Improved Contact Tracing SIR Model for Randomly Mixed Populations*

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Abstract Contact tracing allows for more efficient quarantine and isolation, and is thus a key control measure in combating infectious diseases. Mathematical models that accurately describe the contact tracing process are important tools for studying the effectiveness of contact tracing. Recently, we developed a novel contact tracing SIR model based on pair dynamics, which uses pairs (two-individual) interactions to approximate triple (three-individual) interactions to close the model. However, the pair approximation used in the model is only a crude estimate. We extend this model to improve the approximation. Specifically, the new model tracks infectious individuals who have or have not infected others, as they play different roles in triples. We conduct a theoretical analysis to calculate the control reproduction number. The results of the new model are compared with those of the original model by numerical analysis. We find that the two models yield a similar epidemic final size. However, the original model yields a larger control reproduction number and thus underestimates the effect of contact tracing. This discrepancy increases as contact tracing is strengthened.

Keywords Compartmental disease model, control reproduction number, pair dynamics

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1. Introduction

Since the beginning of the COVID-19 pandemic, governments worldwide have widely adopted physical containment measures in an effort to control the spread [6]. These policies have significantly reduced disease transmission [12]. Contact tracing is an important epidemic prevention measure to reduce the spread of infectious diseases by blocking the chain of infection. Traditional contact tracing involves identifying the close contacts of an infected individual. These contacts are considered at risk of infection and are advised to take actions to reduce transmission, such as self-isolation [1]. Its effectiveness depends on several factors: timely detection

and isolation of indicator cases [9], timely and comprehensive identification of contacts [5], and quarantine compliance [7, 11]. Technology can address some of these limitations by automating the processing of test results or symptom reports and utilizing mobile phones to identify and notify contacts at risk of infection [4].

Due to its importance, the mathematical modelling of contact tracing has been studied using multiple approaches. A contact network model for contact tracing was developed by [8, 16], as close contacts can be naturally modeled by contact networks. However, network models require information about the contact network, which is often difficult to obtain. During the COVID-19 pandemic, much effort has been dedicated to collecting this information [15]. However, human contacts may be spatially, culturally, and economically specific, limiting the generalizability of these contact network studies to other regions. A traditional compartmental model that incorporates quarantine and isolation was first proposed by [3] to study the 2003 SARS pandemic. This model assumes that a fraction of the cases are contact traced. It has been adapted to study the COVID-19 pandemic [13]. However, it is difficult for these models to precisely describe contact tracing because traditional compartmental models assume that the population is randomly mixed and do not trace individual contacts. Branching process models for contact tracing have recently been developed [14] to study the COVID-19 pandemic. These models can precisely describe the contact tracing process for a single patient, thus yielding a precise control reproduction number. However, it is difficult to use these models to study disease dynamics without involving large-scale agent-based simulations.

Bednarski et al. [2] established a novel compartmental SIR contact tracing model for a randomly mixed population, thus avoiding the need for contact network information. This model tracks contacts using pairs, which are formed by disease transmission. The authors recognized that disease transmissions form a tree of transmissions. They borrowed the edge dynamics idea from network models to study contact tracing as a dynamic process on this tree.

Like the network models in [10, 18], the dynamics of pairs depend on interactions between the individuals in the pair and other individuals, i.e., triple interactions, which in turn depend on four-individual interactions and so on. To truncate this infinite chain of dependences and simplify the model, triple interactions are approximated by pairs, using the triple closure method introduced in [10]. However, this is only a crude approximation, as it ignores the fact that not all infectious individuals play the same role in triple interactions. The specific approximation and its problems are explained in more detail in Subsection 2.1.

The goal of this paper is to improve this model by more accurately approximating triples. To do this, in Section 2, we extend the Bednarski et al. model to track infectious individuals who have or have not infected others. We calculate the control reproduction number and compare the simulation results of our new SIR model with the previous contact tracing SIR model [2] in Section 3.

2. Modelling contact tracing

2.1. The simple SIR contact tracing model

The SIR contact tracing model [2] divides the population into susceptible (S), infectious (I), diagnosed (T), contact tracing initiated (X), and recovered without being diagnosed (R) compartments. The infection process dynamically generates a