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# Bayesian inference for synaptic connectivity rules in anatomically realistic cortical connectomes

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A key goal in connectomics research is to discover local synaptic connectivity rules which can explain the global organization of cortical circuits. Identifying and selecting such rules remains a challenging problem, as even advanced experimental techniques can only provide partial measurements of neural circuits.

We approach identification and selection of synaptic connectivity rules as a Bayesian inference problem: Given partial measurements of structural features at different scales, we use Bayesian inference to identify which parameters of synaptic connectivity models are quantitatively consistent with experimental observations.

One challenge of applying these approaches is the fact that the underlying models might not be tractable with conventional Bayesian approaches: In particular, when models are defined only indirectly through a complex simulator, or are constrained by aggregate data, it is often impossible to compute the likelihood  $p(x|\theta)$  of the data  $x$  given model parameters  $\theta$ . In contrast to classical likelihood-free approaches, recent advances based on conditional density estimation [1, 2, 3] can scale to high-dimensional observations. We use automatic posterior transformation (APT) [3] to estimate the posterior distribution of the parameters of hypothesized synaptic connectivity rules, given observed connectivity measurements.

We illustrate the approach on a dense structural model of the rat barrel cortex. This model is based on anatomical measurements of geometry, soma distributions, and morphologies [4]. We perform inference on a synaptic connectivity rule that predicts the presence of synapses based on pre- and postsynaptic target densities. In the tractable case of a small sub-volume with fully observed synapse counts the posterior is estimated accurately. When using only empirically measured connection probabilities the resulting posterior successfully reveals the underlying rule parameters and how they are constrained by the observed data.

By scaling this inference to larger sub-volumes and by enabling the comparison of hypothesized synaptic connectivity rules, we will ultimately provide tools to relate structural features of neuronal networks to the underlying synaptic organization.

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