

Adding an exposed compartment may improve biological realism, but it also introduces an additional parameter that must be estimated. Roda et al. (2020) argued that more complex epidemic models may experience identifiability problems because several different parameter combinations can reproduce similar observed data. Consequently, a more detailed model is not automatically more reliable, particularly when the additional parameters are uncertain. This supports the use of simpler models when they can reproduce the quantities relevant to the research question.

Heng and Althaus (2020) investigated the shapes of epidemic curves produced by the SEIR model. They found that SIR and SEIR curves may have closely related shapes, while the exposed stage mainly stretches the epidemic over time. Their analysis indicates that the

relationship between the latent and infectious timescales is important for determining how much the two models differ. This is directly relevant to the present investigation: when the latent period is short relative to the infectious period, the delay introduced by the exposed compartment should be small, and SIR may provide a close approximation. As the latent period becomes longer, larger differences in the timing and height of the infectious peak are expected.

Previous studies therefore identify three parameters as particularly important for the comparison. The basic reproduction number controls the overall strength of transmission; the infectious period determines how long infectious individuals remain capable of transmitting disease; and the latent period determines the delay before newly infected individuals begin transmitting. Nevertheless, the reviewed literature does not provide a systematic classification of the combinations of these three parameters under which SIR may be treated as an acceptable approximation of SEIR.

Research gap

Most existing studies either analyse the mathematical properties of one model, apply SIR or SEIR to observed epidemic data, or discuss their qualitative differences. Few studies perform paired simulations in which (R_0) and the infectious period is held constant while the latent period is varied systematically. Furthermore, the reviewed literature does not establish a simple quantitative boundary based on both the error in peak size and the difference in peak timing.

The present research addresses this gap by comparing matched SIR and SEIR simulations over multiple values of (R_0), latent period and infectious period. Approximation quality is assessed using the percentage difference in peak infectious population, the difference between peak times and a population-normalised root mean squared error. Particular attention is given to the ratio of latent period to infectious period. It is hypothesised that SIR will approximate SEIR most accurately when this ratio is small and that the approximation error will increase as the latent period becomes larger relative to the infectious period.

Methodology

Research Design

During the development of the study, it became apparent that comparing the models only through individual numerical outputs would make it difficult to examine how changes in the parameters affected the relationship between the SIR and SEIR curves. This led to the idea of developing an interactive online simulator that could calculate and display both models under the same initial conditions.

The simulator was developed in Python and implemented as a web application using Streamlit. It allows the user to change the main model parameters, including the basic reproduction number, latent period, infectious period, population size, initial conditions, simulation duration

and time step. For each parameter setting, the simulator calculates the SIR and SEIR trajectories and displays the infectious-population curves together with the comparison metrics used in this study.

The main purpose of the methodology was to compare paired SIR and SEIR simulations under matching initial conditions. For each parameter combination, both models used the same population size, initial number of infectious individuals, transmission rate and recovery rate. The only structural difference was that the SEIR model included an exposed compartment, while the SIR model did not.

Model Structure

The SIR model divided the population into three compartments: susceptible S, infectious I, and recovered R. The total population was assumed to remain constant:

S(t)+I(t)+R(t)=N.

The model was defined by the following system of differential equations:

$$dS/dt = -\beta \frac{SI}{N},$$
$$dI/dt = \beta \frac{SI}{N} - \gamma I,$$
$$dR/dt = \gamma I.$$

The SEIR model added an exposed compartment E, representing individuals who had been infected but were not yet infectious. In this model,

S(t)+E(t)+I(t)+R(t)=N.

The SEIR system was defined as:

$$dS/dt = -\beta \frac{SI}{N},$$
$$dE/dt = \beta \frac{SI}{N} - \sigma E$$
$$dI/dt = \sigma E - \gamma I,$$
$$dR/dt = \gamma I.$$

Here, β represents the transmission rate, γ represents the recovery rate, σ represents the rate at which exposed individuals become infectious.

Parameter Definitions

The population size was fixed at

N=10,000

The initial number of infectious individuals was set to

I_0=10

For the SEIR model, the initial number of exposed individuals was fixed at

E_0=0

This was done to ensure that the SIR and SEIR models started from comparable initial conditions. If the SEIR model began with additional exposed individuals, then the two models would not be directly comparable.

