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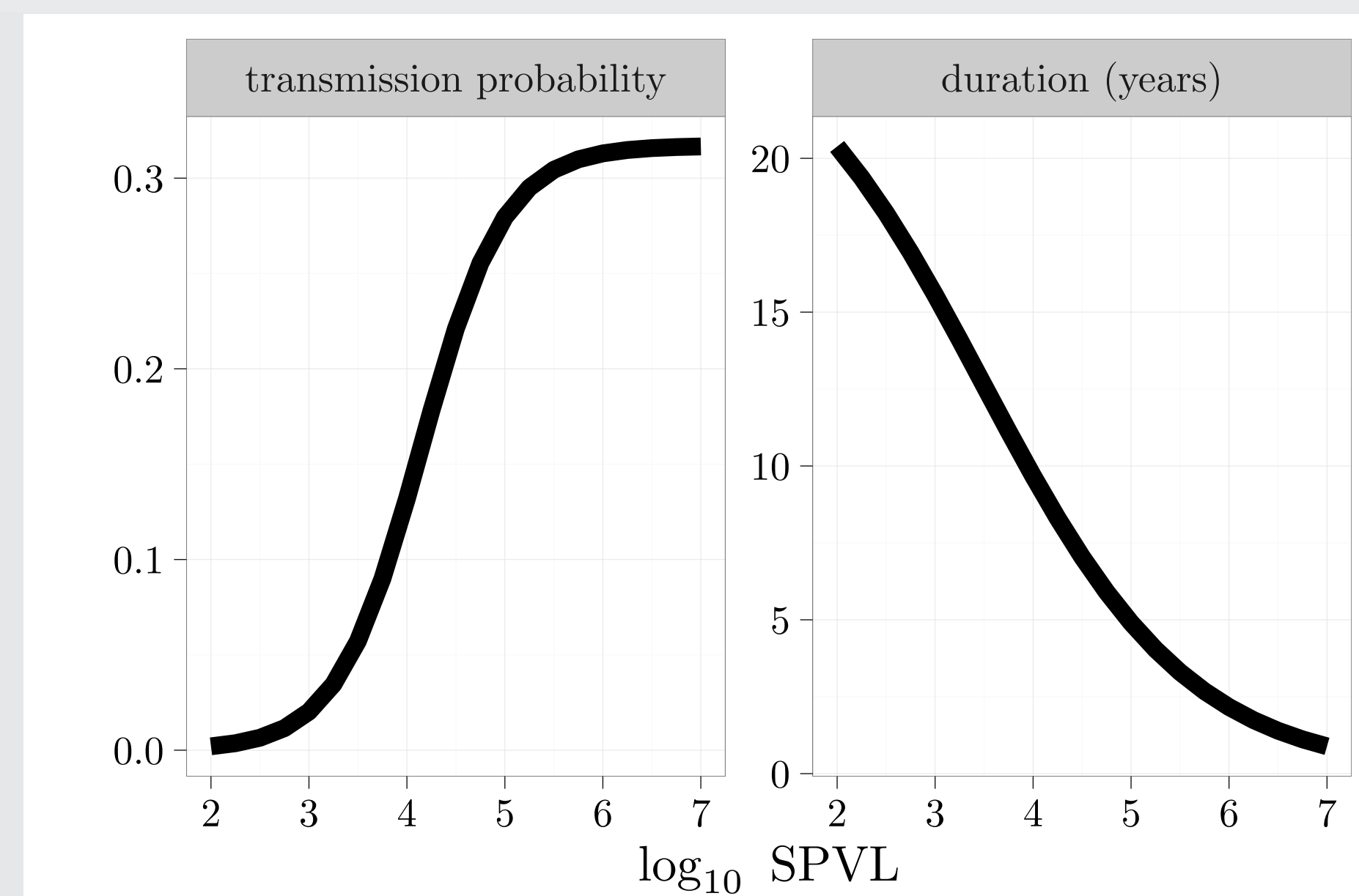
- ▶ virulence evolution mediated by transmission-vs-clearance tradeoff
- ▶ still debated [1, 2]
- ▶ HIV [3]: **set-point viral load** correlated with transmission probability, rate of progression to AIDS (data from Rakai, Uganda)
- ▶ eco-evolutionary virulence dynamics: [4]

