



## Overview

Efficient inference procedure with objective criteria, which infers couplings in neuronal networks from spike data.

- We use the kinetic Ising model (generalized linear model) to efficiently infer synaptic connectivity in the nervous systems.
- We apply our previous method to make original spike trains coarse-grained with objective criteria.
- We propose a novel method to screen relevant couplings objectively based on computational-statistic idea.
- We demonstrate performance of proposed inference procedure using synthetic systems of the Hodgkin-Huxley models and real systems of cultured cortical neurons of rats.
- Our tests include both systems without and with external stimuli, all of which imply the applicability of our methods.

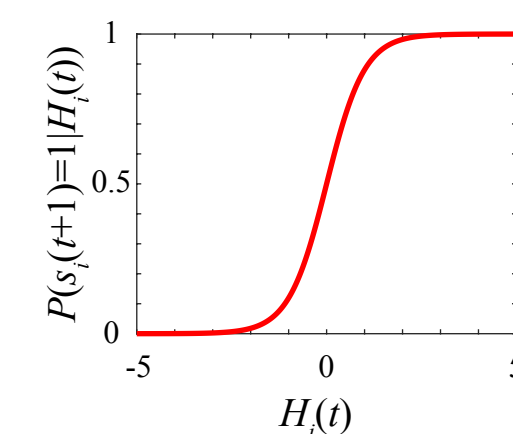
## Kintetic Ising Model

Network of binary neurons  $s_i(t) = \pm 1$  with couplings  $J_{ij}$

### Dynamics

$$P(\mathbf{s}(t+1)|\mathbf{s}(t); \{J_{ij}, \theta_i(t)\}) = \prod_{i=1}^N \frac{\exp[s_i(t+1)H_i(t; \{J_{ij}, \theta_i(t)\})]}{\exp[H_i(t; \{J_{ij}, \theta_i(t)\})] + \exp[-H_i(t; \{J_{ij}, \theta_i(t)\})]}$$

