Group models
MATH 8xyz – Lecture 16

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Outline

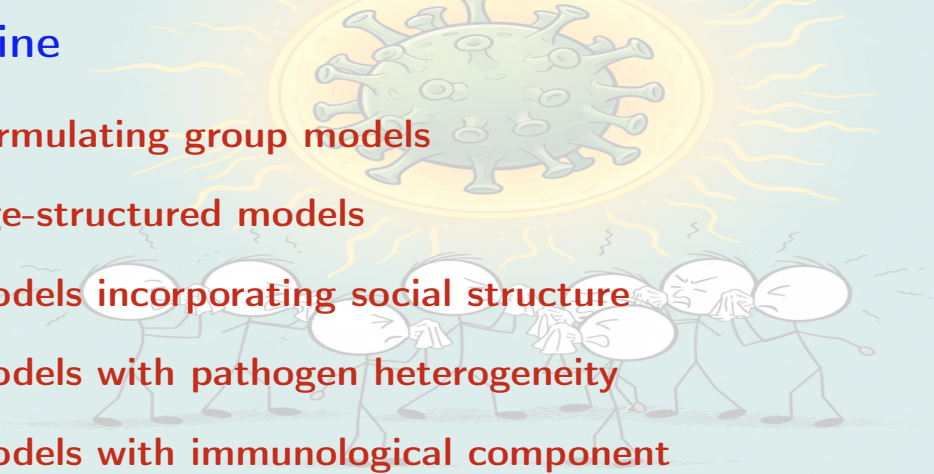Formulating group models

Age-structured models

Models incorporating social structure

Models with pathogen heterogeneity

Models with immunological component

Analysing group models

Simulating group models

Formulating group models

▶ Age-structured models ▶ Models incorporating social structure ▶ Models with pathogen heterogeneity ▶ Models with immunological component

Limitations of single population ODE models

▶ Basic ODEs assume all individuals in a compartment are roughly the same ▶ Individuals can spend differing times in a compartment, but they are all the same ▶ As seen with COVID-19, different age groups are impacted differently

Groups can be used for many things

- ▶ Groups allow to introduce structure in a population without using PDEs
  - ▶ Age structure
  - ▶ Social structure
  - ▶ Pathogen heterogeneity
  - ▶ Host heterogeneity (e.g., super spreaders)

- ▶ In this lecture, we do not consider spatial heterogeneity; this is done in Lecture 05 ▶ We start by considering a few examples

Age-structured models

▶ ODEs are not the best way to incorporate structure such as age ▶ Will come back to this in Lecture 09, but give one example here

A multi-group SIS model with age structure

▶ Feng, Huang & C^3 (2004) ▶ For $i = 1, \ldots, n$ different subgroups:

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) S_i = -\mu_i(a)S_i(t,a) - \Lambda_i(a, I(t,\cdot))S_i(t,a) + \gamma_i(a)I_i(t,a)$$

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) I_i = -\mu_i(a)I_i(t,a) + \Lambda_i(a, I(t,\cdot))S_i(t,a) - \gamma_i(a)I_i(t,a)$$

where

$$\Lambda_i(a, I(\cdot, t)) := K_i(a)I_i(a,t) + \sum_{j=1}^{n} \int_0^{\omega} K_{ij}(a,s)I_j(s,t) \, ds$$

Boundary and initial conditions

For $i = 1, \ldots, n$:

$$S_i(t, 0) = \int_0^\omega b_i(a)[S_i(t, a) + (1 - q_i)I_i(t, a)] \, da$$

$$I_i(t, 0) = q_i \int_0^\omega b_i(a)I_i(t, a) \, da, \quad 0 < q_1 < 1$$

$$S_i(0, a) = \psi(a)$$

$$I_i(0, a) = \varphi(a)$$

(q_i fraction of newborns that is infected)

Basic reproduction number in group $i = 1, \ldots, n$:

$$\mathcal{R}_i = \int_0^\omega b_i(a) \exp\left(- \int_0^a \mu_i(\tau)d\tau \right) \, da$$

Remarks

▶ Authors obtain some results in terms of global stability ▶ Need simplifications to move forward ▶ No numerics, because numerics for such models are hard

Going the ODE route

- ODEs are way less satisfactory but can be used as-is and are much easier numerically
- Caveat: ODE models with age structure are intrinsically wrong, since sojourn times in an age group is exponentially distributed instead of Dirac distributed!

