Vector-borne diseases

MATH 8xyz – Lecture 10

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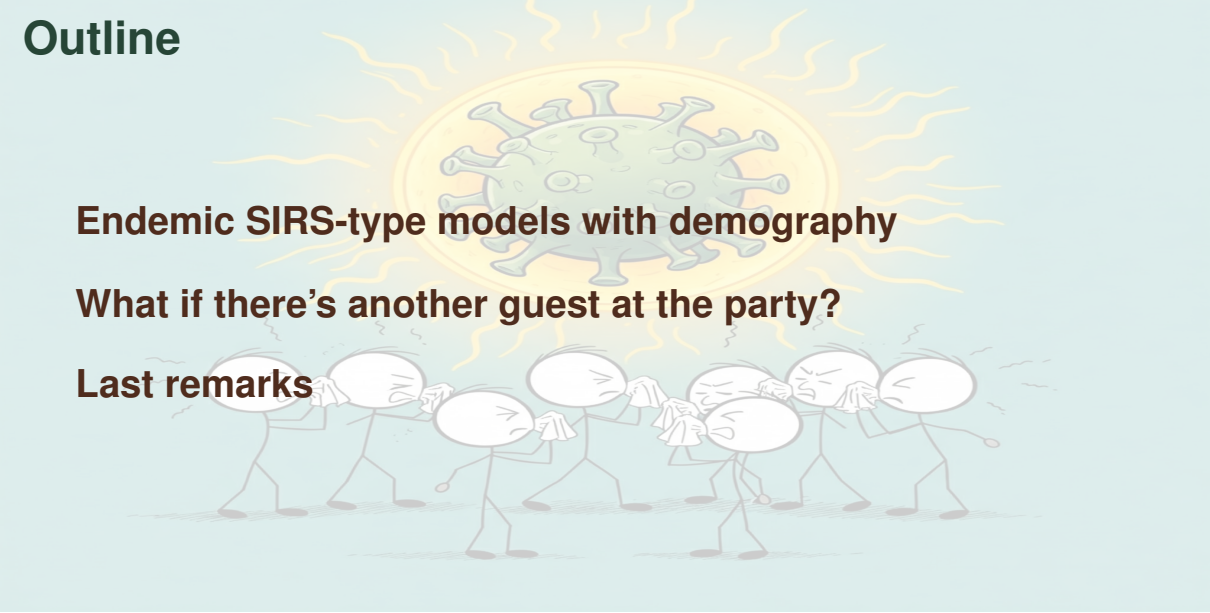
The University of Manitoba campuses are located on original lands of Anishinaabeg, Ininew, Anisininew, Dakota and Dene peoples, and on the National Homeland of the Red River Métis. We respect the Treaties that were made on these territories, we acknowledge the harms and mistakes of the past, and we dedicate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

Outline



Endemic SIRS-type models with demography

What if there's another guest at the party?

Last remarks

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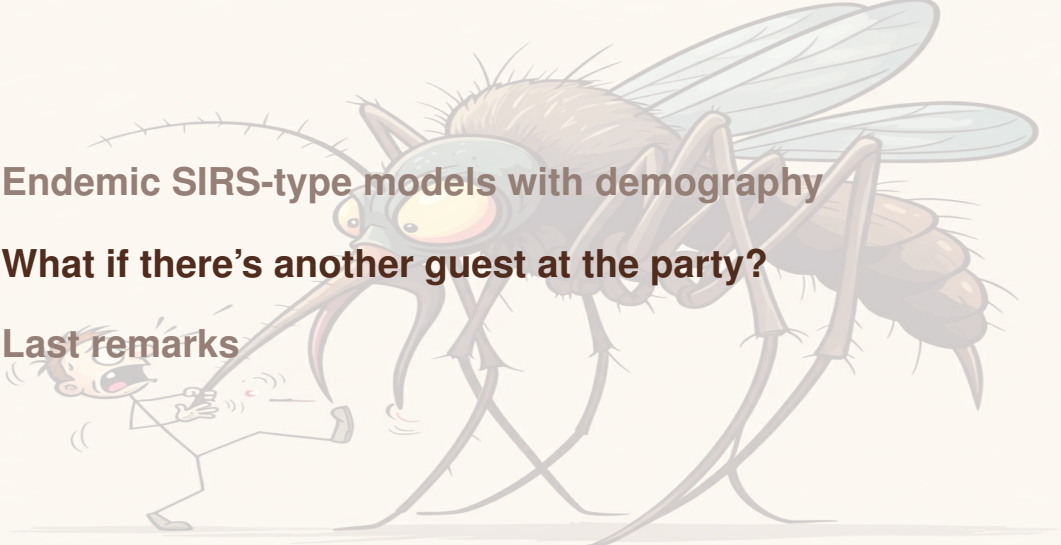


What if there's another guest at the party?

