

MCMaster HIV virulence evolution in structured epidemic models University Ben Bolker and Sang Woo Park

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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.

Tradeoff theory transmission probability duration (years) 0.30.21510 -0.12.55.07.50.0

 \log_{10} set-point viral load

- 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]

Epidemiological structure Susceptible Infectious infection Uncoupled Coupled infection

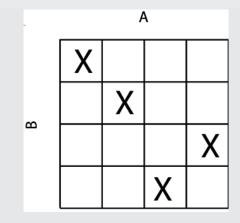
Champredon et al. 2013 [5]

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

Simplified disease model (single stage only)

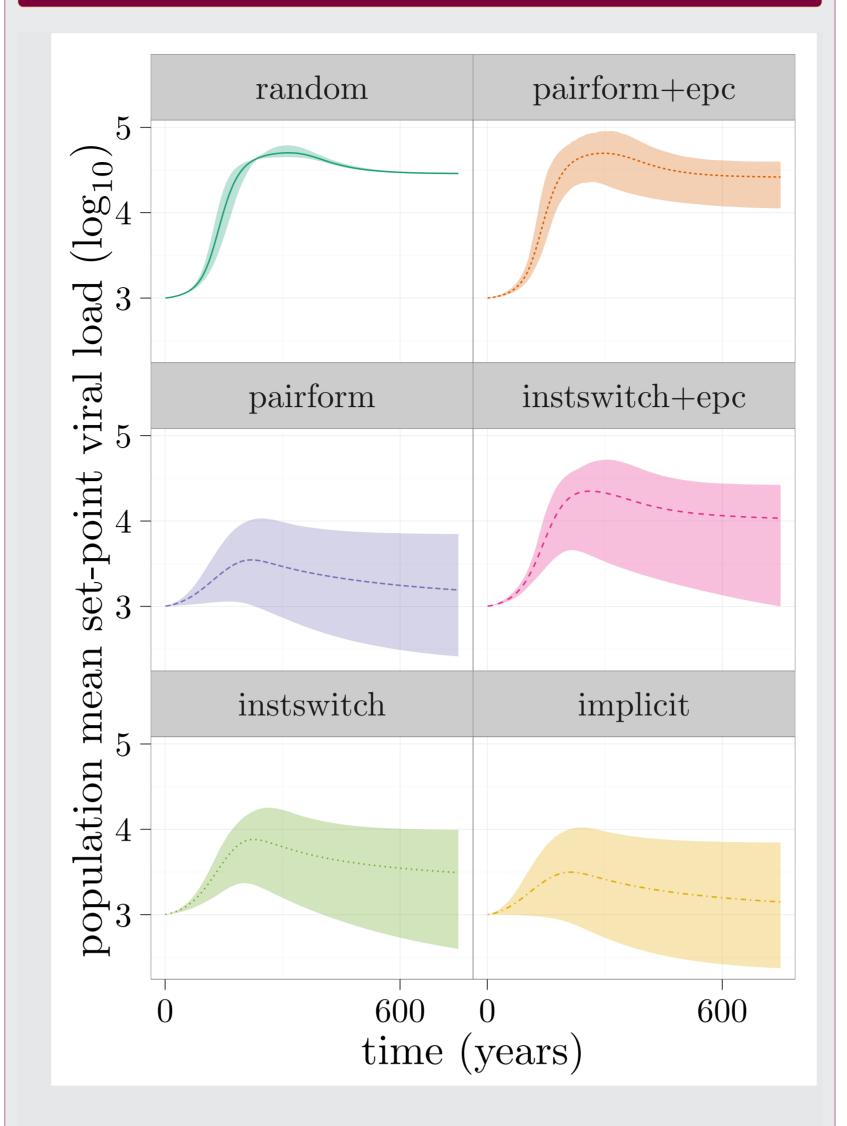
- **pair formation**: instantaneous or delayed?
- extra-pair contact (epc): present or absent?
- ▶ implicit model: no explicit partnerships, force of infection expression derived from \mathcal{R}_0 of pair-formation model (without epc)
- random-mixing model: standard SIR model

