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Network Neuroscience Feature with a Biomarkers Focus

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ABSTRACT: The significant overlap of behavioural symptoms and other pathophysiological traits makes it difficult to diagnose neurological and psychiatric illnesses, hence there is a constant demand for new biomarkers in clinical neuroscience. The main question raised by this Focus Feature is whether network-based biomarkers may be a useful tool for discriminating across disordered populations or if they could only have a modest ability to discriminate between states due to the high degree of network homogeneity.

KEYWORDS: Neuroscience, Clinical Psychiatry, Connectome, Biomarkers, Personalized medicine.

I. INTRODUCTION

There are numerous ways to answer the issue of whether network-based biomarkers could be useful in clinical settings; in this Focus Feature, we examine many of them. Blomsma and associates (Blomsma et al., 2022) concentrate on the minimal spanning tree (MST) as a technique that may reveal distinctions between disorders of the nervous system or the mind and healthy controls. The subset of edges that maximise connection without producing any loops or cycles is what the authors claim the MST offers as a theoretical method for thresholding adjacency matrices. In order to evaluate the disease specificity and transdiagnostic sensitivity of MST-based metrics, they conduct a systematic evaluation of MST studies utilising various network sizes.

II. NETWORK NEUROSCIENCE & BIOMARKERS

Several patterns could be seen within and between illness categories, despite the fact that there were discrepancies in the results of several investigations. It was interesting to see that the MST measurement of leaf fraction is reliant on network size regardless of the presence of illness, which restricts the use of this metric to research using other techniques. The authors assert the necessity for reporting rules in network neuroscience and stress the need of consistently providing numerical values for network measurements as well as the usage of the analytic tools. The research by Rodriguez-Cruces and associates (Rodriguez-Cruces et al., 2022) employs a different approach to the investigation of biomarkers: With the aim of identifying both common and syndrome-specific network substrates, they evaluated the present state of network neuroscience research in three distinct epileptic syndromes. According to the authors' conclusion, "brain network measures may ultimately serve as powerful intermediary phenotypes to study effects of biological as well as environmental factors on cognitive systems in epileptic patients, including medication effects, disease status, and baseline genetic factors," there are, in fact, common and specific network markers for these syndromes. In addition to multimodal imaging, they advise include comprehensive clinical phenotyping and genetic testing in future research. The authors assert that their work may pave the way for network-based biomarkers to be used in clinical practise for epilepsy together with multisite data collecting. New network-based biomarkers are also presented and assessed in this Focus Feature. In Kulik and colleagues' study (Kulik et al., 2022) of a cohort of multiple sclerosis (MS) patients, they examine relationships between structural and functional connectivity and examine if changes in these relationships can serve as a viable biomarker for cognitive impairment in MS. Receiver operating characteristic (ROC) curves showed that these group-level differences did not substantially distinguish between

cognitively impaired patients and matched healthy controls, despite the fact that there were significant variations in structure-function coupling between them. This finding emphasises how critical it is to record classification accuracy for putative biomarkers, especially when there are large group disparities. Iraj and colleagues (Iraj et al., 2022) examine shared and particular connection patterns between boys and females with schizophrenia using the recently described approach of multiscale independent component analysis (msICA). With the use of this technique, functional sources may be naturally detected across various geographic scales using data. The authors report on common network differences between male and female patients with schizophrenia using three large cohorts, but they also uncover sex-specific effects that were connected with symptom ratings. The authors stress the significance of properly including sex into the creation of biomarkers for schizophrenia that are diagnostic, predictive, and/or monitoring. As a new biomarker for early-stage Alzheimer's disease, Scheijbeler and associates (Scheijbeler et al., 2022) offer a network version of permutation entropy (AD). This measurement incorporates data on nonlinear coupling, local signal complexity, and variability. They do discover group differences between early-onset AD patients and a control group. Furthermore, relative theta power, the most advanced biomarker at the time, was equivalent to the ROC curve analysis's classification accuracy in this situation. This conclusion might be replicated in more extensive samples in future research.

III. CONCLUSION

Clinical neuroscience has potential for network-based biomarkers. Consistently reporting the accuracy, repeatability, sensitivity, and specificity of brain network measurements as biomarkers is a crucial first step in conducting an adequate assessment of these measurements. The discovery of biomarkers useful for differential diagnosis and prognosis will benefit from the growing accessibility of big databases with multimodal data to crosslink various techniques. We hope that the research presented in this Focus Feature will help guide future investigations into this crucial subject.

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