Comparison of the Hawkes and SEIR models for the spread of Covid-19

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Abstract
Two models that capture the spread of infectious diseases, the Hawkes point process model and the SEIR compartmental model, are compared with regard to their use in modeling the Covid-19 pandemic. The physical plausibility of the SEIR model is weighed against the parsimony and flexibility of the Hawkes model. The mathematical connection between Hawkes and SEIR models is described.
1 Introduction

The SARS-CoV2 (Covid-19) pandemic spread from China to at least 188 countries or regions in the first six months of 2020 [15]. The characteristics of the Covid-19 virus have been estimated and forecasted by numerous researchers with highly variable results. Estimates of properties such as reproduction rate (or time-varying reproduction number), numbers of individuals infected, hospitalization rates, fatality rates, and efficacy of containment measures have varied widely [4, 22]. Accurate real-time estimates of the spread of Covid-19 are difficult to achieve without population-wide testing [18, 6]. Nevertheless, it is important for researchers to accurately estimate and forecast the dynamics of Covid-19 so that optimal public policy measures and other responses can be adopted.

Several different frameworks have been proposed for modeling the spread of Covid-19, including compartmental models such as the SEIR (Susceptible → Exposed → Infectious → Removed) differential equation model, and branching point process models such as the Hawkes point process model [70, 37, 6, 10]. This paper compares these two approaches for forecasting Covid-19. Relative to Hawkes models, SEIR models and their variants have been used far more widely to describe the Covid-19 pandemic [7, 24, 31, 42] as well as other infectious diseases such as Ebola [43] and SARS [19]. However, recent studies have suggested that Hawkes models may be more accurate [87]. For general discussion of mathematical and statistical models of epidemiological phenomena, see [60, 28].

This paper is structured as follows. Following a review of Hawkes and SEIR models in Section 1, we compare their advantages and disadvantages, especially with respect to forecasting Covid-19 cases or deaths in Section 2. In Section 3, we detail the mathematical connection between Hawkes processes and SEIR models, and in Section 4 we provide concluding remarks.

1.1 The Hawkes Model

The Hawkes model or self-exciting point process model is commonly used to model clustered point patterns in applications such as seismology, finance, crime, and infectious diseases [16, 69, 57, 9]. A spatial-temporal Hawkes process is specified by the model

\[ \lambda(s, t) = \mu(s) + K \int_{t' < t} g(s - s', t - t')dN(s', t') \]  

(1)

for \( s \in X \subseteq \mathbb{R}^2 \) and \( t \in [0, T) \), where \( \lambda(s, t|\mathcal{H}_t) \) is the conditional rate at which points (events) are expected to accumulate around spatial-temporal location \( (s, t) \), given information on all previous events. The conditional intensity uniquely characterizes the finite-dimensional distribution of any simple point process (see Prop. 7.2.IV of [16]), and thus equation (1) fully specifies the model.
The function $g$ is typically assumed to be a density, i.e. to be nonnegative and to integrate to 1 over all time and space, and is called the *triggering density*. Common choices for $g$ are the exponential or Pareto densities in time, and the Gaussian or Pareto densities in space [69]. The constant $K$ is called the *productivity*.

Provided $g$ is a density function, $K$ is the expected number of points triggered directly by each point, and is thus closely connected to the reproduction number in compartmental models such as SEIR. Each background point, associated with $\mu(s)$, is expected to generate $K + K^2 + K^3 + \ldots = 1/(1 - K) - 1 = K/(1 - K)$ triggered points. As a result, in a Hawkes process, the expected fraction of background points is $1 - K$.