The infectious period T_I was used to calculate the recovery rate:

$$\gamma = \frac{1}{TI}$$

The latent period T_E was used to calculate the exposed-to-infectious transition rate:

$$\sigma = 1/T_E$$

The transmission rate was calculated from the basic reproduction number:

$$\beta = R_0\gamma.$$

This follows from the standard relationship:

$$R_0 = \frac{\beta}{\gamma}$$

The study tested several values of R_0, latent period and infectious period. The main parameter ranges were:

R_0 values: 1.2, 1.5, 2.0, 2.5, 3.0
Latent periods: 1, 2, 4, 6, 8, 10, 12, 15, 20 days
Infectious periods: 3, 5, 7, 10, 15, 20 days

The ratio

$$\frac{T_E}{T_I}$$

was also calculated for each simulation. This ratio was important because the hypothesis of the study was that SIR would approximate SEIR better when the latent period was short relative to the infectious period.

Numerical Method

For all simulations included in the main analysis, the simulation duration was fixed at 1500 days. The differential equations were solved numerically using the Euler method. Time was divided into small steps of size:

dt=0.05

At each time step, the program calculated the number of individuals moving between compartments.

For the SIR model, the number of new infections and recoveries were calculated as:

$$new\ infections = \beta\frac{SI}{N}dt,$$
$$new\ recoveries = \gamma Idt.$$

The compartments were then updated as:

$$S_{next} = S - new\ infections,$$
$$I_{next} = I + new\ infections - new\ recoveries,$$
$$R_{next} = R + new\ recoveries.$$

For the SEIR model, the transitions were:

$$new\ exposures = \beta\frac{SI}{N}dt,$$
$$new\ infectious = \sigma Edt,$$
$$new\ recoveries = \gamma Idt.$$

The updated compartments were then calculated as:

$$S_{next} = S - new\ exposures,$$
$$E_{next} = E + new\ exposures - new\ infectious,$$
$$I_{next} = I + new\ infectious - new\ recoveries,$$
$$R_{next} = R + new\ recoveries.$$

A small value of dt was used to improve the accuracy of the numerical approximation and to produce smoother epidemic curves.

Comparison Metrics

The SIR and SEIR models were compared using three main metrics.

First, the peak infectious population was calculated for each model:

$$Ipeak = max\ I(t).$$

The percentage error in peak size was then calculated as:

$$Peak\ error\ = \frac{|Ipeak,SIR - Ipeak,SEIR|}{Ipeak,SEIR} \cdot 100\%$$

Second, the day of the peak was recorded for each model. The difference in peak timing was calculated as:

$$\Delta t_{peak} = |t_{peak,\,SIR} - t_{peak,\,SEIR}|$$

This metric was included because two models may predict a similar peak size but still differ significantly in when the peak occurs.

Third, the root mean squared error was calculated to measure the difference between the full infectious-population curves:

$$RMSE\ = \sqrt{\frac{1}{n}\sum_{k=1}^{n}(I_{SIR,k} - I_{SEIR,k})^2}$$

To make this value easier to compare across population sizes, it was normalised by the total population:

$$NRMSE\ = \frac{RMSE}{N}.$$

NRMSE was reported as a supplementary measure of overall curve difference but was not included in the binary acceptance criterion.

Acceptance Criterion

A working acceptance criterion was defined for this investigation. The SIR model was considered an acceptable approximation of the SEIR model if both of the following conditions were satisfied:

$$Peak\ error \leq 10\%$$

and

$$\Delta t_{peak} \leq 15\ days.$$

This criterion was not treated as a universal epidemiological standard. Instead, it was used as a consistent rule for comparing all parameter combinations in this study. The 10% difference in peak magnitude was intended to demonstrate a relatively small deviation, while the 15-day threshold provided a complementary restriction on differences in epidemic timing.

Interactive Web Application

In addition to the Python simulation script, an interactive Streamlit web application was developed. The web application allowed users to change the main model parameters, including R_0, latent period, infectious period, population size and simulation duration. The app automatically recalculated the SIR and SEIR curves and displayed the comparison metrics.

The web application was used as an educational and exploratory tool. It helped visualise how changes in the latent period, infectious period and basic reproduction number affected the similarity between the two models. However, the application was not intended for real medical forecasting.

Methodological Limitations

Several simplifying assumptions were made in this methodology. The population was assumed to be closed, meaning that births, deaths and migration were ignored. The models also assumed homogeneous mixing, meaning that every individual had the same probability of contacting every other individual. In addition, the parameters β, γ and σ were assumed to remain constant over time.

