

# MCMaster HIV virulence evolution in structured epidemic models

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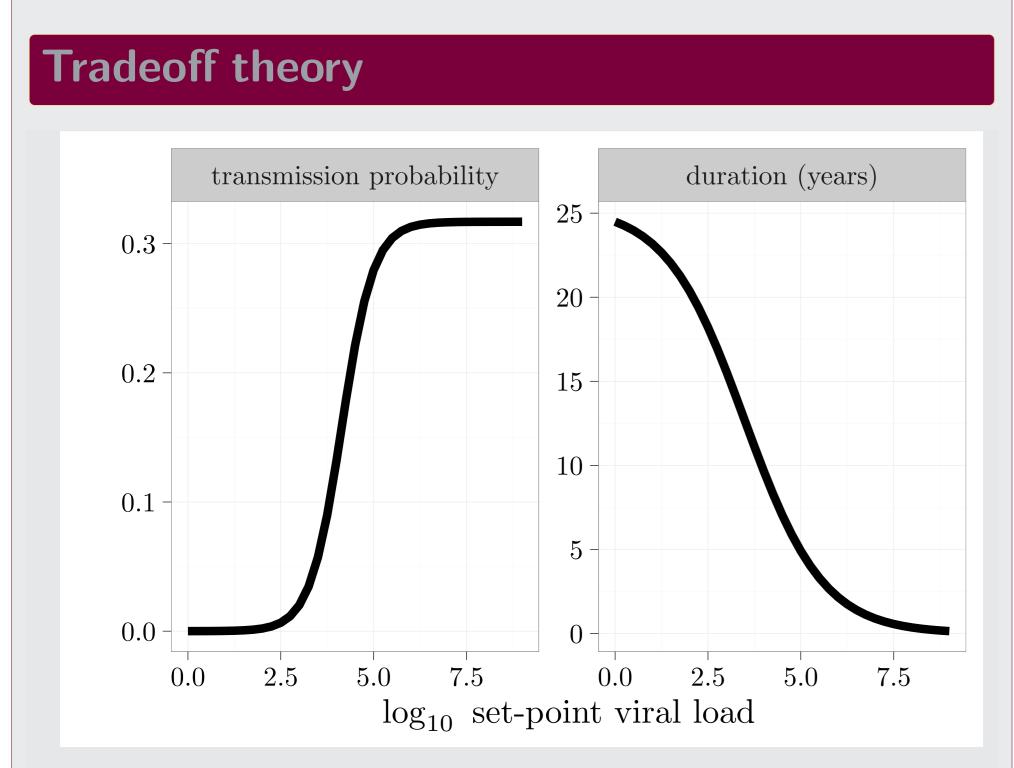
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**Eco-evolutionary dynamics** 



### Summary

Pathogens can evolve rapidly in response to changing conditions (e.g., epidemic stage or public health interventions). Models of **eco-evolutionary dynamics** often neglect important epidemiological processes, such as the dynamics of sexual partnerships. We compared **models with a range of complexity** of partnership dynamics and extra-partnership contact.



- ▶ virulence evolution mediated by transmission-vs-clearance tradeoff
- ▶ still debated [1, 2]
- ► HIV [3]: **set-point viral load** ( $\approx$  "virulence") correlated with transmission probability, rate of progression to AIDS (data from Rakai, Uganda)
- eco-evolutionary virulence dynamics: [4]

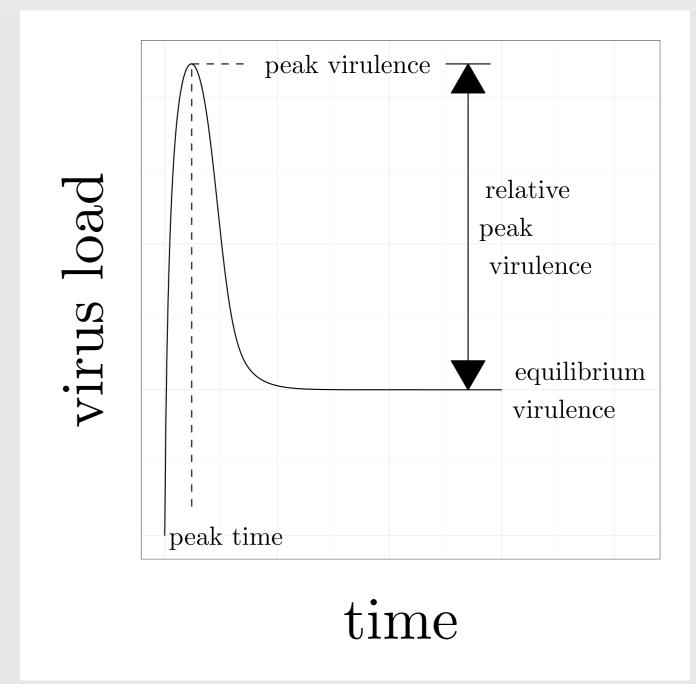
# random pairform+epc of the first pairform pairform instswitch+epc instswitch implicit of the first pairform instswitch instswit