Given a dataset consisting of $n$ points within a space-time observation region $B$, the parameters in Hawkes processes are typically fit by maximum likelihood estimation (MLE), where one obtains parameter estimates $\hat{\Theta}$ maximizing

$$L(\Theta) = \sum_{i=1}^{n} \log(\lambda(s_i, t_i)) - \int_B \lambda(s, t) dt ds.$$  

The resulting estimates have desirable properties. For instance, Ogata (1978) showed that the MLE $\hat{\Theta}$, is, under standard conditions, asymptotically unbiased, consistent, asymptotically normal, and asymptotically efficient, with standard errors readily constructed using the diagonal elements of the inverse of the Hessian of $L$ evaluated at $\hat{\Theta}$ [59]. Further, if the fitted model is missing some relevant covariates, under general conditions the MLE will nevertheless be consistent, provided the effect of the missing covariates is small [74]. The triggering function can also be estimated non-parametrically [49], and some authors have also estimated the background rate $\mu(s)$ nonparametrically, e.g. [91, 65]. Bayesian methods can also be used to estimate parameters and quantify uncertainty in Hawkes process models [68, 53].

A host of variations of the Hawkes model have been proposed [10, 70]. The HawkesN model, as defined in [70], has a Hawkes conditional intensity scaled by the proportion of events which can still occur after time $t$, in order to account for the dynamic decrease in the number of susceptible individuals in a given location [70]:

$$\lambda(t) = (1 - L_c(t)/N)(\mu + K \sum_{t' < t} g(t - t')).$$  

(2)

In the context of a Hawkes process modeling the spread of an infectious disease, $L_c(t)$ is the cumulative number of infections that have been recorded up to time $t$ and $N$ is the total population size.

Hawkes models and their slight variants such as the epidemic-type aftershock sequence (ETAS) model [57, 58], HawkesN [70, 6, 54], and the recursive model [76] have been shown to be useful in modeling infectious diseases such as Ebola [39, 64], chlamydia [75], SARS [82, 9], measles [21], meningococcal disease [51], and Rocky Mountain Spotted Fever [76]. Hawkes models have also been shown to be the best fitting models for forecasting seismicity in rigorous, purely prospective earthquake forecasting studies such as the Collaboratory for the Study of Earthquake Predictability (CSEP) [13, 14, 90, 8, 27, 77].
1.2 The SEIR Model

SEIR models and their variants have been widely used to model and forecast the spread of many contagious diseases including Covid-19 [81, 86, 7, 29, 44, 32, 30, 66, 52, 31]. Such models employ a wide variety of modifications to the classic SEIR model, including using Bayesian inference [52], machine learning [31], mobility networks and ensemble approaches [32], and mixed-effects curve fitting [81] to fit parameters, as well as slight compartmental variants like SuIER which account for unreported cases [30]. Other models explicitly define scenarios for government interventions or enforcement of public health policies in specific populations [44, 7, 29].

SEIR models assume that individuals within each category, or compartment (susceptible, exposed, infectious, and recovered), share pertinent characteristics, and the size of the population of interest $N$ is equal to the total number of individuals in the compartments [40]. SEIR models are a slight extension of SIR (Susceptible $\rightarrow$ Infectious $\rightarrow$ Removed) models, generalized to account for the fact that there is an incubation time for some infectious diseases like Covid-19, during which the exposed host may be asymptomatic and thus not recorded as infected. SEIR models can be either deterministic, in which case they are comprised of a system of differential equations, or stochastic, in which case they are based on a Markov chain framework. Given large populations, sufficient initial spread, and enough time, the deterministic framework should resemble the stochastic framework in expectation, assuming properly specified models [70].

Deterministic SEIR models, such as that described in Figure 1, can provide a reasonable approximation of the characteristics of a contagious disease such as Covid-19. There are numerous variations, but the basic idea conveyed in Figure 1 common to compartmental models is that there is some rate at which people shift from one portion of the population to another, e.g. from the susceptible population to the exposed population, and these rates may be fixed or allowed to vary over time subject to certain constraints. Deterministic models such as that shown in Figure 1 can be extended to allow parameters governing the force of infection, number of cases by symptom onset, and death rate, with movement between compartments commonly specified as binomial random variables. Such a model has been suggested for the transmission of Ebola, for instance [43]. Number of cases or deaths are commonly specified as a negative binomial random variable [45, 35].