$$H_i(t) = \theta_i(t) + \sum_{j=1}^N J_{ij}s_j(t)$$



### Maximum Likelihood with Mean-Field Approximation

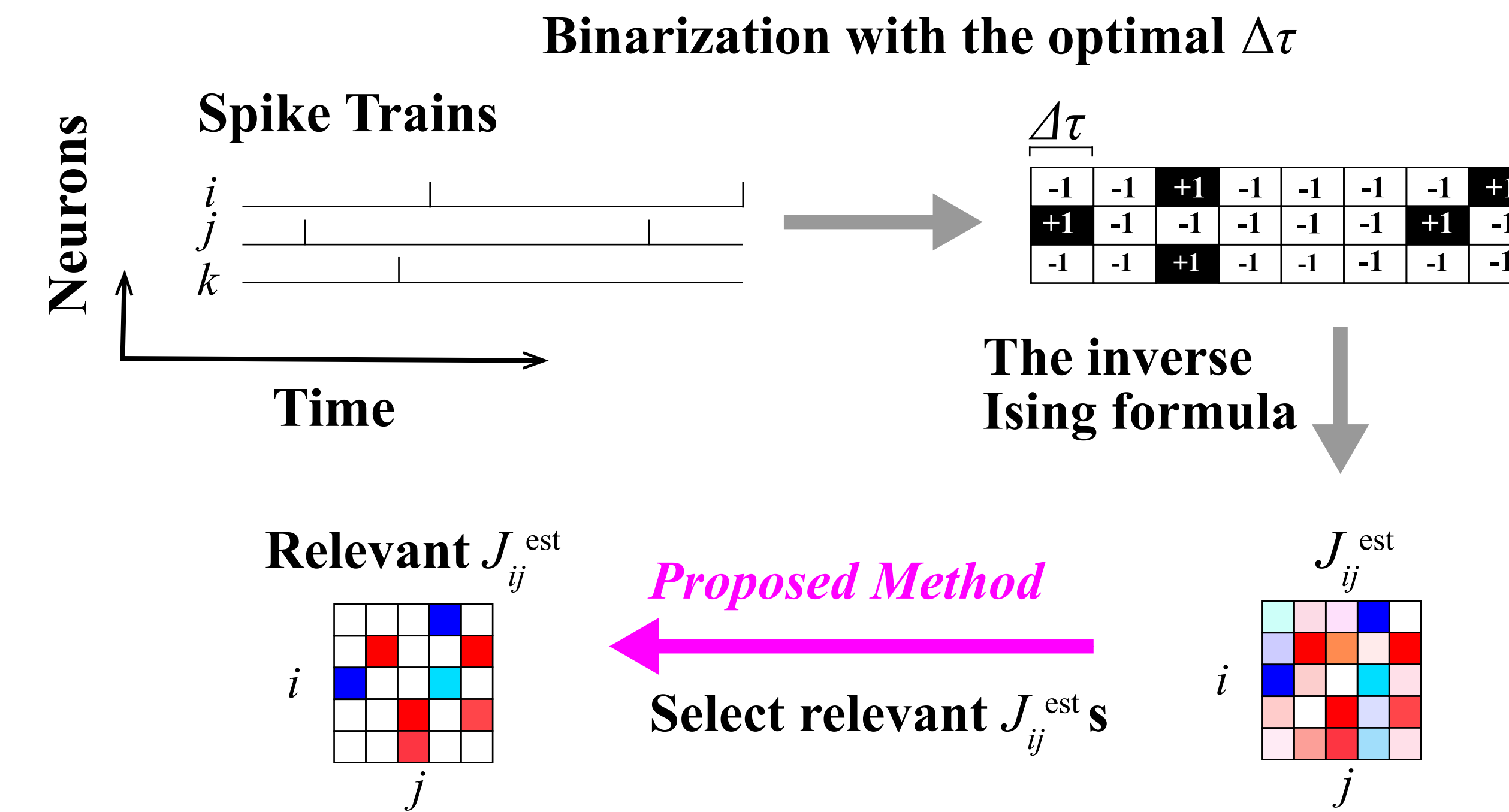
#### Mean-field inverse formula

$$\hat{J}^{\text{MF}} = A^{-1}DC^{-1},$$

$$\begin{aligned} \mu_i(t) &= \langle s_i(t) \rangle, \\ A_{ij}(t) &= (1 - \mu_i^2(t)) \delta_{ij}, \\ C_{ij}(t) &= \langle s_i(t)s_j(t) \rangle - \mu_i(t)\mu_j(t), \\ D_{ij}(t) &= \langle s_i(t+1)s_j(t) \rangle - \mu_i(t+1)\mu_j(t). \end{aligned}$$

[1] Y. Roudi & J. Hertz, *Physical Review Letters* 106, 048702 (2011);  
 M. Mézard & J. Sakellariou, *Journal of Statistical Mechanics* (2011) L07001.

## Inference Procedure



## Coarse-graining of Signals

We set a null hypothesis:  
*every neuron fires independently of other neuron states.*  
 Then, we choose the time bin size such that we can reject the hypothesis *with the strictest criteria.*  
 This idea induces the formula [2]

$$\Delta\tau_{\text{opt}} = \arg \max_{\Delta\tau} \left\{ \left( \frac{\mathcal{T}}{\Delta\tau} - 1 \right) \sum_{i \neq j} \hat{I}_{\Delta\tau}(s_i(t+1); s_j(t)) \right\},$$

where  $I$  is the gross mutual information of the whole trains:

$$\hat{I}_{\Delta\tau}(s_i(t+1); s_j(t)) = \sum_{(\alpha, \beta) \in \{+, -\}^2} r_{\alpha\beta}(i, t+1; j, t) \log \frac{r_{\alpha\beta}(i, t+1; j, t)}{r_{\alpha}(i, t+1)r_{\beta}(j, t)}$$

[2] Y. Terada, T. Obuchi, T. Isomura, & Y. Kabashima, arXiv: 1803.04738 (2018).

## Screening of Relevant Couplings

We consider *randomizing* the original trains, and then the couplings for the randomized trains obey

$$\hat{J}_{ij}^{\text{ran}} = \sum_k (A^{-1})_{ii} D_{ik} (C^{-1})_{kj} \approx (A^{-1})_{ii} D_{ij} (A^{-1})_{jj} = \frac{1}{(1 - \mu_i^2)(1 - \mu_j^2)} D_{ij}.$$

By the central limit theorem, this means the probability for obtaining a larger coupling than  $\Phi_{\text{th}}$  is

$$P(|\hat{J}_{ij}^{\text{ran}}| \geq \Phi_{\text{th}}) \approx 1 - \text{erf} \left( \Phi_{\text{th}} \sqrt{\frac{(1 - \mu_i^2)(1 - \mu_j^2)(M - 1)}{2}} \right),$$

where  $M$  is # of the windows and  $\text{erf}(\cdot)$  is the error function.

