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Stochastic models for epidemics with and without inclusion of superspreaders

Felicia Benedetti Yu*

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Abstract

In this thesis we investigate the effects of inclusion of superspreaders in a SIR epidemic model. We create a standard SIR epidemic model and a two-type SIR epidemic model with the same basic reproductive number R_0 , to describe an epidemic in a homogeneous population and in a heterogeneous population respectively. Then, with the help of branching process approximation of these models we calculate the probability that the epidemic in the two cases stays small, and conclude that it is higher in the case of superspreaders. We then investigate the expected size, when observing an emerging epidemic at some future generation, k in the homogeneous and heterogeneous case respectively. We could then conclude that we will expect the size of the epidemic in generation k to be bigger if the population contain superspreaders.

^{*}Postal address: Mathematical Statistics, Stockholm University, SE-106 91, Sweden. E-mail: felicia.benedetti98@gmail.com. Supervisor: Pieter Trapman.