

# Overcoming model limitations via empirically-tuned parameters

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## Motivation

- Even the best neuron population models are still only **approximations** of biological processes.
- **Statistical inference** is already used to fit phenomenological models to data.

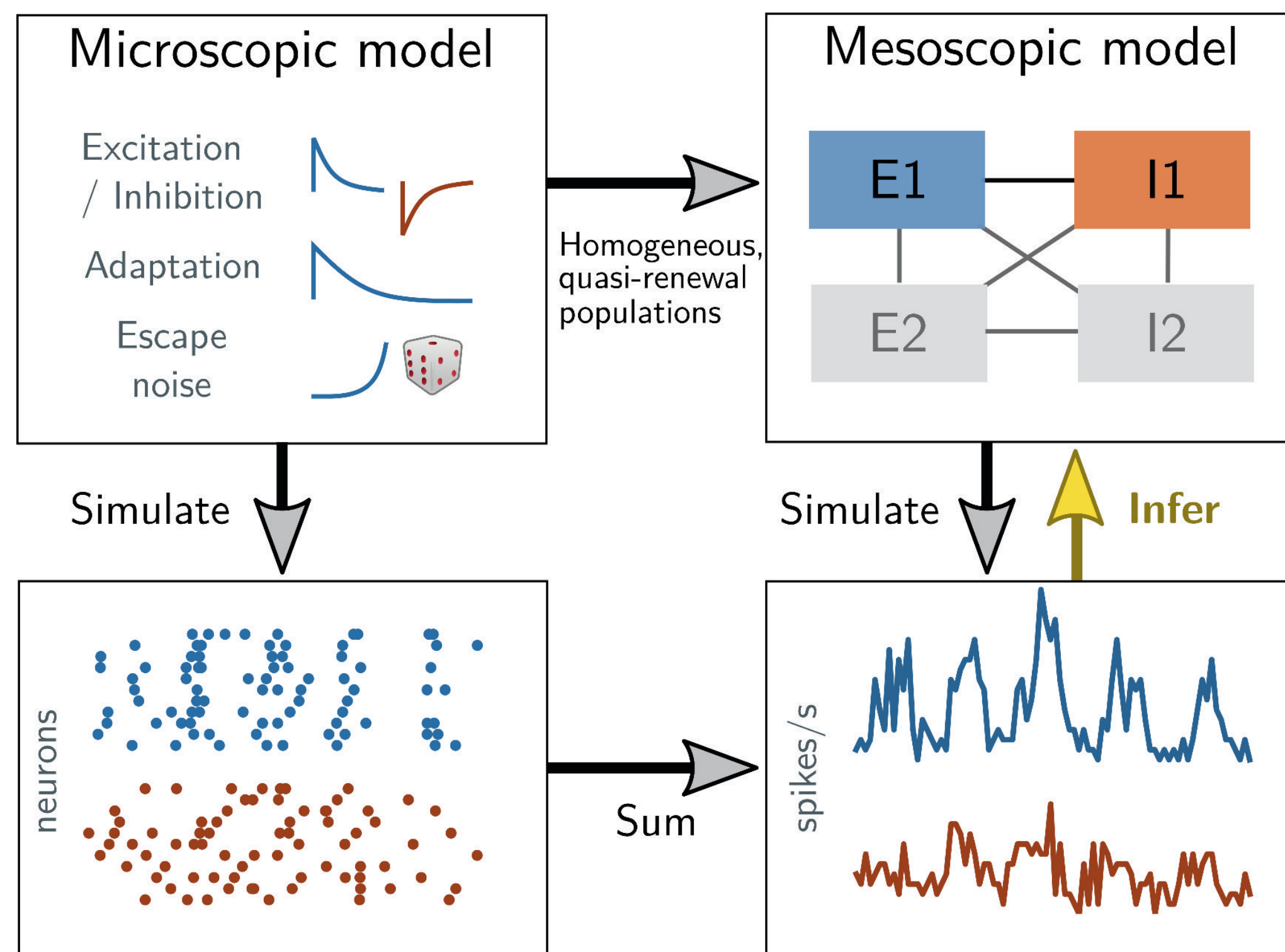
- We can **compensate** for approximations by extending statistical inference to mechanistic models.