## Epidemiological structure
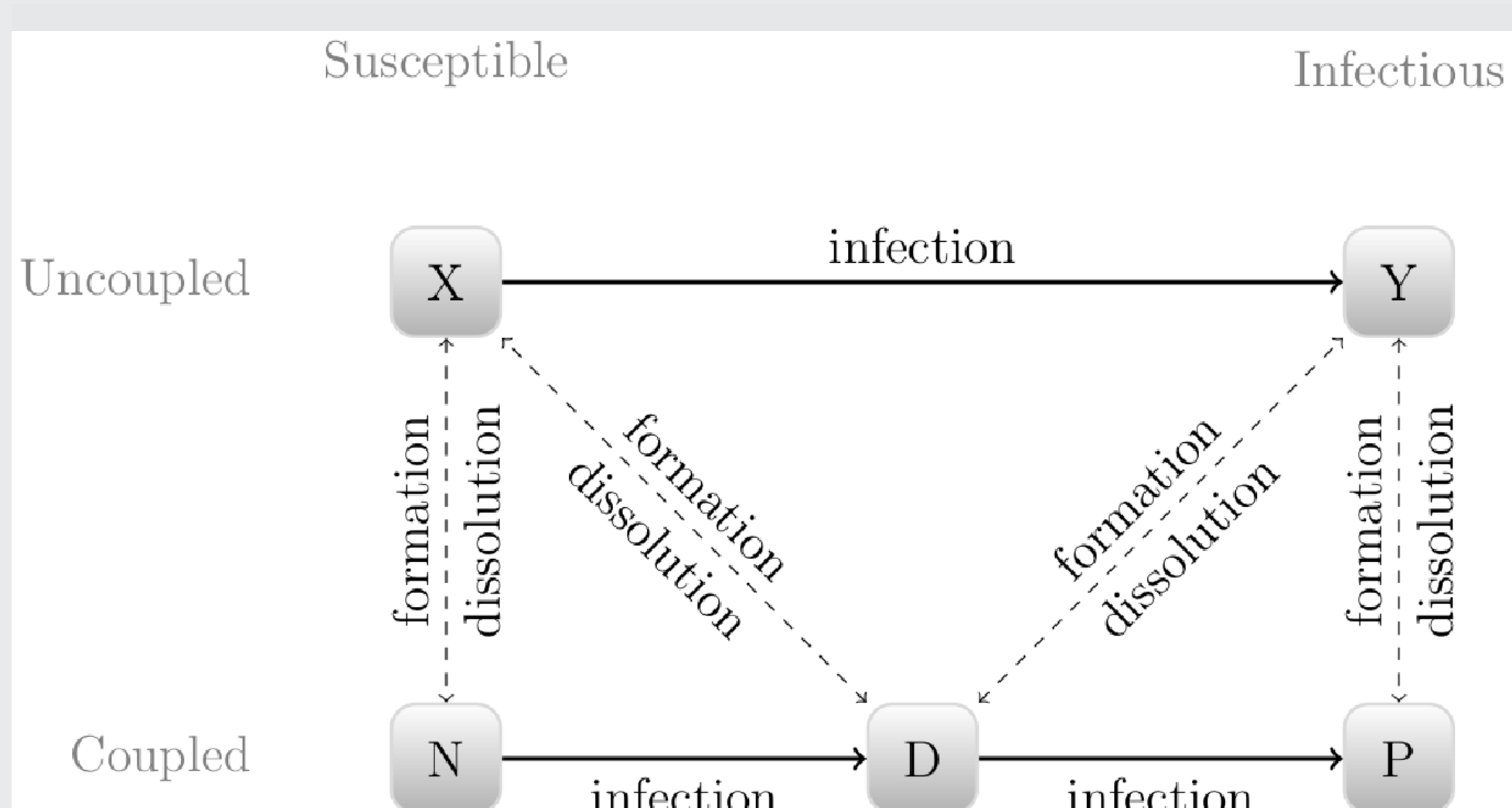
Champredon *et al.* 2013 [5]

Spectrum of model complexity:

