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An Analytical Solution Eliminates Monte Carlo Error in Intervention Analysis for Ising Networks: A Comment on Wang et al. (2026)

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An Analytical Solution Eliminates Monte Carlo Error in Intervention Analysis for Ising Networks: A Comment on Wang et al. (2026)

In-silico interventions on symptom networks have been a pressing topic in the past decade (Henry et al., 2022; Lunansky et al., 2022; Stocker et al., 2023). Instead of searching for the most central nodes in the networks, more sophisticated methods have been developed to test more directly intervening on which nodes in the network can exert the best overall outcomes. A tutorial published in Advances in Methods and Practices in Psychological Science recently by Wang et al. (2026) aimed to take the NIRA method by Lunansky et al. (2022) one step further by introducing more rigorous assumption examination before the simulated intervention, and statistical testing regarding the uncertainty of the simulation results, thereby enhancing the usability of this approach. The post-simulation statistical approaches introduced in this tutorial are very valuable in helping researchers understand how much uncertainty is involved in the Monte Carlo simulation applied in NIRA (and more specifically, the implementation in the NodeIdentifyR package; Lunansky et al., 2022). However, I argue that for networks with a moderate or small number of nodes, which are common in the psychological setting, the simulation with Monte Carlo errors is not needed to calculate the outcome of interventions, as an analytical approach exists that provides solutions without Monte Carlo error.

The theoretical underpinning of this analytical approach has recently been shown in Cui et al. (2026), and interested readers may refer to that article for a more comprehensive discussion. Here, I briefly summarize the main points in Cui et al. (2026) that are particularly relevant for this topic. Ising models have an intrinsic energy property, namely the Hamiltonian. It is defined as follows:

$$\begin{aligned} H(\boldsymbol{a}) &= -\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} w_{i,j}a_i a_j - \sum_i a_i m_i \\ &= -\frac{1}{2}\boldsymbol{a}^T\boldsymbol{W}\boldsymbol{a} - \boldsymbol{a}^T\boldsymbol{m}, \end{aligned} \tag{1}$$

where $\boldsymbol{a} = (a_1, a_2, ..., a_n)^\top$ is a vector representing the activation states of n nodes, with 1

representing activated nodes and 0 representing deactivated nodes, $\boldsymbol{W}$ is an $n \times n$ matrix representing the connectivity (i.e., edge strength) among nodes, and $\boldsymbol{m}$ is a vector of length n representing the thresholds of nodes. The overall occupation probability of a certain activation status of the network, $\boldsymbol{a}$, given $\boldsymbol{W}$ and $\boldsymbol{m}$, is given by:

$$P(\boldsymbol{a}) = \frac{e^{-H(\boldsymbol{a})}}{Z}, \tag{2}$$

where $Z = \sum_{\boldsymbol{a}} e^{-H(\boldsymbol{a})}$. The Metropolis-Hastings algorithm applied in NIRA (Lunansky et al., 2022) converges to this steady-state distribution in the long run (Newman & Barkema, 1999). Therefore, it is possible to calculate the mean number of activated symptoms in the long run for any network parameters $\boldsymbol{W}$ and $\boldsymbol{m}$ with the following:

$$\bar{n}_{\text{activated}} = \sum_{\boldsymbol{a}} P(\boldsymbol{a}) \sum_{i=1}^{n} a_i. \tag{3}$$

Applying this approach to the network in Wang et al. (2026) yields the result in Figure 1. These results align with Fig. 5 in the original article, confirming that the numerical simulation technique approaches the analytical solution, while the analytical solution was obtained without Monte Carlo errors. Consequently, the ranking of nodes by their intervention effects can also be obtained without Monte Carlo uncertainty. The code to obtain this result can be accessed in the Supplementary Materials.