- This allows us to combine the **interpretability** of mechanistic models with the **predictive power** of data-driven models.

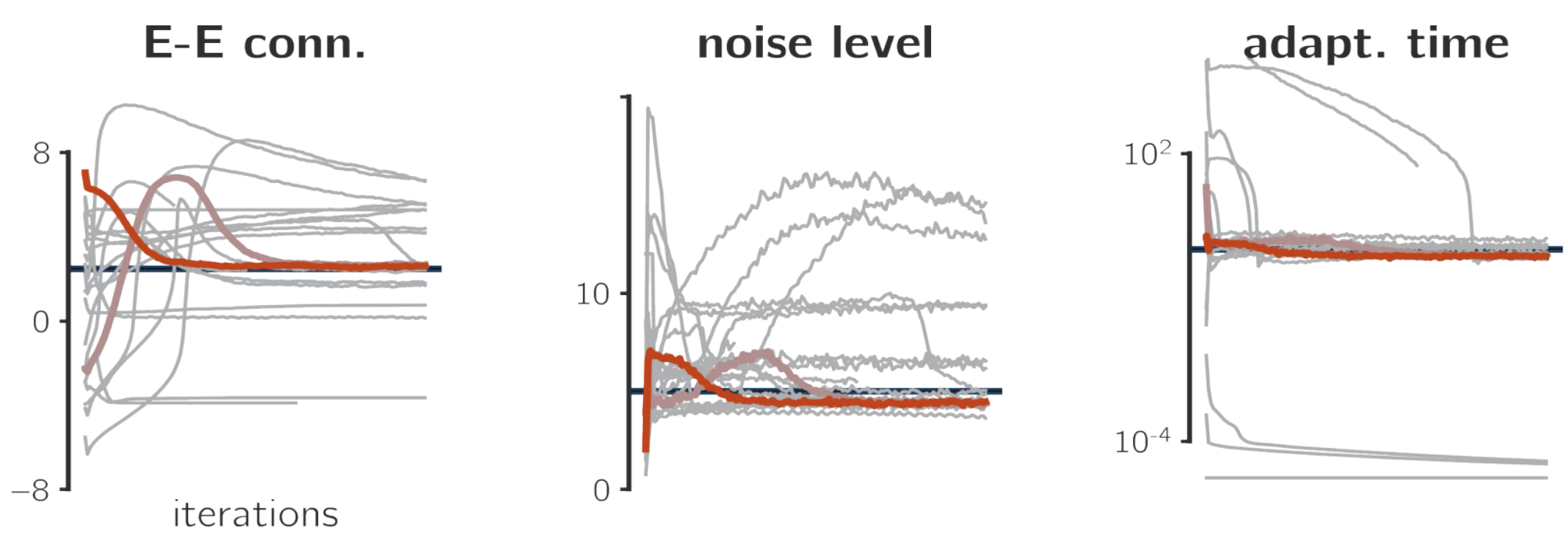
## Approach

Choose data and model with known mismatch:

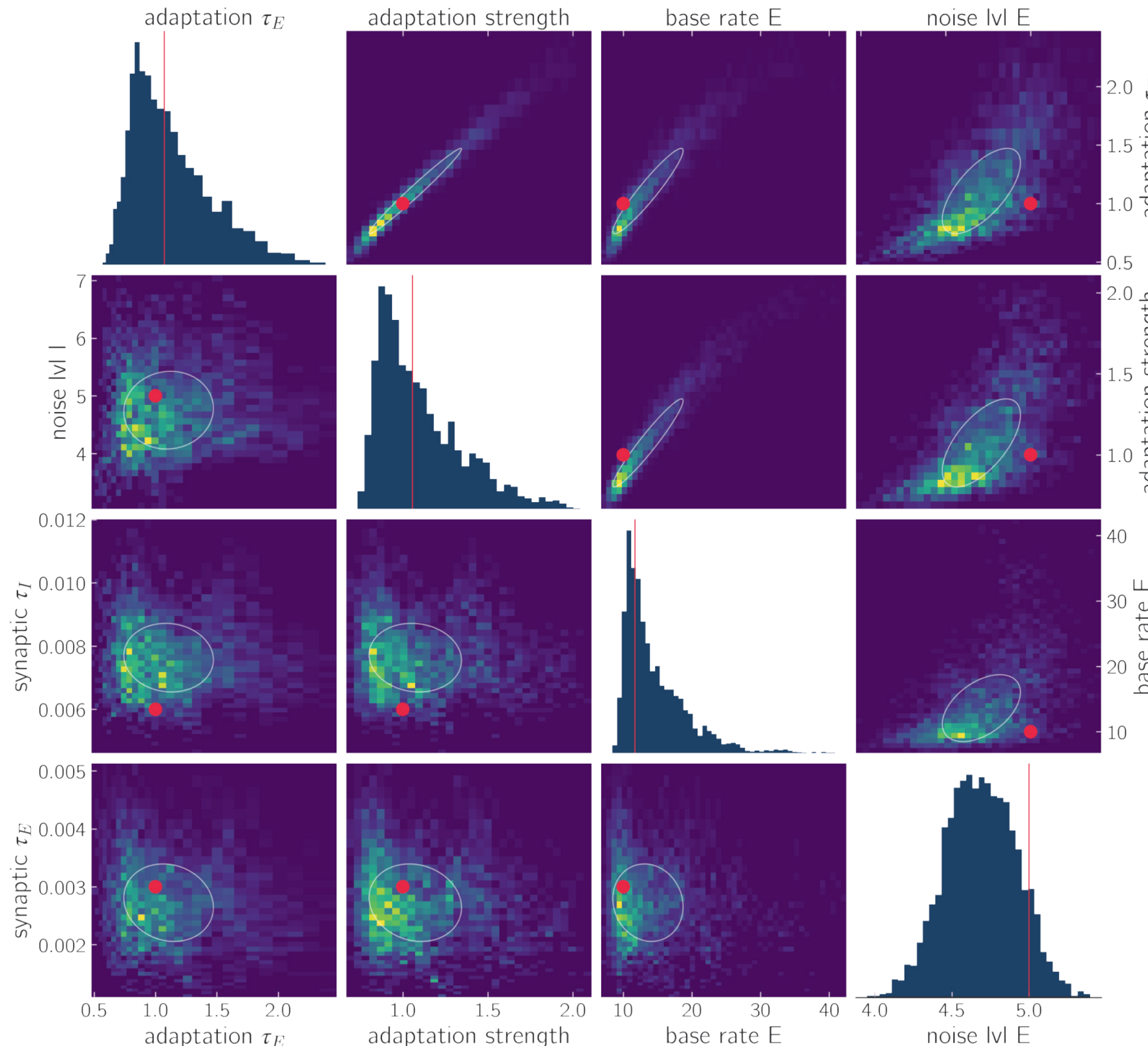
- Synthetic data (microscopic)
- Derived model (mesoscopic)<sup>1</sup>