Parameter uncertainty/exploration



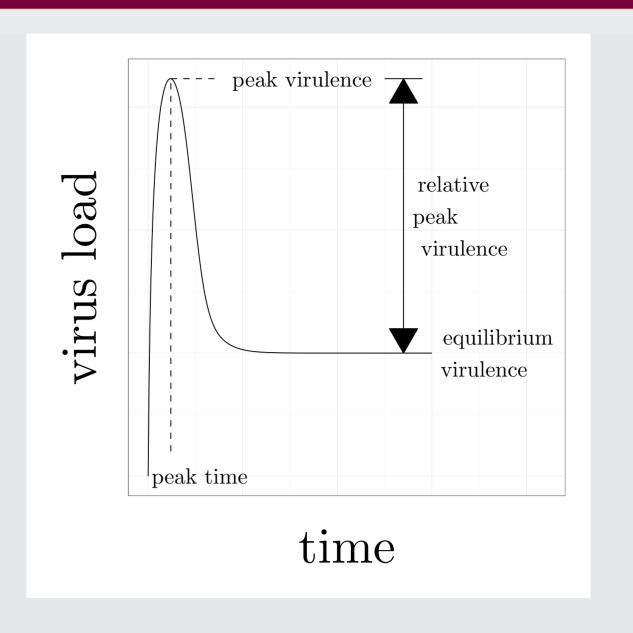
- ► Latin hypercube sampling: parameters from [5]
- parameters calibrated across models to the same initial epidemic growth rate (r)

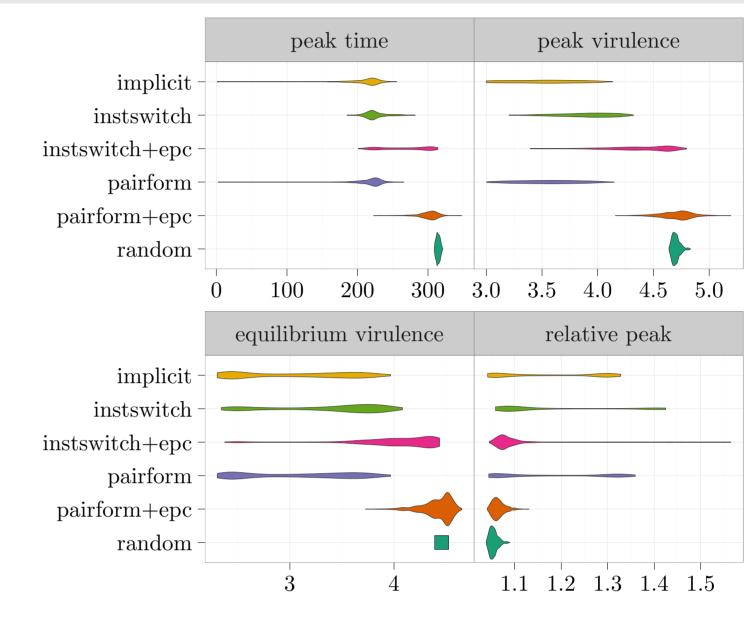
Eco-evolutionary dynamics



- ▶ 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
- random-mixing model underestimates variability

