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A STATE SPACE APPROACH FOR SIR EPIDEMIC MODEL

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ABSTRACT:

In this paper, we construct a SIR(Susceptible -Infected-Recovered) epidemic model using a system of stochastic difference equations. A state space approach is proposed for this model. The Kalman filter (KF) is the most accepted estimation technique that has been widely used for state estimation of nonlinear systems. For this SIR epidemic model, we have developed methodologies for estimation and prediction of infected and non infected population through Kalman filter method. In this state space model, the observation equations are observed from infected cases of Influenza epidemic in India in 2009 and the total system population can be obtained from population survey. Finally, we prove our theoretical results using numerical simulations through MATLAB.

Keywords: Stochastic Difference Equations, Kalman Filter, Stochastic stability.

1. INTRODUCTION:

An epidemic is the rapid spread of infectious disease to a large number of people in a given population within a short period of time, usually two weeks or less. The modelling of infectious diseases is a tool which has been used to study the mechanisms by which diseases spread, to predict the future course of an outbreak and to evaluate strategies to control an epidemic.

A deterministic model is one in which every set of variable states is uniquely determined by parameters in the model and by sets of previous states of these variables; therefore, a deterministic model always performs the same way for a given set of initial conditions. Conversely, in a stochastic model—usually called a "statistical model"—randomness is present, and variable states are not described by unique values, but rather by probability distributions. Tan et al. have proposed a stochastic dynamic model which is referred to as multinomial model.

The classical Kalman filter was first introduced by Rudolph E. Kalman in his seminal paper (Kalman, 1960). The purpose of the discrete-time Kalman filter is to provide the closed form recursive solution for estimation of linear discrete-time dynamic systems, which can be described by equations of the form. In many cases interesting dynamic systems are not linear by nature, so the traditional Kalman filter cannot be applied in estimating the state of such a system. In these kind of systems, both the dynamics and the measurement processes can be nonlinear, or only one them.

State space approach has been done for HIV models by various authors. A state space approach for HIV epidemic model was studied by Hulin Wu. State space models for HIV pathogenesis under treatment by anti-viral drugs in HIV infected individuals was studied by Wai-Yuan Tan.

In Section 2, we formulate a Multinomial model for SIR epidemic. In section 3, we formulate a state-space model for the SIR epidemic model and introduce the Kalman recursive estimation methods in Section 4. In Section 5, we have provided a numerical illustration of Influenza in India in 2009. Conclusion is given in Section 6.

2. STOCHASTIC MODEL FOR SIR EPIDEMIC:

Let $S(t), I(t)$ and $R(t)$ denote the susceptible, infected and recovered populations at time t respectively. We are considering a three dimensional discrete stochastic process[5],[6].

$$X(t) = \left[S(t), I(t), R(t)\right]^T$$

To formulate a dynamic model, let $\eta_S(t)$ denote the conditional probability of $S \to I$ given $X(t)$ during $[t, t+1)$ and we give other notations of transition probability and various other transitions are given below:

S.No	Transition	Transition Probability	Transition Number
1	$S \to I$	$\eta_S(t)$	$N_S(t)$
2	$I \to S$	$\delta_{I1}(t)=0$	$Q_{I1}(t)=0$
3	$I \to R$	$\eta_I(t)$	$N_I(t)$
4	$R \to I$	$\delta_{R1}(t)=0$	$Q_{R1}(t)=0$
5	$S \to Death$	$d_S(t)$	$D_S(t)$
6	$I \to Death$	$d_I(t)$	$D_I(t)$
7	$R \to Death$	$d_R(t)$	$D_R(t)$
8	$immigration \to S$	$\mu_S(t)$	$R_S(t)$

By using the Multinomial Model, we obtain the following Stochastic Difference Equations[1]:

$$\begin{aligned} S(t+1) &= S(t) + R_S(t) - N_S(t) - D_S(t) \\ I(t+1) &= I(t) + N_S(t) - N_I(t) - D_I(t) \\ R(t+1) &= R(t) + N_I(t) - D_R(t) \end{aligned} \tag{1}$$

The distributional properties of the quantities in these equations are given below:

