



CSS/ITALY

ITALIAN CHAPTER OF
COMPLEX SYSTEMS SOCIETY

Contribution ID: 170

Type: **not specified**

Quantifying biases in reconstructed brain networks

Wednesday 17 September 2025 11:20 (20 minutes)

Brain network reconstruction from neuroimaging data is subject to sources of systematic bias. One can arise from the arbitrariness introduced by thresholding procedures used in typical structural and functional network reconstruction techniques. The produced connectivity matrices exhibit variable density, which has been shown to impact the evaluation of many graph metrics [1]. Additionally, potential biases in the estimation of network descriptors may arise depending on the type of statistical approach used to handle the variability across subjects, particularly when attempting to estimate quantities from systems with probabilistic or fluctuating characteristics. In statistical mechanics, the evaluation of a metric can be seen as the application of a highly complex and non-linear function f of the adjacency matrix. In such a case, there is a difference between the exact equation for the model on a sparse network and its mean-field approximation, according to the so-called Jensen's inequality [2].

Here, we quantify how different types of bias impact network measures at macro-, meso-, and microscales, analyzing their dependence on network density.

Specifically, we analyzed a group mean approach, where a network descriptor is estimated from the average connectome, and an ensemble mean approach, where a network descriptor is evaluated from each individual connectome and then averaged (see Fig 1 A-B). For cases that can be treated analytically, we estimate the explicit dependence of topological metrics on network density and we assess the magnitude of the difference between the estimates obtained using different statistical methods. Our analytical results demonstrate that global clustering coefficient estimates have an explicit dependence on network density that is maintained regardless of the statistical approach. Results are confirmed and generalized for a set of measures at different scales through the analysis of neuroimaging data and synthetic network ensembles preserving specific features of real networks. In functional connectomes, we find that the statistical approach affects estimates for all the selected metrics and the difference depends on network density. Furthermore, for high-density values, the results are reconciled, but they are not statistically different from random networks (see Fig 1C).

Our findings set limits on analyses based on the thresholding of connectomes – and more generally, of graphs where edges are defined by correlations – while calling for caution in interpreting results.

[1] M. P. van den Heuvel, S. C. de Lange, A. Zalesky, C. Seguin, B. T. Yeo, and R. Schmidt, *Neuroimage* 152, 437 (2017).

[2] V. Buendia, P. Villegas, S. Di Santo, A. Vezzani, R. Burioni, and M. A. Munoz, *Jensen's force and the statistical mechanics of cortical asynchronous states*, *Scientific Reports* 9, 15183 (2019).

Presenter: D'ANDREA, V.

Session Classification: Session 10