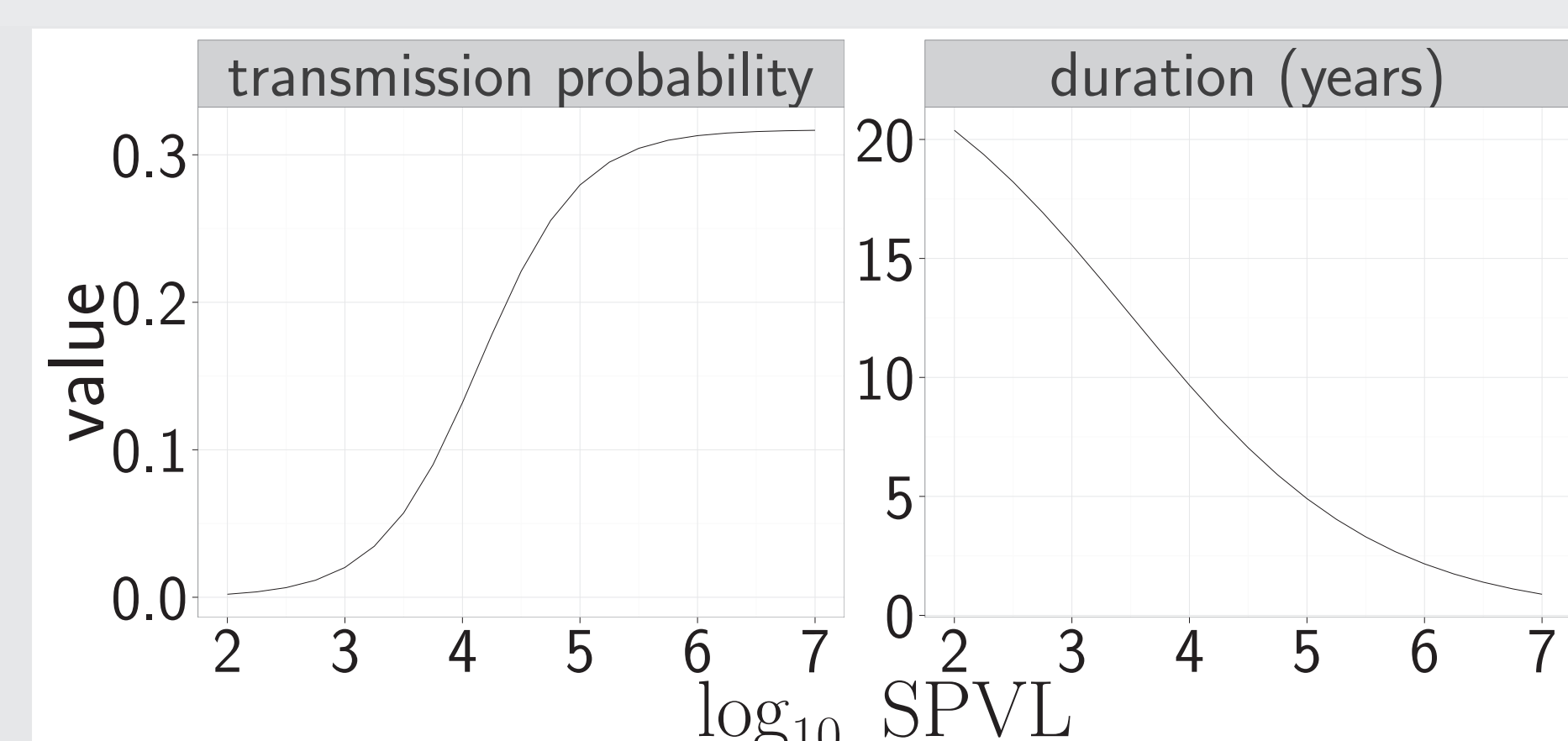


Summary

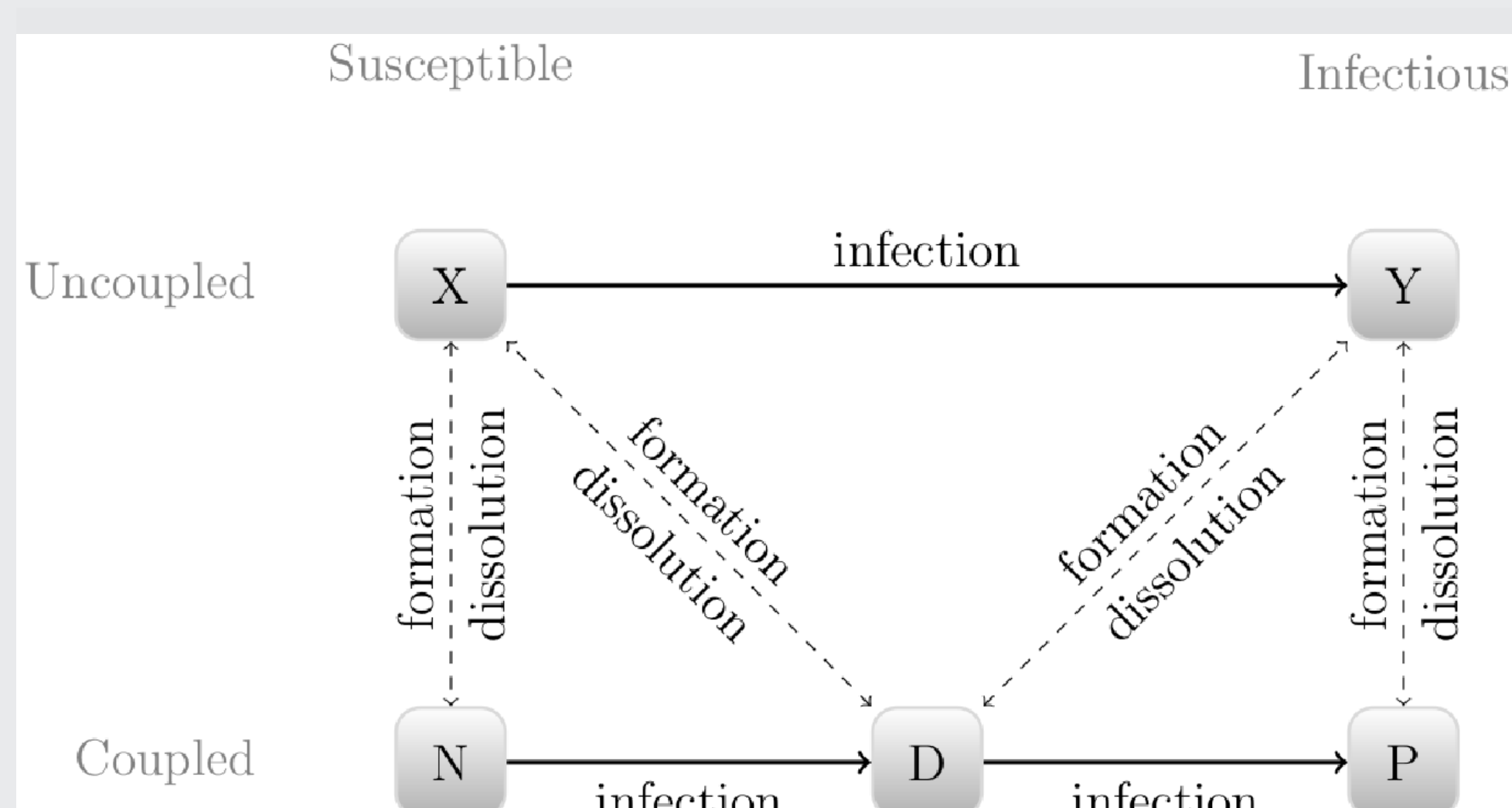
Pathogens can evolve rapidly in response to changing conditions (e.g., epidemic stage or public health interventions). Models of **eco-evolutionary dynamics** often neglect important epidemiological processes, such as the dynamics of sexual partnerships. We compared **models with a range of complexity**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