- $R_S(t)$ □ Binomial$\left[S(t);\mu_S(t)\right]$ independent of $N_s(t)$ and $D_S(t)$.
- $\left[N_S(t), D_S(t)\right] X(t)$ □ Multinomial $\left[S(t);\eta_S(t), d_S(t)\right]$
- $\left[N_I(t), D_I(t)\right] X(t)$ □ Multinomial$\left[I(t);\eta_I(t), d_I(t)\right]$
- $D_R(t)$ □ Binomial$\left[R(t);d_R(t)\right]$

To provide the system of equations in state space model, we rewrite

$$\begin{aligned} S(t+1) &= \left[1+\mu_S(t)-\eta_S(t)-d_S(t)\right]S(t)+\varepsilon_S(t) \\ I(t+1) &= \left[1-\eta_I(t)-d_I(t)\right]I(t)+\eta_S(t)S(t)+\varepsilon_I(t) \\ R(t+1) &= \left[1-d_R(t)\right]R(t)+\eta_I(t)I(t)+\varepsilon_R(t) \end{aligned} \tag{2}$$

Where

$$\varepsilon_S(t) = R_S(t) - \mu_S(t)S(t) - \left[N_S(t) - \eta_S(t)S(t)\right] - \left[D_S(t) - d_S(t)S(t)\right] - \left[Q_S(t) - \delta_S(t)S(t)\right] \tag{3}$$

$$\varepsilon_I(t) = \left[N_S(t) - \eta_S(t)S(t)\right] + \left[Q_{V2}(t) - \delta_{V2}(t)V(t)\right] - \left[N_I(t) - \eta_I(t)I(t)\right] - \left[D_I(t) - d_I(t)I(t)\right]$$

$$\varepsilon_R(t) = \left[N_I(t) - \eta_I(t)I(t)\right] + \left[Q_{V3}(t) - \delta_{V3}(t)V(t)\right] - \left[D_R(t) - d_R(t)R(t)\right]$$

Let $\varepsilon(t)=\left[\varepsilon_S(t),\varepsilon_I(t),\varepsilon_R(t)\right]^T$. It can be shown that $\varepsilon(t)$ and $X(t)$ are uncorrelated and mean of $\varepsilon(t)$ is 0.

The variances and covariances of components of $\varepsilon(t)$ are given by

$$Var\left[\varepsilon_S(t)\right]=V_S(t)=E\left[S(t)\left\{\eta_S(t)+\delta_S(t)+d_S(t)\right\}\left\{1-\left[\eta_S(t)+\delta_S(t)+d_S(t)\right]\right\}\right]$$

$$+E\left[S(t)\left\{\mu_S(t)\right\}\left\{1-\left[\mu_S(t)\right]\right\}\right] \tag{4}$$

$$Var\left[\varepsilon_I(t)\right]=V_I(t)=E\left[I(t)\left\{\eta_I(t)+d_I(t)\right\}\left\{1-\left[\eta_I(t)+d_I(t)\right]\right\}\right] \tag{5}$$

$$Var\left[\varepsilon_R(t)\right]=V_R(t)=E\left[R(t)\left\{d_R(t)\right\}\left\{1-\left[d_R(t)\right]\right\}\right] \tag{6}$$

$$COV\left[\varepsilon_S(t),\varepsilon_I(t)\right]=-E\left[S(t)\left\{\eta_S(t)\right\}\left\{1-\left[\eta_S(t)+d_S(t)\right]\right\}\right]$$

$$(7)\ COV\left[\varepsilon_S(t),\varepsilon_R(t)\right]=0 \tag{8}$$

$$COV\left[\varepsilon_I(t),\varepsilon_R(t)\right]=-E\left[I(t)\left\{\eta_I(t)\right\}\left\{1-\left[\eta_I(t)+d_I(t)\right]\right\}\right] \tag{9}$$

The above stochastic difference equations (2) will be taken as state equations in our state space model.

3. STATE SPACE MODEL:

The state space model in matrix notation is given by

$$\begin{aligned} X(t+1)&=\phi(t)X(t)+\varepsilon_t \\ Y(t)&=H(t)X(t)+\theta_t \end{aligned} \tag{10}$$

where $X(t)$ is the state vector. $Y(t)$ is the observation vector. $\phi(t)$ has been referred to as state transition matrix. $H(t)$ is the observation matrix. ε_t and θ_t are state model noise and observation noise respectively. It is observed that ε_t and θ_t are uncorrelated.