The study also did not include age groups, vaccination, reinfection, stochastic effects or changes in public health behaviour. Therefore, the results should be interpreted as mathematical comparisons between two idealised models rather than predictions for a specific real-world epidemic.

Results and Analysis

Overview of Simulation Results

This section presents the results of the paired SIR and SEIR simulations. All simulations used a population size of 10,000, with 10 initially infectious individuals and 0 initially exposed individuals. The SIR model was evaluated as an acceptable approximation of the SEIR model if two conditions were satisfied: the peak infectious population error had to be no greater than 10%, and the peak-time difference had to be no greater than 15 days.

In total, 20 parameter combinations were tested. Out of these, 3 simulations were classified as acceptable approximations, while 17 simulations were classified as not acceptable. This shows that the SIR model can approximate SEIR under some conditions, but only when the latent period is very short relative to the infectious period.

Acceptable Approximation Cases

Table 1. Acceptable cases

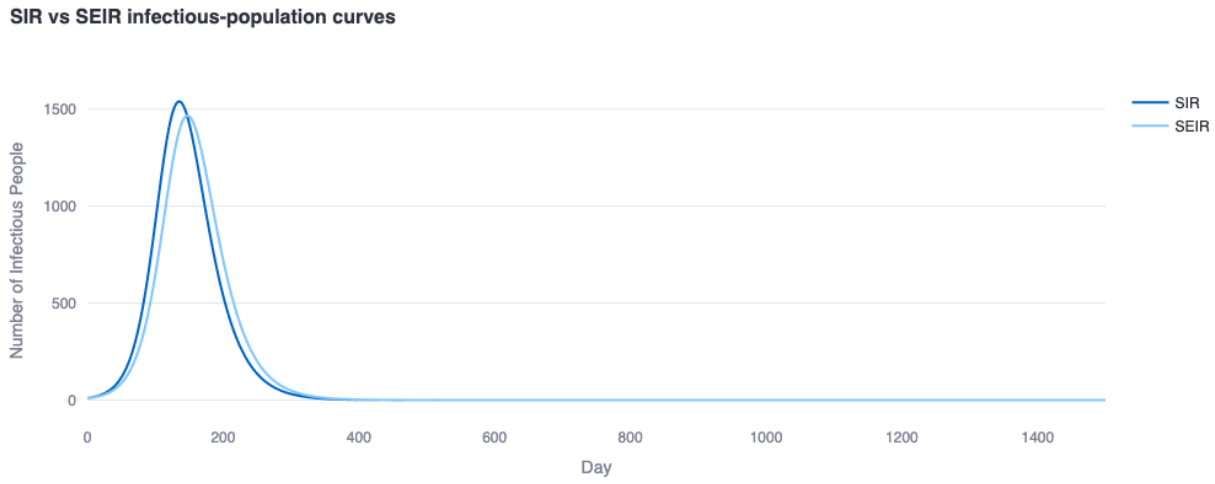
R_0	Latent period	Infectious period	Latent-to-infectious ratio	Peak error %	Peak-time difference	NRMSE	Acceptable
2.0	1	15	0.067	6.73	12.15 days	0.0073	TRUE
2.0	1	20	0.050	5.04	12.30 days	0.0065	TRUE
3.0	1	20	0.050	5.10	9.80 days	0.0129	TRUE

As shown in Table 1, the common feature of all acceptable cases is that the latent period was only 1 day, while the infectious period was relatively long. This produced very small latent-to-infectious ratios, between 0.050 and 0.067. In these cases, the SEIR model still had a delayed infectious peak, but the delay was small enough to remain within the 15-day acceptance limit. The peak-size errors were also below 10%, meaning that SIR estimated the maximum infectious population reasonably well.

However, a small ratio alone did not guarantee acceptance. For example, when R_0 = 1.5, latent period = 1 day, and infectious period = 20 days, the peak error was only 5.01%, but the peak-time difference was 16.2 days. Since this exceeded the 15-day limit, the simulation was still classified as not acceptable.

Figure 1

SIR and SEIR infectious-population curves for R_0 = 2.0, a latent period of 1 day, and an infectious period of 20 days.



The case in Figure 1 was classified as an acceptable approximation because the peak error was 5.04% and the peak-time difference was 12.30 days. Figure 1 shows that the two models produce relatively similar epidemic curves under these conditions, with only a small difference in both peak size and peak timing.

