

Overcoming Model Misspecification in Bayesian Inference of Molecular Signalling Networks

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Abstract

Bayesian inference of molecular signalling networks usually relies on tractability of the marginal likelihood, enabling the set of possible networks to be efficiently explored. As such, linear models with independent errors and conjugate priors are routinely used. However, the dynamics of molecular signalling are nonlinear, and relevant confounders are often unobserved; failure to account for these complexities will almost certainly lead to over-confident inferences in the standard Bayesian framework. To confront this reality, we develop a post-Bayesian approach to inference of molecular signalling networks, guided by the principle that uncertainty should not vanish when the statistical model is misspecified, even in the infinite-data limit. Technically, we extend the predictively-oriented (PrO) posterior of McLatchie et al. (2025) to the setting of latent variable models, empirically investigating the properties of PrO posteriors in the challenging network inference context.

This is joint work with Yinghan Li, Heishiro Kanagawa, Francesca Romana Crucinio, and Matthew A. Fisher.

Keywords: postBayes, neural SBI, multi-level Monte Carlo.

Reference:

Y. Li, H. Kanagawa, F. R. Crucinio, M. A. Fisher, C. J. Oates. Overcoming Model Misspecification in Bayesian Inference of Molecular Signalling Networks. Preprint at arXiv: 2609.24590, 2026.