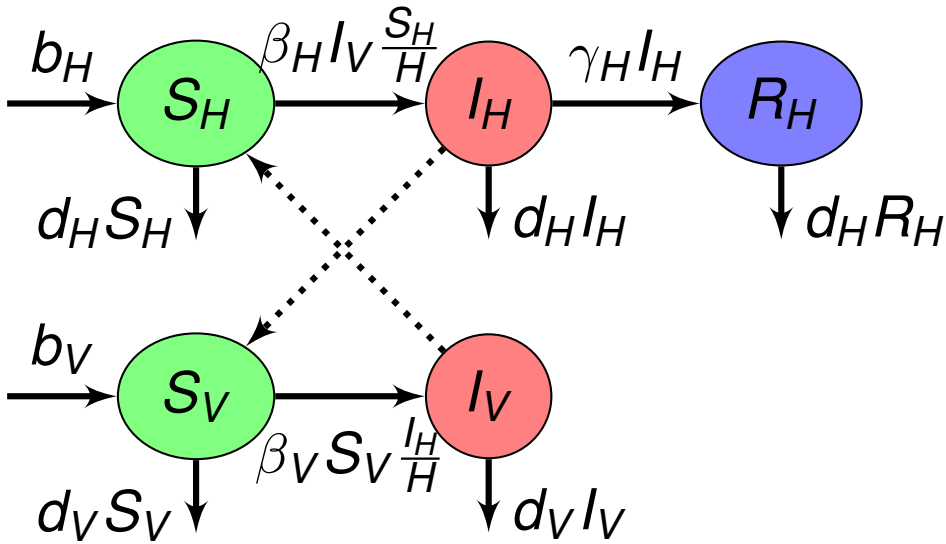
Two Ross-Macdonald-type models

A little complexification of Ross-Macdonald

See, e.g., Simoy & Aparicio, Ross-Macdonald models: Which one should we use?, *Acta Tropica* (2020)

Ross introduced the model in 1911. Later “tweaked” by Macdonald to include mosquito latency period

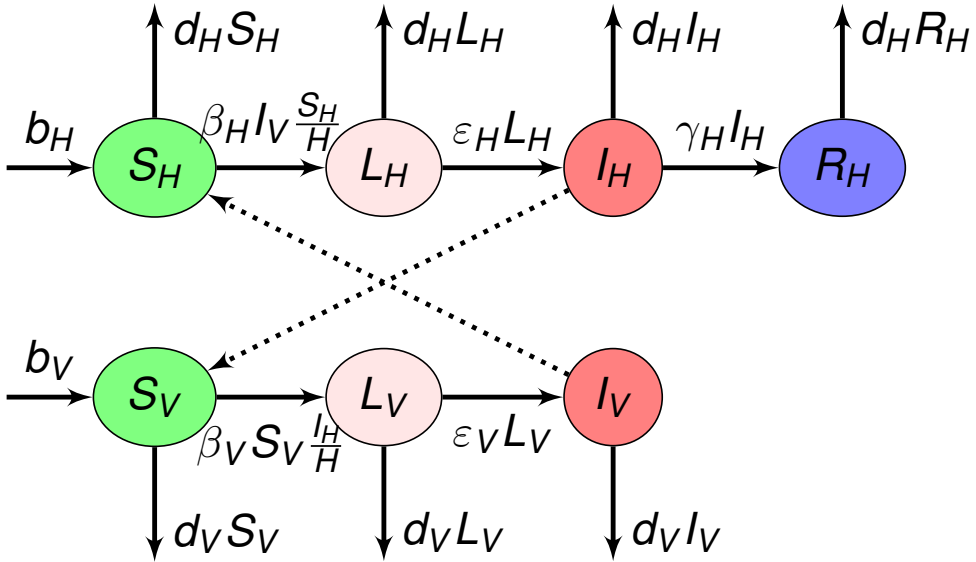
Here, I show a version in the paper cited, with some notation changed


b_H
S_H
$\beta_H I_V \frac{S_H}{H}$
I_H
$\gamma_H I_H$
R_H
$d_H S_H$
$d_H I_H$
$d_H R_H$
b_V
S_V
I_V
$\beta_V S_V \frac{I_H}{H}$
$d_V S_V$
$d_V I_V$