Effect of Latent-to-Infectious Ratio

The strongest trend in the results was the effect of the latent-to-infectious ratio. When this ratio increased, the SIR model became a much poorer approximation of the SEIR model.

This pattern is especially clear when R_0 = 2.0 and the infectious period is 4 days. As the latent period increased from 4 to 12 days, the latent-to-infectious ratio increased from 1.0 to 3.0. Over the same range, the peak error increased from 102.09% to 302.98%, and the peak-time difference increased from 36.0 days to 90.85 days.

Table 2. Effect of latent-to-infectious ratio on approximation accuracy

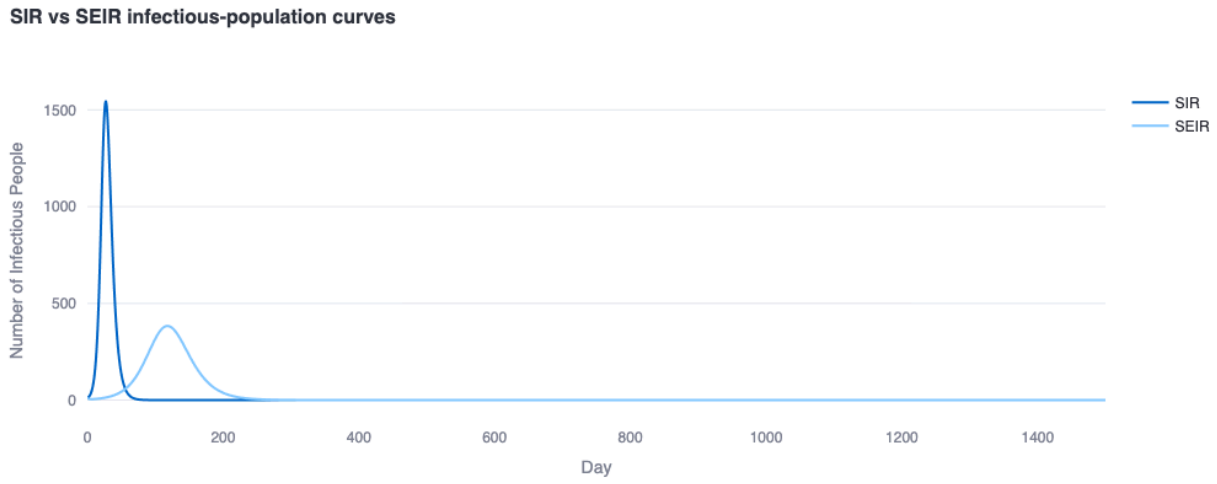
Latent period	Infectious period	Ratio	Peak error %	Peak-time difference
4	4	1.0	102.09	36.00 days
6	4	1.5	152.52	50.55 days
8	4	2.0	202.76	64.35 days
10	4	2.5	252.89	77.75 days
12	4	3.0	302.98	90.85 days

Results in Table 2 show that when the latent period is equal to or longer than the infectious period, SIR greatly overestimates the infectious peak compared with SEIR. This happens because SIR assumes that newly infected individuals become infectious immediately, while SEIR delays their movement into the infectious compartment. As this delay becomes longer, the SEIR curve becomes lower and more spread out over time, while the SIR curve remains much sharper.

As the latent-to-infectious ratio increased, the difference between the two models became substantially larger. For example, when R_0 = 2.0, the latent period was 12 days and the infectious period was 4 days, producing a ratio of 3.0 (**Figure 2**).

Figure 2.

SIR and SEIR infectious-population curves for R_0 = 2.0, a latent period of 12 days, and an infectious period of 4 days.



As shown in Figure 2, the SIR model substantially overestimates the infectious peak and predicts it much earlier than SEIR. The peak error was 302.98%, and the peak-time difference was 90.85 days.

Effect of Infectious Period

The results also show that increasing the infectious period can improve the peak-size approximation when the latent period is held constant. For the simulations with R_0 = 2.0 and latent period = 6 days, the peak error decreased as the infectious period increased. Because R_0 was held constant in this comparison, changing the infectious period also changed γ and consequently β through the relationship β = R_0γ.