Perhaps the most common method for estimating compartmental infectious disease model parameters is by using Bayesian estimation [62, 12]. Prior parameters are often decided on using subject matter experts [52] or parameters fit to prior outbreaks [25]. Bayesian SEIR models have been employed to model infectious diseases such as Ebola [25], Visceral Leishmaniasis [62] and Covid-19 [52]. Prior distributions are typically specified by compartment. For instance, Frasso et al. specified number of deaths as beta-distributed, duration of incubation as normal, and observed cases as negative binomial [25]. Disease characteristics such as reproduction number has been modelled within the context of SIR models with a gamma prior [12]. Joint posteriors are then solved for using a
Figure 1: Diagram of the deterministic SEIR model. Definitions: $N$ is a constant number of individuals in a susceptible population, $\beta \cdot I$ is equal to the force of infection, $\Lambda$ equal to birth rate, $\mu$ equal to death rate, $\gamma$ equal to mortality rate, $\alpha$ equal to the average incubation period. Such a model has reproduction number $R_0 = \frac{\alpha \beta}{(\mu + \alpha)(\mu + \gamma)}$.

MCMC approach such as Metropolis-Hastings or Gibbs sampling [12, 43].

Stochastic versions of the SIR and SEIR models allow researchers to include the effect of networks of individuals, but specification and parameter estimation can be more challenging [3]. Various stochastic SEIR models have been developed to model Covid-19 data. A stochastic SEIR model with parameters fit using grid search, which may be viewed as a relatively agnostic machine learning approach, was implemented in [31], and a stochastic SEIR model hybrid with agent-based simulation was suggested in [42]. The compartmental approach of the SEIR model is slightly modified to accommodate under-detection and differentiated government intervention in the DELPHI model [7]. Their flexibility notwithstanding, the difficulty in estimating time-varying parameters in real time for stochastic SEIR models is well known, especially for large populations [55].

Parameters in SEIR models are often estimated using opinions of expert epidemiologists or using data from other locations or past epidemics [11]. This is attractive in the sense that expert opinion is integrated, but there is ample opportunity for bias as well as mis-specification, and the parameter estimates have a covariance structure that can be difficult to estimate. Further, non-identifiability is a known problem for compartmental models [26]. Although there exists algebraic approaches for testing identifiability such as exhaustive modeling [83], such methods are not implemented in any of the above referenced Covid-19 SEIR models. Crucially, estimated SEIR parameters in the early stages of a epidemic (before peak infection) have been shown to be struc-
2 Comparison of Point Process and Compartmental Models

Hawkes and SEIR models both offer flexible (and somewhat complementary) frameworks for modeling infectious diseases. Hawkes models allow for nonparametric estimation of the triggering function $g$, as well as spatial covariates, and an intrinsic network-effect. SEIR models offer a far more physically plausible framework for describing Covid-19 relative to the Hawkes model. Specifically, SEIR models allow for specification of stochastic movement between compartments based on previous epidemics and expert opinions. The compartmental model framework allows for natural implementation of known networks within the population of interest [55]. Further, quantities of interest to epidemiologists and policy makers such as infection rate within a population can be imputed using SEIR models [43].

Within the context of a SEIR model, the spread or transmission of an infectious disease such as Covid-19 occurs via Markovian diffusion which, under certain regularity conditions, ultimately converges to a stationary distribution. In the context of a Hawkes model, background events trigger future events, and these trigger subsequent events, ultimately resolving due to the decay of the chosen triggering function if the productivity is less than one. In general, a point process is considered to be stationary when for all bounded Borel subsets $A_1, \ldots, A_r$ of the real line, the joint distribution of $\{N(A_1 + t), \ldots, N(A_r + t)\}$ is independent of $t \in \mathbb{R}$ [16]. A Hawkes process with $K > 1$ is not stationary [80]. The HawkesN model is a stationary process for $K > 1$.

The link between Hawkes-like and stochastic SIR models is explored in detail in [70], where it is shown that an exponentially decaying triggering function chosen for a finite population Hawkes model (HawkesN) coincides in expectation with the number of individuals infected in a stochastic SIR model as it approaches stationarity. This connection between SIR and Hawkes models was explored in particular in the context of Covid-19 [6], where it was shown that the HawkesN and SIR models converge if the triggering function is exponential and the reproduction number in the SIR model is constant [6]. SIR and HawkesN models are shown to provide similar fit to Twitter re-tweet diffusions in [70].

