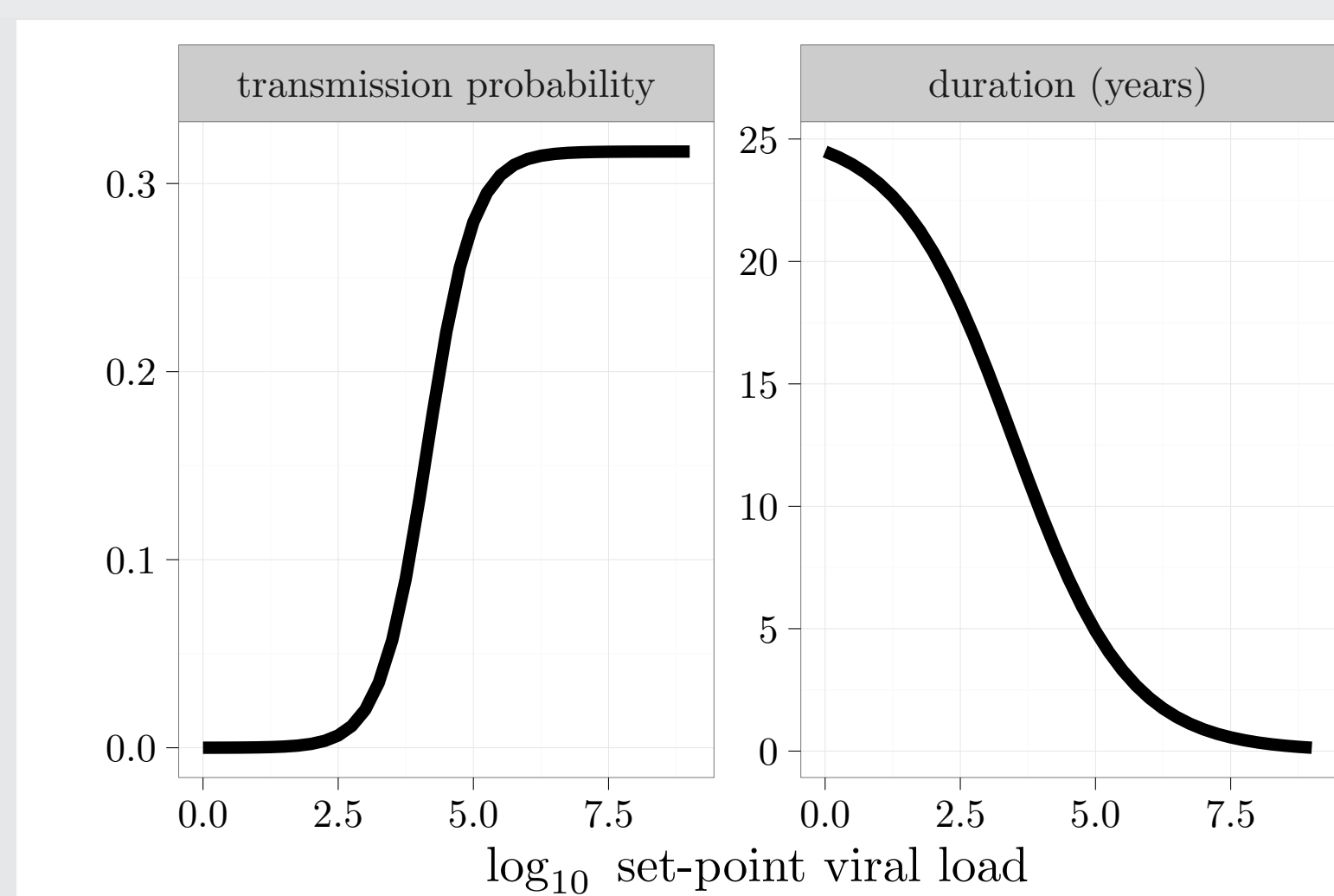




## Summary

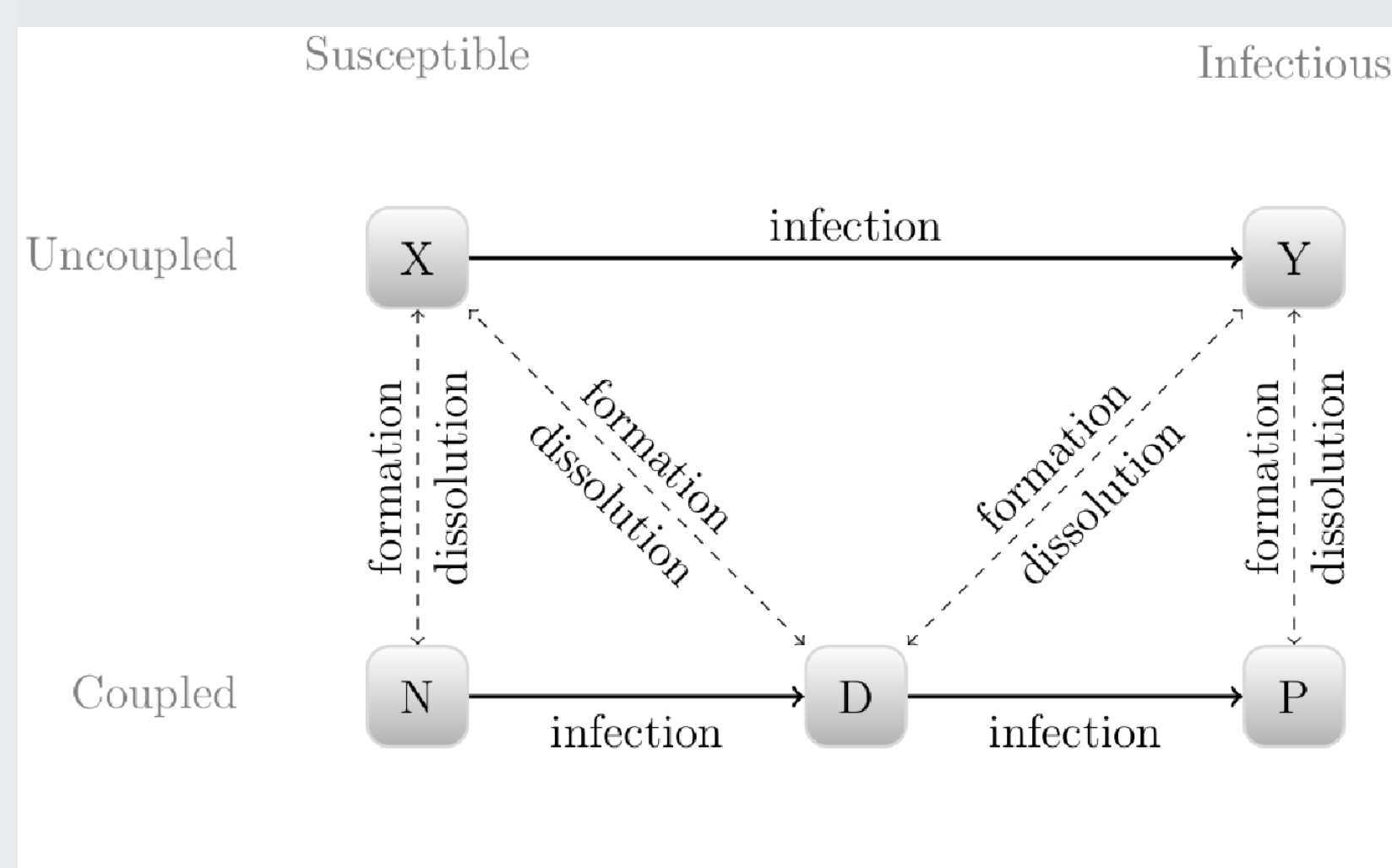
Pathogens can evolve rapidly in response to changing conditions (e.g., epidemic stage or public health interventions). Models of **eco-evolutionary dynamics** often neglect important epidemiological processes, such as the dynamics of sexual partnerships. We compared **models with a range of complexity**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



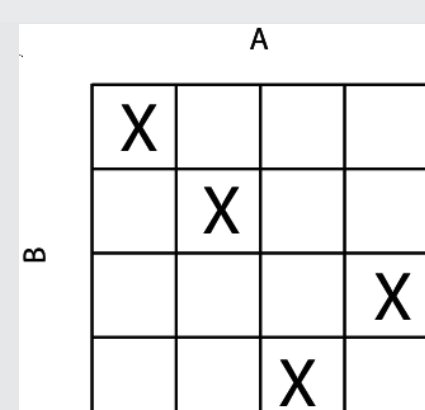
Champredon *et al.* 2013 [5]

