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Decomposing the brain: components and modes, networks and nodes

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Abstract

Smith and colleagues recently presented a temporal independent component analysis (tICA) decomposition of resting-state functional MRI data. Compared to the widely used spatial ICA (sICA), tICA better allows for a brain region to engage in multiple, independent interactions with other regions and will potentially offer new insights into brain function.

In the past two decades, approaches to functional imaging analysis have substantially evolved. Initial work focused on correlating voxel timeseries with a reference signal. The field, however, quickly advanced to multiple regression, allowing voxelwise fits to detailed models of hypothesized temporal activation. Although a very powerful and still broadly used approach, model specification can be challenging in many situations, including when the timing and modulation of signals of interest are unknown or when adequate parameters of the associated hemodynamic response function are unavailable. Since the late 1990s, ICA has been applied to fMRI as a data-driven approach that does not require an explicit temporal model and also, being a multivariate method, estimates parameters from the entire spatiotemporal data set at once [1]. There was initial interest in applying both tICA (optimizing independence over time) as well as sICA (optimizing independence over voxels) to fMRI data and some discussion over the more appropriate model arose [2,3]. Elegant early work used tICA in conjunction with sICA to decompose unique constituents of response signals from audition [4] and more recently in speech processing [5]. However, sICA quickly emerged as the most widely used method, in part due to computational convenience (with many more voxels than time points in fMRI data), better plausibility of stationarity in the spatial domain and natural extensions to a group framework [6], but also due to reproducibility of components across different methods and labs.

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Smith *et al.* revisited the use of tICA, applying it to resting-state data acquired with a state-of-the-art multiplexed sequence with high temporal sampling rate [7]. After regressing out artifacts identified in two applications of sICA to the data, the authors applied tICA to identify temporal functional modes (TFMs). They found that these TFMs differ from networks commonly identified with seed-based correlation, sICA or magnetoencephalography (MEG) deconvolution approaches and interpreted the networks in light of anatomical and functional organization, anticorrelatedness, reproducibility and temporal stationarity. The paper offers a fresh look at resting-state data and motivates us to reexamine current models for decomposing brain data and how these may be improved in future iterations.

On spatial and temporal overlap

In contrast to ‘functional parcellation’ schemes, where one implicitly assumes that each region has a single temporal activation, tICA affords (to a greater degree than sICA) that a region may participate in several TFMs (analogous to how sICA affords temporal overlap [8]). Thus, as seen in Figure 1 of Smith *et al.*, regions of visual cortex contain temporal signatures common to all early visual areas (TFM 2), as well as activation representing an antagonism between cortical areas dedicated to more foveal versus more eccentric stimuli (TFM 4). In sICA, optimization for spatial independence will make these highly overlapping TFMs difficult to decompose (even though, interestingly, some weak antagonism is evident in the resting-state networks shown in Figure 1). TFMs thus appear quite interesting; however, we note that one should be cautious about allowing an analysis method define interpretation. As the authors point out, tICA carries with it the assumption of little temporal overlap between TFMs, and it is unclear what impact violations of this assumption may have on the resulting decomposition and data interpretation.

Certainly, the boundary conditions of when temporal or spatial processes are separated given different assumptions are worthy of more study, and the use of simulations to understand the empirical properties of approaches when assumptions are violated should not be understated [9]. As we have witnessed in our own simulations with sICA (see Figure 7f in [9]), even minor dependencies in the spatial domain can produce subtle but systematic biases in the temporal domain, encouraging us to proceed cautiously when interpreting results from real data. Ultimately, our understanding of TFMs and their utility in research will be borne out by the extent to which they change with behavioral states and different traits. In the best case, TFMs will show unique covariance with basic demographic factors, participant behavior, and increased sensitivity and specificity to various neuropsychiatric disorders than is afforded by other decomposition methods.

Potential causes of non-robustness of tICA

First, as mentioned by the authors, fastICA (the tICA algorithm employed in the study) uses non-Gaussianity to separate the components. However, it appears that the components are not strongly non-Gaussian, thus other more flexible ICA algorithms may be needed. Second, one of the reasons sICA has been so successful with imaging data is that spatial patterns tend to be much more stationary than temporal patterns. The authors make some effort to evaluate non-stationarity; however, a windowed correlation approach does not allow direct estimation of the stationarity of the networks being separated. In addition, the algorithm used assumed that the samples in the time domain are indeed stationary, thus ultimately using an ICA algorithm which does not rely on a stationarity assumption would be more optimal. In addition, it remains to be seen to what degree the preprocessing, including filtering by the spatial ICA results, as well as the algorithm used will affect the results.

Smith *et al.* acknowledge that, given its strong assumptions of temporal independence, tICA may not be the ideal method for decomposing and interpreting brain function. Other approaches with different and perhaps more appropriate assumptions, including canonical correlation analysis [10] and various extensions of ICA, may be useful. In general, concepts of independence are quite powerful and identifying research areas where sICA, tICA or their combination can provide new insights into brain function will be a rich topic of future research. The decomposition of co-occurring activity, as routinely observed in tICA of EEG/MEG is one such area of great relevance, as is the development of improved functional localizers via temporally independent stimulation and tICA decomposition.

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