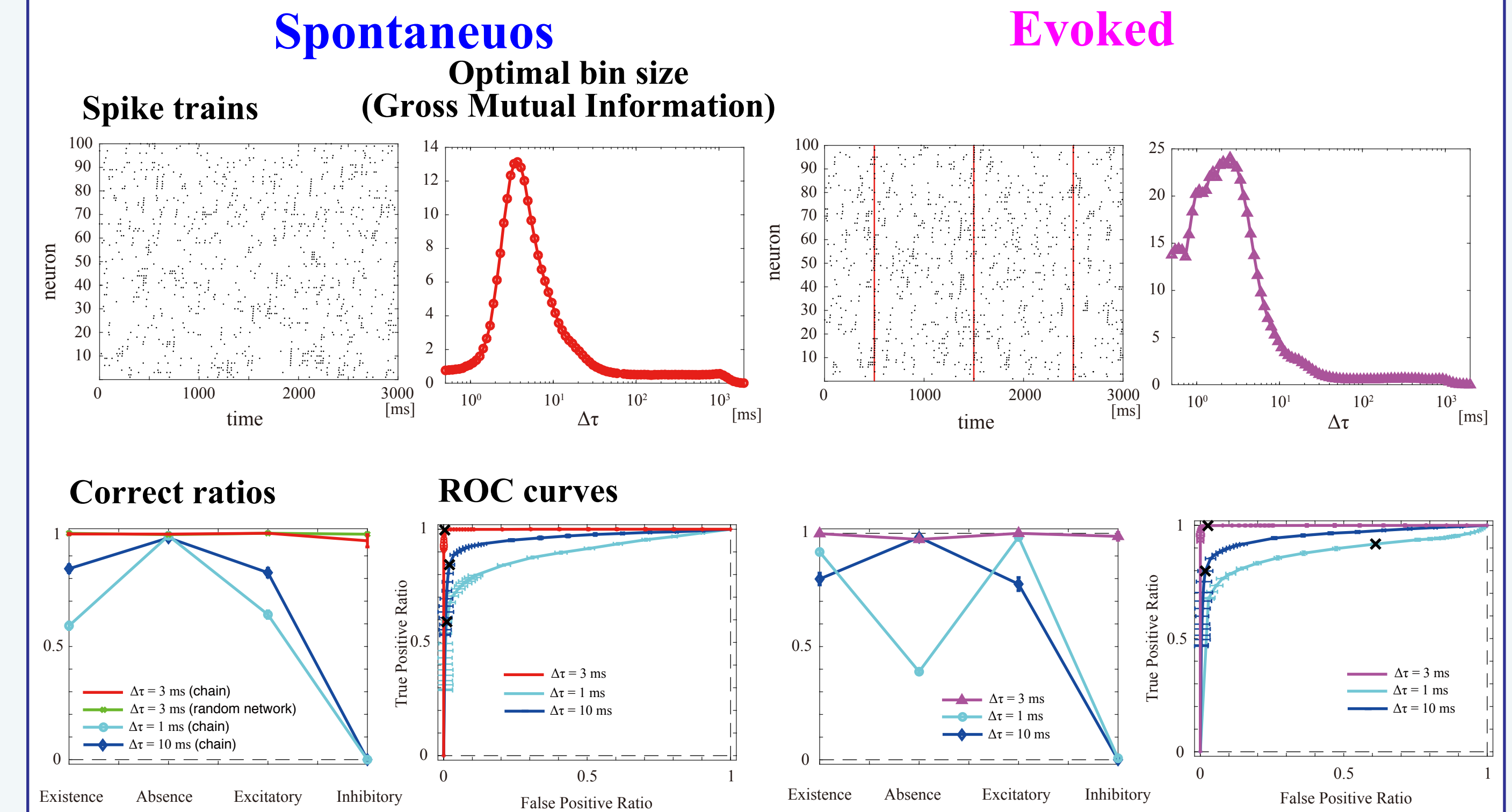
As a result, for the level of significance  $p_{\text{th}}$ , we can use the value

$$(\Phi_{\text{th}})_{ij} = \sqrt{\frac{2}{(1 - \mu_i^2)(1 - \mu_j^2)(M - 1)}} \text{erf}^{-1}(1 - p_{\text{th}})$$