Table 3. Effect of infectious period on approximation accuracy

Infectious period	Latent period	Ratio	Peak error %	Peak-time difference	Acceptable ?
3	6	2.0	202.95	48.25 days	FALSE

5	6	1.2	122.23	52.40 days	FALSE
7	6	0.857	87.51	55.40 days	FALSE
10	6	0.600	61.34	58.60 days	FALSE

As shown in Table 3, the peak error decreased from 202.95% to 61.34% as the infectious period increased from 3 to 10 days. This supports the hypothesis that SIR becomes closer to SEIR when the latent period is shorter relative to the infectious period. However, none of these cases were acceptable because the peak error remained far above 10%, and the peak-time difference remained much greater than 15 days.

An important observation is that the peak-time difference did not decrease in this subset. Instead, it increased from 48.25 to 58.60 days. This suggests that a longer infectious period may reduce the difference in peak height, but it can also stretch the epidemic over a longer time scale, keeping the timing difference large.

Increasing the infectious period while keeping the latent period at 6 days reduced the peak error, although the simulations remained outside the acceptance criteria. The case with R_0 = 2.0, a latent period of 6 days, and an infectious period of 7 days is shown in Figure 3.

Figure 3

SIR and SEIR infectious-population curves for R_0 = 2.0, a latent period of 6 days, and an infectious period of 7 days.

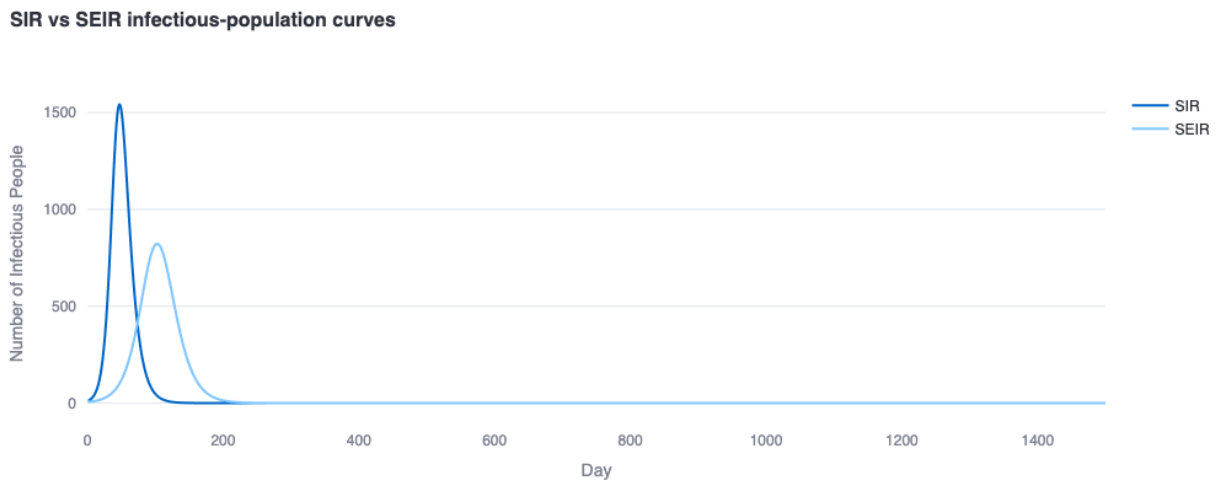


Figure 3 demonstrates a substantial difference between the models. The peak error was 87.51%, and the peak-time difference was 55.40 days, so the approximation was classified as not acceptable.

Effect of R_0

The simulations also tested the effect of changing R_0 while keeping the latent period at 6 days and the infectious period at 7 days. In this group, all parameter combinations were classified as not acceptable.

Table 4. Effect of R_0 on approximation accuracy

R_0	Latent period	Infectious period	Peak error %	Peak-time difference	Acceptable?
1.2	6	7	85.86	131.10 days	FALSE
1.5	6	7	86.33	81.45 days	FALSE
2.0	6	7	87.51	55.40 days	FALSE
2.5	6	7	88.89	44.45 days	FALSE
3.0	6	7	90.35	38.25 days	FALSE

Table 4 shows that peak error stayed high across all R_0 values, ranging from 85.86% to 90.35%. This indicates that when the latent period is already substantial relative to the infectious period, changing R_0 does not make SIR a good approximation of SEIR. However, the peak-time difference decreased as R_0 increased. For example, when R_0 increased from 1.2 to 3.0, the peak-time difference decreased from 131.10 days to 38.25 days. This suggests that stronger transmission speeds up both models, reducing the absolute delay between their peaks, although the difference in peak size remains too large.

