Impact of Production-Inventory Control on the Dynamics of Epidemics

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Abstract

A general production inventory (PI) model is integrated with the traditional disease diffusion (SEIRS) model to understand the role of inventory policies on vaccine preventable epidemic dynamics. An integrated PI-SEIRS model has been described, wherein the demand to the PI component depends on the infected population, and the recovery rate of patients depends on the timely supply of medicines. The performance comparison of PI-SEIRS model and the standalone SEIRS model is carried out using an illustrative influenza epidemic data set. Results show that the supply chain or inventory effects on the epidemic dynamics is significant. A given epidemic can be caused by high infectivity parameter with sufficient supply of medicine or with a low infectivity parameter but insufficient supply of medicine. Also, the use of a standalone SEIRS model overestimates the disease severity, compared to the combined inventory control and epidemics model.

Keywords: infectivity parameter; SEIRS model; PI-SEIRS model; inventory control

1 Introduction

A severe influenza epidemic outbreak is a very real threat for any society or country. The declaration of epidemic further can create unnecessary panic among people and disrupt essential services, business activities, and transportation services due to workforce absenteeism (Bienstock & Zenteno, 2012). Control measures are designed by healthcare decision makers based on the severity of the epidemic. Thus, a good estimation for epidemic severity (disease transmissibility or *infectivity*) parameter is of paramount importance. Past literature (Nsoesie et al., 2013; Samsuzzoha et al., 2013; Chowell et al., 2006) have used dynamic epidemic models to estimate the disease

model parameters. Now, for any vaccine preventable disease, the supply of medicine/vaccine plays an important role in controlling the dynamics of the epidemic (Dasaklis et al., 2012). Hence, it is necessary to incorporate the medicine supply information into epidemic dynamics model as well to estimate the disease parameters with higher precision.

There is a significant gap between epidemic modelling and supply chain modelling literature. There is few literature (Duintjer Tebbens et al., 2010; Thompson & Duintjer Tebbens, 2014; Chick et al., 2008) available that combines these two areas. Most of the previous literature (Arinaminpathy & McLean, 2008, 2009; Lee & Chen, 2007; Yarmand et al., 2014; Ren et al., 2013) in planning and control of epidemic have focused primarily on resource allocation (RA) models but not on the supply chain aspects of resources (Dasaklis et al., 2012). The procurement/ stock management of resources are of importance since without ensuring the availability of resources, RA models are pointless. Duintjer Tebbens et al. (2010), have combined a disease diffusion and a vaccine production model to minimize the total cost of public health and vaccine production for a suitable selection of vaccine filling flows and production flows at each time t. Using game theoretic approach, (Chick et al., 2008) have developed a variant of cost sharing contract between governmental healthcare sector and vaccine manufacturer to improve the overall performance of influenza vaccine supply chain. But these models (Duintjer Tebbens et al., 2010; Thompson & Duintjer Tebbens, 2014) are from the production perspective while this paper addresses the inventory management perspective.

Sterman (2000) has provided a generic stock management system structure that provides the basic environment for decision making experiment in various scenarios like, production inventory control, raw material ordering etc. Various analyses (such as average system cost, service level, stability) on production inventory (PI) system has already been concluded using control theoretic approach (Venkateswaran & Son, 2007; Bijulal et al., 2011). However, these analyses on PI system have been done for time invariant demand mean and are thus not valid for epidemic demand pattern as it follows a bell shaped curve with a long right tail.

This research has two goals. The *first goal* is to bridge the gap between supply chain and epidemic containment literature and aid healthcare decision makers in managing outbreaks more efficiently. The interaction between epidemic outbreak and medicine stock management is a two way feedback process, as unmet vaccine needs will generate more demands and sufficient supply will reduce disease transmission. Hence, SD methodology is adopted to build the integrated model. The *second goal* is to explore the effect of stock management control parameters on disease dynamics and on the quality of disease parameter estimation, since every supply chain involves various delays (such as production delay, transportation delay etc.) and delays cause additional dynamics in system variables which eventually degrade the performance of the supply chain. For vaccine preventable diseases, poor supply of

medicines can also force the epidemic to grow further, even when the severity of the actual disease is low. Thus, it is difficult to determine whether an epidemic has occurred due to higher *infectivity* or poor supply of medicine by only looking at the disease data without analysing the corresponding supply chain. Moreover, it is not clear as to how much of the epidemics impact is reduced by better supply chain management. We hypothesize that the use of a standalone disease transmission model will over-estimate the disease severity, as against a combined inventory control and epidemics model.

We investigate our hypothesis using data from the second wave of *Spanish flu* outbreak that occurred in Sydney in 1919 (Samsuzzoha et al., 2013), for illustration purposes only.

The rest of the paper is organised as follows: Section 2 describes a basic disease transmission model and the proposed integrated model. In section 3 the performance of both the models are analysed, and the impact of supply chain effects on disease dynamics is quantified using the illustrative data set of the *1919 Spanish flu* . Section 4 discusses the observations and future work.