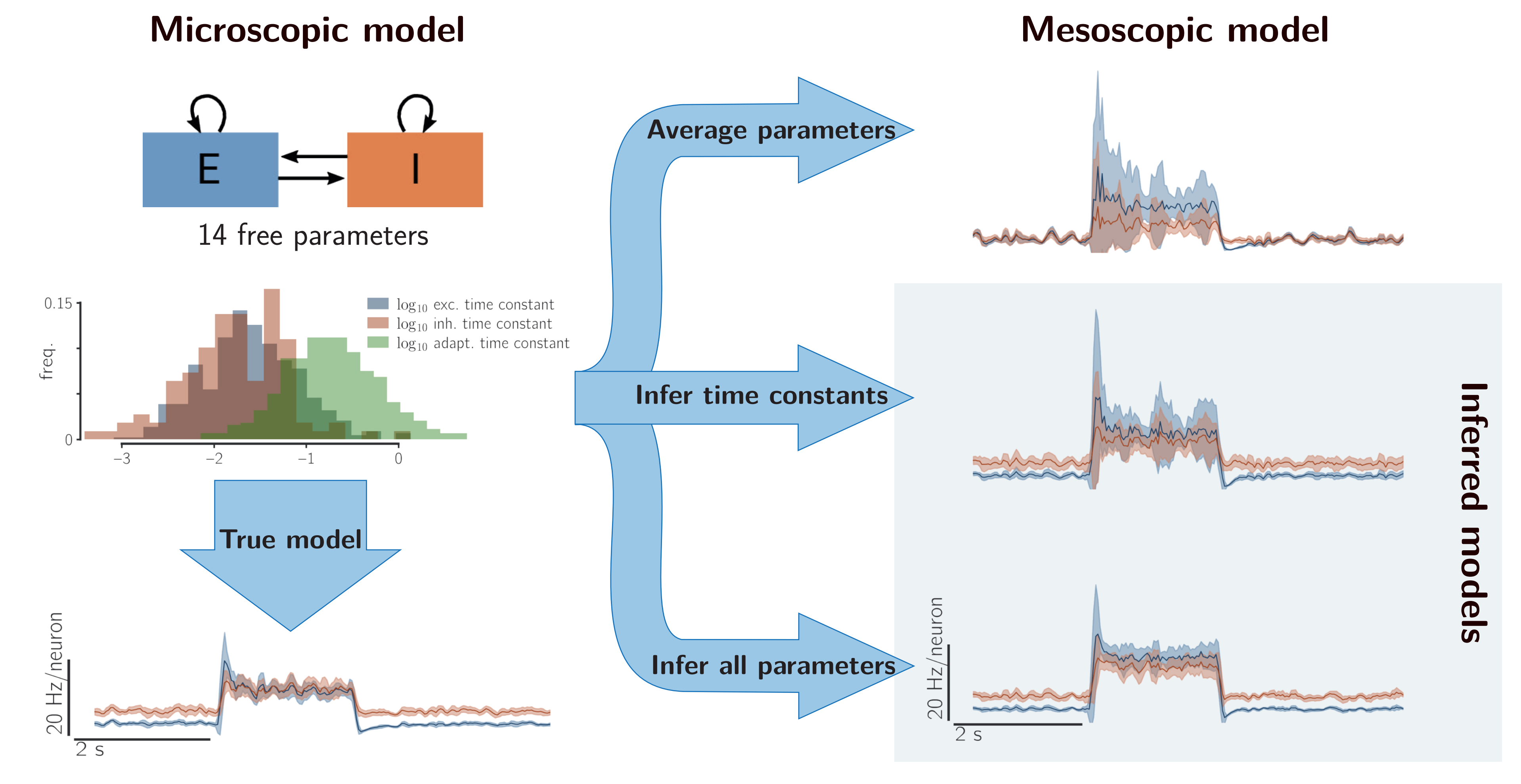
Use statistical inference to recover parameter point estimates...



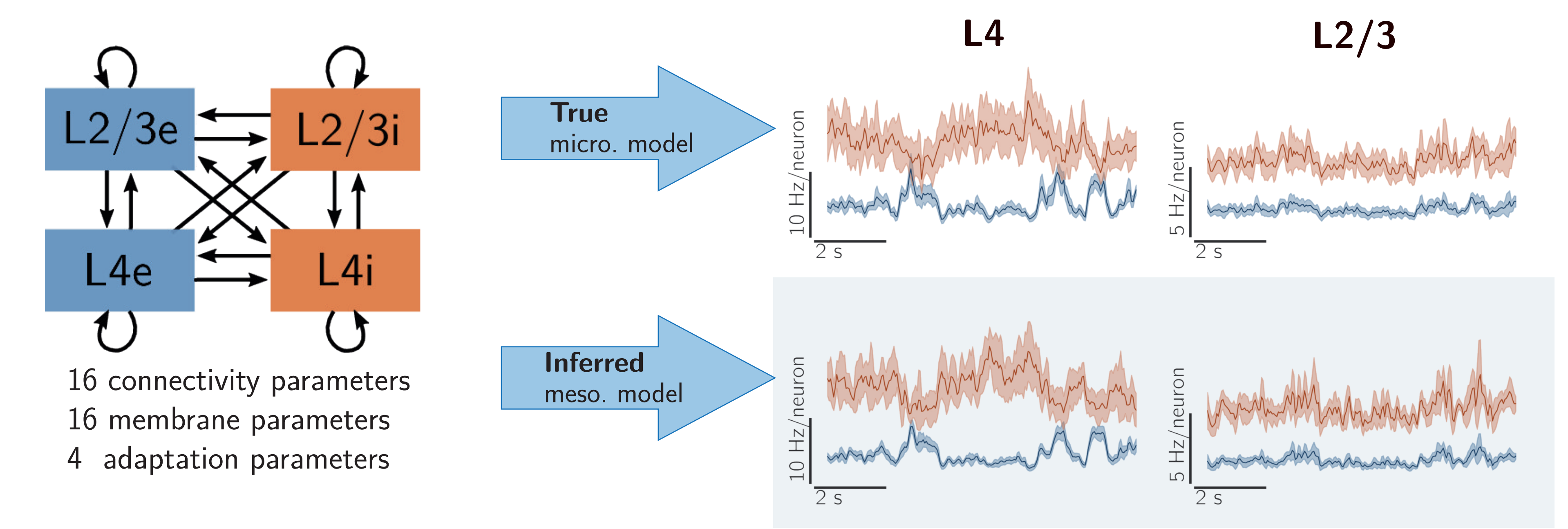
...or their posterior distribution.



