HIV virulence evolution in structured epidemic models

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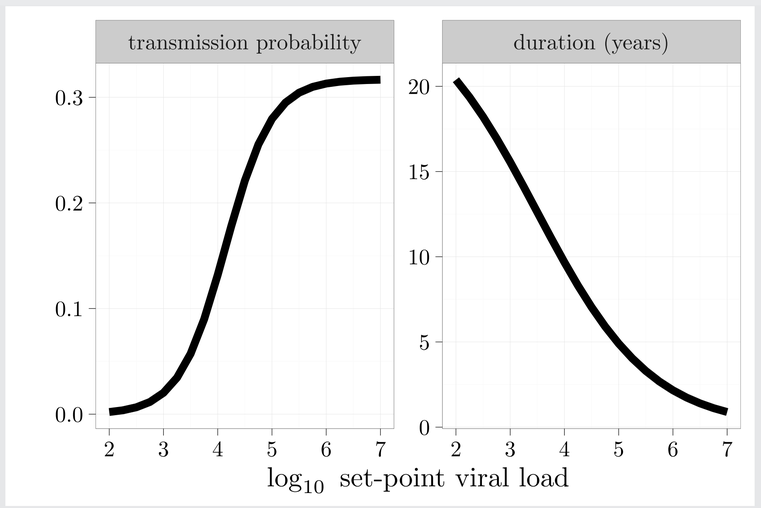
Summary

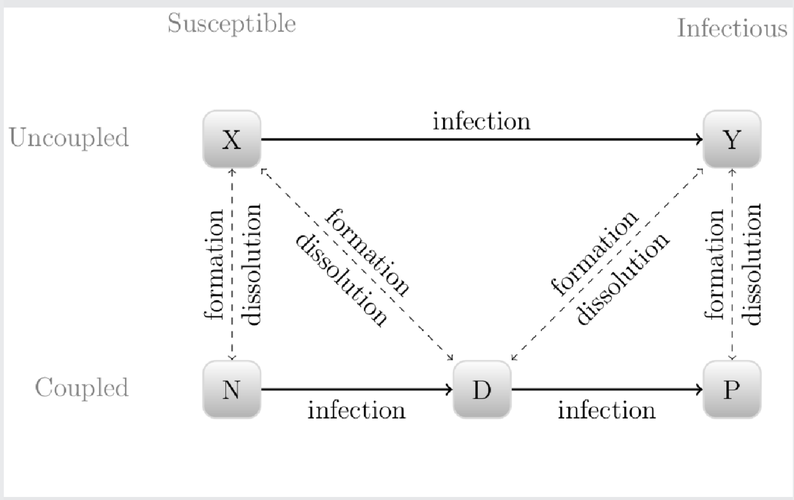
Pathogens can evolve rapidly in response to changing conditions (e.g., epidemic stage or public health interventions). Models of **eco-evolutionary dynamics** often neglect important epidemiological processes, such as the dynamics of sexual partnerships. We compared **models with a range of complexity**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

Tradeoff theory



- 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



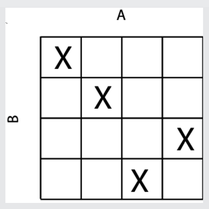
Champredon *et al.* 2013 [5]

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

Simplified disease model (single stage only)

