Our objective is to quantify the transmission of STEC (Shiga toxin-producing *Escherichia coli*) serotypes by analyzing the cross-sectional data on STEC prevalence. This is an important problem that lies at the math/statistics/ecology interface. We consider a family of stochastic transmission models to estimate the transmissibility parameters of the different STEC serotypes. Our discussion was focused on how to: a) estimate transmission coefficient ($\beta$) and recovery rate ($\gamma$) through a single cross-sectional dataset for *E. coli* O157 serotype; b) estimate basic reproduction number ($R_0$) for all the other seven *E. coli* serotypes; and c) investigate uncertainty (i.e. type I and type II errors) in the transmission of different *E. coli* serotypes.

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