2 Model Description

In this section, we first describe the popular SEIRS model for disease transmission, and then the proposed integrated SEIRS and production inventory (PI) models. The PI component represents the vaccine supply chain. The interaction between these two models' functions are as follows: the demands for vaccine (in hospitals) are generated from the epidemic model and fed into the production inventory model. Then, based on output of the production inventory model (i.e., the availability of vaccines in the hospital stock), the patients in the hospital are treated. The symbols, notations and then abbreviations as used in this section are listed in Table 1.

2.1 Standalone SEIRS Model

A variant of the compartmental SEIRS model has been used to describe the dynamics of influenza transmission. In a similar manner to the conventional SD models for epidemic outbreak (e.g., SI, SIR models, discussed in (Sterman, 2000)), this model divides the total population into four groups viz. Susceptible (S), Exposed (E), Infected patient under treatment (I), and Recovered (R). Further, the mixture of population within each compartment is assumed to be homogeneous. The stock and flow diagram of the SEIRS model is shown in Fig.1.

A susceptible (S) individual may get exposed to the disease if he comes in contact with an exposed (E) or infected (I) individual (see Equation (1)). It is assumed that the capability of spreading the disease of an exposed individual is only $k\%$ of an infected individual. The infectivity rate of S is governed by the infectivity parameter γ, which is defined as the product of contact

Table 1: Notations Used

Symbol	Description	Units
γ	Infection probability (pi)$\times$ Contact rate (λ)	(rate) 1/day
N	Total population	people
P	Incubation period	day
TRM	Time to recovery with medicine	day
TR	Time to recovery without medicine	day
TW	Waning time	day
S(t)	Susceptible population at time t	people
E(t)	Exposed population at time t	people
I(t)	Infected patients under treatment at time t	people
R(t)	Recovered population at time t	people
ER(t)	Exposure rate at time t	people/day
AR(t)	Hospital admission rate at time t	people/day
RRM(t)	Recovery rate with medicine at time t	people/day
RR(t)	Recovery rate without medicine at time t	people/day
WR(t)	Waning rate at time t	people/day
α	Fractional rate of adjustment of medicine on order discrepancy	(rate) 1/day
β	Fractional rate of adjustment of medicine in stock discrepancy	(rate) 1/day
ρ	Smoothing factor (constant) for forecast	
L	Production lead time	day
VDT	Vaccine distribution time	day
DCovg	Desired stock coverage	day
SS	Safety stock coverage	day
DS(t)	Desired stock of medicine at time t	units
DO(t)	Desired order of medicine at time t	units
FD(t)	Demand forecast for time period t	units/day
MS(t)	Available inventory or stock at time t	units
MO(t)	Medicine quantity on order at time t	units
AdjMS(t)	Adjustments for inventory discrepancy at time t	units/day
AdjMO(t)	Adjustments for medicine on order discrepancy at time t	units/day
DR(t)	Medicine demand rate at time t	units/day
OR(t)	Medicine order sent from hospital at time t	units/day
PR(t)	Production completion rate at time t	units/day
SR(t)	Shipment rate of medicine at time t	units/day
MaxSR(t)	Maximum Shipment rate of medicine at time t	units/day

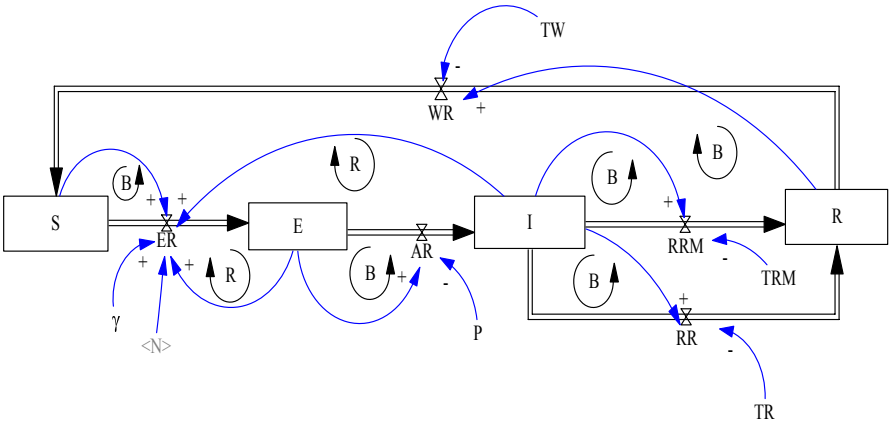


Figure 1: Stock flow diagram of disease diffusion model

rate (λ, the number of people who interact per time period) and infection probability (pi, the chance of getting infection from contacting an infected person). Thus $\gamma = \lambda \times pi$. An exposed individual remains asymptomatic for an incubation time period P (see Equation (2)). As soon as the patient develops symptom or falls sick, he is shifted from the "E" to the "I" compartment for treatment (see Equation (3)). Patients are assumed to recover after an average recovery time (TRM) when medicines are made available and an average time of recovery (TR) without medicine (i.e., natural burnout). It is assumed that $TR > TRM$. After recovering from the disease, an individual loses immunity (this loss could be due to the mutation of the disease virus) and again becomes susceptible to the disease after a time period of "TW" (see Equation (4)).