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

Simplified disease model (single stage only)

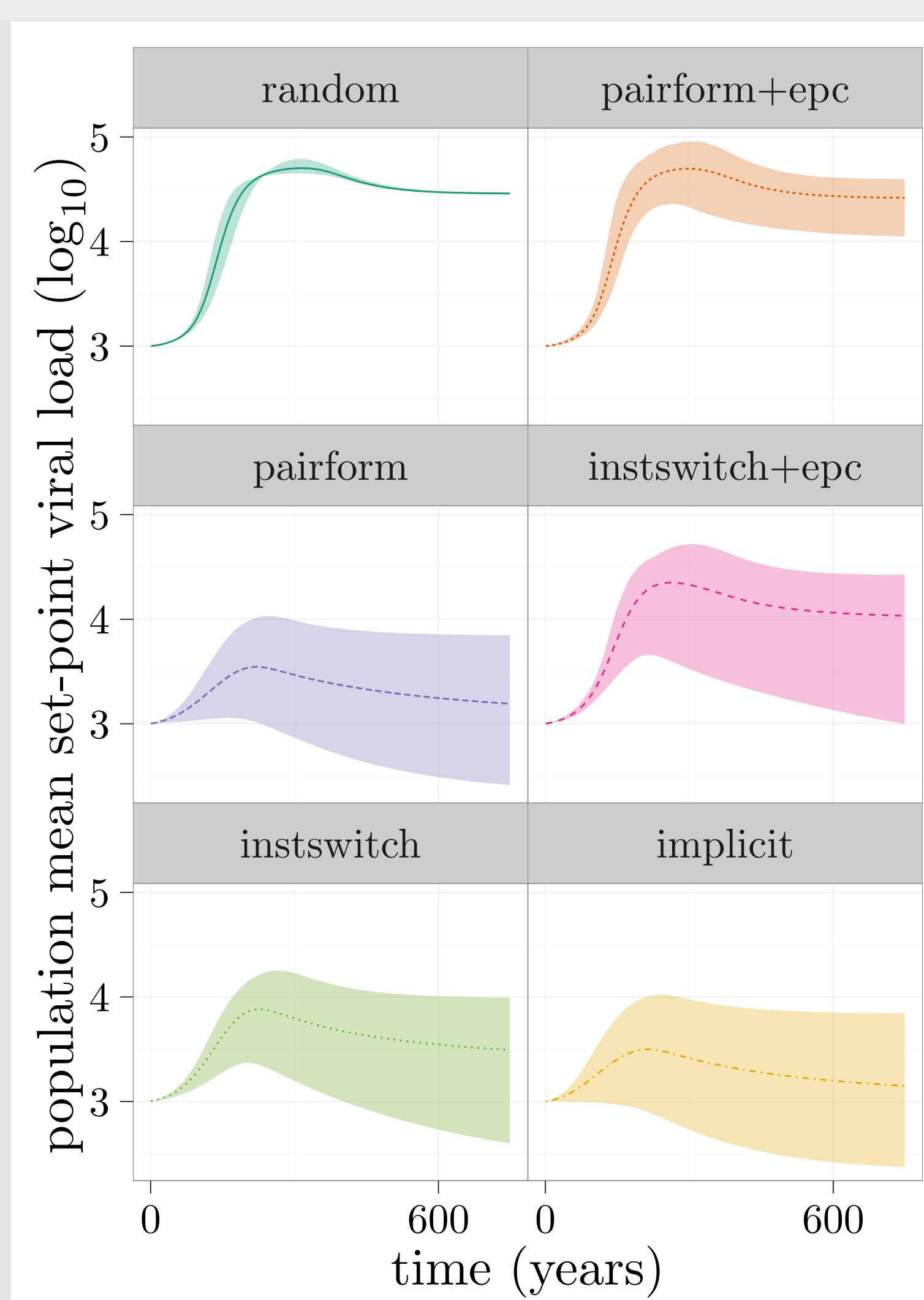
- ▶ **pair formation**: instantaneous or delayed?
- ▶ **extra-pair contact** (epc): present or absent?
- ▶ **implicit model**: no explicit partnerships, force of infection expression derived from  $R_0$  of pair-formation model (without epc)
- ▶ **random-mixing model**: standard SIR model