Reproduction number

$$\mathcal{R}_0 = \frac{\beta_H \beta_V}{(\gamma_H + \gamma_V) d_V} \frac{V^\star}{H^\star} \tag{1}$$

where $H^\star$ and $V^\star$ are the total host and vector populations, respectively


$d_H S_H$
$d_H L_H$
$d_H I_H$
$d_H R_H$
b_H
$\beta_H I_V \frac{S_H}{H}$
S_H
L_H
$\varepsilon_H L_H$
I_H
$\gamma_H I_H$
R_H
b_V
S_V
L_V
I_V
$\beta_V S_V \frac{I_H}{H}$
$\varepsilon_V L_V$
$d_V S_V$
$d_V L_V$
$d_V I_V$

Reproduction number

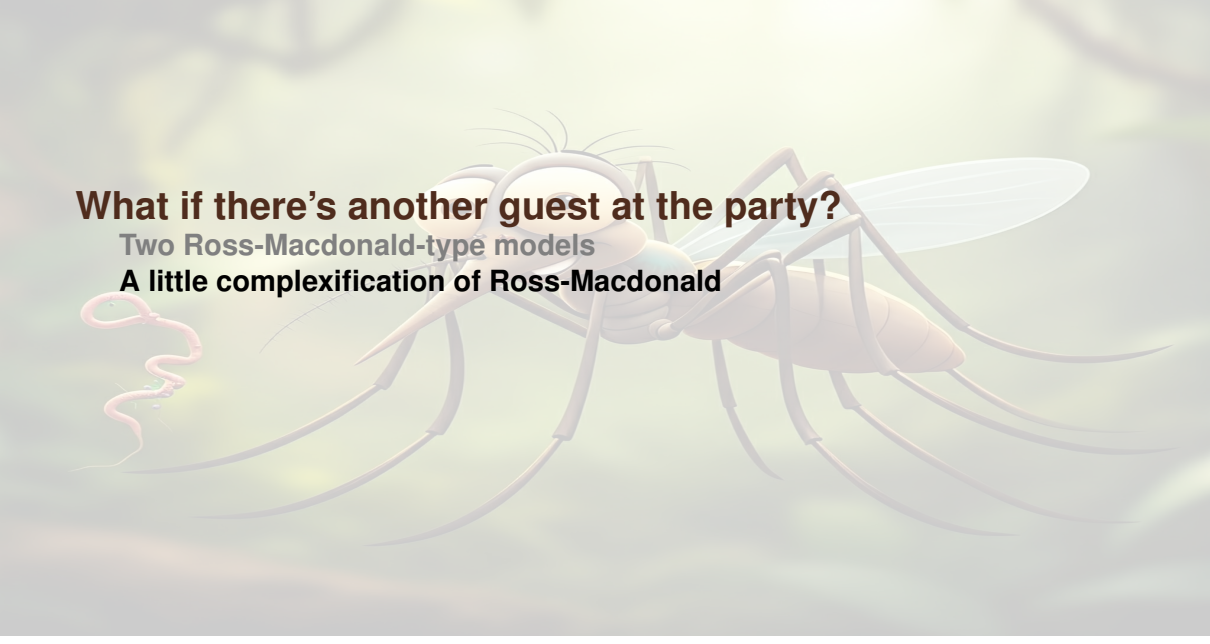
$$\mathcal{R}_0 = \frac{\beta_H \beta_V}{(\gamma_H + \gamma_V) d_V} \frac{\varepsilon_V}{d_V + \varepsilon_V} \frac{\varepsilon_H}{d_H + \varepsilon_H} \frac{V^\star}{H^\star} \tag{2}$$

where $H^\star$ and $V^\star$ are the total host and vector populations, respectively

Here

$$f_X = \frac{\varepsilon_X}{d_X + \varepsilon_X}$$

are the fractions of latent individuals (of type $X = \{V, H\}$) who survive the latency period