## Inference can compensate for homogeneous approximation



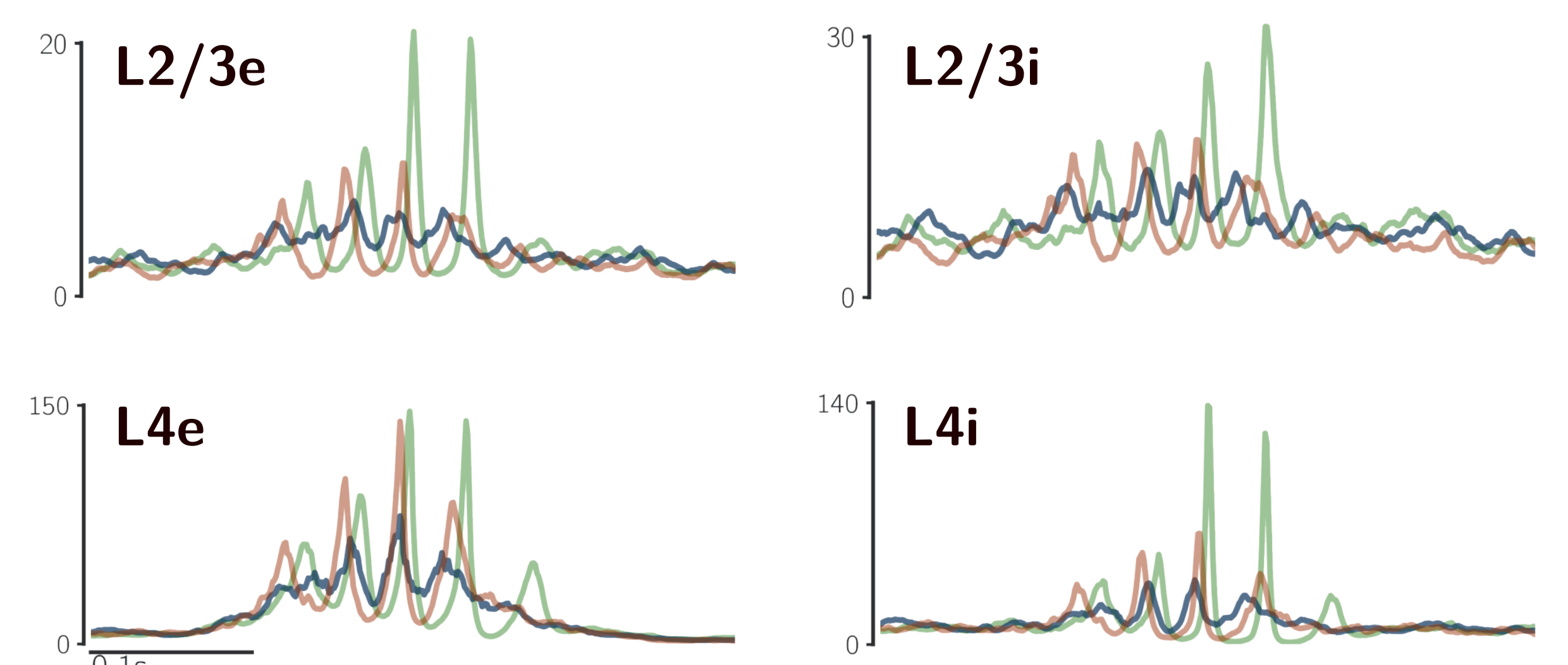
## We can infer dozens of parameters simultaneously



