
MICHAEL LI, University of Alberta

Nonidentifiability Issues in Fitting Transmission Models with Disease Data

Mathematical models that describe the transmission dynamics of infectious diseases are increasingly applied to analyze public health data. When model parameters are estimated from fitting model outcomes to data, questions such as how many parameters can be fitted or whether the best-fit parameter values are unique often occur. These questions are related to the *nonidentifiability* issue: there are infinitely many best-fit values for certain parameters, which needs to be rigorously resolved for reliable data analysis and model predictions. In this talk, I will show that the nonidentifiability issue is intrinsic to the fitting of transmission models to disease data, and present a new method for detecting nonidentifiability and assessing the degree of nonidentifiability. A case study on parameter estimation of a HIV transmission model from surveillance data is used to demonstrate the concept of nonidentifiability and our method.