The governing continuous time domain equations of the *SEIRS* disease diffusion model are as follows:

$$\frac{d(S(t))}{dt} = \frac{R(t)}{TW} - \frac{\gamma \times (k \times E(t) + I(t)) \times S(t)}{N} \quad (1)$$

$$\frac{d(E(t))}{dt} = \frac{\gamma \times (k \times E(t) + I(t)) \times S(t)}{N} - \frac{E(t)}{P} \quad (2)$$

$$\frac{d(I(t))}{dt} = \frac{E(t)}{P} - \frac{I(t)}{TRM} - \frac{I(t)}{TR} \quad (3)$$

$$\frac{d(R(t))}{dt} = \frac{I(t)}{TRM} + \frac{I(t)}{TR} - \frac{R(t)}{TW} \quad (4)$$

2.2 Description of PI-SEIRS Integrated Model

Our integrated model comprises a disease diffusion component and a stock management component.

2.2.1 Production Inventory (PI) Model

A generic stock management model, similar to those discussed in (Sterman, 2000; Venkateswaran & Son, 2007) or class of automatic pipeline variable inventory order based production control system (APVIOBPCS) (Dejonckheere et al., 2003) is adopted for depicting the inventory management of medicines or vaccines at the hospital, as shown in Fig. 2.

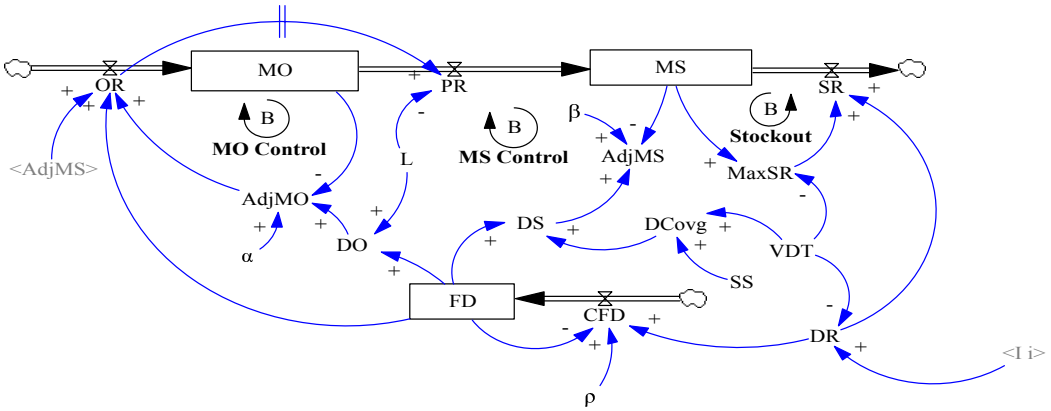


Figure 2: Stock flow diagram of inventory management model

The demand is forecasted (FD) using an exponential smoothing method with smoothing factor ρ, as shown in Equation (5). The hospital ordering strategy is modelled as a generalized order-upto (G-OUT) policy (Bijulal et al., 2011), as shown in Equation (6). The order quantity depends on the forecasted demand FD, the discrepancy in desired and actual orders in pipeline ($AdjMO$) and the discrepancy in desired and actual stock or inventory on hand ($AdjMS$). The discrepancy in orders in pipeline and in stock is adjusted using the tuning parameters α ($1/T_w$, the reciprocal of time to adjust MO) and β ($1/T_i$, the reciprocal of time to adjust MS), respectively. The desired orders in pipeline, as per Little's Law, is computed as a product of lead time L and the FD (see Equation (7)). The desired stock is also governed by the FD and the desired coverage level and safety stock SS (see Equation (8)). Equations (9) and (11) are the inventory balance equations for the orders in pipeline (MO) and (MS), respectively. The production rate (PR) is modelled as a third order material delay to capture the mixing of products and variabilities in production times. The delivery or sales rate SR of medicines, Equations (12) and (13), govern the actual supply of medicines from the stock to the hospital, subject to the actual availability. It is noted that the ordering behaviour of the system can be tuned using the parameters (α, β).

$$\frac{d(FD(t))}{dt} = \rho \times (DR(t) - FD(t)) \quad (5)$$

$$OR(t) = FD(t) + \underbrace{\alpha(DO(t) - MO(t))}_{AdjMO(t)} + \underbrace{\beta(DS(t) - MS(t))}_{AdjMS(t)} \quad (6)$$

$$DO(t) = L \times FD(t) \quad (7)$$

$$DS(t) = (SS + DCovg) \times FD(t) \quad (8)$$

$$\frac{d(MO(t))}{dt} = (OR(t) - PR(t)) \quad (9)$$

$$PR(t) = \text{Delay3}(OR(t), L) \quad (10)$$

$$\frac{d(MS(t))}{dt} = (PR(t) - SR(t)) \quad (11)$$

$$SR(t) = \max\{0, \min\{\text{MaxSR}(t), DR(t)\}\} \quad (12)$$

$$\text{MaxSR}(t) = MS(t)/VDT \quad (13)$$

The demand of medicines DR depends on the number of infected patients under treatment $I^i(t)$, as shown in Equation (14), where VDT is the vaccine distribution time. This serves as the linking constraint from the SEIRS model to the PI model.