A downside of this analytical approach is that its computational cost scales as 2^n, which becomes increasingly expensive as the number of nodes grows. In Table 1, I show the computation time required for the analytical calculation proposed here, with the computational code available in the Supplementary Materials. It should be noted that the implementation is based on the Isinglandr package (Cui et al., 2026), which was not specifically designed for intervention analysis. The code could therefore be made more efficient if customized for this application. However, the order of magnitude of the computation time is expected to remain similar, as the underlying scaling law does not change. The result shows that when the number of nodes (n) is 12, the whole procedure can be completed in around one second on a consumer laptop. For networks with up to 17

nodes, the procedure takes approximately one minute or less. However, under an approximate 2^n scaling, the total computation time would increase to about one hour for 23 nodes and on the order of one day for 27 to 28 nodes. Beyond this range, obtaining the analytical solution becomes increasingly impractical. In contrast, the Monte Carlo simulation approach, although requiring more simulations to maintain a reasonable level of Monte Carlo error for larger networks, scales much more slowly than 2^n. Therefore, for sufficiently large networks (around 28 nodes or more), depending on the computational resources available, the approach used in the original tutorial remains a valuable numerical alternative.

To conclude, as the property that Monte Carlo simulation intends to estimate can be obtained analytically without Monte Carlo error, quantifying the error of Monte Carlo simulation is not necessary for NIRA with a moderate or small number of nodes (roughly below 28). Future research can be devoted to quantifying the influence of sampling error, which is a major source of the uncertainty of NIRA results. This can be accomplished, for example, through a resampling approach on the original dataset. Post-analysis steps similar to those proposed in the target article, such as the quantification of standard errors and the stability analysis of node rankings, would also be helpful for studying the influence of sampling error.

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Table 1

Computation time of the analytical solution across network sizes

Number of nodes	Total computation time (s)
10	0.33
11	0.66
12	1.28
13	2.85
14	5.95
15	12.71
16	28.19
17	60.10

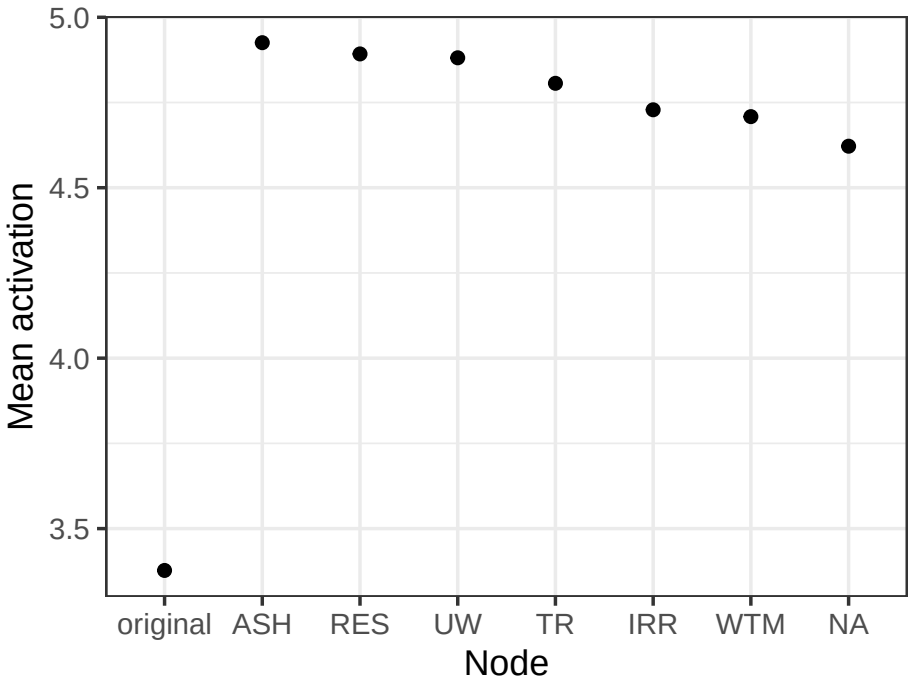

Figure 1

The analytical solution obtained for the Ising network presented in Wang et al. (2026).