$$\begin{aligned} E\left(\varepsilon_t\right)=0, E\left(\theta_t\right)=0 \\ E\left(\varepsilon_t\varepsilon_t^T\right)=Q(t)>0, E\left(\theta_t\theta_t^T\right)=R(t)>0 \\ E\left(\varepsilon_t\varepsilon_s^T\right)=0, E\left(\theta_t\theta_s^T\right)=0\forall t\neq s \end{aligned} \tag{11}$$

For modelling SIR epidemic, we consider four stages:

$$X(t)=\left[S(t),I(t),R(t)\right]^T,\varepsilon(t)=\left[\varepsilon_S(t),\varepsilon_I(t),\varepsilon_R(t)\right]^T \tag{12}$$

We have

$$\phi(t)=\begin{bmatrix}1+\mu_S(t)-\eta_S(t)-d_S(t) & 0 & 0\\ \eta_S(t) & 1-\eta_I(t)-d_I(t) & 0\\ 0 & \eta_I(t) & 1-d_R(t)\end{bmatrix} \tag{13}$$

Let $Y_1(t)$ be the infection prevalance at time *t* and $Y_2(t)$ be the total population size of system at time *t.*

$$\begin{aligned}Y_1(t)&=I(t)+\eta_1(t)\\ Y_2(t)&=S(t)+I(t)+R(t)+\eta_2(t)\end{aligned} \tag{14}$$

$\eta_1(t)$ is associated with the error in reports of infected people, whereas $\eta_2(t)$ is associated with the error in population survey errors. We have $Y(t)=\left[Y_1(t),Y_2(t)\right]^T,\eta(t)=\left[\eta_1(t),\eta_2(t)\right]^T$.

Then we have the observation matrix

$$H(t)=\begin{bmatrix}0 & 1 & 0\\ 1 & 1 & 1\end{bmatrix} \tag{15}$$

Here ε_t and $\eta(t)$ are uncorrelated.

4. RECURSIVE ESTIMATION:

The kalman filter is used to investigate the state estimation of non linear systems.

We use the following notations:

- $\hat{X}_{t+1|t+1}$ - The best linear estimator of the state vector at time $t+1$ based on the observations $Y_1,Y_2.....Y_{t+1}$.
- $\hat{X}_{t+1|t}$ - The one step ahead prediction of the state vector at time $t+1$ based on the dynamic model.
- $P_{t+1|t+1}=E\left(X_{t+1}-\hat{X}_{t+1|t+1}\right)\left(X_{t+1}-\hat{X}_{t+1|t+1}\right)^T$;The covariance matrix of best state estimator.

- $R_{t+1|t} = E\left(X_{t+1} - \hat{X}_{t+1|t} \right)\left(X_{t+1} - \hat{X}_{t+1|t} \right)^T$;The covariance matrix of predictor.
- K_t - Gain matrix.

The kalman filter equations are given by:

$$\hat{X}_{t+1|t+1} = \hat{X}_{t+1|t} + K_{t+1}\left[Y(t+1) - H(t+1)\,\hat{X}_{t+1|t} \right]$$

$$\hat{X}_{t+1|t} = \phi(t)\,\hat{X}_{t|t}$$

$$K_{t+1} = P_{t+1|t} H^T(t+1)\left[H(t+1) P_{t+1|t} H^T(t+1) + R(t+1) \right]^{-1} \tag{16}$$

$$P_{t+1|t} = \phi(t) P_{t|t} \phi^T(t) + Q(t)$$

$$P_{t+1|t+1} = \left[I - K_{t+1} H(t+1) \right] P_{t+1|t}$$

Where I is the Identity matrix.

5. APPLICATION OF SIR EPIDEMIC TO INFLUENZA IN 2009:

Using the Influenza epidemic in India in 2009, we illustrate the state space approach for estimating and projecting the number of infected population.

S.NO	PARAMETERS	SOURCE
1.	$\mu_S(t) = 0.0001$	ASSUMPTION
	$\eta_S(t) = 0.000023, d_I(t) = 0.036$	[3]
	$\delta_S(t) = 0.0013$	[2]
	$d_S(t) = d_V(t) = 0.00623$	
	$\delta_{V2}(t) = 0.9$ $\delta_{V3}(t) = 0.000$ $\eta_I(t) = 0.9$	[4]

		ASSUMPTION
2.	INITIAL VALUES: $X_0 = [50,10,1]^T$ TRANSTITION MATRIX: $\phi(t) = \begin{bmatrix} 0.992 & 0 & 0 \\ 0.0013 & 0.0936 & 0 \\ 0.000023 & 0.0001 & 0.0938 \end{bmatrix}$	DYNAMICAL MODEL
3.	VARIANCE AND COVARIANCE MATRIX OF RANDOM ERRORS: $Q(t)$ $R(t) = diag[4,4]$	EQUATION (8) ASSUMPTION
4.	STATE VARIABLES: $X(t) = [S(t), I(t), R(t)]^T$	ESTIMATED BY KF RECURSION

For the above set of parameters, we get the following behaviour of the Stochastic. Here, we see the evaluation between the true value and the Kalman filter, that is the evaluation between observed value and estimated value.