$$DR(t) = I^i(t)/VDT \quad (14)$$

2.2.2 Disease Diffusion Component

The *SEIRS* model (see Section 2.1) is integrated with a production inventory (PI) model of the hospital to explore the impact of supply chain on epidemic dynamics. In the integrated model, the recovery rate with medicine (RRM^i) depends on the flow of medicine from the stock management model. That is, $RRM^i = \dfrac{\max\{0, \min\{I^i(t), MS(t)\}\}}{TRM^i}$. The updated differential equations governing the SEIRS component of the integrated model is as shown in Equations (15) - (18). The variables of the PI-SEIRS model is distinguished from those of the stand-alone SEIRS model using superscript i, while the meaning of the notations remains the same as defined in Table 1. In addition to the above, we made the following assumptions: the hospital was under stable condition before the occurrence of the epidemic outbreak, and each epidemic patient required one unit of drug to recover. All other general assumptions of the compartmental epidemic models (Sterman, 2000) hold true.

$$\frac{d(S^i(t))}{dt} = \frac{R^i(t)}{TW^i} - \frac{\gamma^i \times \left(k \times E^i(t) + I^i(t)\right) \times S^i(t)}{N^i} \quad (15)$$

$$\frac{d(E^i(t))}{dt} = \frac{\gamma^i \times \left(k \times E^i(t) + I^i(t)\right) \times S^i(t)}{N^i} - \frac{E^i(t)}{P^i} \quad (16)$$

$$\frac{d(I^i(t))}{dt} = \frac{E^i(t)}{P^i} - \frac{\max\{0, \min\{I^i(t), MS(t)\}\}}{TRM^i} - \frac{I^i(t)}{TR^i} \quad (17)$$

$$\frac{d(R^i(t))}{dt} = \frac{\max\{0, \min\{I^i(t), MS(t)\}\}}{TRM^i} + \frac{I^i(t)}{TR^i} - \frac{R^i(t)}{TW^i} \quad (18)$$

3 Experiments and Analyses

In this section we study, using simulation, the appropriateness of standalone SEIRS model and the integrated PI-SEIRS model in modelling the epidemic dynamics. The *second wave of the 1919 Spanish Flu* data set (Samsuzzoha et al., 2013) or *raw data* is used for illustration. The SEIRS model and PI-SEIRS model are both independently calibrated for the *raw data*, using least square regression method, so as to minimize the root mean square error (RMSE). Thus the objective function can be written as shown in Equation (19), where p is the set of all parameters, Γ is the set of ranges of corresponding parameters, and T is the total run time.

$$RMSE = \min_{p \in \Gamma} \sqrt{\frac{\int_{t=0}^{T} \left(I(t) - \hat{I}(t)\right)^2 dt}{T}} \quad (19)$$

The general simulation settings, and simulation-based optimisation method employed is described in (Section 3.1). The SEIRS model results are discussed in (Section 3.2). (Section 3.3) demonstrates the effect of stock control parameters on the final epidemic size using PI-SEIRS model. Finally, the PI-SEIRS model results are discussed in (Section 3.4)

3.1 Simulation Settings and Optimisation

Simulation models for SEIRS and PI-SEIRS were built using *Anylogic®6*. RK4 integration method with time step of 0.001 was used for integration and simulation was run for 70 days (T). For PI-SEIRS's stock management component, we chose $L = 3$ days (Bijulal et al., 2011), $VDT = 1$ day, $SS = 0.1$ day (chosen arbitrarily but lesser system inventory preferred), ρ =1 (to give higher weightage to current demand). For the SEIRS model and the epidemic component of PI-SEIRS model, we have taken $k = 0.85$ (chosen arbitrarily), $TW = 365$ days (Samsuzzoha et al., 2013), $I_0 = 79$, and $R_0 = 0$. Note that the influence of *Waning Rate* (WR(t)) in this illustration is expected to be negligible due to large *Waning Time* (TW). For MO, MS, and FD initial values are chosen as DO, DS and DR respectively.