Tradeoff theory



- **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

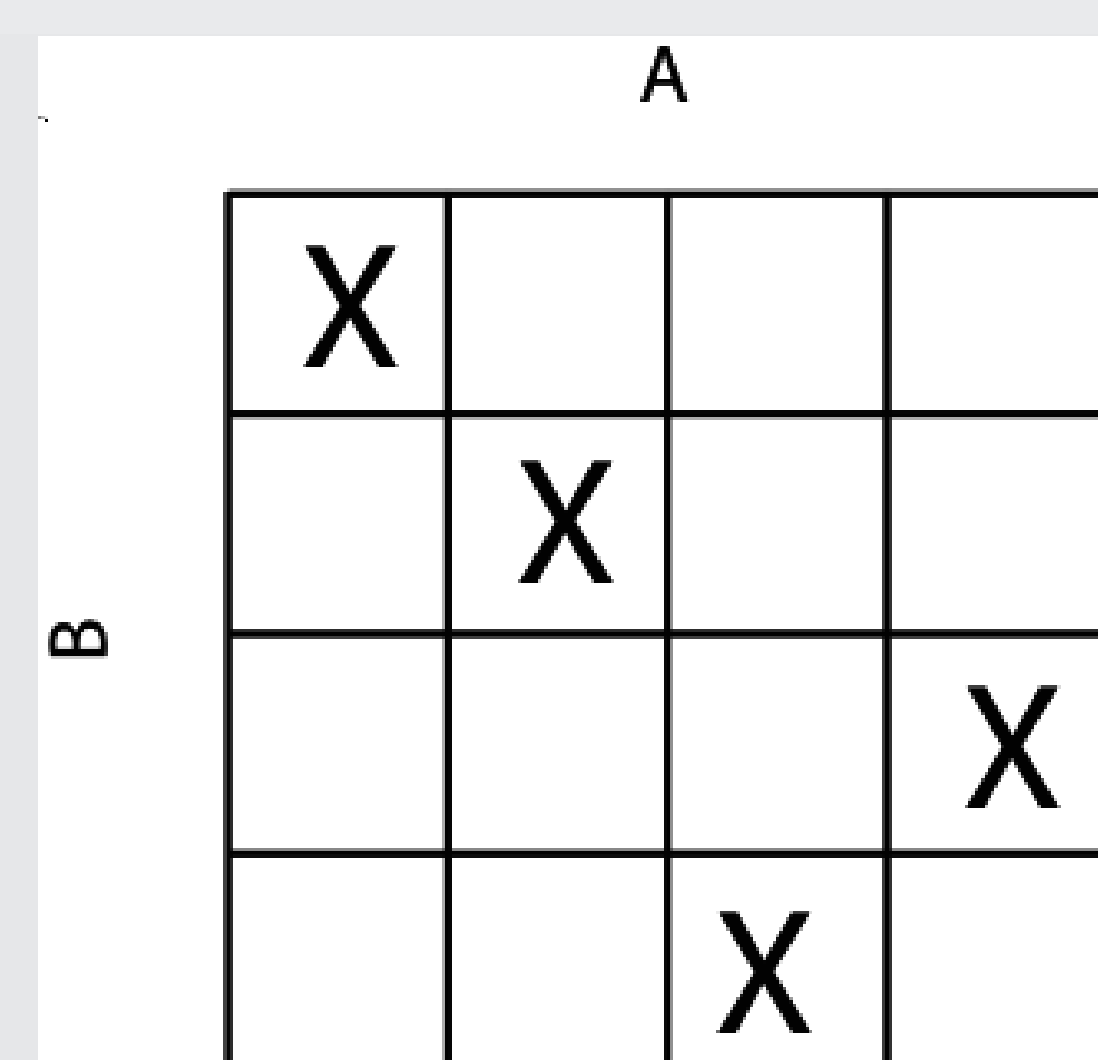


Champredon *et al.* 2013 [5]

Spectrum of model complexity:

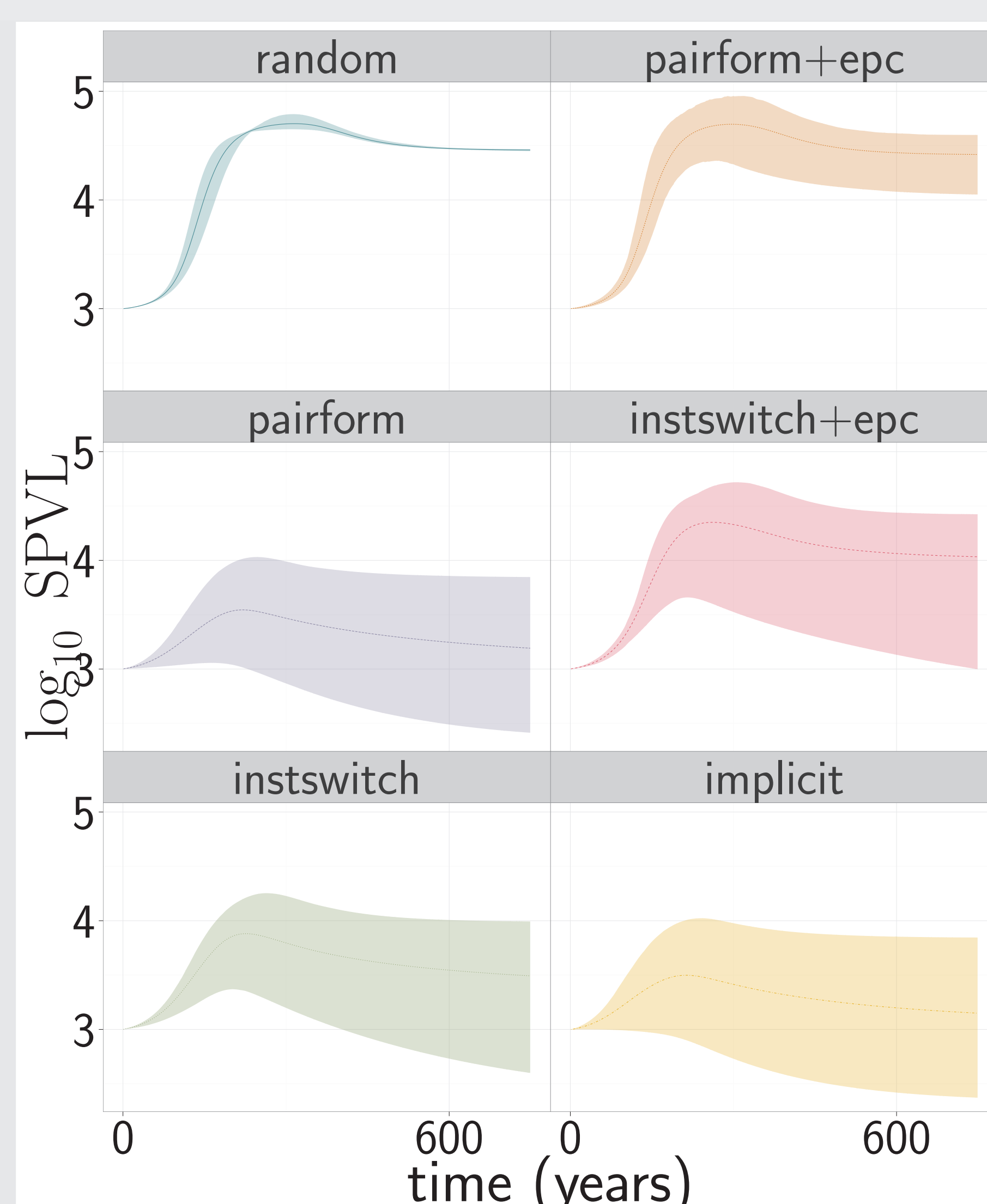
- **pair formation**: instantaneous or delayed?
 - **extra-pair contact (epc)**: present or absent?
 - **implicit model**: no explicit partnerships, force of infection expression derived from \mathcal{R}_0 of pair-formation model (without epc)
 - **random-mixing model**: standard SIR model
- Simplified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