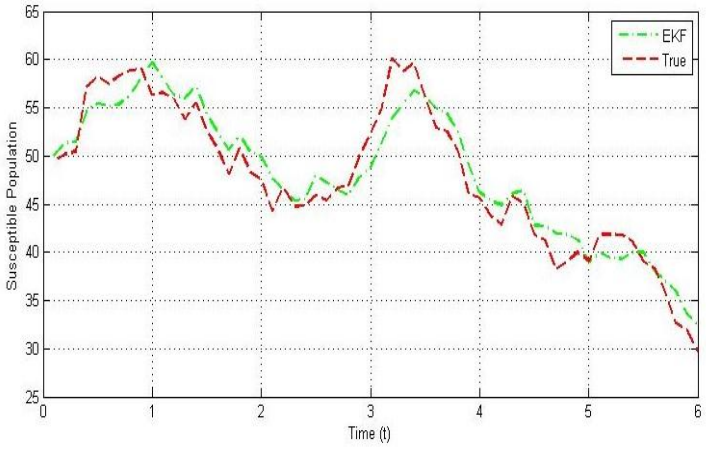

Fig 1: Observed(True) and Estimated(KF) of Susceptible Population.

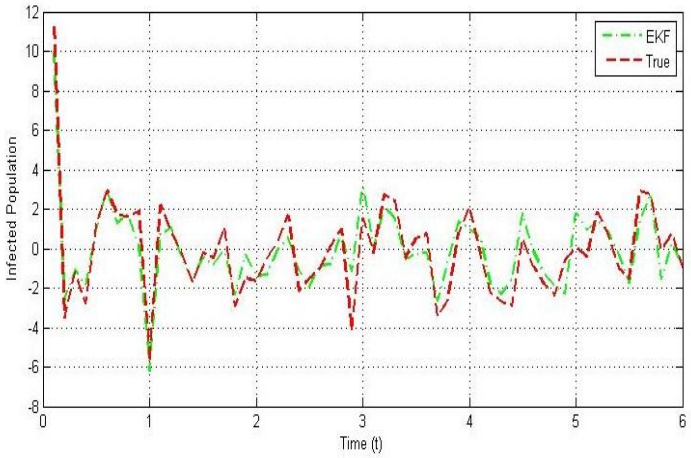

Fig 2: Observed(True) and Estimated(KF) of Infected Population.

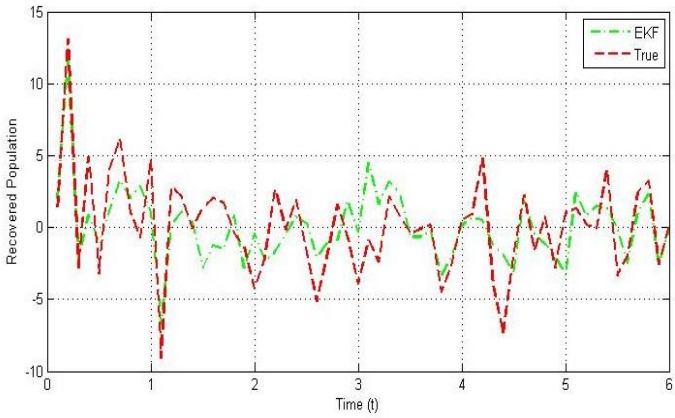

Fig 3: Observed(True) and Estimated(KF) of Recovered Population.

6. CONCLUSION:

In this paper, we have proposed a state space approach for SIR epidemic model. We have applied Kalman filter to our model to estimate and predict the number of susceptible, infected and recovered populations. Finally, we provide a Numerical Illustration of Influenza in 2009 in India and have provided the observed and estimated values of the susceptible, vaccinated, infected and recovered populations.

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