One may also compare features such as the doubling time for both Hawkes and SIR/SEIR models. In the early exponential growth stage, the doubling time for SIR is $\tau = \log(2)/(\gamma(R_0 - 1))$ [1]. The relationship between estimates of $R_0$ and doubling time for simulations of compartmental models is summarized in [50]. The parameter $K$ is intuitively similar to $R_0$, as it represents the expected number of events triggered by a previous event. The doubling time for HawkesN models as a function of $K$ is shown next to the doubling time of a SIR model as a function of $R_0$ in Figure 2. It should be noted that doubling time for Hawkes models quickly approaches zero for $K > 1$, justifying the finite population correction present in the HawkesN in the context of modeling infectious diseases.
such as Covid-19 [70].

Figure 2: Average doubling time for HawkesN model with $\beta = \frac{1}{4}$, $I_0 = 10$, population size $N = 10^6$, and using mean intensity over 100 simulations per $K$ (notated $R_0$ for SIR). Doubling time is defined as $t$ such that $N(t) = 20$.

Hawkes models offer computationally inexpensive parametric and non-parametric estimates for important characteristics of infectious diseases such as Covid-19. Due to computational difficulty, and model-specification convenience, both SEIR and Hawkes models often make assumptions such as fixed population size, or homogeneity individuals within compartments. Despite this, the difficulty of specifying large population size stochastic SEIR models in real time is not trivial. In general, Hawkes models seem to be far simpler to implement than SEIR-type models, and in a pandemic such as the spread of Covid-19, where resources can be scarce and policies and health-allocations must be made in real-time, quick and accurate short term forecasts are highly valuable [85].

Relative to Hawkes processes, SEIR models are more natural mathematical representations of the spread of contagious diseases. However, in implementation SEIR models often require estimation of more parameters and structural modifications. With complexity, there is more opportunity for bias and random errors in parameter estimates, as well as large covariances between pairs of parameter estimates, and in some cases problems of identifiability [20, 71]. More pressingly, each component of the model is susceptible to mis-specification, which can result in highly variable estimates and large forecasting errors [34, 61].

Problems such as these can be particularly severe in the case of Covid-19, where available data used to fit parameters can rely on substantial errors, due to undercounted infected populations and testing policies that vary over time and space [41]. Both Hawkes and SEIR models assume a homogenous population and do not explicitly account for testing errors, but Hawkes and HawkesN models appear to perform better than their SEIR equivalents for modeling the spread of infectious diseases (see Table 1 below).
2.1 Comparison of Covid-19 Results in the Current Literature

SEIR models appear to be far more widely used by State and Federal agencies for forecasting Covid-19 cases and deaths, with a notable exception being the State of New Jersey which is primarily using a multivariate Hawkes model [36]. Table 1 summarizes results comparing the accuracy of Hawkes models and their variants with SEIR models and their variants for forecasting infectious diseases. Point process models have been found to forecast incidence of mumps in Pennsylvania better than compartmental SVEIR models [38]. Further, point process models have been found to improve fit and forecasting performance relative to SEIR models when applied to incidence of pertussis in [87]. Yuan et al. find substantially improved accuracy of Hawkes models over SEIR models for forecasting Covid-19 in the European Union, California, New York, and for the United States as a whole [89].

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<th>Data</th>
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Table 1: Prior results comparing the forecasting accuracy of point process and compartmental models for infectious diseases. Errors reported are the root mean squared error (RMSE) and (**) mean absolute error of daily forecasts. Model selection using (+) Akaike Information Criterion (AIC) and (**) Normalized Discounted Cumulative Gain.