## Not all approximations can be compensated by inference

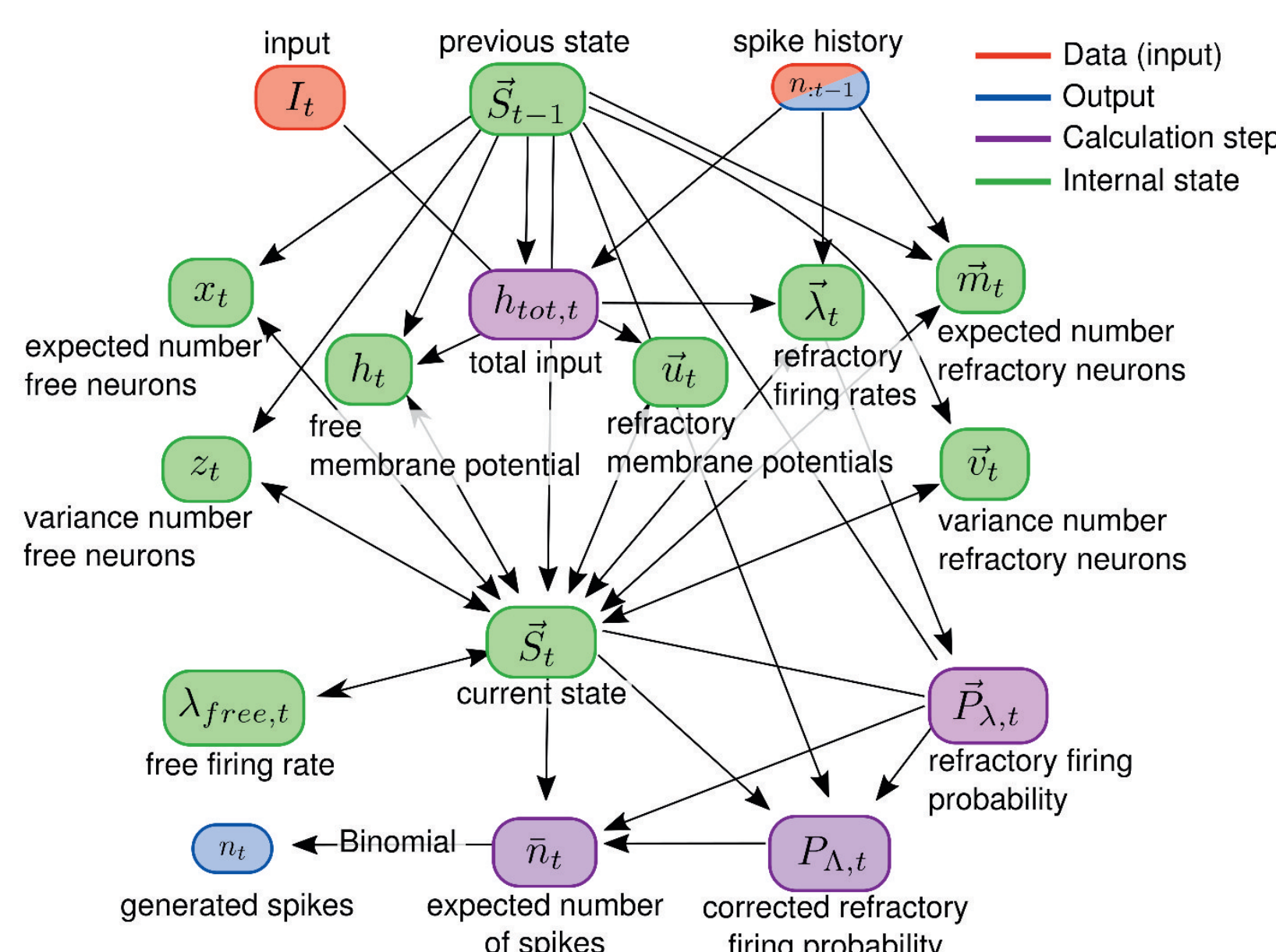
- Extreme inputs can break the quasi-renewal renewal approximation
  - Inference can only work within model constraints
  - More flexible models
- more compensation possibilities

