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The statistical estimation of the basic reproduction number, and other parameters of SEIR stochastic epidemic models. Case study- influenza

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Reliable information about important epidemiological parameters such as the basic reproduction number (BRN) of diseases are driven by stochastic data from the disease systems. Thus, deriving a robust statistical scheme to approximate these disease control parameters is a prelude to planning major disease control measures. A practical setback in deriving "statistically good" estimators on SEIR epidemic models such as influenza is the inability to sort data for the incubating (E) and infectious (I) classes from the general infected population. In this talk, discrete time Markov chain (DTMC) models for SEIR epidemics such as influenza epidemics are derived and studied. The DTMC models are Chain-Binomial models consisting of fixed and random incubating and infectious periods for the disease dynamics. The statistical techniques of maximum likelihood estimation (MLE) and expectation maximization (EM) algorithm are applied (to minimize all practical and computational setbacks) to find reliable estimates for the BRN. The algorithm is executed on influenza data for Georgia, USA, and the numerical results are presented and interpreted. Also, the statistical consistency of the estimators is discussed.