

Modular organization of brain connectivity networks beyond the resolution limit

Carlo Nicolini^{1,2} & Cécile Bordier² & Angelo Bifone²

¹University of Verona, (Italy).

²Center for Neuroscience and Cognitive Systems, Istituto Italiano di Tecnologia, Rovereto (Italy)



Introduction

Neuroimaging methods, like functional MRI, have shown that the brain consists of functionally specialized modules that are hierarchically organized to form highly integrated networks. Graph theory provides a valuable framework for the analysis of the modular structure of this complex architecture. Indeed the brain is represented as a graph comprising N nodes connected by M edges. The nodes correspond to brain regions and the edges to measures of inter-regional interaction [1]. The most widely used metric to investigate modular structure of FC networks is Newmans Modularity [2], which identifies modules within which links are more abundant than expected on the basis of a random network. However, this approach is limited in its ability to detect relatively small communities, a problem known as resolution limit. We have recently demonstrated [3] that a quality function grounded in probability theory dubbed Surprise [4, 5] is resolution-limit free and may be applied to detect tightly knit clusters regardless of their size. Here we demonstrate that Surprise can be applied to detect functional modules in brain connectivity datasets beyond the resolution limit.

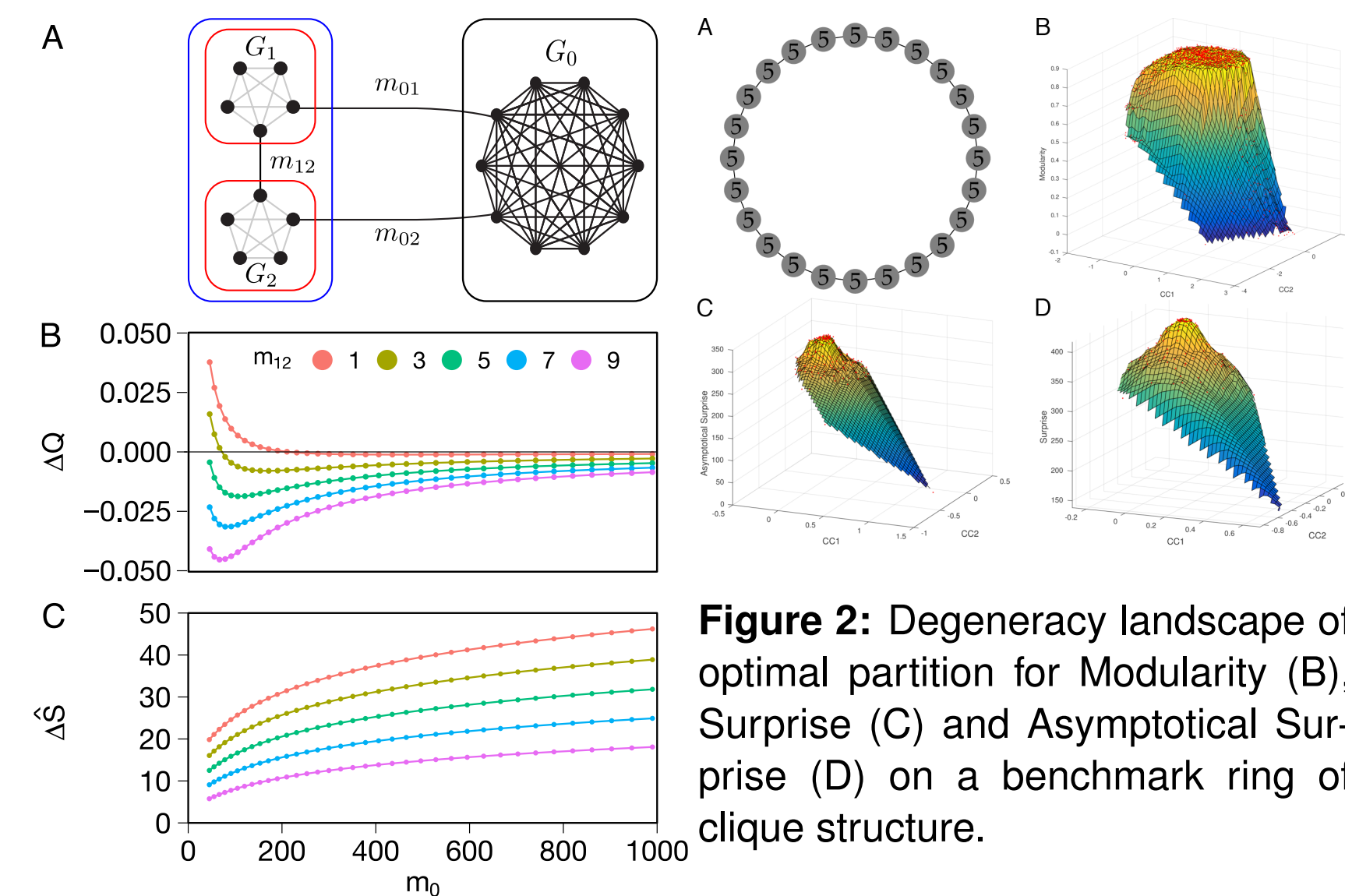


Figure 1: Onset of the resolution limit in optimal partition of a pathological network (A). With larger size of G_0 module, the two cliques G_1 and G_2 are merge by Modularity optimization (B), never merged by Surprise optimization (C).

