SENSOR FUSION FOR NORMALLY DISTRIBUTED NOISE ESTIMATION BY SNAPSHOTS TECHNIQUES USING FOOT AND MOUTH DISEASES MASSIVE DATA SETS IN KARNATAKA STATE

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ABSTRACT

The foot and mouth disease (FMD) is one of the highly contagious viral diseases causing illness in cloven-footed animals. The outbreak of this disease can grave deleterious economic burden on national GDP and global economic level. FMD life data sets are often sparse and unable to guide the policymakers on an outbreak, epidemic attack, vaccination status, impact of vaccination, economic loss and mortality rate. Many intrinsic factors have influenced FMD epidemic viz., Climatic, Intrasectoral transmission, disease residual effect, hygiene of the heard, food, shelter, drinking water etc. Over a period of disease occurrence, impact factors, different variants, and confounders have aroused from the FMD real- life datasets. Due to the paucity of literature, no modified Statistical and Mathematical tools have been availed for reduction of high dimensional massive data sets. In this context of the research gap, the present study aims to fit Sensor fusion noise estimation by Snapshots techniques for the reduction of high dimensional massive real life FMD datasets. The FMD high dimensional life datasets studied pertained to the accrual period from 2005-2014. The data on demographic profile, epidemic factors and economic loss or constraints faced by the farmers were collected through questionnaires. Sensor fusion for noise estimation was simulated by Mathematica-16.50 version. The fitted model estimates incidence rate, outbreak and economic losses within subject noise attributes. The present study recommends the improvement of life quality domain and also nurtures how best the model would be applied in high dimensional data sets with respect to the traditional method.

KEYWORDS: Sensor Fusion, Mathematica, FMD-Foot and Mouth Disease & Dimensional Life Datasets

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INTRODUCTION

The foot and mouth is a scourge in an Indian farmer perspective. Many states have been traumatically facing the incursive difficult situation for perceiving the prevention programmes of FMD outbreak (Ref). Different analytical models were used to understand the disease dynamics and forecast the decision and control measures

