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Studying the Recovery Algorithm for the Time-dependent Transmission Rate(s) in Epidemic Models

While the recovery rate of a disease can be measured in a controlled laboratory setting and these values used to estimate the value during the actual disease outbreak, the same is not true for the transmission rate. The transmission rate is known to be difficult to measure due to its dependence on the probability of transmission between individuals and social contact rates. On the other hand, there is a wealth of information that could be extracted regarding disease transmission and recovery if the time-dependent transmission function were known. For example, it would be possible to test hypotheses such as whether the school year causes increased disease incidence due to increased contacts among children.

Determining the time-dependent transmission function that exactly reproduces disease incidence data can yield useful information about disease outbreaks, including a range potential values for the recovery rate of the disease and could offer a method to test the "school year" hypothesis (seasonality) for disease transmission. Recently two procedures have been developed to recover the time-dependent transmission function, $\beta(t)$, for classical disease models given the disease incidence data. These two procedures to recover $\beta(t)$ can be extended to a broad class of *SIR*-type compartment models, including the *SIR* model with waning immunity, the *SIR* model with a time-dependent indirect transmission rate, to the discrete time setting, the stochastic setting, and assuming an specific exit distribution from the infected class.

We first review the $\beta(t)$ recovery procedures and give the resulting formulas, using both methods, for the susceptible-infected-recovered (*SIR*) and susceptible-exposed-infected-recovered (*SEIR*) models. Using a modification of one procedure, the two formulas are shown to be identical. Second, we explore several technical issues that appear when implementing the procedure for the *SIR* model; these are important when generating the time-dependent transmission function for real-world disease data. Third, we extend the recovery method to heterogeneous populations modeled with a certain *SIR*-type model with multiple time-dependent transmission functions.

We demonstrate the $\beta(t)$ recovery procedure for two population classes assuming that the length of the disease outbreak is short compared with the time required to "grow up" from the child class into the adult class. Thus there is no movement from one class to another. With two classes, there is a possibility of four different transmission rates within and between the two groups, and two different recovery rates.

For two populations, we assume that the incidence data functions, $I_1(t)$ and $I_2(t)$, are known, allowing us to solve for two transmission functions. If additional information is known about the disease spread then it may be possible to solve for the four transmission functions completely.

We consider two possible scenarios resulting in two distinct transmission functions. First, we assume that the disease spread is different between adults and among the two classes than among the children only. Second, we consider the scenario when the transmission matrix is separable (has proportionate mixing), where the number of contacts between individuals in two different groups is assumed to be proportional to the activity levels and sizes of the groups. In particular, the "infectivities" of each group are the same and only the "susceptibilities" of the groups are different.

We apply the $\beta(t)$ recovery procedure to data from the 2002–2003 influenza season and for the six seasons from 2002–2003 through 2007–2008, for both one population class and for two age classes. We discuss the consequences of the technical conditions of the procedure applied to the influenza data. We show that the method is robust in the heterogeneous cases, producing comparable results under the two different hypotheses. We perform a frequency analysis, which shows a dominant 1-year period for the multi-year influenza transmission function(s).