## Parameter uncertainty/exploration



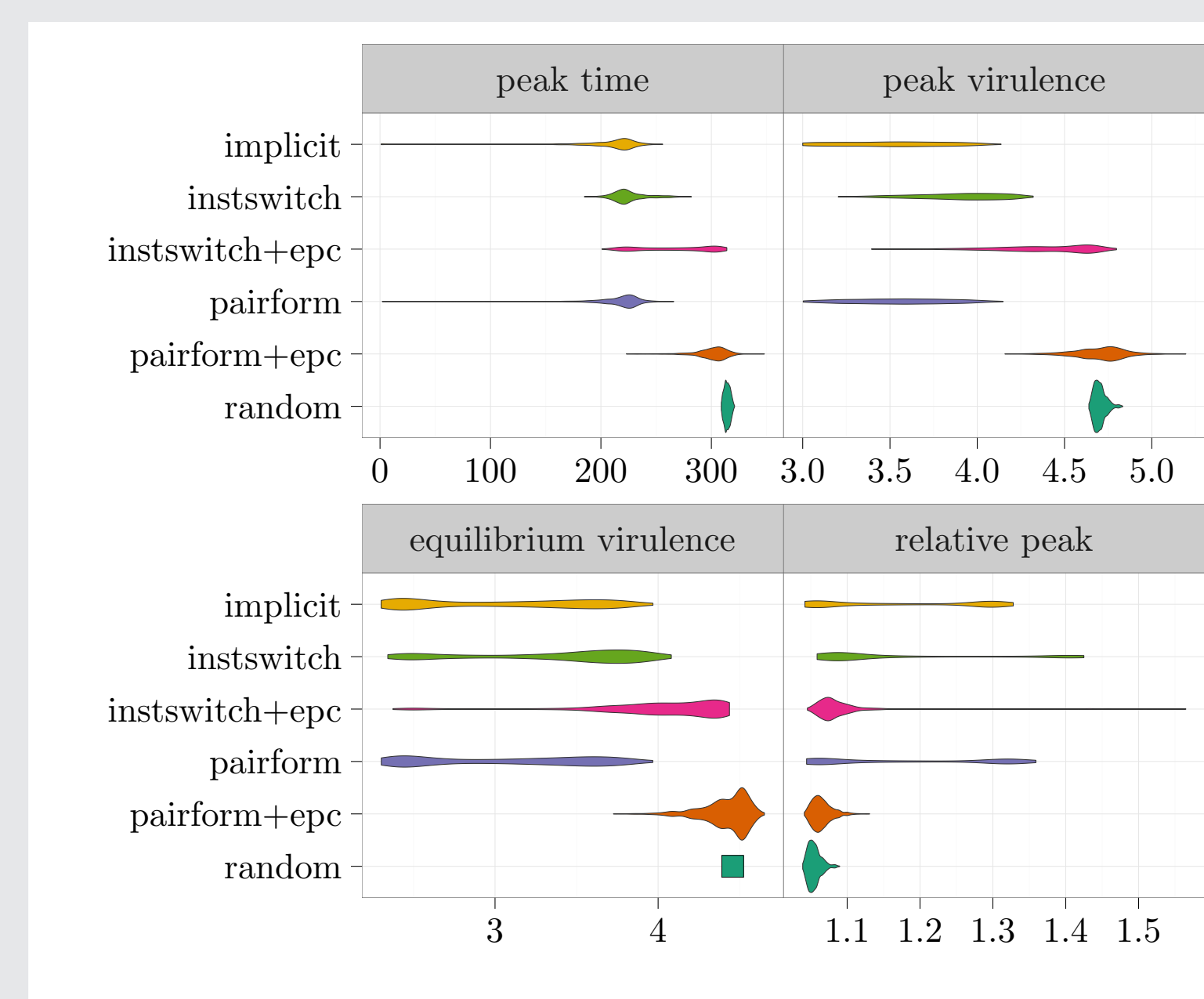
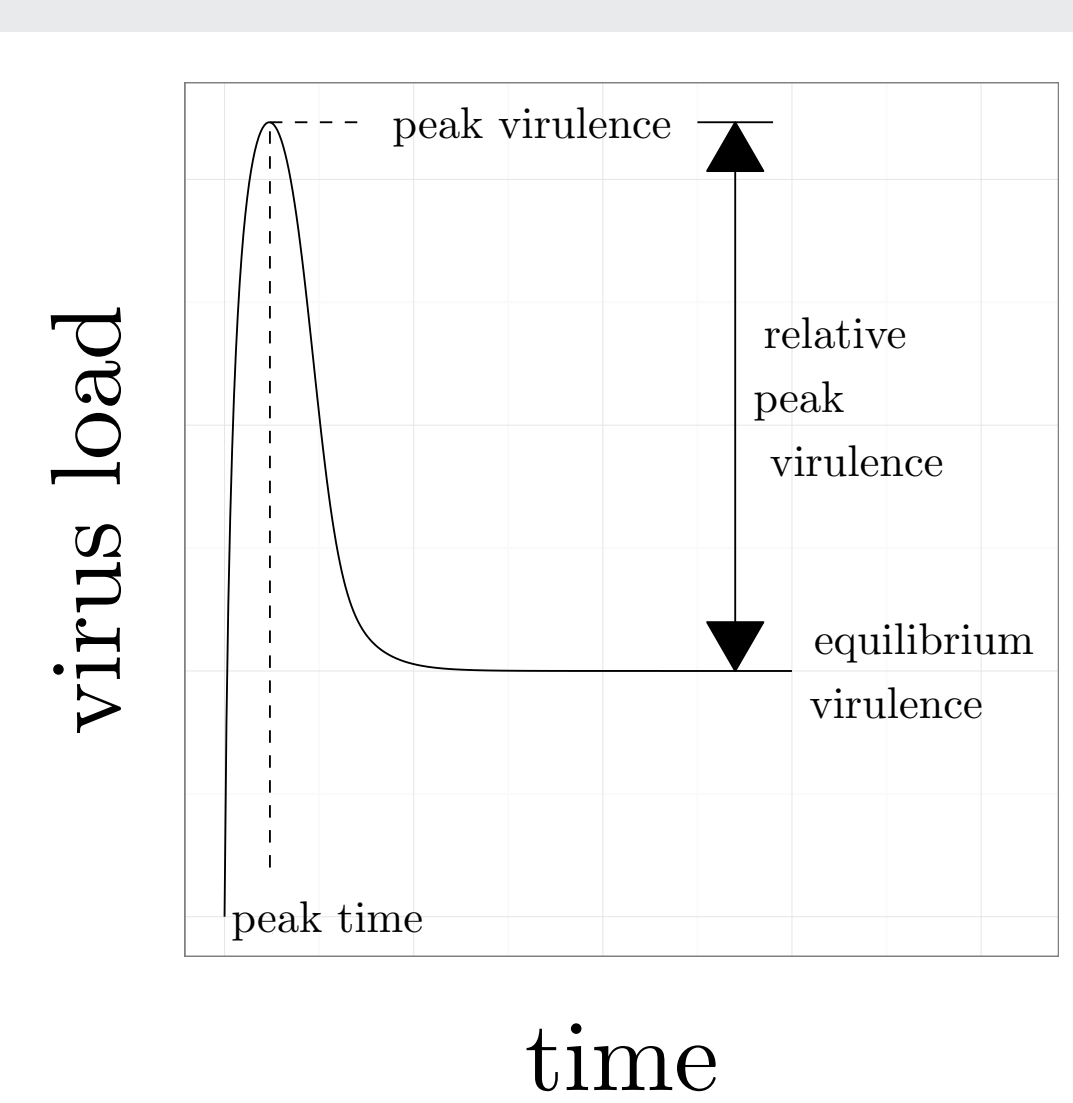
- ▶ Latin hypercube sampling: parameters from [5]
- ▶ parameters calibrated across models to the same **initial epidemic growth rate** ( $r$ )