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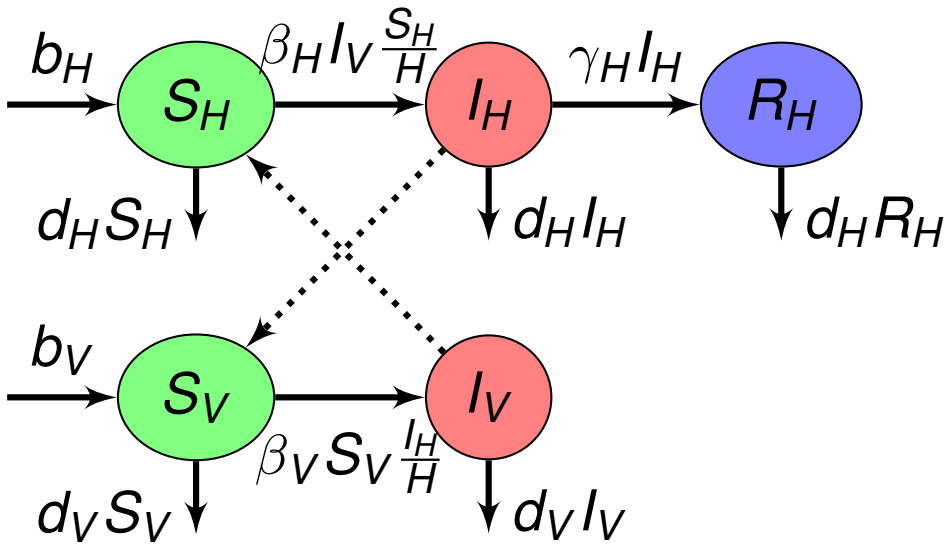
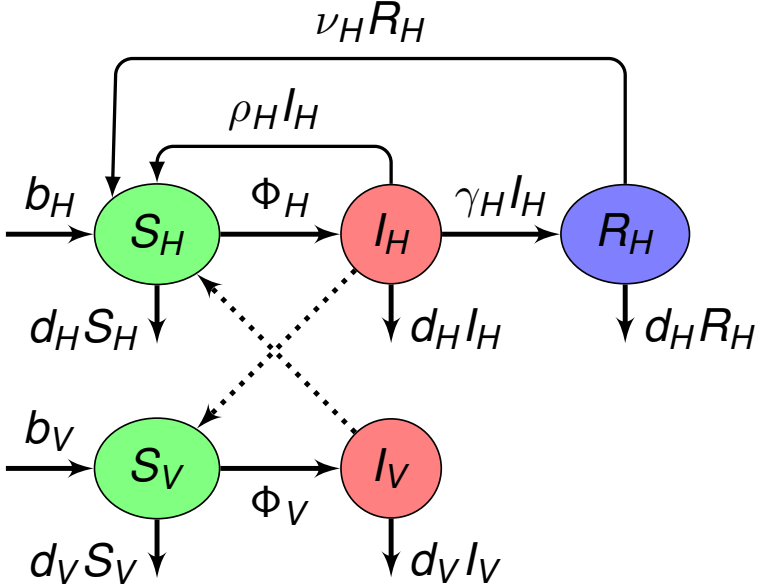
Two Ross-Macdonald-type models

A little complexification of Ross-Macdonald

Recall this guy?



Let us add a few arrows



Arino, Ducrot & Zongo, A metapopulation model for malaria with transmission-blocking partial immunity in hosts, Journal of Mathematical Biology (2012)

Incidence functions take the form

$$\Phi_H = b_H(H, V)\sigma_{VH}\frac{I_V}{V}$$

and

$$\Phi_V = b_V(H, V)\left(\sigma_{HV}\frac{I_H}{H} + \hat{\sigma}_{HV}\frac{R_H}{H}\right)$$

where b_H and b_V are numbers per unit time of mosquito bites a human has and the number of humans a mosquito bites, respectively

Parameters of the incidence function

- σ_{HV} probability of transmission of the parasite (in gametocyte form) from an infectious human to a susceptible mosquito
- $\hat{\sigma}_{HV}$ probability of transmission of the parasite (in gametocyte form) from a semi-immune human to a susceptible mosquito
- σ_{VH} probability of transmission of the parasite (in sporozoite form) from an infectious mosquito to a susceptible human

Additional parameter that can be factored in (all per unit time)

- a_H maximum number of mosquito bites a human can receive
- a_V number of times one mosquito would "want to" bite humans
- a average number of bites given to humans by each mosquito

People to read for malaria models (IMOBO)

See also the work of

- Gideon Ngwa at the University of Buea
- Nakul Chitnis at the Swiss Tropical and Public Health Institute

Many others...

