## FINAL AND PEAK EPIDEMIC SIZES FOR SEIR MODELS WITH QUARANTINE AND ISOLATION

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ABSTRACT. Two SEIR models with quarantine and isolation are considered, in which the latent and infectious periods are assumed to have an exponential and gamma distribution, respectively. Previous studies have suggested (based on numerical observations) that a gamma distribution model (GDM) tends to predict a larger epidemic peak value and shorter duration than an exponential distribution model (EDM). By deriving analytic formulas for the maximum and final epidemic sizes of the two models, we demonstrate that either GDM or EDM may predict a larger epidemic peak or final epidemic size, depending on control measures. These formulas are helpful not only for understanding how model assumptions may affect the predictions, but also for confirming that it is important to assume realistic distributions of latent and infectious periods when the model is used for public health policy making.

1. Introduction. Quarantine (of exposed individuals) and isolation (of infectious individuals) are two of the most commonly implemented control measures for infectious diseases, especially in the case of SARS. Mathematical models such as the SEIR type of epidemiological models have been used to assess the effectiveness of various control strategies (see, for example, [2], [6], [9]). Some of the models are made mathematically simpler by assuming exponentially distributed latent and infectious periods, while others are made more complicated (and more realistic) by replacing the exponential distribution with gamma distributions (see [4], [10]). The gamma distribution assumption (GDA) is considered to be more realistic than the exponential distribution set. It has been shown that models under GDA and EDA may generate different disease dynamics (see [5], [7]).

When a mathematical model is used to study disease control, it is common to consider certain quantities (derived from the model) that can provide information about the effect of control measures on disease prevalence. These quantities include the (control) reproductive number, final epidemic size, maximum (peak) value of an epidemic, etc. Although formulas for the maximum and final epidemic sizes have been derived previously for some SIR or SEIR types of epidemic models (see [1], [3], [8]), formulas for models with quarantine, isolation, or both or with GDA have not been available. In this article, we derive these formulas for two such models,

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