METHODS

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graph TD
    Data([Data]) --> EpidModel[Epid-Model]
    EpidModel --> EconomicModel([Economic Model])
    Data --> Sectoral([Sectoral])
    Sectoral --> ProductionParam[Production parameter]
    ProductionParam --> FMDOutBreak[FMD-Out break]
    FMDOutBreak --> ProductivityEffect[Productivity effect]
    ProductivityEffect --> ControlCost([Control cost])
    ControlCost --> DiseasesImpact[Diseases Impact Indicators]
    ControlMeasures{Control measures} --> PPP[PPP]
    PPP --> Vaccination[Vaccination]
    Vaccination --> ControlCost
    Vaccination --> SurvivalStatus[Survival-Status]
    SurvivalStatus --> DiseasesImpact
    GovtInvolvement([Govt involvement]) --> SurvivalStatus
    IntraSectTransmission((Intra sect Transmission)) --> SurvivalStatus
    IntraSectTransmission --> ControlCost
    EconomicModel --> ControlCost
  
```

Figure 1: Schematic Model of FMD Outbreak

DISEASES /INFECTION SUSCEPTIBLE MODEL

NAAS Rating: 4.13

population level. The diseases progression rates were formulated on different characteristics - 'F_j', where j is Infected animals pertaining to a particular farm with 'F' individuals. The susceptible population was simulated by the following formula:

$$\text{Diseases progression rate for farm } j = \text{Susceptibility}_j \times \sum_{\text{farm } i} \text{Infectivity}_i \times k(d_{ij})$$

Where,

$$\text{Susceptibility}_j = \sum N^i_s, S_s, \text{infectivity}_i = \sum N^i_s, T_s$$

Here, N_i s -gives the number of livestock species 's' on farm 'i' obtained from census data sets, S and T are the species-specific to the susceptibility and transmission rates, and K is the transmission kernel values, which was defined how the infectivity declined with distance, d_{ij}, between farms i and jth. Hence, 'K' describes the transmission mechanisms that can be existed on real -life data sets, although this model was explained the distinct merits of kernel parameterized values which were generated from the FMD-epidemic life data sets. The model will be intended to explain the spatial aspects of a spread of diseases, economic loss, Intrasectoral transmission mechanisms, vaccination coverage, PPP participation, productivity effect, survival status of the animals, prevention measures and government involvement for control of FMD outbreak at distinct spatial distribution.

PHARMOKINTIC MODEL FOR FMD

Both linear and non- linear models are helpful to measure the pharmokinetics dynamics (PK dynamics). Majority of the pharmaceutical companies would be availing this model for therapeutic evaluation approach and formulation of new drug delivery systems.

MODEL FORMULATION:

The rate of changes in drug concentrations with time 't' derived by using first order differential equations

$$\frac{dc_p}{dt} = -\frac{V_m * C_p}{K_m + C_p}, \text{ The rate changes of drug amount with time "t" equation (1)}$$

$$\frac{dx}{dt} = -\frac{V_m * C_p}{K_m + C_p}$$

By dividing the rate of elimination by drug concentrations provided by the value of drug clearance or metabolized activity.

$$\text{Clarence or metabolized activity becomes} = \frac{\frac{dx}{dt}}{c_p} = \frac{V_m * C_p}{K_m + C_p} * \frac{1}{C_p}$$

$$\text{Finally, the above equation becomes, metabolize} = \frac{-V_m}{K_m + C_p}$$

Our fitted model allowed making for analysis of varied parametric variation by using simulation process at time “t” After drug therapy; the prognosis was measured in terms of a total score by using standard WHO proforma (0-100 scale). A fitted model could be extended in the following nonlinear form $Y_t = a^{b^x}$ Where, t = time period for taking the drug metabolize or clearance, X= Animal prognosis score (Scale 0-100).

The rate of change of prognosis after the therapy at time “t”

$$\text{Log } Y_t = X \log b + \log a$$

$$\text{Differentiate with respect “t” } \frac{dy}{dt} = \frac{dx}{t} \log b + \log a$$

Model $\Delta = TB + A$ Where, Δ = Changes in time for drug metabolized in the body system, T – total drug delivered during the follow up period and A – parameter Constant.

FORMULATION OF EPIDEMIOLOGICAL PROBABILITY MODEL

We assumed that, the r.v. ‘X’ follows a binomial distribution $X \sim b(n, \pi)$ means, the component of ‘X’ variable corresponding to the number of success and ‘n’ be the independent variant of success or failure is equal to π then the expected value becomes

$$E(X_i) = n_i \pi_i, \text{ where } E(\cdot) \text{ denotes expectation of the random variable – equation (1)}$$

Where, n_i is the number of FMD’s infected animals were vaccinated at i^{th} location or epidemic geographical zone.

π_i Is the success of an individual animal cured after FMD vaccination .

$(1 - \pi_i)$ is the failure of individual animals were not cured and died after vaccination event

$$E(X_i) = n_i (1 - \pi_i) \text{ --- Equation (2)}$$

$\text{Var}(X_i) = n \pi_i (1 - \pi_i)$, Where $\text{Var}(\cdot)$ denotes the variance of the random variables of an individual group of animals (out broken in high incidence zone).

$$\text{The density function of FMD –outbreak was } P(X_i = k_i) = \binom{n_i}{k_i} \pi_i^{k_i} (1 - \pi_i)^{n_i - k_i}$$

Where k_i is random variable i.e. Number of animals vaccinated

n_i = Total number of animals was infected at epidemic area or zone