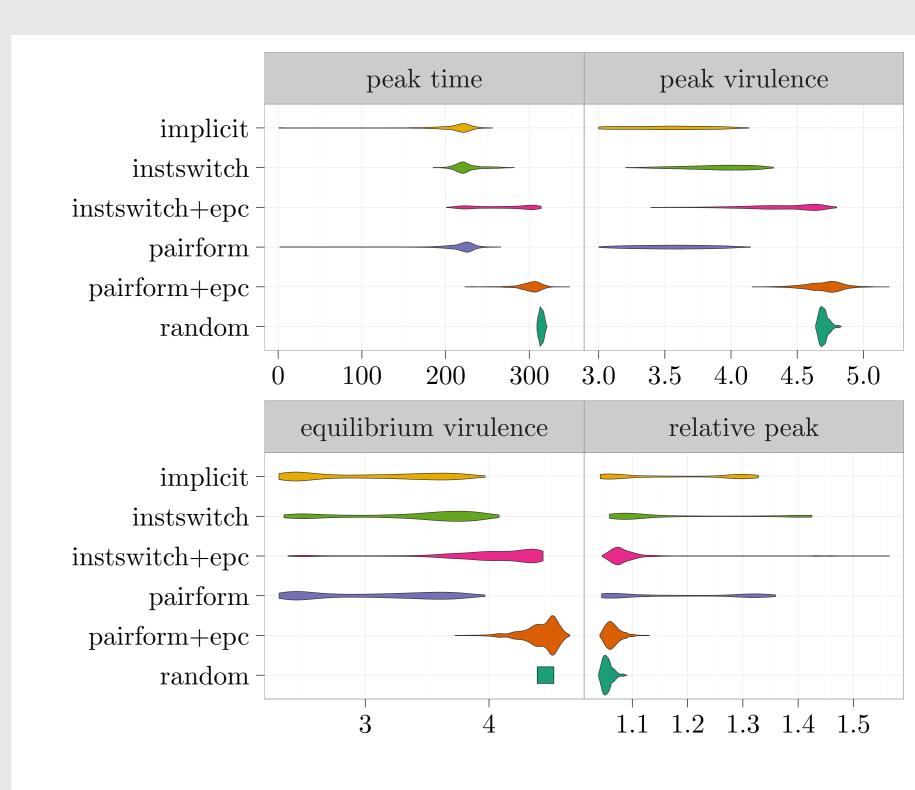
- ▶ 80% of total variability in peak SPVL is among- vs. within-model
- ▶ least (random) and most (pairform+epc) models most similar: single individuals and extra-pair contact wash out effects of structure

time (years)