Comparison of Best and Worst Cases

The best approximation in the tested data occurred when R_0 = 2.0, the latent period was 1 day, and the infectious period was 20 days. In this case, the latent-to-infectious ratio was 0.05, the

peak error was only 5.04%, and the peak-time difference was 12.30 days. This case met both acceptance criteria and was therefore classified as acceptable.

The worst case occurred when R_0 = 2.0, the latent period was 12 days, and the infectious period was 4 days. In this case, the latent-to-infectious ratio was 3.0, the peak error was 302.98%, and the peak-time difference was 90.85 days. This case was clearly not acceptable.

Interpretation in Relation to the Hypothesis

Overall, the results support the hypothesis that the SIR model becomes a closer approximation of SEIR as the latent period becomes shorter relative to the infectious period. All acceptable cases in the tested parameter set had latent-to-infectious ratios between 0.050 and 0.067. However, the low-ratio case with R_0 = 1.5 and a ratio of 0.050 failed the peak-time criterion, showing that a small ratio alone did not guarantee acceptance.

Discussion

Interpretation of the Main Findings

The main finding of this investigation is that the effect of the exposed stage depends strongly on its duration relative to the infectious period. When the latent period was very short, the delay introduced by the SEIR model had a limited effect on peak size and timing. As the latent period became longer relative to the infectious period, the difference between the models increased substantially.

However, the results also show that a small latent-to-infectious ratio does not automatically guarantee an acceptable approximation. For example, when R_0 = 1.5, the latent period was 1 day and the infectious period was 20 days, the peak error was only 5.01%, but the peak-time difference was 16.2 days. Since this exceeded the 15-day limit, this simulation was still classified as not acceptable.

This suggests that the relationship between SIR and SEIR depends not only on the latent-to-infectious ratio, but also on how quickly the epidemic develops overall. Even if the peak sizes are similar, the peak timing may still differ enough for the SIR model to fail the acceptance criterion.

Why SIR Only Worked for Small Latent-to-Infectious Ratios

The observed pattern can be explained by the delay introduced by the exposed compartment in SEIR. When this delay is small relative to the infectious period, its effect on the infectious curve is limited. As the latent period becomes longer, the delay becomes increasingly important, producing a later and lower SEIR peak compared with SIR. This is clearly shown in the

simulations where R_0 = 2.0 and the infectious period was 4 days. As the latent period increased from 4 to 12 days, the peak error increased from 102.09% to 302.98%, while the peak-time difference increased from 36.0 to 90.85 days.

This pattern shows that SIR strongly overestimates the infectious peak when the latent period is substantial. Since SIR assumes immediate infectiousness, it concentrates transmission earlier in the epidemic. SEIR spreads the transmission process over a longer time because individuals must first pass through the exposed stage. Therefore, SEIR tends to produce a later and lower infectious peak, while SIR produces an earlier and sharper peak.

Role of the Acceptance Criterion

The acceptance criterion had an important effect on the interpretation of the results. In this investigation, SIR was considered acceptable only if both conditions were met:

peak error ≤ 10%

peak-time difference ≤ 15 days

This criterion is useful because it evaluates both the peak and timing of the epidemic peak. A model that predicts the correct peak size but the wrong peak day may still be misleading, especially if the model is used to plan healthcare resources or interventions.

The choice of acceptance thresholds affected the final classification. In particular, some simulations produced relatively small peak-size errors but failed because their peak-time differences exceeded the selected limit. This shows why evaluating both magnitude and timing provides a more demanding comparison than using peak error alone. Because the thresholds were defined as working criteria rather than universal epidemiological standards, different thresholds could produce different classifications.

The results show why using two criteria is important. Some simulations had relatively small peak-size errors but still failed because the peak-time difference was too large. This means that relying only on peak error would make the SIR model appear more accurate than it actually is. Therefore, including peak timing made the comparison more balanced.

Relationship to Previous Literature

The findings are consistent with the theoretical difference between SIR and SEIR described in the literature review. The SIR model is useful because it is simple and interpretable, but it assumes that infected individuals become infectious immediately. The SEIR model adds biological realism by including a delay between infection and infectiousness.

The results also support the idea that adding an exposed compartment mainly affects the timing and shape of the epidemic curve. In the simulations, SEIR curves were generally delayed compared with SIR curves. This agrees with the explanation that the exposed compartment stretches the epidemic over time.

The findings also connect with the argument that more complex models are not always automatically better. In cases where the latent period was very short compared with the infectious period, the simpler SIR model produced an acceptable approximation. This supports the use of simpler models when they are sufficient for the research purpose. However, when the latent period was large, the SEIR model was clearly more appropriate because SIR could not reproduce the delayed infectious peak.