Where $P(\cdot)$ denotes the probability of an event, and $\binom{n_i}{k_i} = \frac{n_i!}{(n_i - k_i)! k_i!}$ significant sample proportions $\rho = \frac{x_i}{n_i}$
 $= -E(P_i) = \pi_i$,

$$-Var(P_i) = \frac{\pi_i(1 - \pi_i)}{n_i}$$

When 'n' is sufficiently large (No .of FMD infected animals that increases at larger extent), the distribution with mean ' π ' and variance ' $\frac{\pi(1-\pi)}{n}$ ', $p \sim N(\pi, \frac{\pi(1-\pi)}{n})$ equation (3)

Equation (3) is very useful for drawn the inference about the population parameter ' π ', because due to an entire population of FMD –outbreak could beholds good for the approximation of normality.

The estimator 'p' will be fall within 1.96 SD of ' π ' that means to say 95 % of the outbreak distributed homogeneously. Therefore, the population parameter ' π ' was found between the intervals

$$p \pm 1.96 \{ \pi_i (1 - \pi_i) / n \}^{1/2}$$

Illustrated E.g. (1) : Based on spatial distribution data,we will be assumed that,the response rate of FMD vaccination is about 35% 45%,65% respectively with 95% precision rate and 15% is the true π ,then the number of animals were cured is $1.96 \left\{ \frac{(0.35)(0.65)}{n} \right\}^{1/2} = 0.15$, $n = \frac{(1.96)^2 \pi(0.35)(0.65)}{(0.15)^2} = 39$.

SENSOR FUSION WITH NORMALLY DISTRIBUTED NOISE ESTIMATED BY SNAPSHOTS TECHNIQUES METHOD

FMD outbreak, attack, and mortality rate were visualized by combining sensor measurements is called *sensor fusion*. If each sensor measurements was corrupted by independent noise, and also each measurement was provided additional information's. The information of a measurement has been equated to the inverse of its variance. Each individual parameter was combined in accordance with Bayes's theorem. In present section of the paper, we considered four measures z_1, z_2, z_3 & z_4 with corresponding variances $\sigma_1^2, \sigma_2^2, \sigma_3^2, \sigma_4^2$

According to FMD data sets formulation we have been estimated the true value of different parameters.

$$\hat{x}_i = z_1(\text{Outbreaks}) \frac{\sigma_2^2}{\sigma_1^2 + \sigma_2^2} + z_2(\text{Attackrate}) \frac{\sigma_1^2}{\sigma_1^2 + \sigma_2^2} + z_3(\text{Mortality}) \frac{\sigma_2^2}{\sigma_2^2 + \sigma_3^2} + z_4(\text{Economic loss}) \frac{\sigma_2^2}{\sigma_2^2 + \sigma_4^2} + \dots + z_m \frac{\sigma_2^2}{\sigma_2^2 + \sigma_{m+1}^2}$$

With variance $\hat{\sigma}_i^2 = \frac{\sigma_1^2 \sigma_2^2}{\sigma_1^2 + \sigma_2^2}$, this can be written in recursive forms up to data estimations

$$(\hat{x}_i, \hat{\sigma}_i^2) \text{ With measurement parameters } (\hat{x}_i, \hat{\sigma}_i^2) \text{ form } (\hat{x}_{i+1}, \hat{\sigma}_{i+1}^2)$$

$$\hat{x}_{i+1} = \hat{x}_i + k_i(z_i - \hat{x}_i) \quad \hat{\sigma}_{i+1}^2 = (1 - k_i) \hat{\sigma}_i^2$$

This above recursive equation could be considered as the scalar kalman filter equation and k_i is also known as the optimal kalman gain if only one measurement exists, the central measurement could be identified by original measurement.

Table 1: Descriptive Statistics of Outbreak, Attack and Mortality

Year	Outbreaks Mean $\pm$ SD	Attack Mean $\pm$ SD	Mortality Mean $\pm$ SD
2003	26.17 $\pm$ 7.74	473.25 $\pm$ 44.97	03.42 $\pm$ 1.73
2004	18.17 $\pm$ 7.52	406.75 $\pm$ 48.57	05.83 $\pm$ 1.85
2005	98.00 $\pm$ 9.95	2668.08 $\pm$ 57.43	40.33 $\pm$ 4.41
2006	65.75 $\pm$ 5.39	1658.08 $\pm$ 56.67	13.00 $\pm$ 3.26
2007	86.45 $\pm$ 5.73	2646.00 $\pm$ 66.28	38.91 $\pm$ 5.66
2008	27.85 $\pm$ 6.75	555.38 $\pm$ 64.88	07.08 $\pm$ 2.98
2009	16.42 $\pm$ 1.04	502.08 $\pm$ 64.89	29.67 $\pm$ 6.92
2010	07.64 $\pm$ 3.43	178.36 $\pm$ 31.67	01.36 $\pm$ 1.43
2011	14.08 $\pm$ 5.95	244.50 $\pm$ 31.99	03.33 $\pm$ 4.68
2012	17.17 $\pm$ 6.99	598.42 $\pm$ 46.04	04.75 $\pm$ 0.59
2013	10.75 $\pm$ 3.16	582.33 $\pm$ 49.14	06.50 $\pm$ 0.63

(a)

(b)

Figure (a): Variation of Risk Factors ($p < 0.01$)

(b): Variation of Climatic Factors ($p < 0.01$)

(c)

Figure (c): Epidemic Variation ($p < 0.05$)

Figure (d): Variation of Attack Rate ($p < 0.05$)
(e): Variation of Death Rate ($p > 0.05$)

Figure (f): Variation of Economic Loss by the Farmers ($p < 0.05$)

Figure (g): Variation of Vaccination Coverage ($p > 0.05$)

The FMD data sets used unidirectional vision systems by their sole sensor fusion system, while calibration of variance is being partly compared with life data sets. Predominantly varying parameters were needed to cope with many combined sensor measurements for estimating the relation between epidemic, attack and death rate of animals in epidemic areas. At this point in time, in order to get or achieve very good reliable results, the relation between above- mentioned parameters is to be known. The risk factors of FMD for a given co variants profile like vaccination status and coverage, climatic factors of affected area, relapsed cases encountered at selected study area, seasons of outbreak (Rainy, summer and winter) and effect of FMD for semi competing risk factors on economic viability of the farmers *etc* need to be clearly emphasized . Many authors have pointed out that the principles of data fusion as an inference problem: given two heterogeneous input datasets with different statistical characteristics, how do we optimally estimates the quantity of interest, and obtain uncertainty measurements in accordance with these inferential spatial FMD life data sets. Keeling et al. (2005) proposed that the level of expected fusion sensor and their reliability was estimated by partial differential equations