Methods

Here, we propose the suitability of Surprise S and Asymptotical Surprise S_a , two recently proposed fitness function based on probability theory that are nearly resolution limit free.

$$S = \sum_{i=m_c}^m \frac{\binom{p_c}{i} \binom{p-p_c}{m-i}}{\binom{p}{m}} \quad S_a = m D_{KL} \left(\frac{m_c}{m} \parallel \frac{p_c}{p} \right) \quad (1)$$

We developed an optimization approach to an extension of Surprise to weighted networks named FAGSO (Fast Agglomerative Surprise Optimization) to find maximum Surprise/Asymptotical-Surprise partitions of benchmark resting state networks. The optimization method works by ag-

glomerating edges with the highest Jaccard index and iterates merging their endpoints until no further increment in Surprise is possible.

We benchmark Surprise against widely applied algorithms, and quantitatively assess its performance in synthetic correlation networks with different levels of noise, and in human resting state functional connectivity data.

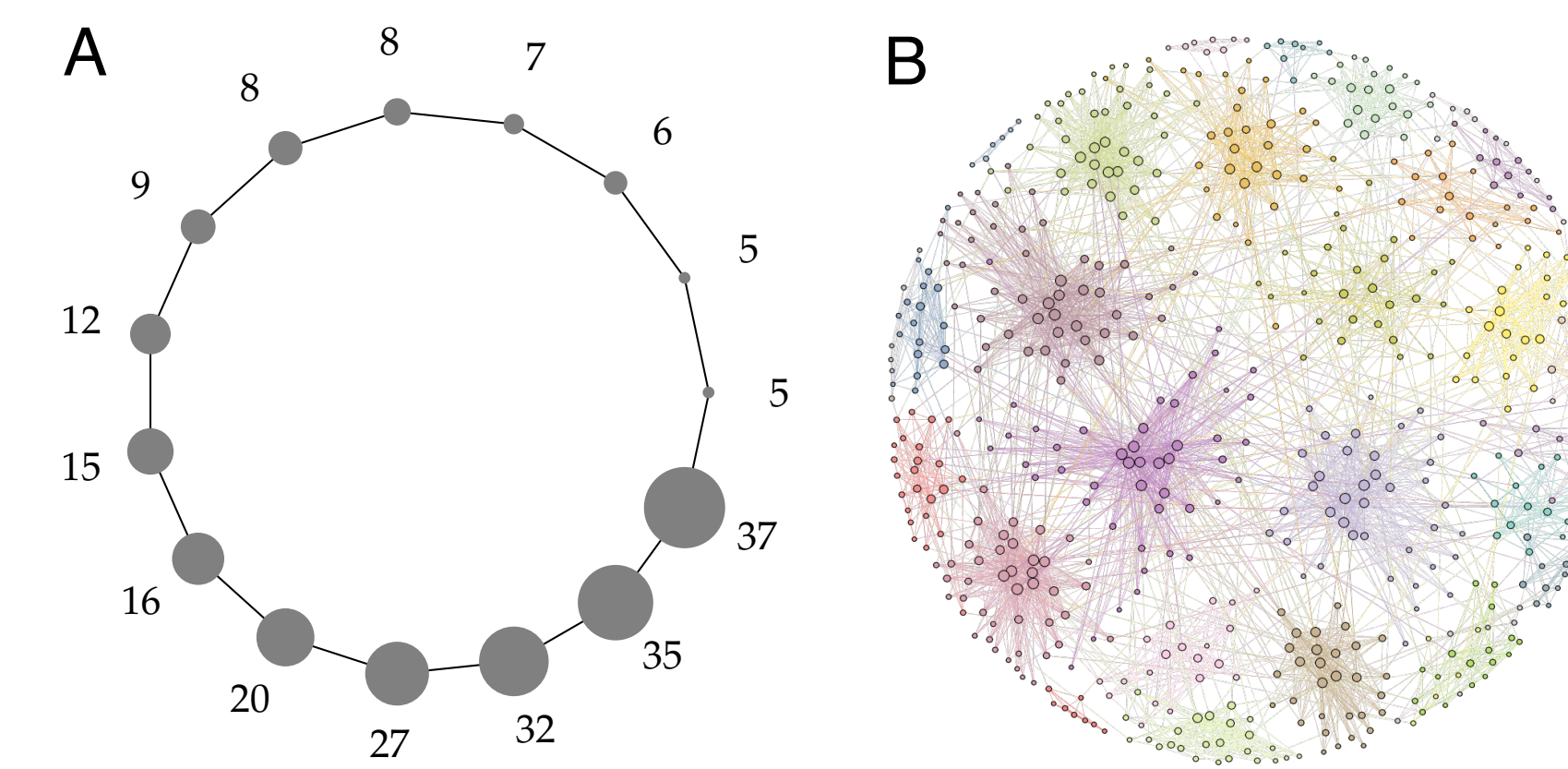


Figure 3: xxx

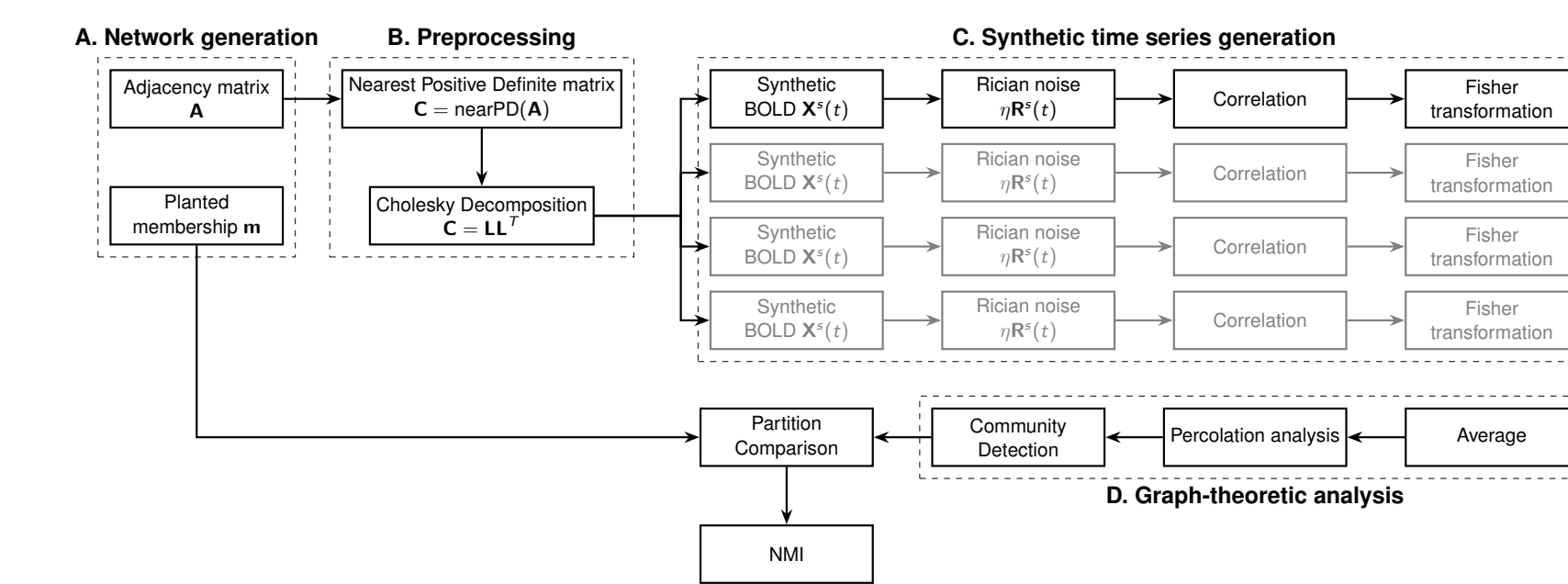


Figure 4: Pipeline of generation

Results

In synthetic networks, Surprise shows better sensitivity and specificity in the detection of ground-truth structures, partic-

ularly in the presence of noise and variability such as those observed in experimental functional MRI data. Surprise maximization in human resting state networks reveals the presence of a rich structure of modules with heterogeneous size distribution undetectable by current methods. Moreover, Surprise leads to different, more accurate classification of the networks connector hubs, the elements that integrate the brain modules into a cohesive structure.

Conclusions

Our results indicate that the resolution limit may have substantially affected previous analyses of brain connectivity networks. Surprise represents a promising alternative to current methods, and demonstrates the presence of functional modules of very different sizes in resting state networks. This calls for a revisitation of some of the current models of brain modular organization.

References

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