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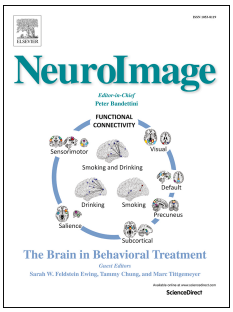

Disambiguating brain functional connectivity

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Disambiguating brain functional connectivity

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Correlation and regression are widely used to characterize the extent to which sets of signals are related, and how these relations might change over time or across experimental conditions. For example, functional connectivity (FC) analyses use correlation and related measures to identify networks of brain regions showing shared activity, to characterize differences within and between networks across different states (Friston, 1994, 2011; Cole et al., 2016; Smith et al., 2011; van den Heuvel and Hulshoff Pol, 2010; Shirer et al., 2012). FC methods include seed-region correlation (Biswal et al., 1995) psychophysiological interaction (PPI) analysis (Friston et al., 1997; O'Reilly et al., 2012), data decomposition methods such as ICA (McKeown and Sejnowski, 1998; Beckmann and Smith, 2004; Cole et al., 2010), and network-matrix evaluations (Smith et al., 2013). These approaches can provide rich summaries of the large-scale patterns of synchronised brain activity, identifying distinct functional systems and their inter-relations. Differences in these patterns across states may indicate differences in inter-regional neural connectivity, and can be used for the decoding of brain and clinical states (Richiardi et al., 2011; Duff et al., 2013; Demertzi et al., 2015; Smith et al., 2015). Differences across subjects may be heritable (Colclough et al., 2017). However, correlation is sensitive to various changes in signal dynamics, making it an