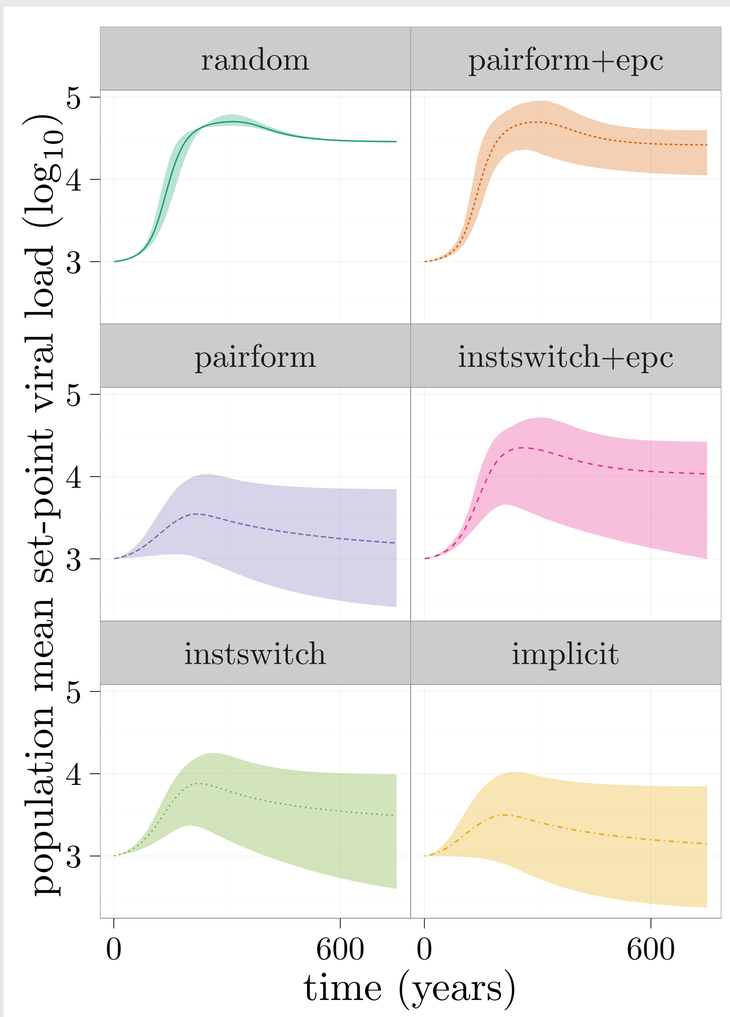
- **pair formation**: instantaneous or delayed?
- **extra-pair contact** (epc): present or absent?
- **implicit model**: no explicit partnerships, force of infection expression derived from $\mathcal{R}_0$ of pair-formation model (without epc)
- **random-mixing model**: standard SIR model

Parameter uncertainty/exploration



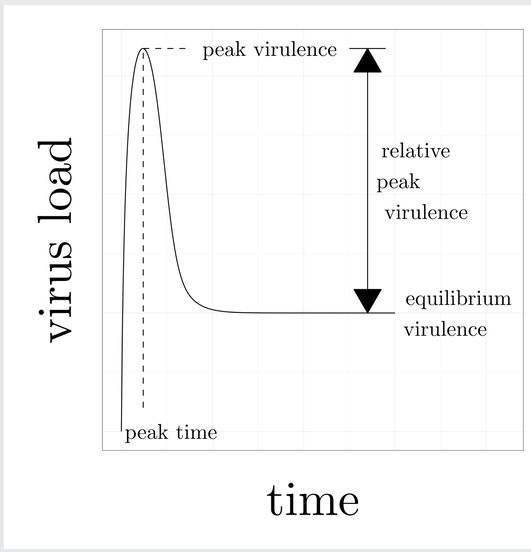
- Latin hypercube sampling: parameters from [5]
- parameters calibrated across models to the same **initial epidemic growth rate** (r)