Limitations of the Investigation

Several limitations should be considered when interpreting these results. First, the investigation used idealised mathematical simulations rather than real epidemic data. The results therefore show how the models behave under controlled parameter combinations, not how a specific disease would spread in a real population.

Second, both models assumed a closed population. Births, deaths, migration and reinfection were not included. The models also assumed homogeneous mixing, meaning that every individual had the same probability of contacting every other individual. This is a simplification, since real populations have age groups, social networks, geographic structure and different levels of contact.

Third, the parameters were kept constant over time. In reality, transmission rates may change because of behavioural changes, public health interventions, vaccination or seasonal effects. The models also did not include stochastic variation, so the same parameter values always produced the same epidemic curve.

Fourth, the number of tested parameter combinations was limited. The results show a clear trend, but they do not define a universal boundary for when SIR approximates SEIR. A larger parameter sweep could test more values of R_0, latent period and infectious period to identify the approximation boundary more precisely.

Finally, the acceptance criterion itself is a limitation. The thresholds of 10% peak error and 15 days peak-time difference were chosen as practical rules for comparison. Different thresholds could lead to a different number of acceptable cases.

Implications for Model Selection

This investigation examined when the SIR model can provide an acceptable approximation of SEIR under matched initial conditions. Across the tested parameter combinations, approximation quality depended strongly on the relationship between the latent and infectious periods. The closest agreement occurred when the latent period was very short relative to the infectious period, while larger ratios produced increasingly large differences in peak size and timing.

The findings therefore support the hypothesis that the latent-to-infectious ratio is an important determinant of SIR–SEIR similarity. However, the low-ratio cases also showed that this ratio alone does not fully determine whether an approximation satisfies both peak-size and peak-time criteria. Within the tested parameter set, all acceptable cases had very small ratios, but not every small-ratio case was acceptable.

These results suggest that SIR can be useful when model simplicity is important and the latent stage has little influence on the quantities of interest. When the delay between infection and infectiousness is substantial, SEIR provides a more appropriate representation. Future work could extend the analysis using a denser parameter grid, alternative acceptance criteria, or real epidemic data.

Conclusion

This investigation examined when the SIR model can provide an acceptable approximation of SEIR under matched initial conditions. Across the tested parameter combinations, approximation quality depended strongly on the relationship between the latent and infectious periods. The closest agreement occurred when the latent period was very short relative to the infectious period, while larger ratios produced increasingly large differences in peak size and timing.

The findings therefore support the hypothesis that the latent-to-infectious ratio is an important determinant of SIR–SEIR similarity. However, the low-ratio cases also showed that this ratio alone does not fully determine whether an approximation satisfies both peak-size and peak-time criteria. Within the tested parameter set, all acceptable cases had very small ratios, but not every small-ratio case was acceptable.

These results suggest that SIR can be useful when model simplicity is important and the latent stage has little influence on the quantities of interest. When the delay between infection and infectiousness is substantial, SEIR provides a more appropriate representation. Future work could extend the analysis using a denser parameter grid, alternative acceptance criteria, or real epidemic data.

Appendix

Appendix A: Full Simulation Results

Table A1 shows the complete set of parameter combinations tested in this investigation. The SIR model was considered an acceptable approximation if the peak error was no greater than 10% and the peak-time difference was no greater than 15 days.

Table A1. Full SIR–SEIR comparison results

Run	R_0	Latent period	Infectious period	Ratio	Peak error %	Peak-time difference	NRMSE	Acceptable?
1	2.0	1	7	0.143	14.51	11.60	0.0094	FALSE
2	2.0	2	7	0.286	29.19	21.65	0.0148	FALSE
3	2.0	4	4	1.000	102.09	36.00	0.0164	FALSE
4	2.0	6	4	1.500	152.52	50.55	0.0167	FALSE
5	2.0	8	4	2.000	202.76	64.35	0.0166	FALSE
6	2.0	10	4	2.500	252.89	77.75	0.0164	FALSE
7	2.0	12	4	3.000	302.98	90.85	0.0163	FALSE
8	1.2	6	7	0.857	85.86	131.10	0.0035	FALSE
9	1.5	6	7	0.857	86.33	81.45	0.0110	FALSE
10	2.5	6	7	0.857	88.89	44.45	0.0284	FALSE
11	3.0	6	7	0.857	90.35	38.25	0.0334	FALSE
12	2.0	6	3	2.000	202.95	48.25	0.0144	FALSE
13	2.0	6	5	1.200	122.23	52.40	0.0186	FALSE
14	2.0	6	7	0.857	87.51	55.40	0.0214	FALSE
15	2.0	6	10	0.600	61.34	58.60	0.0239	FALSE
16	2.0	1	10	0.100	10.12	11.85	0.0084	FALSE
17	2.0	1	15	0.067	6.73	12.15	0.0073	TRUE
18	2.0	1	20	0.050	5.04	12.30	0.0065	TRUE
19	1.5	1	20	0.050	5.01	16.20	0.0027	FALSE
20	3.0	1	20	0.050	5.10	9.80	0.0129	TRUE

