Group models

MATH 8xyz – Lecture 16

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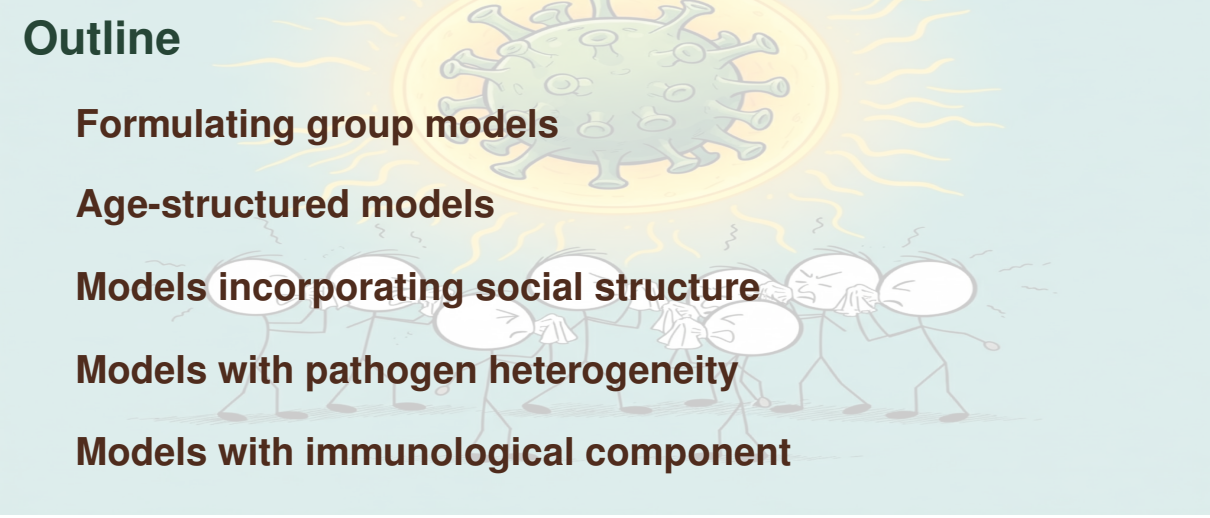
The University of Manitoba campuses are located on original lands of Anishinaabeg, Ininew, Anisininew, Dakota and Dene peoples, and on the National Homeland of the Red River Métis. We respect the Treaties that were made on these territories, we acknowledge the harms and mistakes of the past, and we dedicate ourselves to move forward in partnership with Indigenous communities in a spirit of Reconciliation and collaboration.