and simulation techniques to ascertain the comparison of FMD risk factors. Obviously, a majority of the parameters were found to be positively associated with sensor fusion estimation when compared with real -life datasets. Since then several other papers and books have been published on the topic, which has reinforced what Keeling et al (2005) proved.

However, the complexity of data analysis, model assumptions need to be well thought-out for the hypothesis testing. Frailties of our fitted model are to reduce the extent of the spurious relation between the outcomes within the subjects. In this unrouted mechanism, the fusion sensor noise estimation model fashioned and originated real FMD-data attributes. There are some latency characteristics were found to be statistically insignificant ($p > 0.05$) and operates on their trimmed attributes (in our instances through pooling of nonconfounders). The present fitted model eventually drew up lesser accuracy and low sensitivity of the defined parameters, and also it could be acted as a navigator tool for specified un-umpired data matrix on computational convenience.

In the course of analysis of small biological datasets, both linear and nonlinear models were best fit and statistically significant ($p < 0.05$) when compared to fusion sensor simulation model (risk analysis, drug response, estimation of survivability etc.). When the animal suffered from FMD with a terminal illness and as the relapsed case with the same incidence, the experimental data tend to be massive observation (generated from the therapeutic, economic feasibility, milk yield data, and health quality domain) and ends up with more complexity. While in the case of large data generated from invio or invitro situation, the analysis will be not equated full-blown. Hence, the experimental data needs to be customized and amplified with some sort of reduction of variance.

This prioritized resulted model has the ability to provide within- subject dependence over time along with a quantification of uncertainty from the specified sensor noise attributes. The fitted model will be informed in various ways to recommend the improvement of life quality domain, and also nurtured how best the model could be applied highdimensional data sets with respect to the traditional method (improved version). The simulated results oversaw the substantial variation among outbreak, epidemic and death rate of FMD in larger datasets on varied parameters. The dependence structure was estimated across covariate profile (see figure (a),(b) &(c), (d),(e) & (f) & (g)). The figures revealed that the fitted models were coping with lesser standard error and indoctrinate parameters persuaded at the time of analysis. As per the models, the results were found to be statistically significant ($p < 0.05$) with incidence and death rate of the animal at a specified farm.

DISCUSSIONS

Fusion sensor model included more information than linear and nonlinear model. This type of model can be especially important in massive life datasets in Medical and Veterinary Sciences. Sensor fusion model has reconciled and visualized large sets of FMD disease information. It is quite possible that, with continuous analysis for the epidemic, risk and clinical factors related life- threatening diseases regulated by retrieved information collected from field level as well as competent authority. The present study conceptualized a new model for analyzing massive dynamic life data sets and augmented with data reduction techniques by an analytical approach. Our proposed method gives a visualization of the FMD - risk factors, economic and epidemic factors surpassed with secured projected information. This model allows for a better understanding of its structure and evaluation overhauled with expedited /spearheaded information for policymakers and researchers for implementation of controlled programmes. As per the findings, the linear, nonlinear- epidemiological simulation model procedures unified with quelled more standard error compared to fusion sensor model and was

statistically significant ($p < 0.05$) with varied parameters and variance. This model can be applied in any massive dynamic data sets such as Agriculture, Medical, astronomical, nuclear physics, space science and so on. In case of networking - operating characteristics signal based analysis (Sensored fusion data generated from the satellite), data need to be customized. Eventually, the data generated at large population level with defined geographical location mediated more standard error and also it was not improvised. This unfabricated data need to be customized separately for reduction of standard error or heterogeneity of the observations.

CONCLUSIONS

The model is able to reproduce reproduction number and algorithms. The present study recommends the improvement of life quality domain and also nurtures how best the model would be applied in high dimensional data sets with respect to the traditional method. It serves as a tool for the policymakers, researchers, epidemiologists, and clinicians for the implementation of prevention programmes. Further, practical and analytical approach based studies may fill the gap of spurious estimation.

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