Calibration of the models using least square regression was carried out using the optimisation solver *OptQuest*®, a commercial tool. This simulation based optimisation works as follows. The optimisation solver (i.e. *OptQuest*) chooses a set of parameter values and passes it on to the simulation (SD) model. The model runs the simulation, evaluates the objective function (i.e. *RMSE*), and returns the same to the optimisation solver. The solver, then *intelligently* chooses the next set of parameters for evaluation by the simulation model. This iterative scheme continues until a pre-defined stopping criteria is met, and the best result obtained is reported. *OptQuest* is based on scatter search, tabu search and neural networks. Since *OptQuest* internally uses a probabilistic scheme to search the solution space, multiple runs of the simulation-based optimisation might converge to different best solutions. In our experiments, the simulation-based optimization was run for 5500 iterations (stopping criteria).

3.2 *SEIRS* Model Calibration with *Raw Data* Set

The standalone SEIRS model was calibrated using the *raw data* set of the *second wave of 1919 Spanish Flu* by tuning the parameter set $p = \{S_0,\ E_0,\ \gamma,\ P,\ TRM,\ TR\}$. Based on the characteristic of a disease, some basic parameters (related to length of stay (LOS)) of the epidemic model can be confirmed either from the healthcare experts' opinion or from past data. Unfortunately, for the *1919 Flu* outbreak, most of the LOS parameters (such as TRM, TR) are unknown. Hence, they were also included as a decision parameter in our model. The range of input parameters used are $S_0 \in [3000, 5000]$, $E_0 \in [20, 90]$, $\gamma \in [0, 1]$, $P \in [1, 4]$, $TRM \in [4, 6]$, $TR \in [6, 8]$.

Ten different experimental run were performed for simulation-based optimization to minimize $RMSE$ and the results are presented in Table 2. Based on the results, it is observed that the average $RMSE$ is 13.057 with a 95% confidence interval half width of 0.009, and the corresponding infectivity parameter $\gamma \in (0.307 \pm 0.013)$. The 95% confidence of the other parameters are $P \in (1.99 \pm 0.242)$, $TRM \in (5.06 \pm 0.268)$, $TR \in (7.04 \pm 0.194)$, $S_0 \in (4024 \pm 275.846)$, $E_0 \in (46 \pm 6.508)$.

3.3 Impact of Inventory on Final Epidemic Size

In this section, the effect of inventory control on the final epidemic size is analysed using the PI-SEIRS model. The final epidemic size (R_∞) is defined as the total number of people who were infected during the outbreak, as shown below:

$$R_\infty = \int_0^T I(t)dt \tag{20}$$

In order to show the impact of ordering policies on R_∞, a total of 961 (α, β) pairs were generated combining 31 values for each of α and β between

Table 2: Results of calibration of SEIRS model

Experiment	RMSE	γ	P	TRM	TR	S_0	E_0
1	13.059	0.302	2.1	5	7.1	3951	49
2	13.064	0.298	2.1	5.6	6.6	3777	48
3	13.066	0.297	2.2	5.2	7	3798	51
4	13.043	0.328	1.5	5.1	6.8	4312	32
5	13.028	0.349	1.3	4.3	7.4	4964	29
6	13.065	0.297	2.1	5.5	6.9	3716	47
7	13.057	0.308	2.1	4.7	6.9	4234	52
8	13.066	0.297	2.2	5.2	7	3798	51
9	13.057	0.305	1.9	5.1	7.5	3858	42
10	13.069	0.293	2.4	4.9	7.2	3832	58

0 to 3 with step size 0.1. The parameters $(S_0^i, E_0^i, \gamma^i, P^i, TRM^i, TR^i)$ of the epidemic component of the PI-SEIRS model is assumed to be the same as the results obtained for Experiment 1, Table 2, for all (α, β) combinations. Simulations were carried out for all (α, β) pairs, the R_∞ calculated and a contour plot of the same plotted in Fig. 3. The figure shows that the ordering policies (α, β) affect R_∞ significantly. Moreover, the set of optimal (α, β) lies in $\alpha < \beta$ region (i.e., the region shown by 2375), where β is high and α is small.

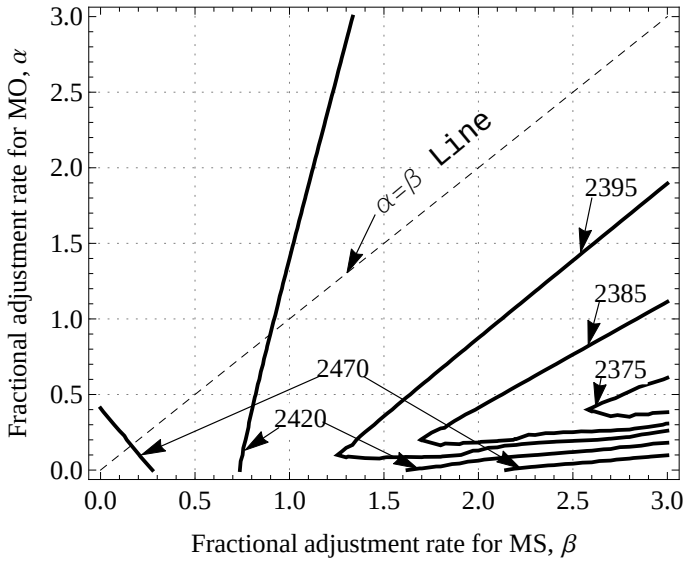


Figure 3: Contour plot of R_∞ with $\gamma = 0.302$

Figure 4 compares the change in R_∞ over time for selected values of (α, β), and the standalone SEIRS model. It is again noted that the epidemics com-