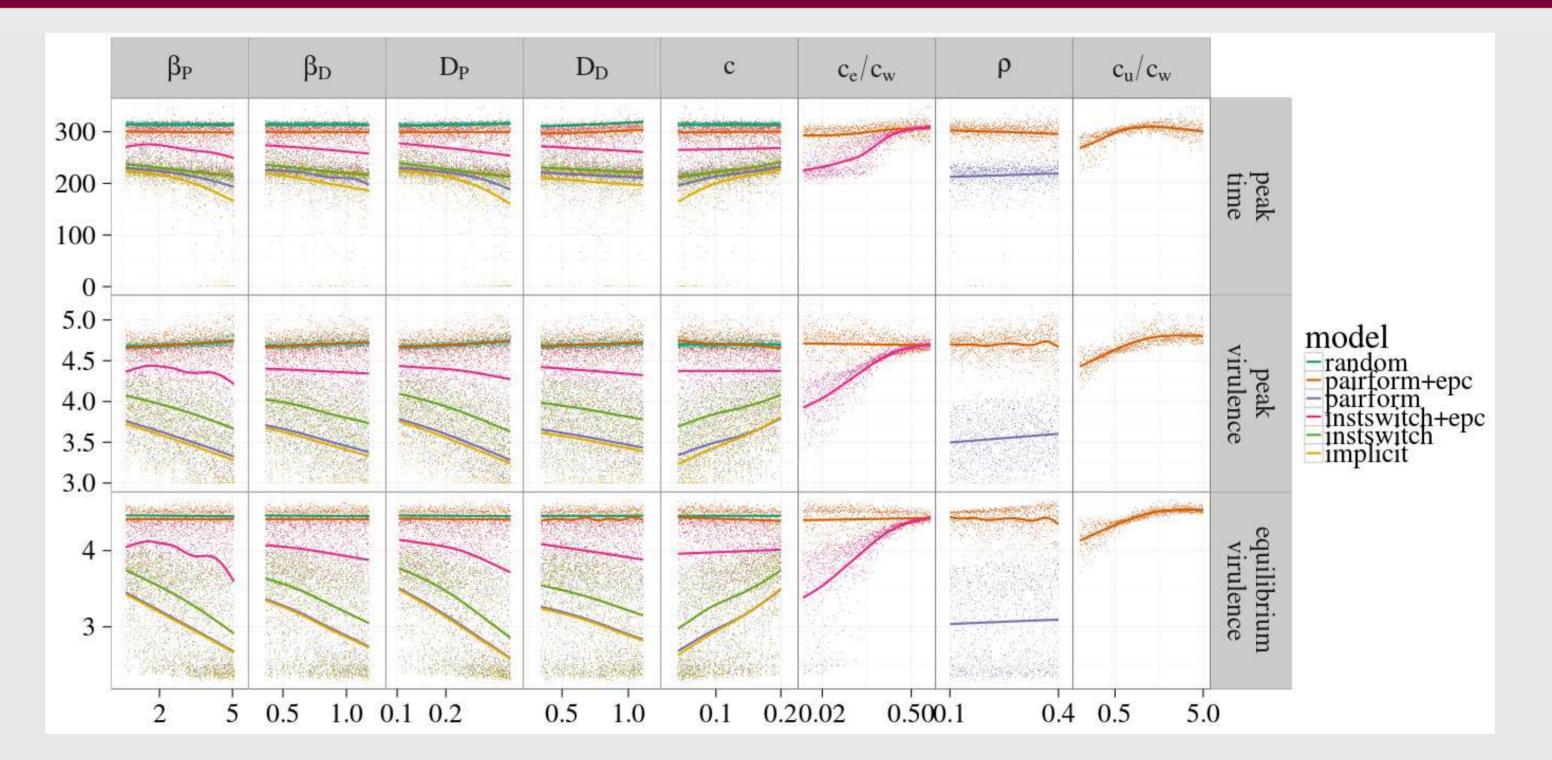
Univariate summaries





- peak timing: epc > finite pair-formation effects
- equilibrium virulence: interaction

Sensitivity



 \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; ρ : partnership formation rate; c_u/c_w : uncoupled contact rate ratio

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
- \blacktriangleright Variation among models (model structure) \gtrsim variation within models (parameter uncertainty)
- ► Large differences in evolutionary dynamics among different epidemiological models ightarrowcaution in predicting evolutionary responses
- ► neglected: disease life history details, sex workers, age-structured mixing ... agent-based models?

References

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