The full table contains 20 simulations. Three simulations were classified as acceptable approximations, while 17 were classified as not acceptable.

Appendix B: Web-Based Simulator

An interactive web-based simulator was developed using Python and Streamlit. The simulator allowed the user to change the main parameters of the SIR and SEIR models, including population size, initial infectious population, basic reproduction number, latent period, infectious period, simulation duration and numerical time step.

The simulator automatically calculated the SIR and SEIR curves and displayed the main comparison metrics, including peak infected population, peak day, peak error percentage, peak-time difference, normalised RMSE and the final acceptable/not acceptable classification.

The public version of the simulator was made available online:

https://sir-seir-simulator-4hzz4b2i7yg854asbf2tsn.streamlit.app/

Appendix C: Main Computational Procedure

The following pseudocode summarises the main computational process used in the simulator.

1. Set initial parameter values:

   population size

   initial infected

   initial exposed

   R_0

   latent period

   infectious period

   simulation duration

   time step

2. Calculate model rates:

   γ = 1 / infectious period

   σ = 1 / latent period

   $\beta = R_0 \times \gamma$

3. Run SIR simulation:

   calculate new infections

   calculate new recoveries

update S, I and R compartments

4. Run SEIR simulation:

calculate new exposures

calculate exposed-to-infectious transitions

calculate new recoveries

update S, E, I and R compartments

5. Compare infectious-population curves:

calculate SIR peak infected

calculate SEIR peak infected

calculate peak error percentage

calculate SIR peak day

calculate SEIR peak day

calculate peak-time difference

calculate NRMSE

6. Classify approximation:

if peak error ≤ 10% and peak-time difference ≤ 15 days:

acceptable approximation = TRUE

else:

acceptable approximation = FALSE

Appendix D: Notes on Model Assumptions

The simulations used the same simplifying assumptions described in the methodology. The population was assumed to be closed, meaning that births, deaths and migration were ignored.

The population was also assumed to mix homogeneously, meaning that all individuals had the same probability of contacting each other.

The models did not include vaccination, reinfection, age structure, stochastic variation, changing public health behaviour or time-dependent transmission rates. Therefore, the results should be interpreted as a mathematical comparison between SIR and SEIR rather than as a prediction for a specific real-world epidemic.

References

[1] Heng, K., & Althaus, C. L. (2020). The approximately universal shapes of epidemic curves in the Susceptible-Exposed-Infectious-Recovered (SEIR) model. *Scientific Reports, 10*, Article 19365. https://doi.org/10.1038/s41598-020-76563-8

[2] Kamrujjaman, M., Saha, P., Islam, M. S., & Ghosh, U. (2022). Dynamics of SEIR model: A case study of COVID-19 in Italy. *Results in Control and Optimization, 7*, Article 100119. https://doi.org/10.1016/j.rico.2022.100119

[3] Maassen, J. P. (2020). The SIR and SEIR epidemiological models revisited. *Preprints*, 202005.0090. https://doi.org/10.20944/preprints202005.0090.v1

[4] Roda, W. C., Varughese, M. B., Han, D., & Li, M. Y. (2020). Why is it difficult to accurately predict the COVID-19 epidemic? *Infectious Disease Modelling, 5*, 271–281. https://doi.org/10.1016/j.idm.2020.03.001

[5] Smith, D., & Moore, L. (2004). The SIR model for spread of disease: The differential equation model. *Mathematical Association of America*. https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model

[6] Weiss, H. (2013). The SIR model and the foundations of public health. *MATerials MATemàtics, 2013*(3), 1–17. https://ddd.uab.cat/record/108432