More complex models may be needed for malaria

Timing of processes is critical in malaria

Plasmodium life cycle in the mosquito is commensurate with mosquito lifetime

Need models that are able to account for that, because ODEs are not really good at this (see beginning of Stochastic systems lecture)

Mathematics becomes more complicated

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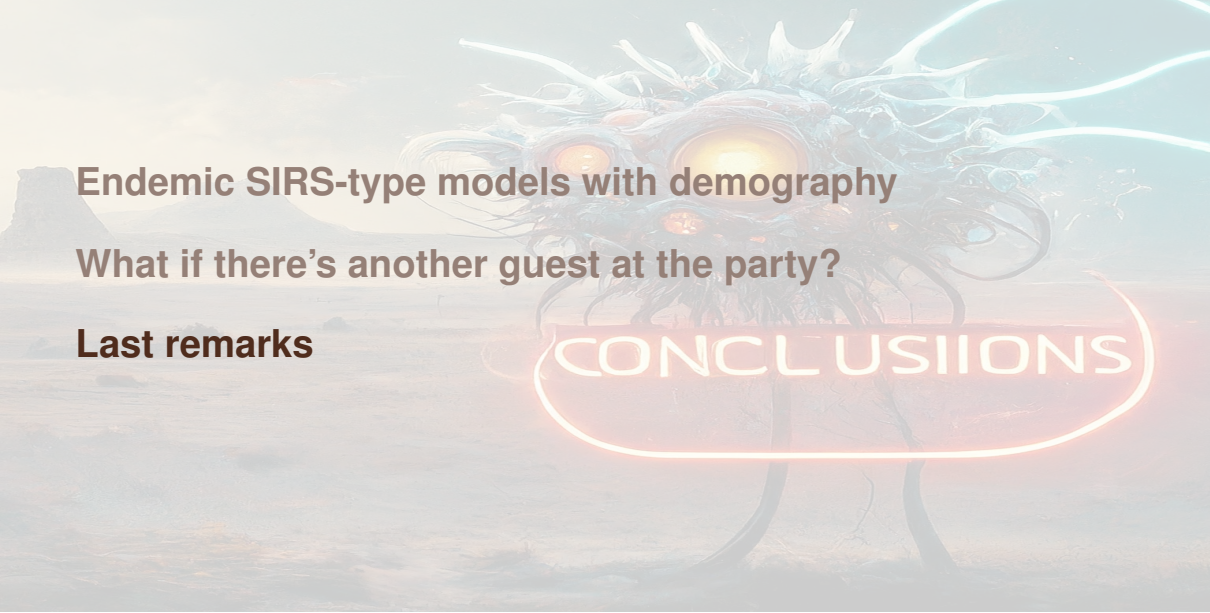

To simplify or not to simplify?

- In the KMK epidemic model (**??**) and the SIRS endemic model (**??**), since the total population is constant or asymptotically constant, it is possible to omit one of the state variables since $N^\star = S + I + R$

- We often use $R = N^\star - S - I$

- This can greatly simplify some computations

- Whether to do it or not is a matter of preference

To normalise or not to normalise?

- In the KMK epidemic model (**??**) and the SIRS endemic model (**??**), since the total population is constant or asymptotically constant, it is possible to normalise to $N = 1$

- This can greatly simplify some computations

- However, I am not a big fan: it is important to always have the "sizes" of objects in mind

- If you do normalise, at least for a paper destined to mathematical biology, always do a "return to biology", i.e., interpret your results in a biological light, which often implies to return to original values

Where we are

- An *epidemic* SIR model (the KMK SIR) in which the presence or absence of an epidemic wave is characterised by the value of $\mathcal{R}_0$
- The KMK SIR has explicit solutions (in some sense). **This is an exception!**
- An *endemic* SIRS model in which the threshold $\mathcal{R}_0 = 1$ is such that, when $\mathcal{R}_0 < 1$, the disease goes extinct, whereas when $\mathcal{R}_0 > 1$, the disease becomes established in the population
- Some simple variations on these models
- A few models for vector-borne or water-borne diseases

Bibliography I