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

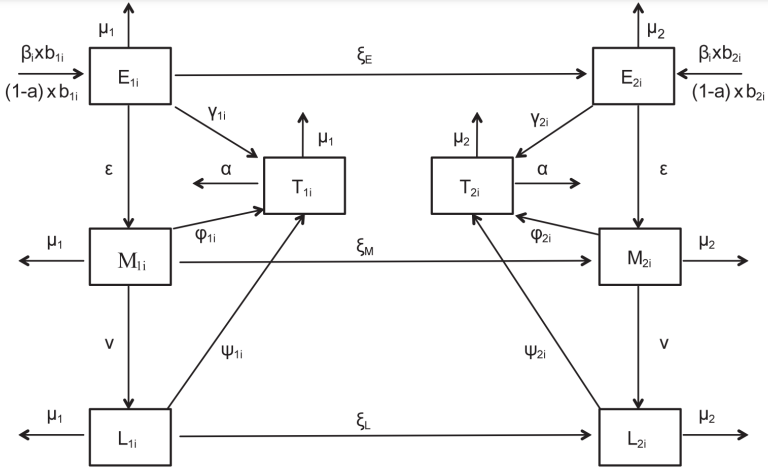
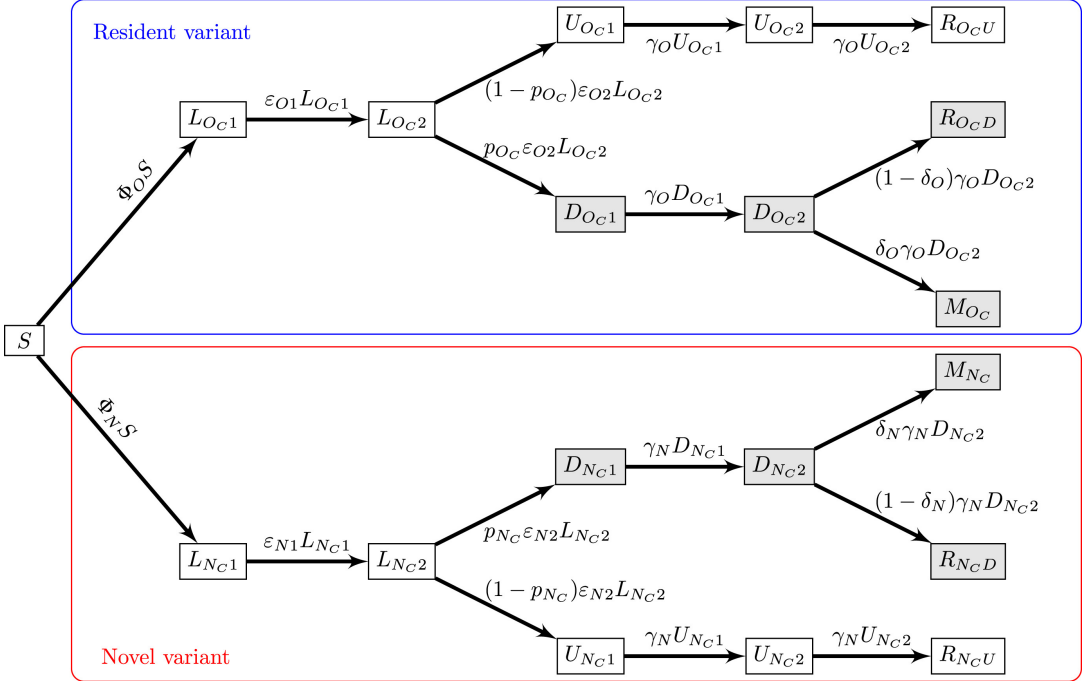


Figure 1 The overall schematic diagram of the LTBI model. The foreign-born population in Canada between 1986 and 2002 was stratified by three incidence groups denoted by *i* (low = L, <15; medium = Me, 15–50; and high = H, >50 cases/100 000). The two age groups for the foreign-born population are denoted by subscripts 1 (<35 years) and 2 (≥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


Resident variant
S
$\Phi_O S$
L_{O_C1}
$\varepsilon_{O1} L_{O_C1}$
L_{O_C2}
$(1-p_{O_C})\varepsilon_{O2} L_{O_C2}$
U_{O_C1}
$\gamma_O U_{O_C1}$
U_{O_C2}
$\gamma_O U_{O_C2}$
$R_{O_C U}$
$p_{O_C}\varepsilon_{O2} L_{O_C2}$
D_{O_C1}
$\gamma_O D_{O_C1}$
D_{O_C2}
$(1-\delta_O)\gamma_O D_{O_C2}$
$R_{O_C D}$
$\delta_O \gamma_O D_{O_C2}$
M_{O_C}
$\Phi_N S$
L_{N_C1}
$\varepsilon_{N1} L_{N_C1}$
L_{N_C2}
$p_{N_C}\varepsilon_{N2} L_{N_C2}$
D_{N_C1}
$\gamma_N D_{N_C1}$
D_{N_C2}
$\delta_N \gamma_N D_{N_C2}$
M_{N_C}
$(1-\delta_N)\gamma_N D_{N_C2}$
$R_{N_C D}$
$(1-p_{N_C})\varepsilon_{N2} L_{N_C2}$
U_{N_C1}
$\gamma_N U_{N_C1}$
U_{N_C2}
$\gamma_N U_{N_C2}$
$R_{N_C U}$
Novel variant