Sampling strategy



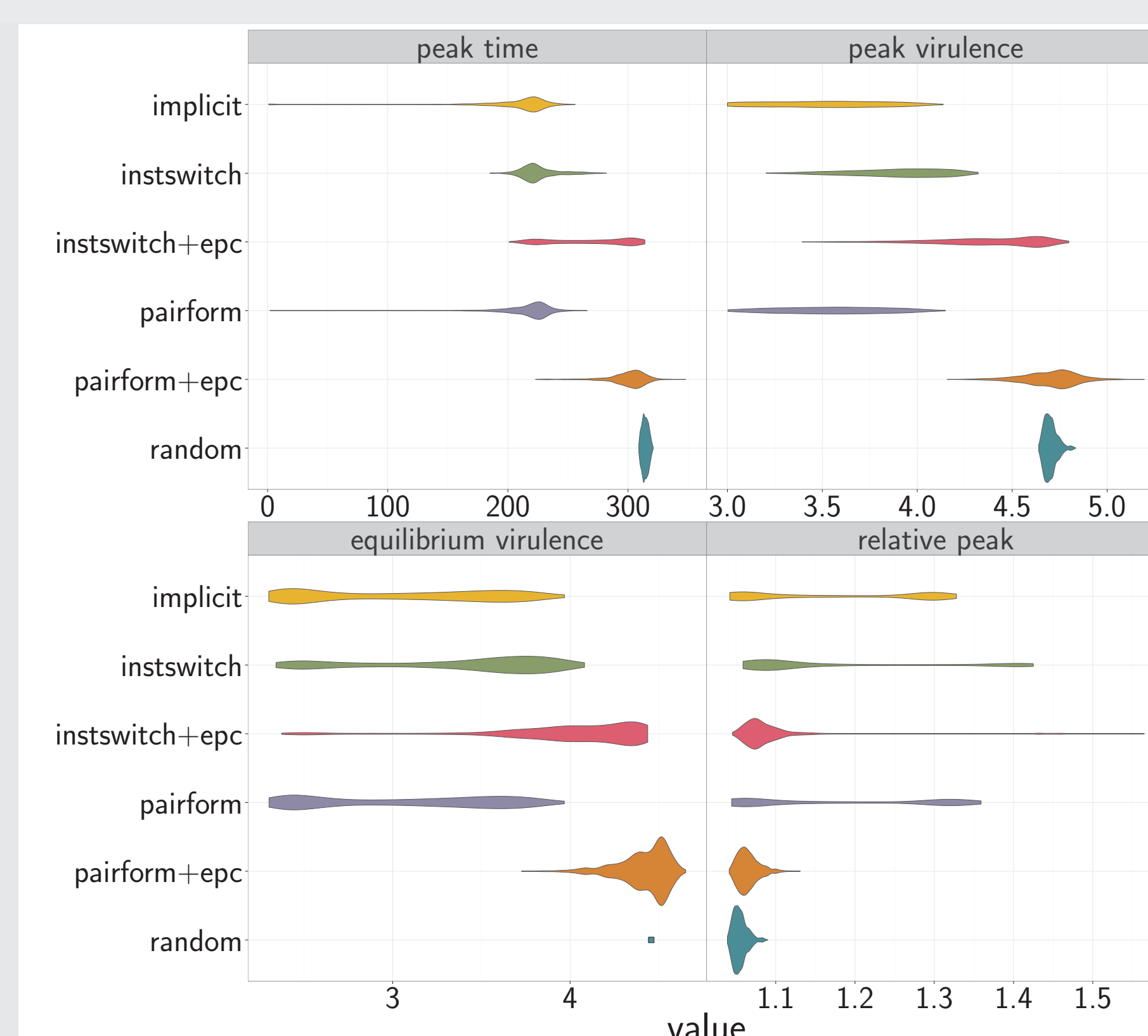
- Latin hypercube sampling: parameters from [5]
- parameters calibrated across models to the same **initial epidemic growth rate (r)**