- ▶ **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

Simplified disease model (single stage only)

Sampling strategy
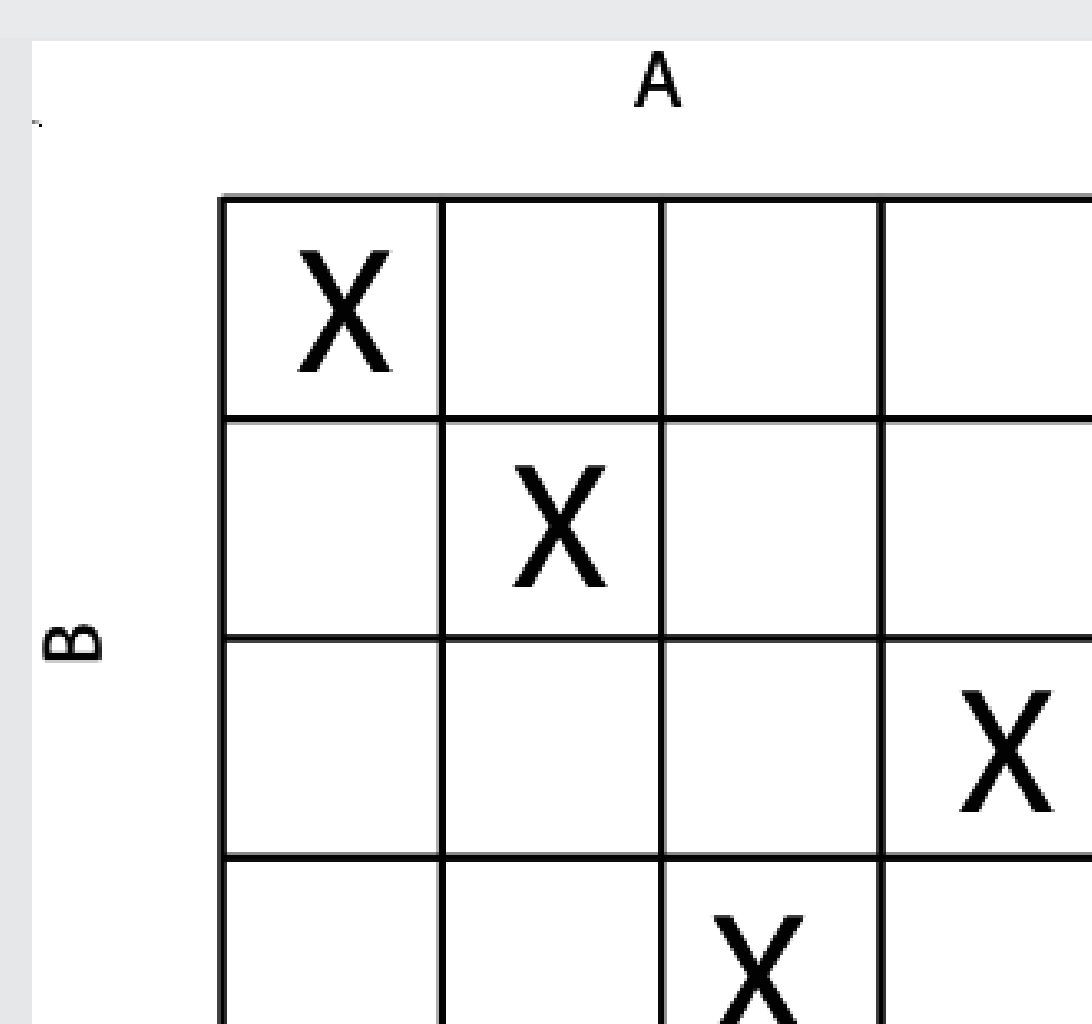

Eco-evolutionary dynamics
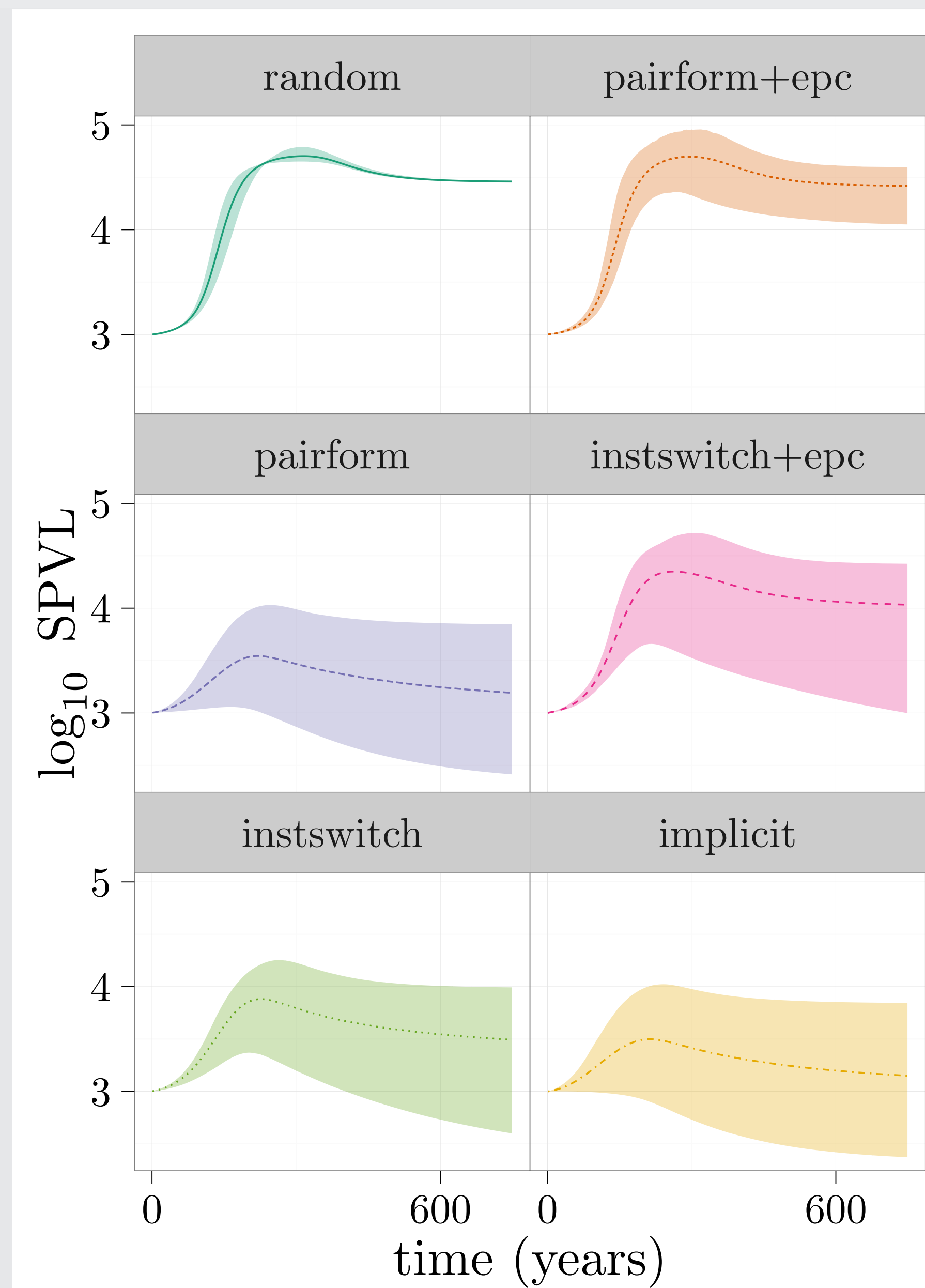
- ▶ significant variation across model structures
- ▶ least (random) and most (pairform+epc) models **most similar**: single individuals and extra-pair contact wash out effects of structure
- ▶ implicit model is **most different**
- ▶ random-mixing model underestimates (?) variability

