

Math Club Presentation of

Structural and practical identifiability analysis
of a multiscale immuno-epidemiological model

By Dr. Tuncer

We perform the identifiability analysis of a multiscale model of seasonal influenza with multiscale data. We show that the well studied target cell limited within-host model is not structurally identifiable. So, we reformulate the model and work with a scaled within-host model which is structurally identifiable. We find that the scaled within-host model is practically identifiable with respect to two distinct viremia data sets while fitting with weighted or unweighted least squares. We introduce a methodology on how to study the structural identifiability of multiscale epidemic models specifically nested immuno-epidemiological models. All parameters of the multiscale model are practically identifiable. Furthermore, we find that the practical identifiability of the multiscale model is significantly better when fitted to viremia and incidence data as opposed to when fitted to viremia and cumulative incidence data. Comparing first and second order numerical methods for solving the partial differential equations suggests that using a higher order numerical method does not affect the identifiability of the parameters. Further simulations suggest that the choice of the linking functions has some impact on identifiability when viremia and incidences are fitted but no impact when viremia and cumulative incidences are fitted.

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SE 215
5pm-6pm