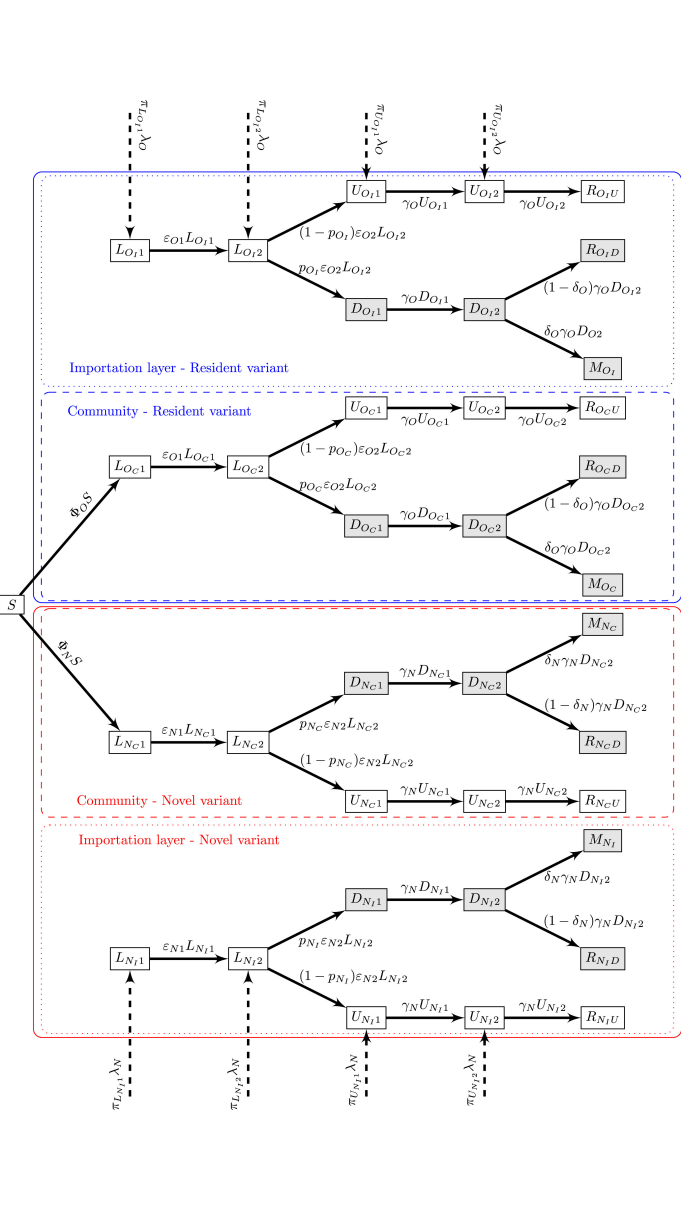
Coupling is through the force of infection

► 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 $X \in \{O, N\}$:

$$\Phi_X = \beta_X(\eta_X L_{Xc2} + \xi_X(D_{Xc1} + D_{Xc2}) + U_{Xc1} + U_{Xc2})$$

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


$\pi_{L_{O_I1}}\lambda_O$
$\pi_{L_{O_I2}}\lambda_O$
$\pi_{U_{O_I1}}\lambda_O$
$\pi_{U_{O_I2}}\lambda_O$
U_{O_I1}
$\gamma_O U_{O_I1}$
U_{O_I2}
$\gamma_O U_{O_I2}$
R_{O_IU}
L_{O_I1}
$\varepsilon_{O1} L_{O_I1}$
L_{O_I2}
$(1-p_{O_I})\varepsilon_{O2} L_{O_I2}$
R_{O_ID}
$p_{O_I}\varepsilon_{O2} L_{O_I2}$
$(1-\delta_O)\gamma_O D_{O_I2}$
D_{O_I1}
$\gamma_O D_{O_I1}$
D_{O_I2}
$\delta_O\gamma_O D_{O2}$
M_{O_I}
Importation layer - Resident variant
Community - Resident variant
U_{O_C1}
$\gamma_O U_{O_C1}$
U_{O_C2}
$\gamma_O U_{O_C2}$
R_{O_CU}
L_{O_C1}
$\varepsilon_{O1} L_{O_C1}$
L_{O_C2}
$(1-p_{O_C})\varepsilon_{O2} L_{O_C2}$
R_{O_CD}
$\phi_{O_C} S$
$p_{O_C}\varepsilon_{O2} L_{O_C2}$
$(1-\delta_O)\gamma_O D_{O_C2}$
D_{O_C1}
$\gamma_O D_{O_C1}$
D_{O_C2}
$\delta_O\gamma_O D_{O_C2}$
S
M_{O_C}
M_{N_C}
$\phi_{N_C} S$
$\delta_N\gamma_N D_{N_C2}$
D_{N_C1}
$\gamma_N D_{N_C1}$
D_{N_C2}
$(1-\delta_N)\gamma_N D_{N_C2}$
L_{N_C1}
$\varepsilon_{N1} L_{N_C1}$
L_{N_C2}
$p_{N_C}\varepsilon_{N2} L_{N_C2}$
R_{N_CD}
$(1-p_{N_C})\varepsilon_{N2} L_{N_C2}$
U_{N_C1}
$\gamma_N U_{N_C1}$
U_{N_C2}
$\gamma_N U_{N_C2}$
R_{N_CU}
Community - Novel variant
Importation layer - Novel variant
M_{N_I}
$\delta_N\gamma_N D_{N_I2}$
D_{N_I1}
$\gamma_N D_{N_I1}$
D_{N_I2}
$(1-\delta_N)\gamma_N D_{N_I2}$
L_{N_I1}
$\varepsilon_{N1} L_{N_I1}$
L_{N_I2}
$p_{N_I}\varepsilon_{N2} L_{N_I2}$
R_{N_ID}
$(1-p_{N_I})\varepsilon_{N2} L_{N_I2}$
U_{N_I1}
$\gamma_N U_{N_I1}$
U_{N_I2}
$\gamma_N U_{N_I2}$
R_{N_IU}
$\pi_{L_{N_I1}}\lambda_N$
$\pi_{L_{N_I2}}\lambda_N$
$\pi_{U_{N_I1}}\lambda_N$
$\pi_{U_{N_I2}}\lambda_N$