Models incorporating social structure

▶ Example: TB in foreign-born population of Canada ▶ Varughese, Langlois-Klassen, Long, & Li (2014) ▶ New immigrants to Canada come predominantly from countries in which TB is very active ▶ People develop TB in the first few years of their presence in Canada ▶ Want to investigate this, together with effect of various screening measures
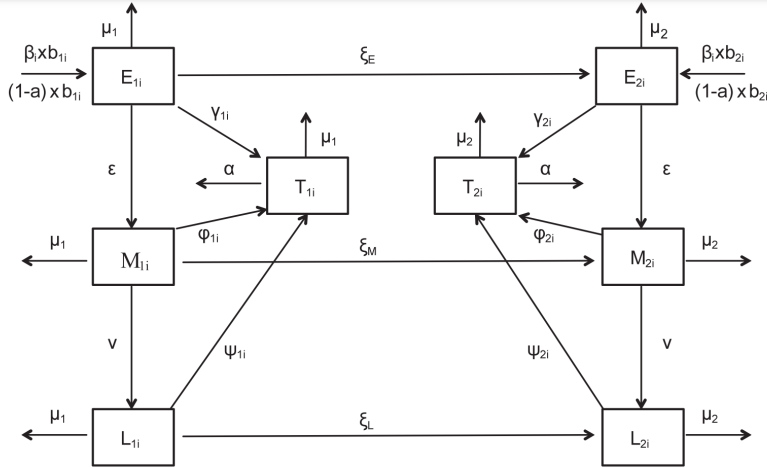
Figure 1 The overall schematic diagram of the LTBI model. The foreign-born population in Canada between 1986 and 2002 was stratified by three incidence groups denoted by i (low = L, <15; medium = Me, 15–50; and high = H, >50 cases/100 000). The two age groups for the foreign-born population are denoted by subscripts 1 (<35 years) and 2 ($\geq$35 years). Compartments E, M, and L describe foreign-born persons who arrived within 2 years, 3–5 years and >5 years, respectively. The T compartment represents the foreign-born population that developed active TB disease. The parameter b describes the average number of people

Models with pathogen heterogeneity

▶ Example: Importation of a new SARS-CoV-2 variant ▶ Arino, Boëlle, Milliken & Portet (2021) ▶ Consider what happens when a new variant N arrives in a situation where another variant O is already circulating
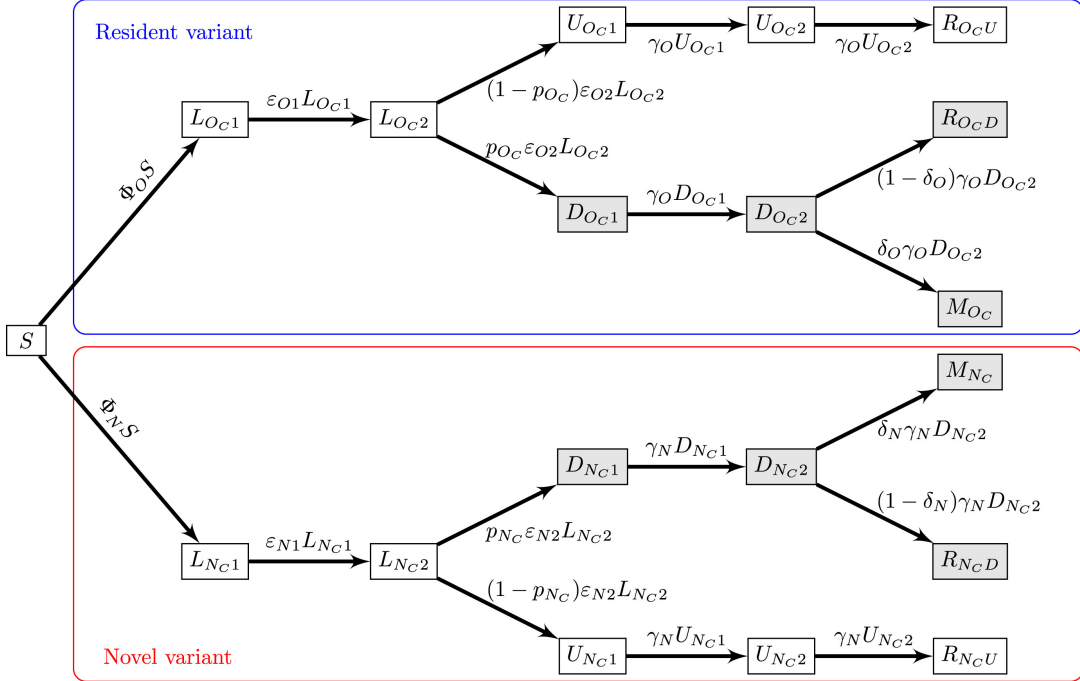
Coupling is through the force of infection