Hawkes models are directly compared to SIR and SEIR models to explain the spread of Covid-19 in California, Indiana, and New York in [6]. The Akaike information criterion (AIC) is used to evaluate the candidate models, and by this metric, Hawkes performs more poorly relative to its compartmental counterparts for Covid-19 death data, and with mixed results for Covid-19 case data. However, fitted parameters are found to vary materially across locations, and relative fit of parameters across models is concluded to not be strongly indicated. Rather than concluding on the merits of either type of model, the authors note the difficulty of using limited data at the beginning of an epidemic such as that of Covid-19 [6].
In the context of the Covid-19 pandemic, compartmental models such as SIR and SEIR have been noted to generally have low accuracy for long-term forecasts, and machine learning models have been proposed as a superior alternative [2]. Compartmental models also may be poorly calibrated for forecasting more than five days out: forecast numbers of Covid-19 cases in Italy six days in the future based on the SEIR model were 14% too low on average [2]. Various compartmental models for forecasting Covid-19 yield slightly different projections of future cases or future deaths [72]. However, estimates of variability vary widely, with prediction interval widths often varying by a factor of 3 [7, 24].

Some variation is to be expected in both mean predicted deaths and size of prediction interval between the models as each are designed differently, and with varying assumptions. Estimates of the initial reproduction number $R_t$ for COVID-19 vary around 3.28 (1.4, 6.5) [63]. Of course, values of $R_t$ are observed to vary substantially depending on social distance policies. In China, estimates of $R_t$ decreased from 2 to 1 when public health measures were put in place [88]. Estimates of $R_t$ in Singapore correspondingly decreased over time by between 78.2% and 99.3% [37]. Similar results were observed in Europe as a result of public health measures [23].

SEIR forecasts of future confirmed cases or deaths depend critically on estimates of the total numbers of asymptomatic or mildly symptomatic cases, which are highly uncertain [78, 5] and extremely difficult to estimate accurately [48, 79]. Jewell et al. [37] note that more detailed and complex models may be more sensitive to assumptions regarding the incubation and infectious periods and other estimates of transmission characteristics. Further, SIR and SEIR models are highly sensitive to assumptions regarding social movement and the estimated impacts of containment policies [67]. SIR and SEIR models are known to be particularly sensitive to assumptions about the distribution of latent and infectious periods [47, 84]. Further, as discussed above, nonidentifiable parameters can be an issue for compartmental models, and methods for dealing with non-identifiability of parameters tend to work better for simpler models than for more complex compartmental models [71].

3 Further Connections Between Hawkes and SEIR Models

The productivity constant $K$ in the Hawkes model is the obvious analogue of the reproduction rate $R_0$ in SEIR, with both interpretable as the expected number of direct transmissions per infected individual. Further, several variations of the Hawkes process in Equation 1 have deeper connections to SEIR-type compartmental models. The point process governed by Equation 2 is a continuous time analog of a discrete stochastic SIR model when $g(t)$ is specified as exponential [70]. When $g(t)$ is chosen to be gamma distributed, the Hawkes process also can approximate staged compartment models, like SEIR, if the average waiting time in each compartment is equal [47]. More complex parametric (or non-parametric) inter-infection time distributions $g(t)$ may be employed within the Hawkes process framework in situations where disease dynamics cannot be
captured by a SIR or SEIR model. In the early exponential growth stage of an epidemic, before finite population and social distancing effects play a role, the linear Hawkes process in Equation 1 can readily be used to model new infections (see Figure 3).

Figure 3: Left: (Red) SEIR differential equation \( \frac{dS}{dt} = -\beta SI/N; \frac{dE}{dt} = \beta SI/N - \mu E; \frac{dI}{dt} = \mu E - \gamma I; \frac{dR}{dt} = \gamma I \), where \( \beta = \gamma R_0, \gamma = .1, R_0 = 2, \mu = 1, \) and \( N = 5 \cdot 10^8 \). (Blue) linear Hawkes process \( \lambda_t = \mu + \sum_{t>t_i} K g(t-t_i) \) fit to the SEIR curve of new infections using non-parametric expectation-maximization [54]. Right: Non-parametric histogram estimate for \( g(t) \) corresponding to the Hawkes process fit.