Univariate summary

Sensitivity

model
— random
— pairform+epc
— pairform
— instswitch+epc
— instswitch
— implicit
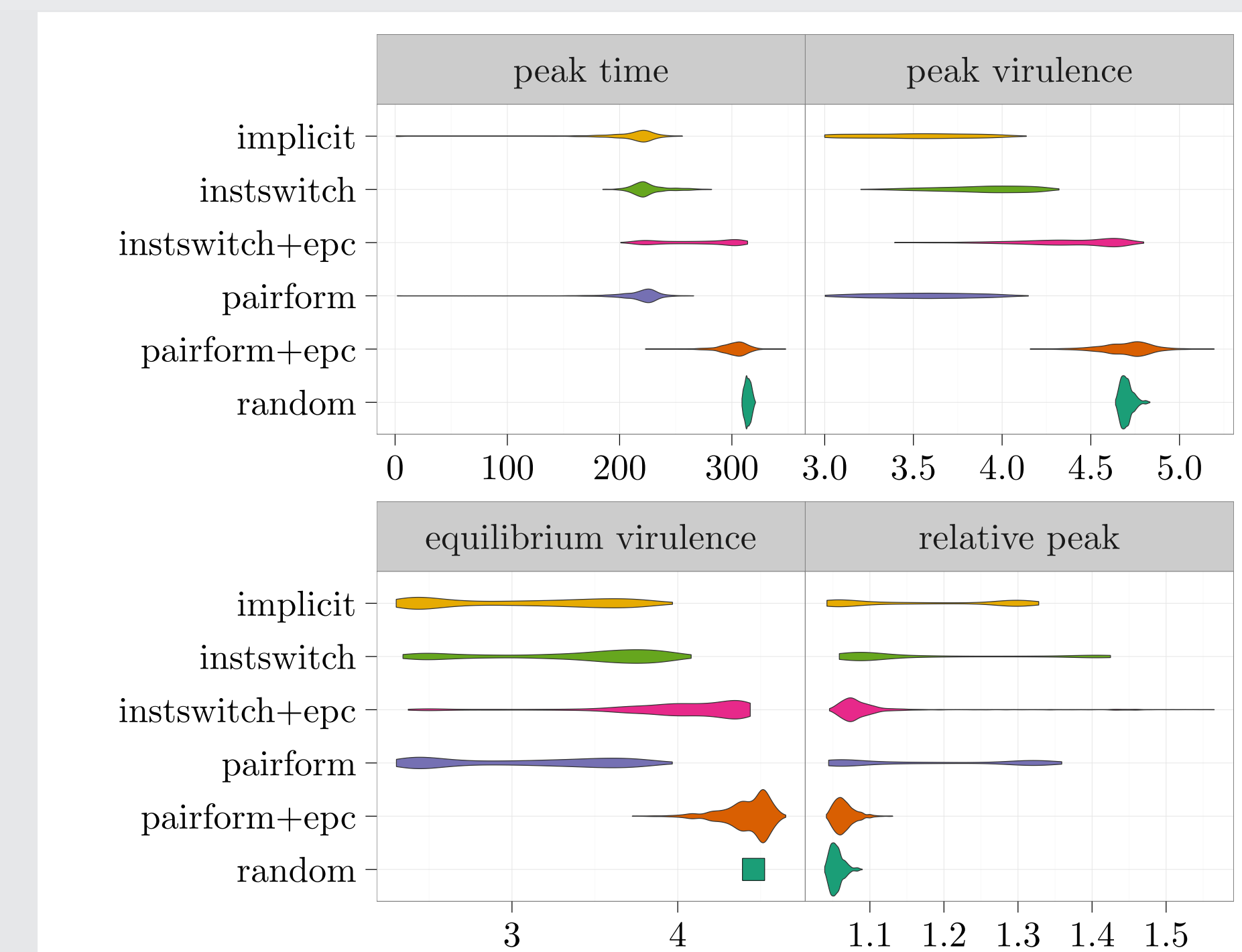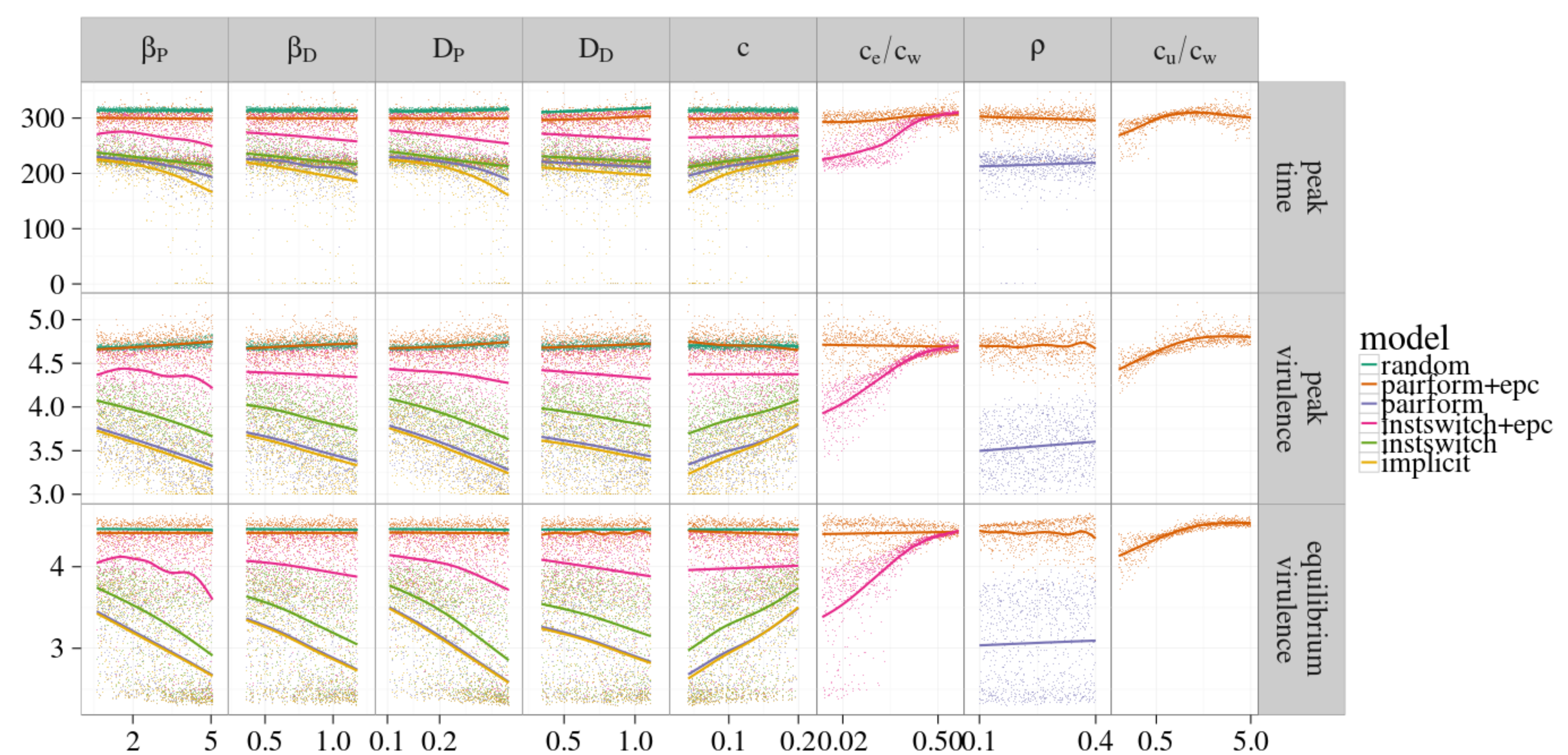
Conclusions and open questions

- ▶ Random-mixing models gave the closest match to the most realistic models; extra-pair contact washed out the effects of epidemiological structure
- ▶ Variation among models (model structure) ≈ variation within models (parameter uncertainty)
- ▶ Large differences in evolutionary dynamics among different epidemiological models suggest caution in predicting evolutionary responses

References

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[2] Alizon S, Michalakis Y. Adaptive virulence evolution: the good old fitness-based approach. Trends in Ecology & Evolution. 2015 Jan;30(5):248–254.

[3] Fraser C, Lythgoe K, Leventhal GE, Shirreff G, Hollingsworth TD, Alizon S, et al. Virulence and Pathogenesis of HIV-1 Infection: An Evolutionary Perspective. Science. 2014 Mar;343(6177):1243727.

[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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