- True micro. model
- Theoretical meso. model
- Inferred meso. model



## Method

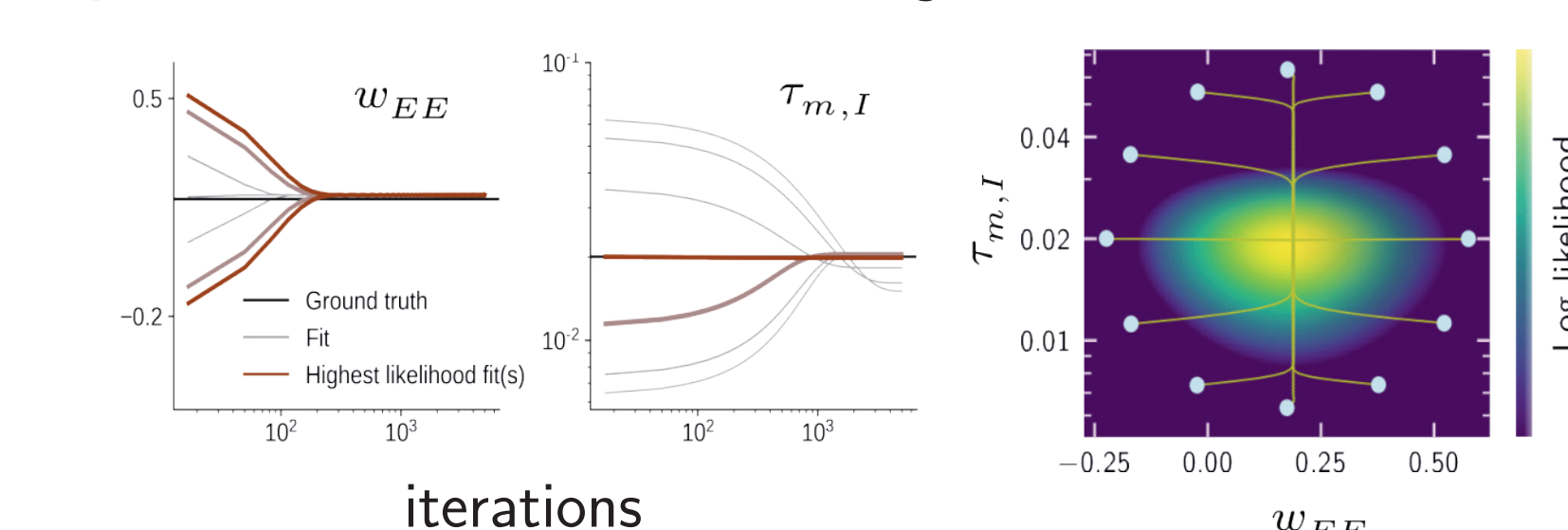
### Mesoscopic generalized integrate-and-fire model<sup>1</sup>



### Maximum likelihood inference

- Likelihood function
- parameters:  $\theta$
  - current state:  $S(t)$
  - data (# spikes):  $n(t)$
  - model:  $P(n(t)|S(t-1), \theta)$
  - $S(t-1) \rightarrow S(t)$
  - likelihood:  $L(\theta) = \prod_t P(n(t)|S(t-1), \theta)$

### Optimization via stochastic gradient ascent



## Why use inference to determine parameters ?

- **Systematic:** no hand-tuning of parameters
- **Principled:** recovered parameters maximize the likelihood
- **Scalable:** can infer dozens of parameters
- **Flexible:** model equations do not change
- **Ready:** code library available on github



## Computational tools

Gradient ascent fits performed with ADAM<sup>2</sup> algorithm, using Theano<sup>3</sup> for automatic differentiation and optimization. Posteriors obtained via Hamiltonian Markov Chain Monte Carlo, using PyMC3.<sup>4</sup>

## References

- [1] T. Schwalger, et al., PLOS Comp. Biol. 13(4)(2017)
- [2] D. P. Kingma, J. Ba, arXiv:1412.6980 (2014)
- [3] T. T. D. Team et al., arXiv:1605.02688 [cs] (2016)
- [4] J. Salvatier, et al., PeerJ Computer Science 2 (2016)