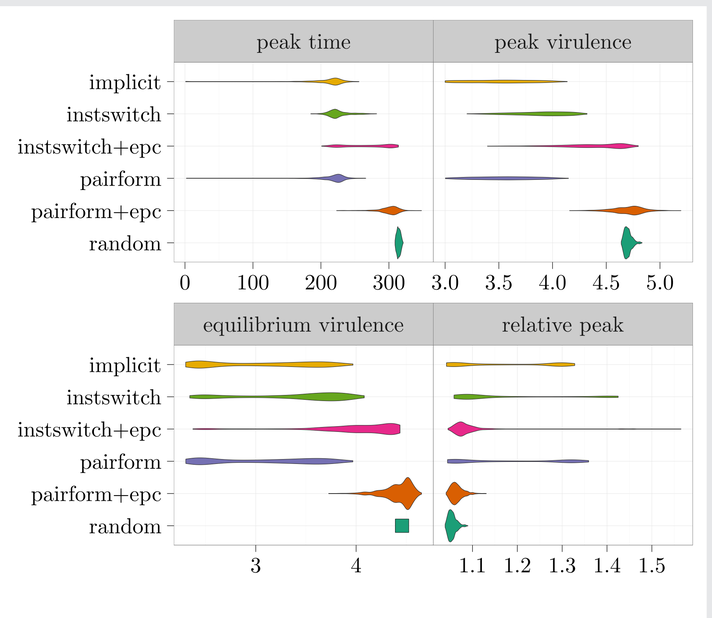
Eco-evolutionary dynamics



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

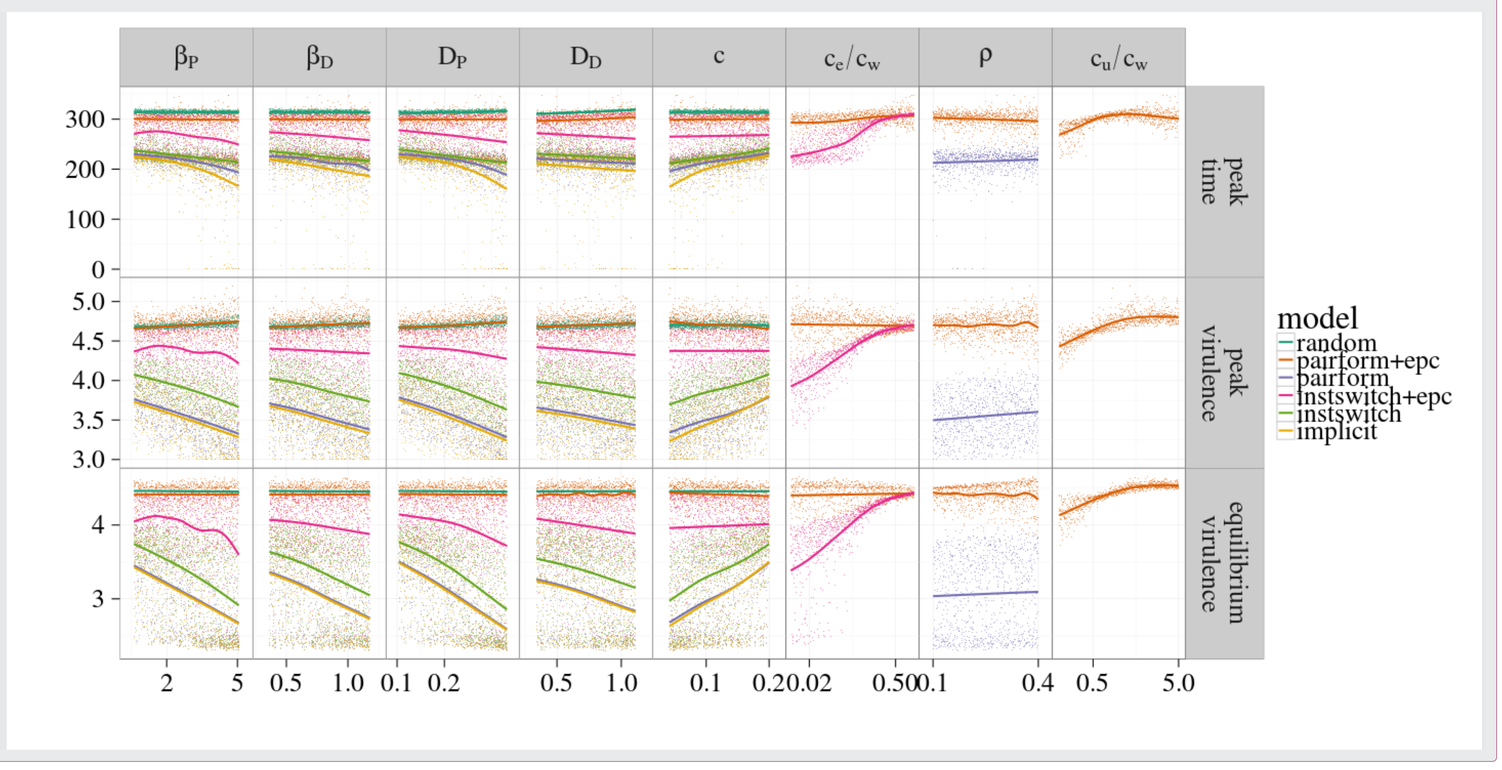
Univariate summaries





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

Sensitivity



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) $\approx$ variation within models (parameter uncertainty)
- Large differences in evolutionary dynamics among different epidemiological models $\rightarrow$ caution in predicting evolutionary responses
- **neglected:** disease life history details, sex workers, age-structured mixing ... agent-based models?

References

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[4] Shirreff G, Pellis L, Laeyendecker O, Fraser C. Transmission Selects for HIV-1 Strains of Intermediate Virulence: A Modelling Approach. PLoS Computational Biology. 2011 Oct;7(10):e1002185. WOS:000297262700019.

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Acknowledgements

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