## Eco-evolutionary dynamics



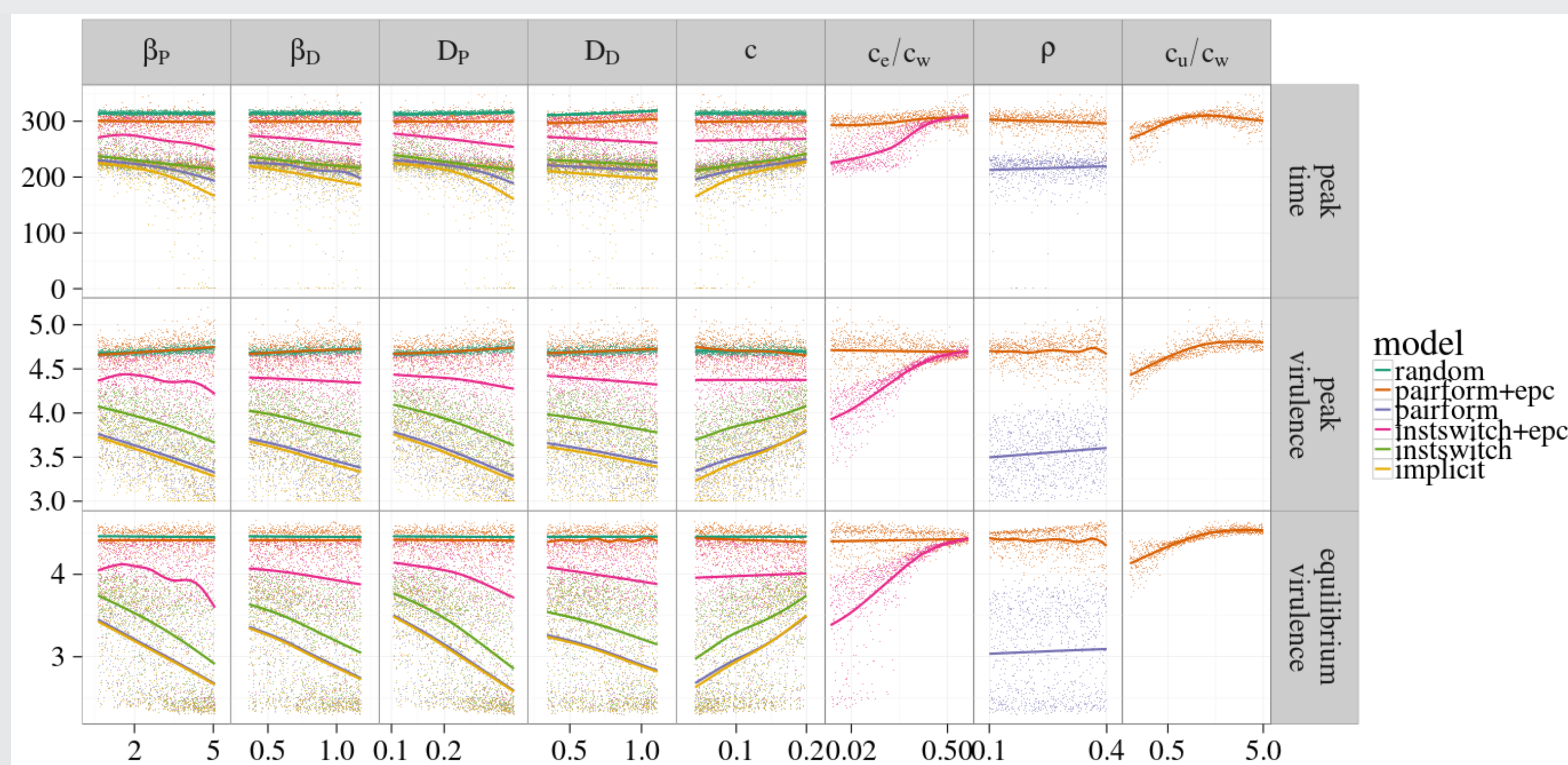
- ▶ **80% of total variability** in peak SPVL is among- vs. within-model
- ▶ least (random) and most (pairform+epc) models **most similar**: single individuals and extra-pair contact wash out effects of structure
- ▶ random-mixing model underestimates variability

## Univariate summaries



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

## Sensitivity



- ▶  $\beta_{P,D}$ : 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

## 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)  $\gtrsim$  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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## Acknowledgements

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