Force of infection with importation layer

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

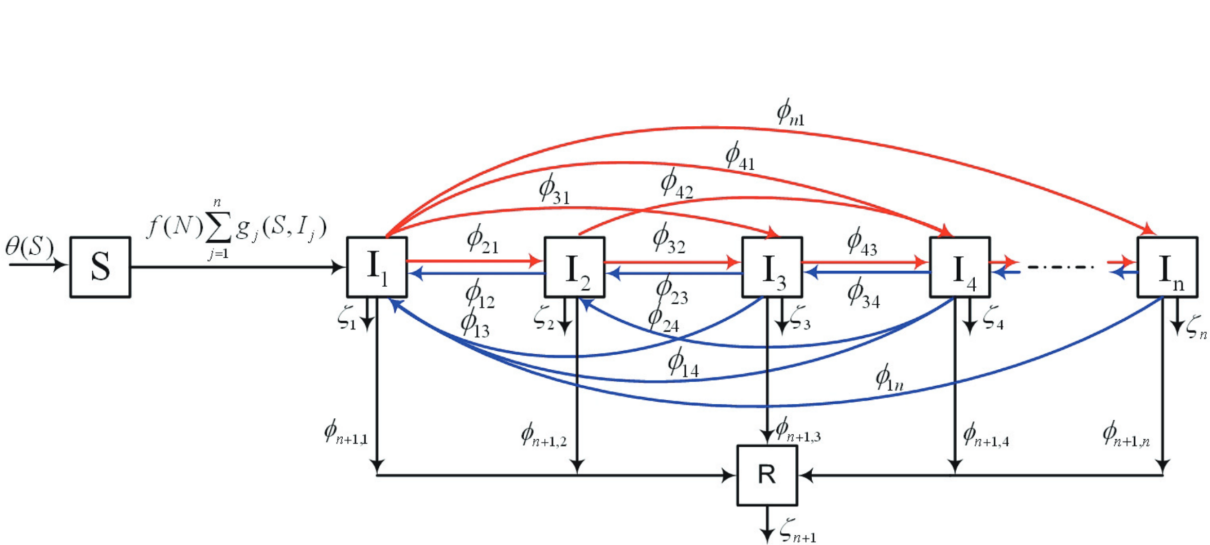
$$\Phi_X = \Phi_{X_l} + \Phi_{X_l}$$

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


$\theta(S)$
S
$f(N)\sum_{j=1}^{n} g_j(S, I_j)$
I_1
I_2
I_3
I_4
I_n
R
ϕ_{21}
ϕ_{12}
ϕ_{32}
ϕ_{23}
ϕ_{43}
ϕ_{34}
ϕ_{31}
ϕ_{13}
ϕ_{42}
ϕ_{24}
ϕ_{41}
ϕ_{14}
ϕ_{n1}
ϕ_{1n}
ζ_1
ζ_2
ζ_3
ζ_4
ζ_n
$\phi_{n+1,1}$
$\phi_{n+1,2}$
$\phi_{n+1,3}$
$\phi_{n+1,4}$
$\phi_{n+1,n}$
ζ_{n+1}

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