Rebuttal of Paper 418

Reviewer 1

We sincerely appreciate your effort in reviewing and commenting on our work. Please allow us to clarify a few points that seemingly have not been conveyed clearly enough.

1. The proposed prediction method appears to be a simple heuristic with no theoretical justification. Also, many technical details are missing. Here are few examples.

This paper does not explain the existence of the so-called equilibrium and how to find the equilibrium if it exists.

Re: Section 3.2 provides the details on the conditions for obtaining a system equilibrium state from Line 211 to Line 260. An equilibrium state can be simply viewed as a state in which all parts of the system are in balance, hence no internal cause/force to drive changes, for example a zero-sum game with all opponents having equal strength. The equilibrium state is estimated by extracting the feature information of attributes (E), and combining trained L (Equations (10) and (11)), which is detailed in Section 4.2.

Why is it enough to evaluate the distribution over different parts of the system? What is exactly the dynamics of the underlying system? In other words, how does the system evolve? What is the mathematical model governing the dynamics of the system?

Re: The dynamic is unknown. The goal of the proposed ESE is to determine the dynamic of the system and then predict the future state. If the mathematical model of the system is available, then there is no need for ESE.

L is not clearly defined. It is also very hard to understand the training process of L in Algorithm 1. The explanation should be improved.

Re: Thank you for the comments. We will certainly improve the explanation in the final version. The algorithm itself is quite simplistic as it is basically a recursive function that will converge when there is no longer change in the state.

The explanation regarding the predictor should be improved greatly. The equations (15)–(18) are just provided without any reasoning or clear explanations.

Re: Equations (16)-(18) are step by step derived from Equation (15). We can provide more detailed explanations of this process in the appendix, for readers that require more information.

2. Experiment results should be improved.

Figure 1 is not so informative. DiS and TED should provide similar results since the difference is just whether they are based on l1 norm or l2 norm. Instead, this paper should clearly explain how to obtain \gamma*.

Re: Thank you for your comment. The details of how to obtain gamma * are in Section 4.2, from lines 297 to 357. For Figure 1, as introduced in the second and third paragraphs of Section 6.1, it shows an important function of ESE, which is to observe the non-equilibrium special periods in the system through abnormal changes in EI.

Figure 2 should also be improved. It does not really show how each part of the system changes over time. The figure should be given to indicate the system dynamics over a longer period of time for each region.

Re: The Figure 1 in the main paper actually is an example of dynamics over time but for the whole area, not for one individual region. They are actually available in the supplementary files, but not presented in the paper as there are 79 figures. The examples as below (Figure 1 and 2):
    The other figures are given in The URL is given in the abstract.

The comparison with other prediction methods seems to be a bit unfair. There is no clear justification on why the input length needs to be chosen to be the same for all prediction methods. The other prediction methods work better with smaller input lengths, which are obviously less costly. In addition, the prediction length could be optimized for each prediction method in which case ESE is no longer the best.

Re: The comparison actually favors other methods as ESE is not a time series model for a single region. It is just to show that ESE can be comparable even it is transformed as a time series. Hence we use the same input length and the same prediction target on all methods. The strength of ESE is not in individual prediction but in holistic prediction of many parts in one go.
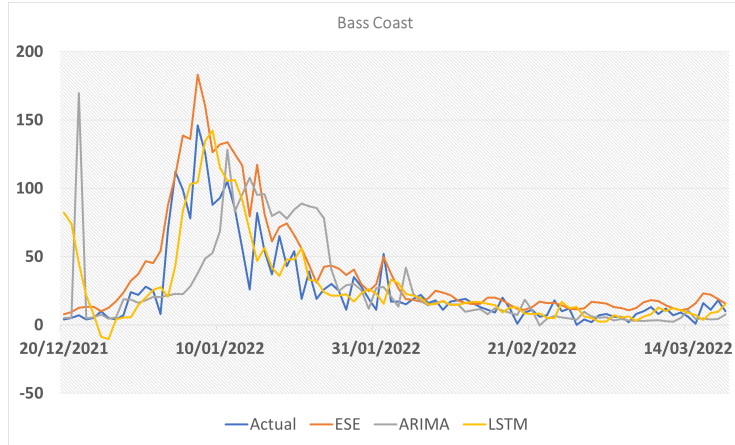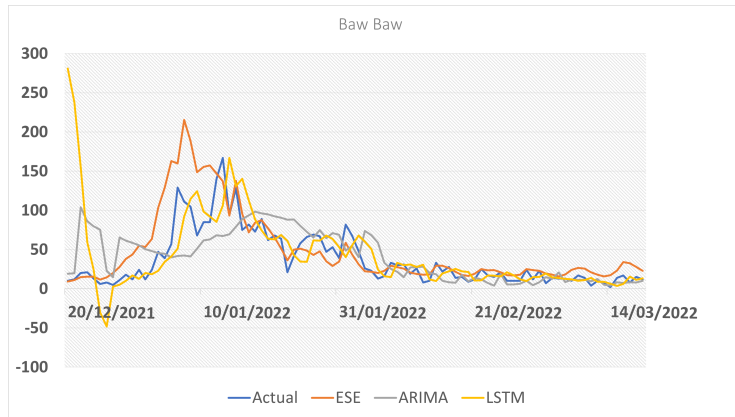
Figure 1: Comparison Plot: Bass Coast

Figure 2: Comparison Plot: Baw Baw

3. The motivation of this work is unclear. It is unclear why existing epidemic models are not enough to capture the system dynamics in different regions. How about the network-based compartment models and metapopulation models in epidemiology? They have been proposed to capture the system dynamics in different regions.

Re: In Section 2.2, we mentioned citations about the current mainstream existing epidemic models, such as [12] [28] [48], and also introduced the citations for many network-based prediction tools, such as [20] [30] [38] [45] [46]. We will make them clearer in the final version.