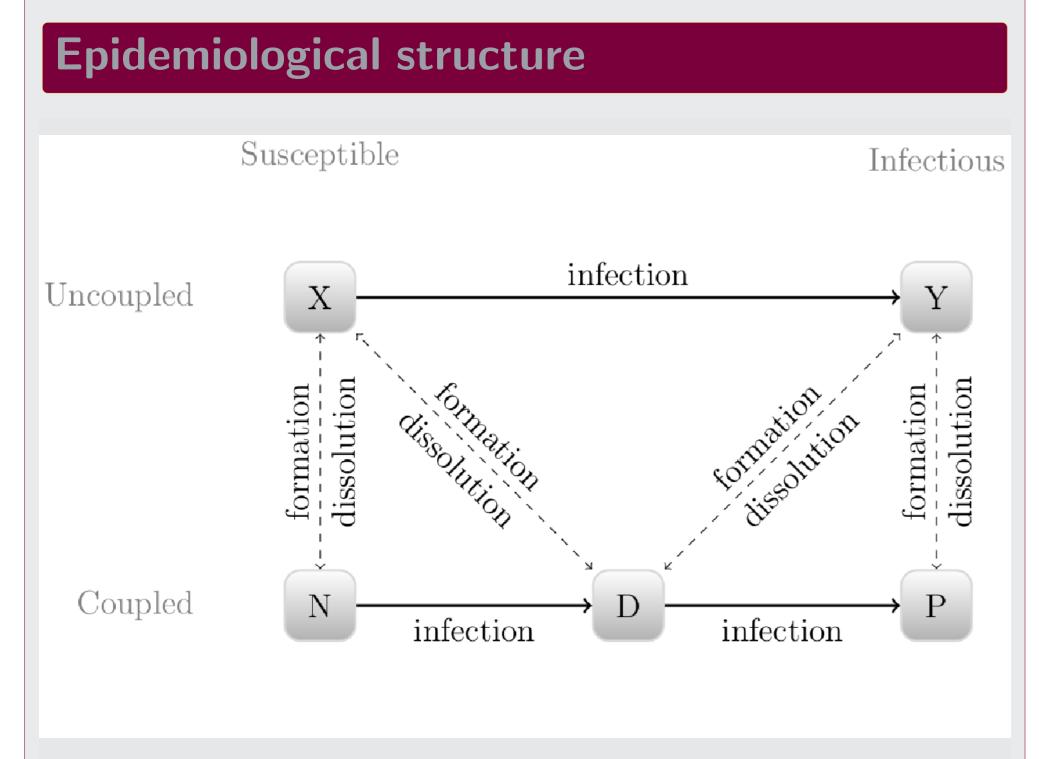
- implicit model is most different
- random-mixing model underestimates variability

## Univariate summaries





- peak timing: epc > finite pair-formation effects
- equilibrium virulence: interaction
- ► low-equilibrium outcomes for intermediate-complexity models



### Champredon et al. 2013 [5]

infection from (1) infected partner (*SI* couples); (2) other coupled inf.; (3) uncoupled inf.

Simplified disease model (single stage only)

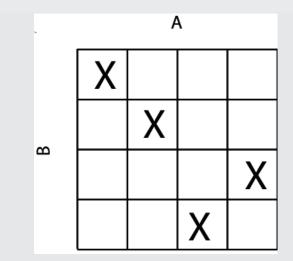
Simplified disease model (single stage only)

- **pair formation**: instantaneous or delayed?
- extra-pair contact (epc): present or absent?
- ▶ implicit model: no explicit partnerships, force of infection expression derived from  $\mathcal{R}_0$  of pair-formation model (without epc)
- random-mixing model: standard SIR model

### Sensitivity $\beta_{P}$ $c_e/c_w$ $c_{\rm u}/c_{\rm w}$ 300 200 100 5.0 model 4.5 -random pairform+epc 4.0 instswitch+epc instswitch implicit 3.5 3.0 -1.0 0.1 0.2 0.1 0.20.02 0.500.1 0.5 0.4 0.5

 $\triangleright$   $\beta_{P,D}$ : early/late-stage transmission probability;  $D_{P,D}$ : early/late-stage duration; c: partnership dissolution rate;  $c_e/c_w$ : extra- vs within-pair contact ratio;  $\rho$ : partnership formation rate;  $c_u/c_w$ : uncoupled contact rate ratio

### Parameter uncertainty/exploration



- ► Latin hypercube sampling: parameters from [5]
- parameters calibrated across models to the same initial epidemic growth rate (r)

### **Conclusions and open questions**

- ► Random-mixing models best matched the most realistic models; extra-pair and uncoupled individuals washed out the effects of epidemiological structure
- ► Implicit models did worst
- ► Variation among models (model structure) ≥ variation within models (parameter uncertainty)
- ► Large differences in evolutionary dynamics among different epidemiological models → caution in predicting evolutionary responses
- ► neglected: disease life history details, sex workers, age-structured mixing . . . agent-based models?

### References

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