A new approach to model immune response in immune epidemiological models

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We consider an SI-epidemic model in which susceptible individuals are unstructured while infected individuals are structured by two immunological variables, $x$ representing infection, and $y$ representing immune response. Those two are assumed to evolve in time according to a deterministic 2-dimensional dynamical system: $\dot{x} = F(x,y)$, $\dot{y} = G(x,y)$. It is further assumed that the initial value problem posed with arbitrary $x_0 > 0, y_0 > 0$ is uniquely solvable, and that the smooth solution can be expressed in the phase plane via the functional relation $H(x,y) = 0$. The density of infected individuals, $\dot{i} = i(t,x,y)$, is modeled as in Gandolfi et al. [1],

$$\frac{\partial i}{\partial t} + \frac{\partial (F(x,y)i)}{\partial x} + \frac{\partial (G(x,y)i)}{\partial y} = -\left(\mu_0 + \mu_i(x,y)\right)i(t,x,y),$$

and the number of susceptibles, $S$, evolves by $S'(t) = \Lambda - \left(\mu_0 + \lambda(t)\right)S(t)$, where $\lambda = \lambda(t)$ is the force of infection. Some theoretical results will be shown, as well as results from simulations.

References


*Mini-Symposium: Modeling Infection Dynamics Across the Scales