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## Sensitivity Analysis of the Effective Reproduction Number in a Sarawak Rabies Epidemic Model

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Abstract—For past decades, investigations on the transmission dynamics of canine-mediated rabies as well as the best practice for rabies control efforts have utilised mathematical models. In this paper, sensitivity of the effective reproduction number to model parameters is investigated by employing Normalised Forward Sensitivity Index. A Susceptible-Exposed-Infectious-Vaccinated (SEIV) model for rabies is formulated and the effective reproduction number is derived through the Next Generation Matrix method. The sensitivity analysis has identified dog-to-dog transmission rate and rate of newborn dogs as the most impactful parameters that contribute to the number of secondary infections. The result highlighted the significance of dog population management to curtail rabies transmission. This is crucial in aiding public health decision-makers as these influential parameters can be targeted for rabies control and intervention strategies.

## Keywords—rabies, sensitivity, SEIV, epidemic, Sarawak

## I. INTRODUCTION

Although rabies is an ancient zoonosis, howbeit considered as one of the 18 neglected tropical diseases as listed by the World Health Organization (WHO) [1]. The latest estimate of human mortality due to rabies is reported to be as high as 60000 people annually across 150 countries [2]. Most of these mortalities are due to the rabid dog exposures, which makes up 99% of all rabies spillover to human population. For past decades, investigations on the transmission dynamics of canine-mediated rabies as well as the best practice for rabies control and interventions have utilised mathematical models [3], [4], [5]. Sensitivity analysis comprises either Local Sensitivity Analysis (LSA) or Global Sensitivity Analysis (GSA) [6]. Whereas LSA examines sensitivity relative to a single parameter value, GSA addresses sensitivity throughout the entire parameter space [7]. Generally, local sensitivity analysis is simpler, faster and calibrated parameters are required in order to apply LSA.

In this paper, we are interested in studying the sensitivity of the epidemic threshold value i.e., the effective reproduction number, to the model parameters using local sensitivity analysis (LSA). This is crucial in aiding public health decision-making process as parameters that are found to be the most influential on can be targeted for rabies control and intervention strategies. In order to identify the most impactful parameters in regard to the effective reproduction number, we employed a local sensitivity analysis (LSA) namely Normalised Forward Sensitivity Index. Jane Labadin Faculty of Computer Science and Information Technology Universiti Malaysia Sarawak Kota Samarahan, Sarawak, Malaysia ljane@unimas.my

To the best of our knowledge, sensitivity analysis on the effective reproduction number in a rabies model is scarcely available. This paper's primary objective is to identify the most important parameters for rabies disease transmission using local sensitivity analysis approach. In the following Section II, we formulate the compartmental model. The effective reproduction number is derived using the Next Generation Matrix method and the list of baseline parameter values is presented in Section IV utilising the Root-Mean-Square-Error (RMSE). In Section V sensitivity analysis with regards to the parameter values is performed using Normalised Forward Sensitivity Index. Brief discussion is presented in the last section.

## II. MODEL FORMULATION

With the aim of modelling the transmission dynamics of rabies virus, we consider two interacting population of dogs and humans. In accordance to their disease status, we partition the dog population into four exclusive compartments: susceptible dogs  $S_d$ , exposed dogs  $E_d$ , infectious dogs  $I_d$  and vaccinated dogs  $V_d$ . Similarly, the human population is categorised into four sub-classes: the susceptible humans  $S_h$ , exposed humans  $E_h$ , infected humans  $I_h$  and vaccinated humans  $V_h$ . The rabies transmission model is derived by assuming several assumptions:

- a) All populations are closed, sufficiently large and mix homogeneously.
- b) All individuals are born equally susceptible to rabies.
- *c)* Only dogs can spread rabies further, whether among themselves or between populations.
- d) All infected dogs are equally infectious.
- e) Infected dogs are not immediately infectious.
- *f)* Infected humans do not immediately show clinical symptoms.
- g) Upon recovery, rabies does not confer lifelong immunity.
- *h)* Aside from the vaccinated dogs, dogs in other compartments may be subjected to culling.

The transmission and progression of rabies virus between the two populations of dog and human, which are governed by 15 epidemiological non-negative parameters (TABLE I), can be visualized in the schematic transmission diagram in Fig 1.

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