Basic eco-evolutionary dynamics

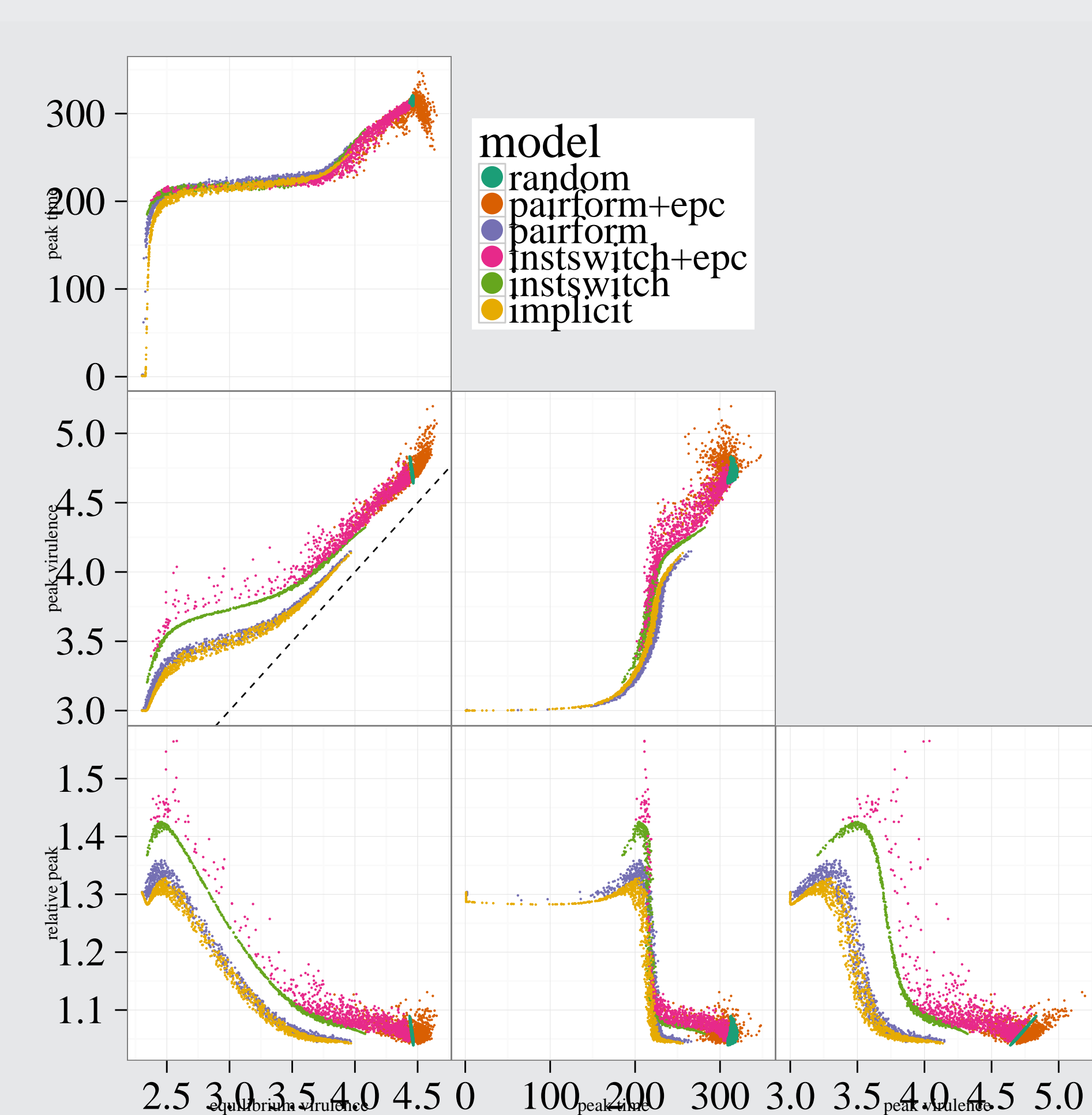


- significant variation across model structures
- least (random) and most (pairform+epc) models **most similar**: single individuals and extra-pair contact wash out effects of structure
- implicit model is **most different**
- random-mixing model underestimates (?) variability

Univariate summary



Bivariate summary



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) \approx variation within models (parameter uncertainty)
- Large differences in evolutionary dynamics among different epidemiological models suggest caution in predicting evolutionary responses