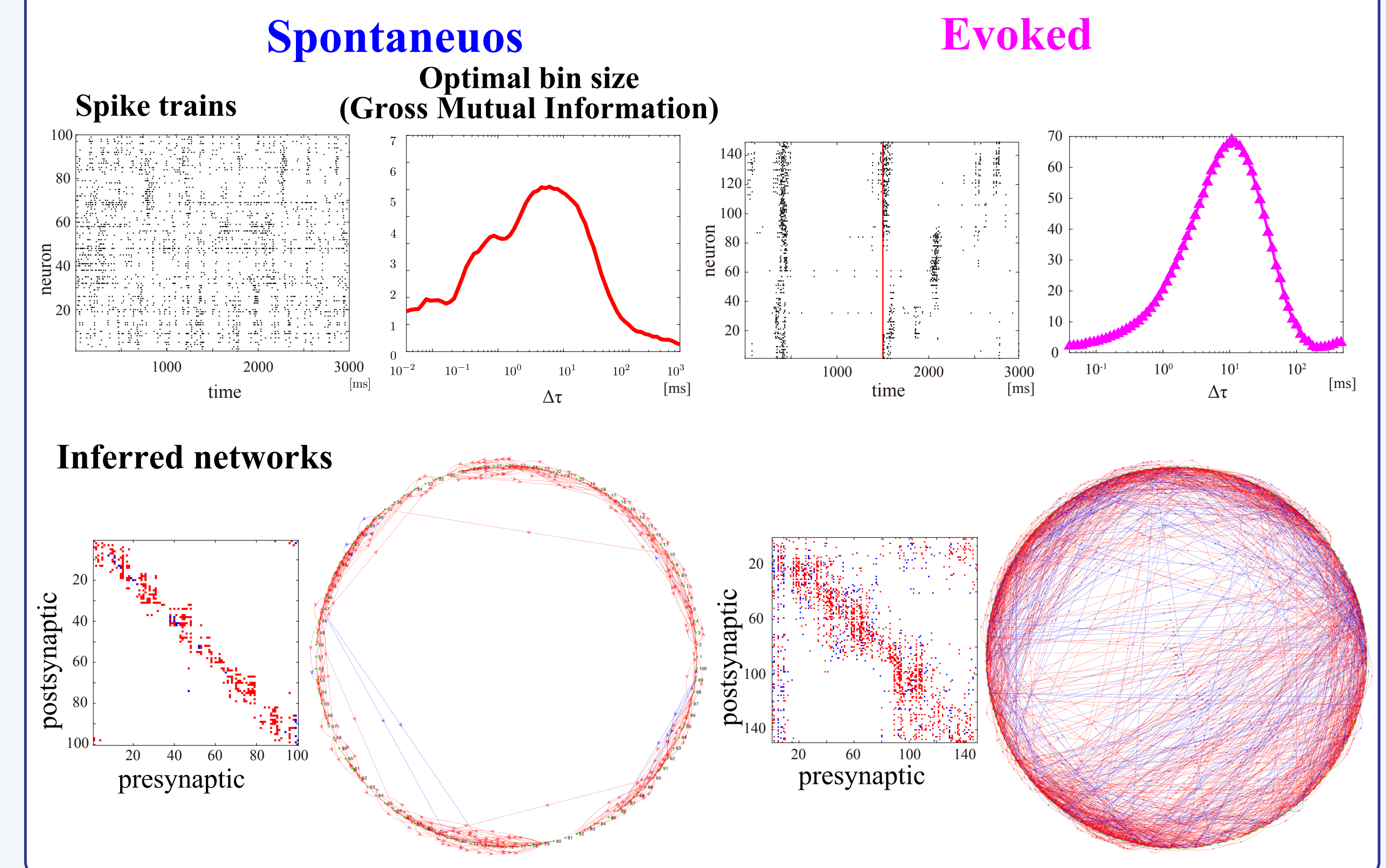
as a criterion of the relevant value.

## Performance

### - Hodgkin-Huxley models in chain networks



### - Networks of cortical neurons cultured in circular environment



## Conclusion & Open code

The sign patterns of the connectivity are reconstructed well in both of the synthetic and real systems. Our fast improvement makes it possible to process huge data with reasonable computational cost.

**Public code of our methods (Matlab)**

[http://toyozumilab.brain.riken.jp/terada/KI\\_inference/KI\\_package.zip](http://toyozumilab.brain.riken.jp/terada/KI_inference/KI_package.zip)