▶ For now, we have discussed incidence functions $f(S, I, N)$ ▶ Here, we use a force of infection Φ_X, for $X \in \{O, N\}$ ▶ Force of infection uses S outside of function: it is the pressure that applies to S individuals to make them infected ▶ Of course, the two are equivalent, but in some contexts, it makes sense to use this ▶ Here, for $X \in \{O, N\}$:

$$\Phi_X = \beta_X(\eta_X L_{X_c2} + \xi_X(D_{X_c1} + D_{X_c2}) + U_{X_c1} + U_{X_c2})$$

Adding more groups - Importation layer

▶ How can we evaluate how much importations contribute to propagation within a location? ▶ If an individual arrives in a new location while bearing the disease, we put them in a special group, the importation layer ▶ In importation layer, individuals make contacts with others in the population, but they remain in the importation layer until recovery or death

S

$\Phi_N S$ $\Phi_O S$

Importation layer - Novel variant

$\pi_{L_{N_{f1}}}\lambda_N \rightarrow L_{N,1}$

$\varepsilon_{N1}L_{N,1} \rightarrow L_{N,2}$

$\pi_{L_{N_{f2}}}\lambda_N$

$p_N\varepsilon_{N2}L_{N,2} \rightarrow U_{N,1}$

$(1-p_N)\varepsilon_{N2}L_{N,2} \rightarrow D_{N,1}$

$\pi_{U_{N_{f1}}}\lambda_N \rightarrow U_{N,1}$

$\gamma_N U_{N,1} \rightarrow U_{N,2}$; $\gamma_N D_{N,1} \rightarrow D_{N,2}$

$\pi_{U_{N_{f2}}}\lambda_N \rightarrow U_{N,2}$

$\gamma_N U_{N,2} \rightarrow R_{N,U}$

$(1-\delta_N)\gamma_N D_{N,2} \rightarrow R_{N,D}$

$\delta_N\gamma_N D_{N,2} \rightarrow M_N$

Community - Novel variant

$L_{N_c,1}$

$\varepsilon_{N1}L_{N_c,1} \rightarrow L_{N_c,2}$

$p_{N_c}\varepsilon_{N2}L_{N_c,2} \rightarrow U_{N_c,1}$

$(1-p_{N_c})\varepsilon_{N2}L_{N_c,2} \rightarrow D_{N_c,1}$

$\gamma_N U_{N_c,1} \rightarrow U_{N_c,2}$; $\gamma_N D_{N_c,1} \rightarrow D_{N_c,2}$

$\gamma_N U_{N_c,2} \rightarrow R_{N_c,U}$

$(1-\delta_N)\gamma_N D_{N_c,2} \rightarrow R_{N_c,D}$

$\delta_N\gamma_N D_{N_c,2} \rightarrow M_{N_c}$

Community - Resident variant

$L_{O_c,1}$

$\varepsilon_{O1}L_{O_c,1} \rightarrow L_{O_c,2}$

$p_{O_c}\varepsilon_{O2}L_{O_c,2} \rightarrow D_{O_c,1}$

$(1-p_{O_c})\varepsilon_{O2}L_{O_c,2} \rightarrow U_{O_c,1}$

$\gamma_O D_{O_c,1} \rightarrow D_{O_c,2}$; $\gamma_O U_{O_c,1} \rightarrow U_{O_c,2}$

$\delta_O\gamma_O D_{O_c,2} \rightarrow M_{O_c}$

$(1-\delta_O)\gamma_O D_{O_c,2} \rightarrow R_{O_c,D}$

$\gamma_O U_{O_c,2} \rightarrow R_{O_c,U}$

Importation layer - Resident variant

$L_{O,1} \leftarrow \pi_{L_{O_{f1}}}\lambda_O$

$\varepsilon_{O1}L_{O,1} \rightarrow L_{O,2} \leftarrow \pi_{L_{O_{f2}}}\lambda_O$