While the Hawkes process can approximate SEIR in some situations with an appropriately chosen kernel \( g(t) \), queue-Hawkes processes [17] can also be used to model an exposed latent class of events. Let \( N \) be population size, \( N_E^t \) be the cumulative sum of infections (whether recovered or not) up to time \( t \). Then we may define a hybrid model incorporating features of both SEIR and Hawkes, which we call a SEIR-Hawkes process, where the intensity of newly exposed cases is given by

\[
\lambda^E(t) = \left(1 - \frac{N_E^t}{N}\right) \sum_{t>t_j^I} R_0 \gamma \exp \left(-\gamma(t-t_j^I)\right),
\]

and the times of infection are generated via

\[
P(t_j^I > t_E^j + c) = \int_c^\infty \mu \exp \left(-\mu(s-t_E^j)\right)ds.
\]

Realizations of the SEIR-Hawkes process can be generated via Lewis’ thinning method for simulation [56, 46]. We first simulate an upper-bounding Hawkes process with intensity

\[
\nu^E(t) = \sum_{t>s_j^I} R_0 \gamma \exp \left(-\gamma(t-s_j^I)\right).
\]

\[
P(s_j^I > s_j^E + c) = \int_c^\infty \mu \exp \left(-\mu(s-s_j^E)\right)ds.
\]
Because the Hawkes process in Equation 5 has a branching process representation [33], the process can be simulated iteratively; for each event pair \((s^I_j, s^E_j)\), by

1. Generating a Poisson random variable \(M\) with mean \(R_0\).
2. Generating \(l = 1, ..., M\) events with inter-event times \(s^E_l - s^I_j\) given by an exponential random variable with parameter \(\gamma\).
3. Generating \(l = 1, ..., M\) events with inter-event times \(s^I_l - s^E_l\) given by an exponential random variable with parameter \(\mu\).

Thinning then proceeds sequentially by accepting each event pair \((s^I_j, s^E_j)\) with probability \(\lambda^E(s^E_j)/\nu^E(s^E_j)\) where \(\lambda^E\) is computed using only accepted events in the history and \(\nu^E\) is computed using all simulated events. In Figure 4 we simulate the SEIR-Hawkes process with parameters \(\mu = 1\), \(\gamma = .1\), \(R_0 = 2\), \(N = 1000\) and \(N^E_0 = 10\) (\(t^E_1 = ...t^E_{10} = 0\)) and compare to the forward-Euler approximate solution (\(dt = .01\)) of a SEIR differential equation \(dS/dt = -\beta SI/N\), \(dE/dt = \beta SI/N - \mu E\), \(dI/dt = \mu E - \gamma I\), \(dR/dt = \gamma I\), where \(\beta = \gamma R_0\).

Figure 4: SEIR differential equation simulation (red) and 50 realizations of the SEIR-Hawkes process. Parameters for the SEIR model are \(R_0 = 2\), \(\mu = 1\) for the \(E \rightarrow I\) rate, \(\gamma = .1\) for the \(I \rightarrow R\) rate, and population size \(N = 1000\).

4 Conclusion

The SEIR model is currently far more widely used to model epidemic diseases such as Covid-19 than the Hawkes model, and its parameterization is physically plausible, with parameters that are readily interpreted in the epidemiological community. The SEIR model also appears to forecast epidemics adequately in most cases, especially in the early spread of the disease. However, the Hawkes model seems to offer more accurate forecasts, with approximately 20-30% smaller errors on average in most cases. Among the several reasons listed in Section 2 for this discrepancy, the most significant seem to be mis-specification.
in the SEIR model and its sensitivity to errors in estimates of latent quantities such as the number of asymptomatic individuals and the distribution of incubation times. In general, when maximal accuracy is desired, models for forecasting observations should typically be only as complex as necessary to represent the main features of interest in the data, with minimal dependence on unobserved or noisy data [39].

There are close connections between SEIR and Hawkes models, and indeed the two types of models can be constructed to be equivalent or to converge to one another in special cases. The SEIR-Hawkes model described here may provide further linkage between the two paradigms in cases where one seeks the accuracy of point process modeling without sacrificing the physical plausibility and interpretation of SEIR parameters, and the model is shown here to emulate characteristics of SEIR models closely.

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References