ponent of PI-SEIRS model and the SEIRS model parameters are exactly the same, with $\gamma = 0.302$. $SEIRS$ results in lowest R_∞ since it assumes infinite inventory and instantaneous supply of medicine, thus giving a lower bound on R_∞. Similarly, the worse case (giving an upper bound on R_∞) is obtained by substituting $\alpha = 0, \beta = 0$ (i.e. inventory discrepancies are not adjusted) in the PI-SEIRS model.

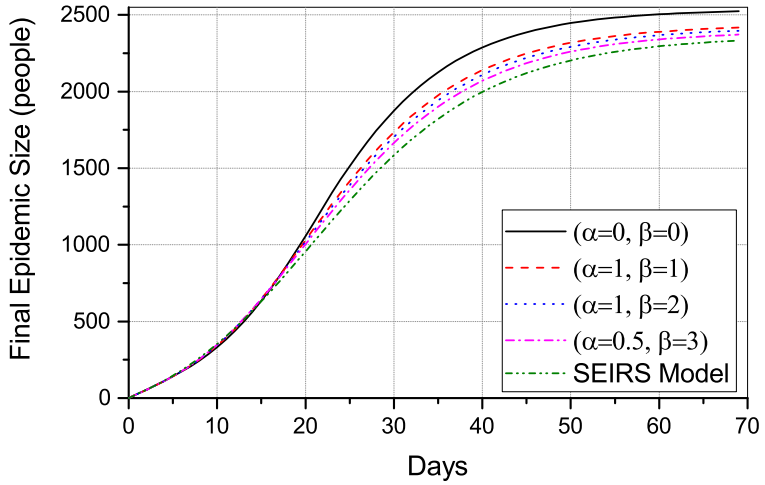


Figure 4: Comparison of R_∞ of SEIRS model and PI-SEIRS model for different ordering policies with $\gamma = 0.302$.

The percentage (%) increase in the final R_∞ value at different settings of (α, β), relative to that obtained using SEIRS is computed using Equation (21), and tabulated in Table 3.

$$\frac{(R_{\infty,(\alpha,\beta)} - R_{\infty,SEIRS}) \times 100}{R_{\infty,SEIRS}} \tag{21}$$

These results clearly show that inventory control aspects does influence the dynamics of the epidemics, with a net increase in R_∞ of 1.693% to 8.208%. A 'natural' order setting of $(\alpha = \beta = 1)$, where discrepancies in order and discrepancies in inventory are adjusted as per their exact shortages, also results in a 3.676% increase in R_∞.

3.4 *PI-SEIRS* Model Calibration with *Raw Data* Set

The integrated PI-SEIRS model is calibrated using the raw data set of the *second wave of 1919 Flu* by tuning the parameter set $p = \{S_0^i,\ E_0^i,\ \gamma^i,\ P^i,\ TRM^i, TR^i,\ \alpha,\ \beta\}$. The range of used input parameters are $S_0^i \in [3000, 5000]$,

Table 3: Increment of R_∞ (in %) from lower bound ($R_{\infty,SEIRS}$) based on different ordering policies.

Ordering Policy (α, β)	Increment of R_∞ (in %)
(0.5,3)	1.693
(1,2)	2.782
(1,1)	3.676
(0,0)	8.208

$E_0^i \in [20, 90]$, $\gamma^i \in [0, 1]$, $P^i \in [1, 4]$, $TRM^i \in [4, 6]$, $TR^i \in [6, 8]$, and $0 \leq \alpha, \beta \leq 2$. The root mean square error $RMSE^i$ is minimized, with objective as shown below.

$$RMSE^i = \min_{(S_0^i, E_0^i, \gamma^i, P^i, TRM^i, TR^i, \alpha, \beta) \in \Gamma} \sqrt{\frac{\int_{t=0}^{T} \left(\hat{I}(t) - I^i(t)\right)^2 dt}{T}} \tag{22}$$

Ten different experimental run were performed for simulation-based optimization to minimize $RMSE^i$ and the results presented in Table 4. Based on the results, it is observed that the average $RMSE^i$ is 13.044 with a 95% confidence interval half width of 0.026, and the corresponding infectivity parameter $\gamma^i \in (0.267 \pm 0.003)$. The 95% confidence of the other parameters are $P^i \in (3.34 \pm 0.227)$, $TRM^i \in (4.69 \pm 0.240)$, $TR^i \in (7.34 \pm 0.268)$, $S_0^i \in (3520 \pm 93.628)$, $E_0^i \in (78 \pm 6.036)$. α, β take only two (0 & 0.2) and four (1.1, 1.2, 1.9, 2) values respectively. Based on the results from Table 4 it can be seen that multiple combinations of $(\alpha, \beta, \gamma^i)$ exist that can give a close fit to the *raw data*, thus highlighting the importance of the medicine supply chain on epidemic dynamics.

