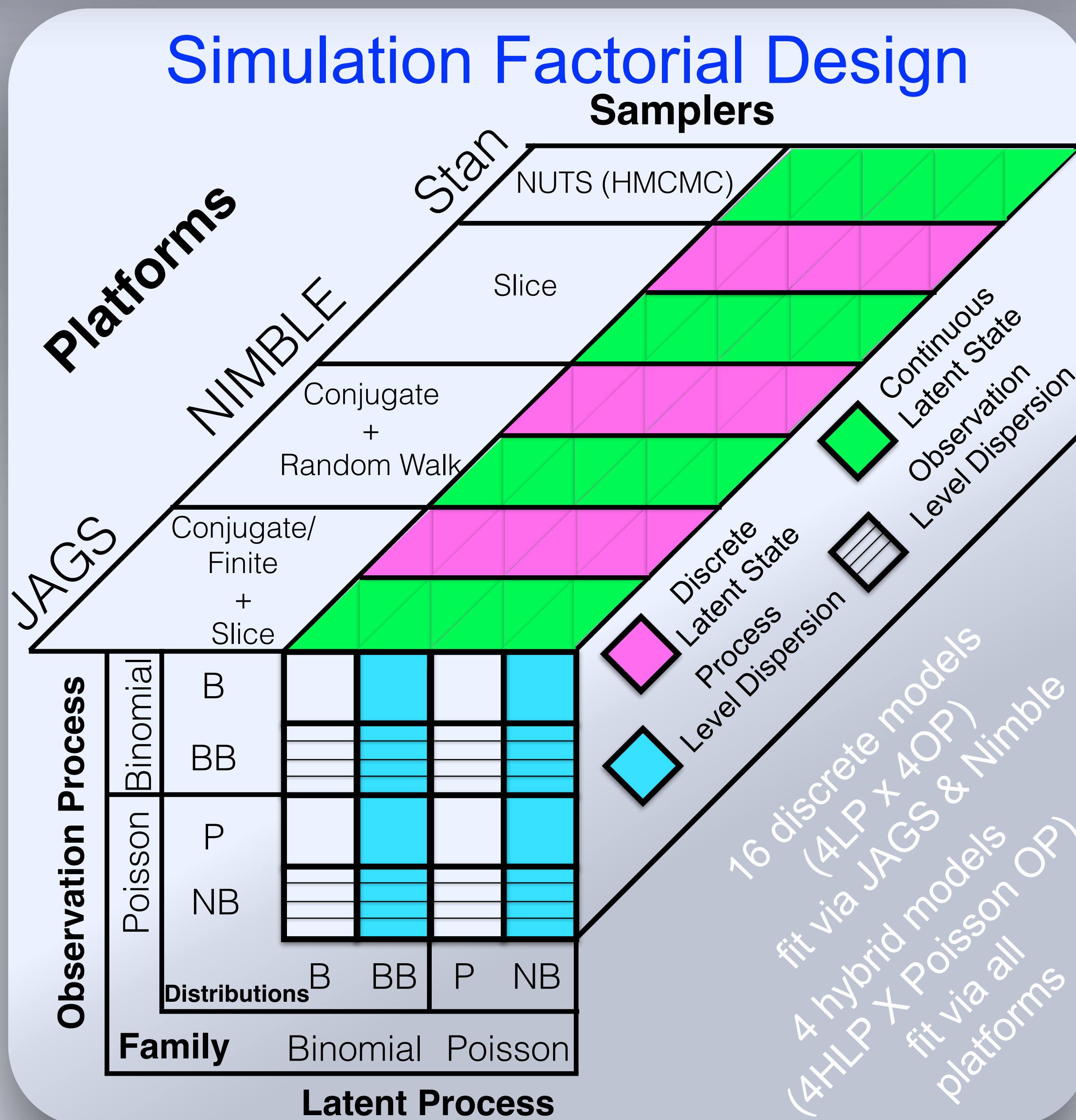


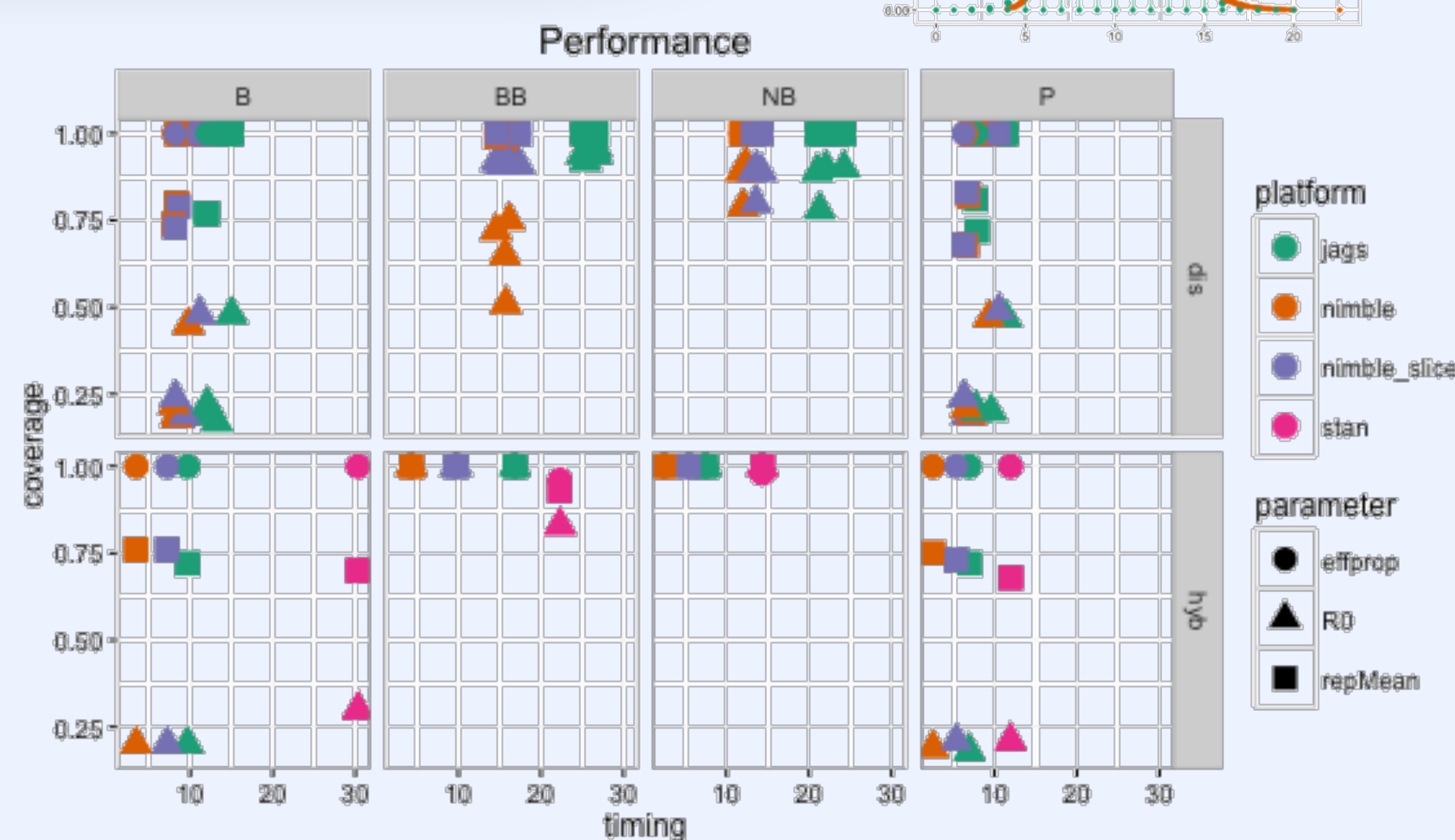
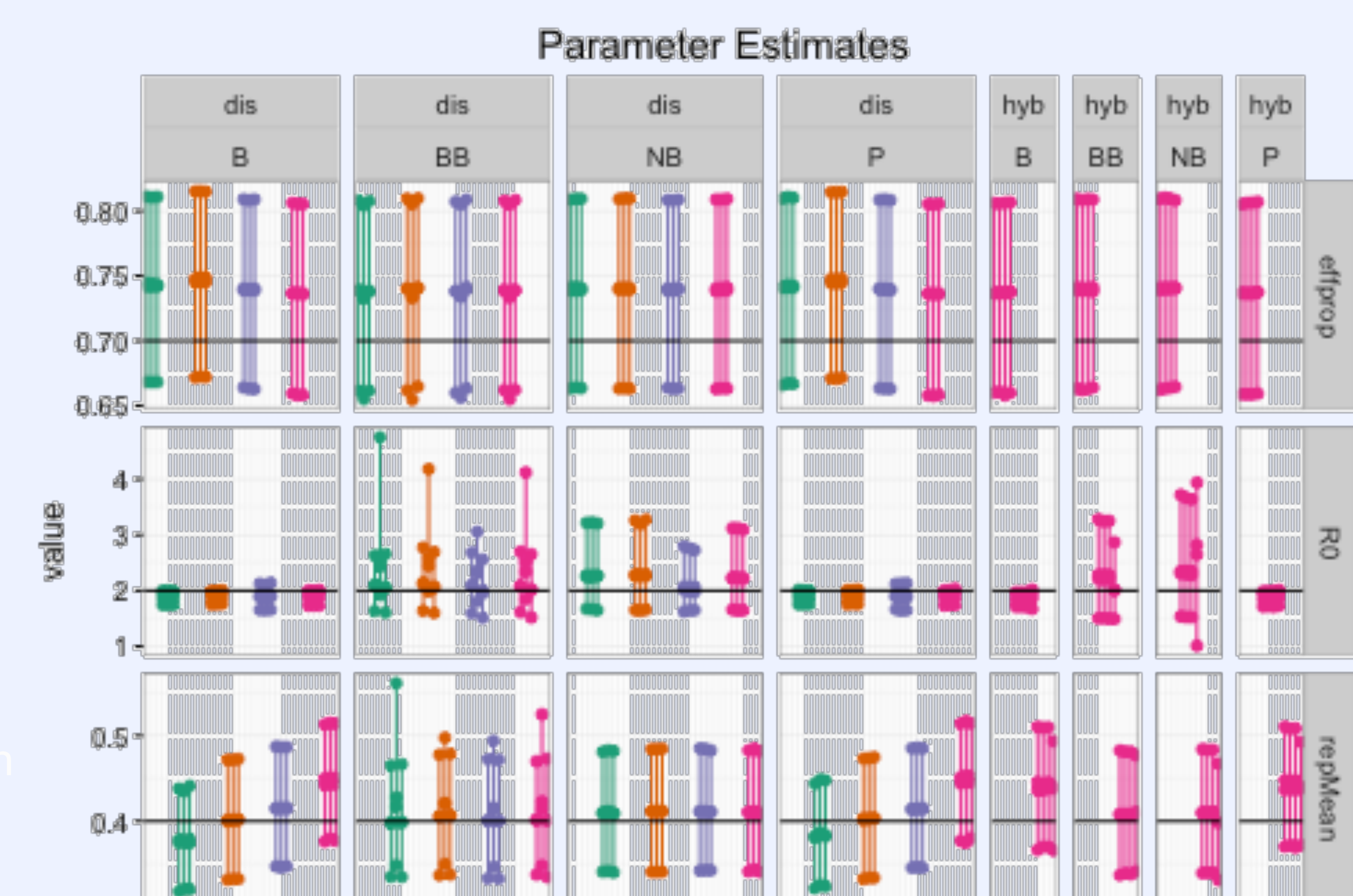
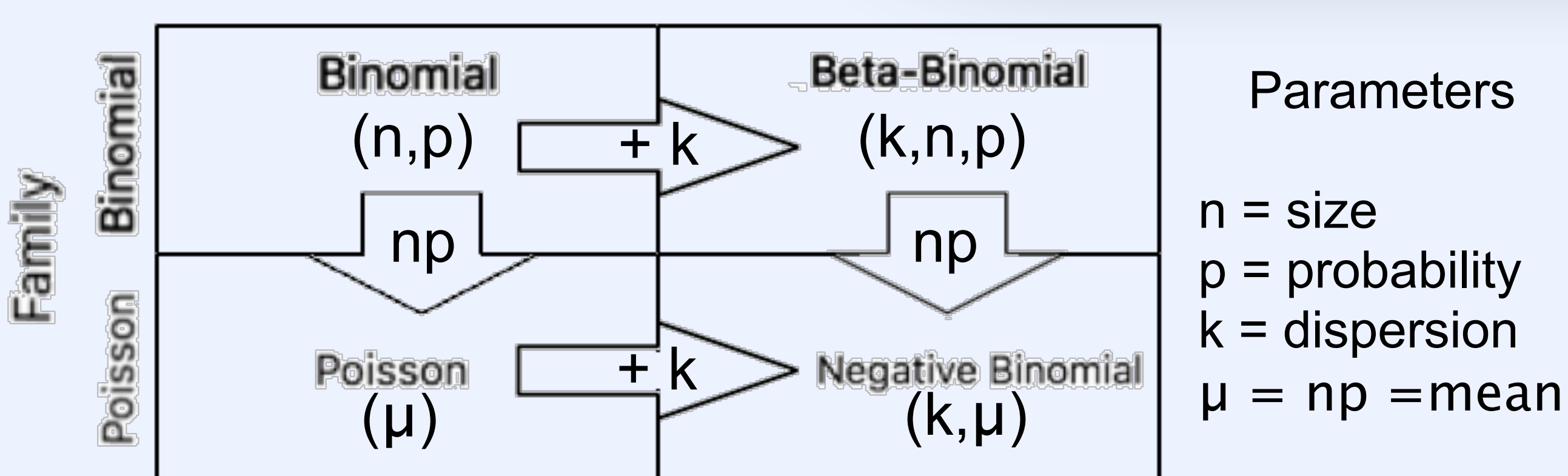
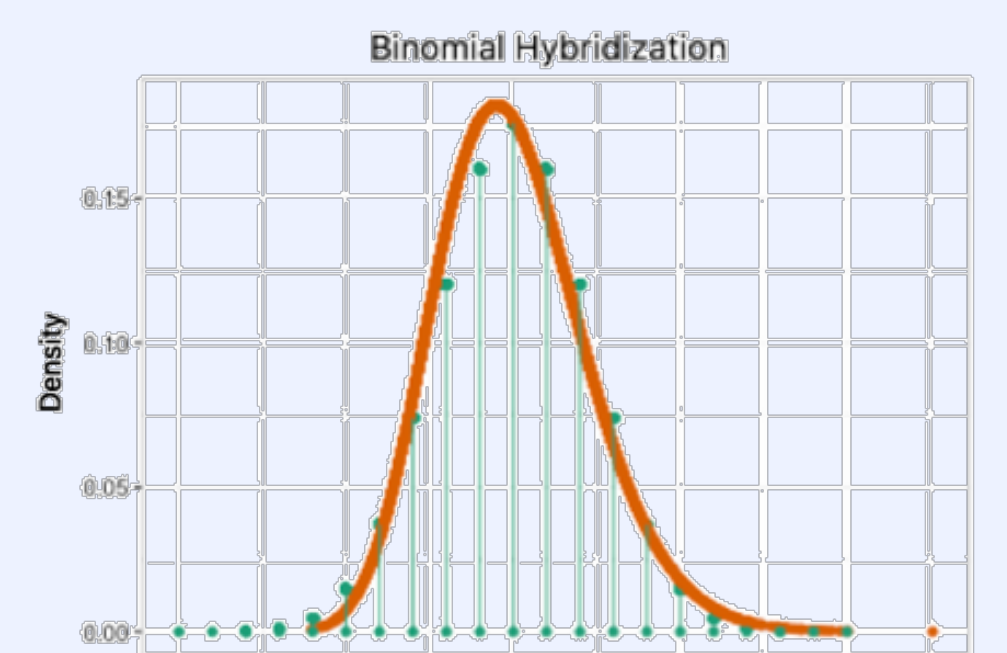
Overview

Mathematical and statistical models are widely used in studying emerging infectious disease outbreaks (e.g., forecasting, planning or evaluating interventions), and yet, we have relatively little solid evidence about the comparative performance of standard computational-statistical frameworks in these contexts. Using the classic stochastic Reed-Frost epidemic model as a baseline, we characterize and explore tradeoffs in computational efficiency and estimation accuracy among different flavours of Markov chain Monte Carlo (MCMC) estimation.

Methods



- JAGS uses conjugate sampling when possible, and discrete/real slice samplers otherwise.
- NIMBLE is a more recent high performance platform that has a variety of discrete and real samplers (Random-walk (RW), RW block, slice, elliptical slice, cross level)
- Stan uses a powerful modern MCMC technique (Hamiltonian MCMC) that CANNOT be used with discrete latent states and it does not have a discrete sampler (eg. slice)
- We **hybridize** discrete distributions in the model with continuous analogues with equivalent 1st and 2nd moments



Conclusion

- Hybridizing via moment matching can overcome discrete-variable obstacles
- Hybridizing also improved overall performance without losing accuracy in JAGS and NIMBLE