$p_O\varepsilon_{O2}L_{O,2} \rightarrow D_{O,1}$

$(1-p_O)\varepsilon_{O2}L_{O,2} \rightarrow U_{O,1} \leftarrow \pi_{U_{O_{f1}}}\lambda_O$

$\gamma_O D_{O,1} \rightarrow D_{O,2}$; $\gamma_O U_{O,1} \rightarrow U_{O,2} \leftarrow \pi_{U_{O_{f2}}}\lambda_O$

$\delta_O\gamma_O D_{O,2} \rightarrow M_O$

$(1-\delta_O)\gamma_O D_{O,2} \rightarrow R_{O,D}$

$\gamma_O U_{O,2} \rightarrow R_{O,U}$

Force of infection with importation layer

For $X \in \{O, N\}$:

$$\Phi_X = \Phi_{X_I} + \Phi_{X_I}$$

where, for $X \in \{O, N\}$ and $Z \in \{I, C\}$:

$$\Phi_{X_Z} = \beta_X(\eta_X L_{X_Z 2} + \xi_X(D_{X_Z 1} + D_{X_Z 2}) + U_{X_Z 1} + U_{X_Z 2})$$

Models with immunological component

▶ Global dynamics of a general class of multistage models for infectious diseases. Guo, Li & Shuai (2012) ▶ Viruses such as HIV reside in the body for a very long time, potentially for life ▶ Throughout the course of this residence, virus loads change and with it symptoms and infectiousness
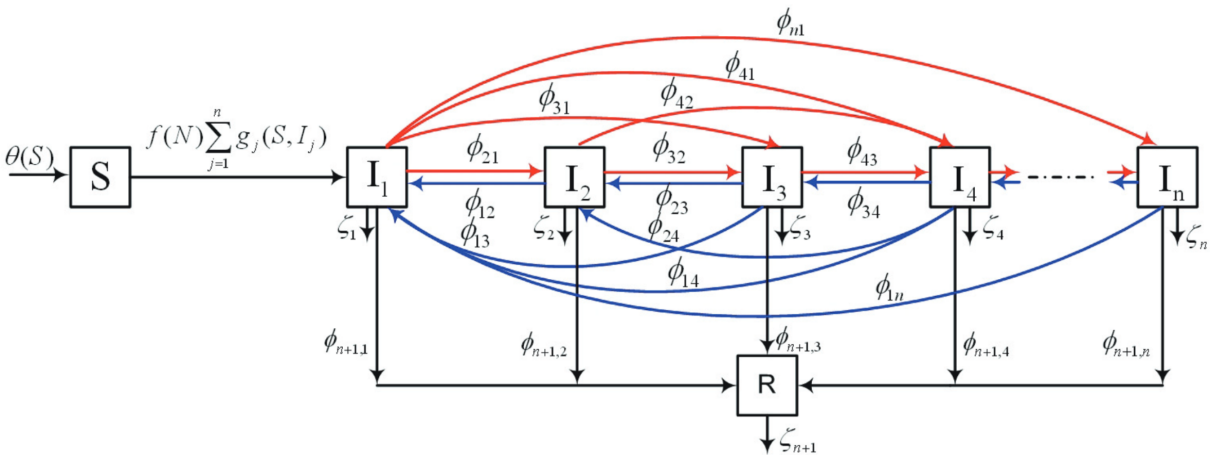
Analysing group models

▶ For general considerations about a method, see Lu & Shuai (2010) ▶ Techniques use combination of classical ODE stability theory, linear algebra and graph theory ▶ They show GAS when $\mathcal{R}_0 \leq 1$ and GAS under conditions when $\mathcal{R}_0 > 1$ ▶ Use Lyapunov function $L = \sum_{i=1}^{n} w_i I_i$ for DFE when $\mathcal{R}_0 \leq 1$ ▶ For EEP, use a Goh type Lyapunov function:

$$V = \tau_1 \int_{S^*}^{S} \frac{\Phi(\xi) - \Phi(S^*)}{\Phi(\xi)} d\xi + \sum_{i=1}^{n} \tau_i \int_{I_i^*}^{I_i} \frac{\psi(\xi) - \psi(I_i^*)}{\psi(\xi)} d\xi$$

▶ Use Kirchhoff's matrix tree theorem to show that V' is negative definite

Simulating group models

▶ This is very similar to metapopulation models which are described in Practicum 02 ▶ The variant importation model simulations will be discussed in the stochastic lectures

Bibliography I