Table 4: Results of calibration of PI-SEIRS model

Experiment	$RMSE^i$	γ^i	P^i	TRM^i	TR^i	S_0^i	E_0^i	α	β
1	13.053	0.265	3.4	5.1	6.8	3,384	78	0.2	2
2	13.01	0.273	3.2	4.5	6.9	3,783	76	0	1.2
3	13.069	0.265	3.2	5.1	7.2	3,394	74	0.2	2
4	13.109	0.267	3	5	7.2	3,566	70	0	1.1
5	13.016	0.264	3.7	4.3	7.6	3,526	89	0.2	1.9
6	13.033	0.265	3.5	4.6	7.4	3,466	82	0.2	2
7	13.089	0.273	2.8	5	7.3	3,577	62	0	1.2
8	13.025	0.271	3.2	4.6	7.2	3,659	76	0.2	2
9	12.998	0.261	3.8	4.2	8	3,464	90	0	1.2
10	13.035	0.262	3.6	4.5	7.8	3,379	82	0	1.2

A comparison of the results from the SEIRS model (Table 2) and the PI-SEIRS model (Table 4) reveals the following. The use of the PI-SEIRS model provides a comparable, if not better fit to the *raw data* with an average RMSE of 13.044, which is slightly lower than 13.057 obtained for the SEIRS model. However, for the PI-SEIRS model, the average infectivity parameter γ^i is found to be 0.267 which is significantly lesser than the average of 0.307 obtained using the SEIRS model. This supports our hypothesis that a given epidemic/disease dynamics can be caused by high infectivity parameter with infinite or sufficient supply of medicine (SEIRS model) or a lower infectivity parameter with insufficient supply of medicine (PI-SEIRS model).

Fig. 5 plots and compares the dynamics of the infected population as obtained using calibrated SEIRS model and PI-SEIRS, with the *raw data*. As illustrated, multiple configurations result in very similar epidemics behaviour. The corresponding dynamics of two key stock management component variables, MS and MO are also shown in Fig. 6.

In this section, the epidemic component of PI-SEIRS model is calibrated with *raw data* within a given range of ordering policies (α, β) to explore the impact of medicine supply chain on γ^i.

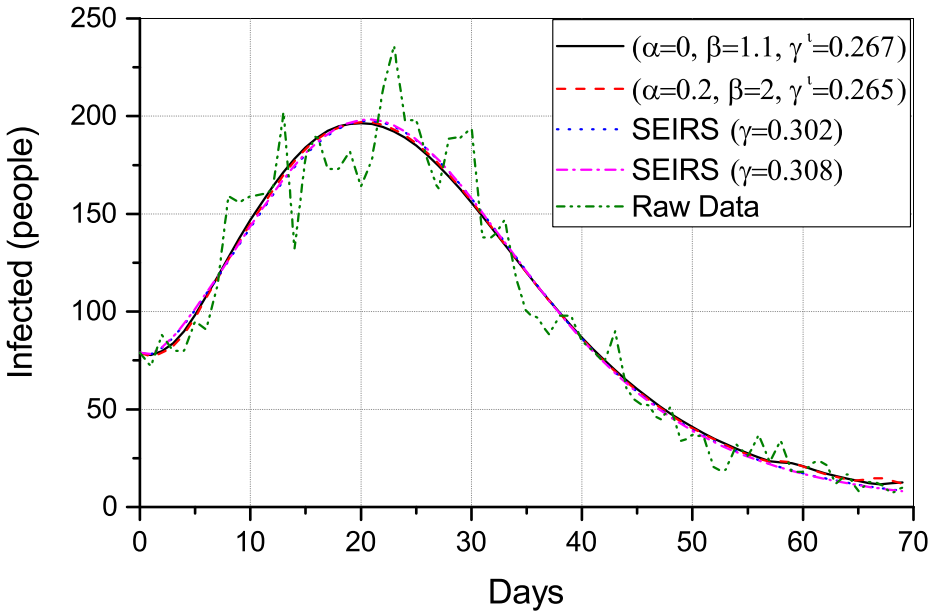
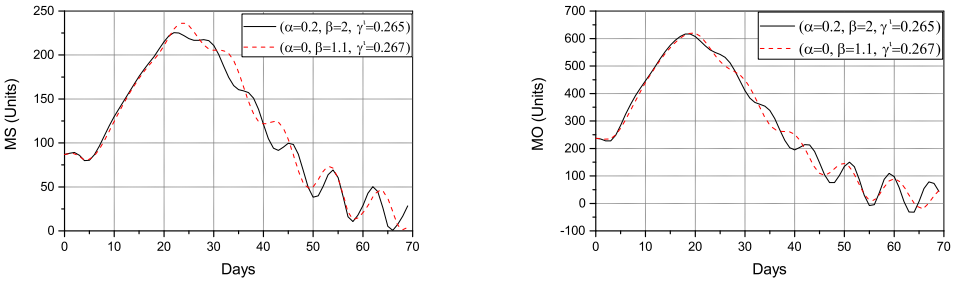