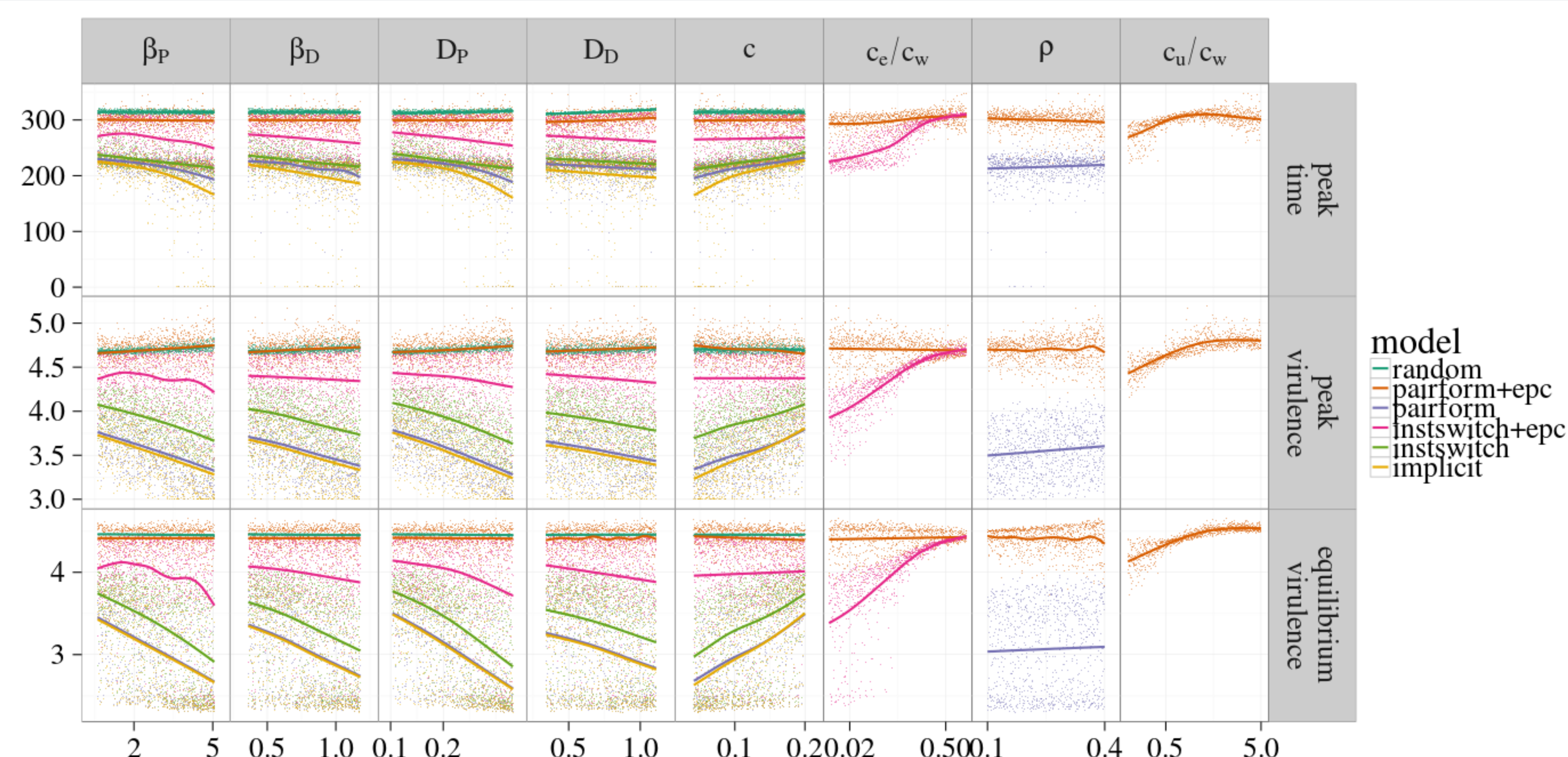
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Acknowledgements

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Sensitivity



model
— random
— pairform+epc
— pairform
— instswitch+epc
— instswitch
— implicit