Figure 5: Infected data comparison from SEIRS and PI-SEIRS model



(a) (b)

Figure 6: Inventory MS, MO dynamics of calibrated PI-SEIRS model

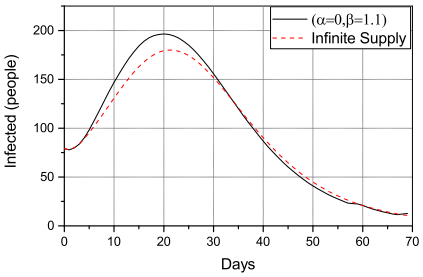
3.4.1 Effect of Improved Medicine Supply on Epidemic Dynamics

In this section, we highlight the scope of reduction in epidemic peaks through better inventory/ supply chain management. We compared the differences in infected curves for $(\alpha, \beta, \gamma^i)$ tuple scenario and γ^i with infinite inventory scenario. The results of this section are based on the data corresponding to 4^{th} & 6^{th} row of Table 4. For example, for γ^i with infinite inventory scenario, we simply substitute the values of γ^i and other epidemic component parameters (i.e., $S_0^i, E_0^i, P^i, TRM^i, TR^i$) of the PI-SEIRS model in the *SEIRS* model. Similarly, the plots of infected population for $(\alpha, \beta, \gamma^i)$ tuple scenario are obtained from the PI-SEIRS model, substituting all the parameters mentioned above.

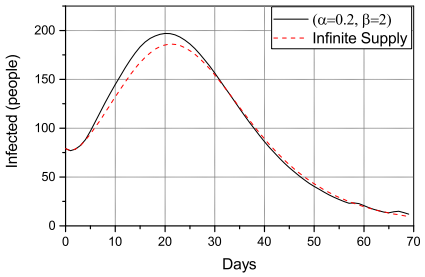
Fig. 7(a) shows that with sufficient supply of medicine an epidemic peak can be reduced by 8.303% while in Fig. 7(b), it is 5.536%. The reason for such difference in reduction size may be because in Fig. 7(b), we are already using better inventory policy (see Fig. 3) compared to Fig. 7(a), and hence increasing the supply of medicine further would reduce the peak of epidemic a little. We require more analysis on the selection of control parameters to further improve the system.

4 Conclusions and Future Work

An integrated PI-SEIRS model has been proposed which combines the general production inventory model with an influenza disease diffusion model. The performance of the PI-SEIRS model has been analysed using an illustrative data set based on the *1919 Spanish flu*. It is noted that these results are expected to be valid for any other disease epidemic data. Experimental results show that the inventory control parameters (α and β) significantly affect infectivity parameter estimation and disease dynamics. Further, it is seen that



(a) $\gamma^i = 0.267$, Exp. 4 from Table 4



(b) $\gamma^i = 0.265$, Exp. 6 from Table 4

Figure 7: Comparison of Infected population of PI-SEIRS and SEIRS Model with (a) and (b)

for vaccine preventable disease epidemic, a standalone epidemic model will lead to over estimation of *infectivity* parameter (see Fig. 5; $\gamma^i = 0.265, 0.267$ and $\gamma = 0.302, 0.308$ resulted in the same infected curve). Hence, the integration of epidemic model and stock management model (PI-SEIRS) is important for vaccine preventable diseases for estimating unknown epidemic model parameters. We conclude that epidemic infected data alone is not sufficient to estimate the disease severity (*infectivity*) parameter indeed we also need to consider supply chain operations information to improve accuracy. The implications of these results are that better inventory management techniques can help in reducing and controlling epidemic dynamics.

Some limitations of the work: included the assumption that the production lead time and *infectivity* parameter as deterministic constants, but in reality they may be stochastic. We have also not considered perishability issues or a capacity constraint of medicine ordering. Future work can be carried out in several directions. Additional empirical/ simulation/ field studies are needed to quantify the magnitude of inventory aspects in managing the impact of vaccine preventable disease epidemics. Specific questions arising thereof include: is there scenario where the primary reason for the epidemics occurrence is the mismanagement of the supply chain? If so, what kind of inventory ordering policies should be adopted? The current work has used a general PI model, which is designed to operate under stable demand conditions. Thus, in the case of epidemics driven demand pattern, further work is needed to develop a more suitable forecasting and PI model. In the standalone SEIRS model, the time to recover with medicine (TRM) parameter can be seen as a sum of *average waiting time* for medicine and *recovery time* after getting medicine. In future, one can undertake the explicit (separate) modelling of these two delays within the PI-SEIRS model framework. Further, the cost aspects (of the medicine supply chain), the service level aspects (of providing treatment by hospitals), and resource constraints (at the hospitals) can be studied in

conjunction to understand the interaction effects.

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